# P-15 <sup>™</sup> User's Guide for Software Version 7.0



KLA-Tencor PN:0104396-000 AA

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At the time of printing, the P-15 complies with the essential requirements of the EC (Electromagnetic Compatibility) Directives listed below

EC Directives	EC 89/392/EEC
	EC 89/336/EEC
	EC 73/23/EEC
Harmonized Safety Standards	EN 50082-2:1995
	EN 50081-2:1993
	EN 55011:1991
Harmonized Electromagnetic Standards	EN 60204-1:1992
	EN 61010-1:1993

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KLA-Tencor Corporation Film and Surface Technology Division 160 Rio Robles San Jose, California USA 95134 e-mail: gss.documentcontrol@kla-tencor.com

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# INTRODUCTION

#### **INSTRUMENT OVERVIEW**

The KLA-Tencor P-15 Profiler is a highly sensitive surface profiler that measures step height, roughness, and waviness on sample surfaces. Roughness can be measured with up to a 0.5 Å resolution over short distances. Waviness can be measured over the entire surface of a sample (assuming a sample size within the system's scan limits). The P-15 system uses stylus-based scanning to achieve high resolution and can correlate local submicron features with global surface measurements. It has a scan area of 200 X 200 mm.

The P15 system offers the option between three head configurations, each with a different vertical range: the MicroHead IIsr (standard range), MicroHead IIIf (low force), and the MicroHead xr (extended range).

- The **MicroHead IIsr** (standard range) has a vertical range of 327 µm and is capable of scanning at forces between 1 mg. and 50 mg.
- The MicroHead IIIf (low force) has a vertical range between 6.5 μm and 130 μm. It is capable of scanning with a stylus force between 0.05 and 50 mg. Low force is useful when scanning soft materials such as gold, indium, or photoresist.
- The **MicroHead IIxr** (extended range) extends the vertical range to 1000µm. It is capable of scanning at forces between 0.5 mg. and 50 mg.

The dual-view optics provide the user with an opportunity to view the sample from the top down and from the side. The top-down view is for accurate scan positioning. The side-view optics are used to view the stylus tip as it passes over sample attributes.

The P-15 is an automated surface scanner that can profile a wide range of topographies, including the following:

• CMP

Recess measurement

Large-feature dishing

- Pattern-dependant erosion
- Surface topography characterization

Global planarity

Data Storage

Measurement of surface roughness

Slider - pole-tip recession and texture bump characterization

#### **CAPABILITIES AND PERFORMANCE**

The Profiler software application runs in the Microsoft Windows environment. It offers the following capabilities and performance features. (See *Table 1.1*).

 Table 1.1
 Capabilities and Performance

Feature	Description
Microscopic and Macroscopic Feature Resolution	Combines macroscopic and microscopic surface analysis, and measures features as small as 0.25 $\mu\text{m}.$
Correlation Scanning	Provides a data reference for comparing the measurements of multiple microscopic features by re-scanning portions of a macroscopic long scan on the microscopic scale.
Die Grid Navigation	Offers an alternative method to that of positioning the sample by XY coordinates. Instead, it selects die location for measuring lithographic patterns in different dies.
Poletip Recession Analysis	Delivers nanometer-level accuracy in determining the height difference between the poletip and the airbearing surface by using the extremely flat scans of the P-15 systems.
Expandable Data Points	Guarantees that the horizontal resolution is limited by the stylus radius and not by the number of data points, by using a number of data points per profile. The number of data points is expandable up to 1 million (maximum).
Advanced Data Acquisition and Manipulation	Measures step height accurately on curved surfaces by being able to fit and level a scan.
	Automates data analysis relative to the feature by detecting the edge or apex of a profile feature.
	Measures many roughness and waviness parameters, with user-selectable cutoff filters to isolate roughness and waviness.
	Calculates statistics for multiple data sets (optional).
Data Recalculation Using different or additional scan parameters	Software versions 6.2 and newer save raw data from the scan for reanalysis of the scan. This allows the user to enter the original scan recipe and reset some of the scan parameters and then reanalyze the scan data using those parameters. Results can be saved in the database.
Database Management	Stores, manages, imports, and exports measurement recipes and scan data using a full-featured database manager.
Network-capable	Allows fast data transfers to a host computer, and can be networked to desktop computers. In addition, the optional SECS II Interface provides
	bi-directional communication between the instrument and a host computer.

## HARDWARE FEATURES AND OPTIONS

Table 1.2 presents the P-15 system's hardware features and options.

Table 1.2Hardware Features

Feature	Description
Dual-View Optics	All three head configurations offer dual-view optics. This provides Two distinct views of the scan surface. The first is a top-down view set of optics with two exchangeable lenses, 115-465x and 185-750x for fast, accurate positioning of the scan. The second is the side view optic set. The 90-410x optics provide the user a way to view the in-progress scan as the stylus moves over surface features.
Motorized Level and Rotation	Enables automatic mechanical leveling of the sample, and programmable sample rotation using a motorized rotary stage, enabling programmed $\theta$ -position repeatability of 4 µm (0.16 mil) at 4 in. from the center.
Vacuum Sample Hold-down	Secures a sample in the center of the stage.
Computer	Includes a 20-GB hard drive, and 256-MB RAM, and 52x speed CD-ROM.
	Also includes an Ethernet network adapter card, and a 3.5-in. floppy disk drive with 1.44-MB capacity.
	Note: Computer specification subject to change.
Monitor	Includes a 38.1-cm (15-in.) SVGA video monitor or 15-in. flat panel monitor that provides a magnified sample video image.
	Note: Computer monitor specification subject to change.
Keyboard	Includes a keyboard with a full set of standard AT keys, as well as some instrument-specific control keys.
	The keyboard has a trackball for fast cursor movement, stage, and measurement head motion control, and convenient menu option selection. The trackball and keyboard can be used interchangeably for these functions.
Printer Port	A parallel printer port is available for local printing.
Network-capable	Allows fast data transfers to a host computer, and can be networked to desktop computers.
	In addition, the optional SECS II Interface provides bi-directional communication between the instrument and a host computer.

Table 1.3 P-15 Options

Feature	Description
Desktop Program	Allows offline analysis and maintenance of scan data. This frees the profiler for measurement and allows the user to conveniently conduct data analysis in an office environment. The Desktop Program can be loaded onto a desktop or laptop PC running Windows.
Sequence Scanning	Automatically executes up to 600 sequential scans per sample by grouping scans into one sequence recipe file.
Pattern Recognition Software	Provides the system with the capability to perform pattern recognition of surface features used to quickly locate scan features on samples with multiple identical scan sites.
Enhanced MaxView 3D™ Imaging	Creates a photo-like presentation of sample topography. Its advanced manipulation and measurement tools provide the ability to better delineate and characterize surface features.
MicroHead IIIf Measurement Head	Low Force head, described in the Instrument Overview.
MicroHead IIxr Measurement Head	Extended Range head, described in the Instrument Overview.
Answer! Custom Software Macros	Extends the data analysis capabilities of the system.
Color Camera	Replaces the standard black and white camera. Not available with pattern recognition option. Factory installed only.
Color Printer	HP 950Cxi Printer w/cable, or equivalent model.
Stress Measurement	Measures and computes the average, maximum and center stress of surface films in MPa.
GEM/SECS Interface	SECS II Interface provides bi-directional communication between the instrument and a host computer.

# **BASIC SKILLS**

## **OVERVIEW**

Before beginning use of the P-15 system, it is important to become familiar with basic skills — such as starting and shutting down the system, and operating the system buttons, keyboard, trackball, Microsoft Windows, Profiler application, and other components.

This chapter describes:

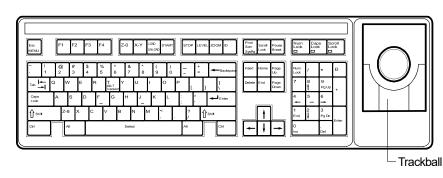
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- Using the Trackball on page 2-3
- Powering Up the Profiler on page 2-4
- Security Log On on page 2-4
- Starting the Windows Profiler Application on page 2-5
- Navigating Between Program Level Screens on page 2-7
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## USING THE KEYBOARD

### Introduction

The keyboard is an input device for communicating with the Profiler. The system interface and scan processes are viewed on the monitor.

Except where noted, the keyboard, the trackball, or a combination of both can be used to perform commands or enter data. (See *Figure 2.1*).



#### Figure 2.1 Keyboard

The keyboard is used to operate the instrument in functions such as entering parameters to establish the Profiler scan procedure, starting a scan, and transferring data files (importing and exporting data files).

1. To perform special functions, press the appropriate key(s) or the corresponding hot key(s). (See *Table 2.1*)

Key	Hot Key	Description
Esc	Esc	Closes the dialog box. Minimizes the menu, if a drop-down menu is displayed.
SHIFT-TAB		Puts text cursor in the previous field.
Тав		Puts text cursor in the next field.
PRINT SCRN	CTRL+P	Prints data from the current page.
DELETE		Deletes any characters in a data field.
Arrow keys [↑] [↓]		For menu items, they select the previous item ( <b>UP ARROW</b> ) or the next item ( <b>DOWN ARROW</b> ).
		Moves cursor up or down in text fields.

 Table 2.1
 Keyboard Functions

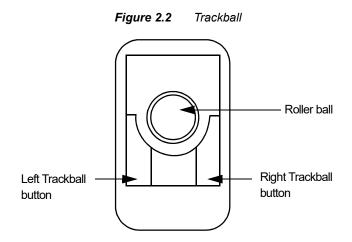
Key	Hot Key	Description
ARROW KEYS [ $\leftarrow$ ] [ $\rightarrow$ ]		Moves the measurement and leveling cursors left or right in the Analysis window.
		Selects the previous item (LEFT ARROW) or the next item (RIGHT ARROW) in a drop-down menu.
		Moves the cursor left or right in text fields.
Enter		Launches currently selected icon. Selects menu item from drop-down menu. Completes the entry of any dialog. Same as clicking <b>OK</b> .
SPACEBAR		In the Analysis window, pressing the <b>SPACEBAR</b> activates first the right, then the left, then both cursors together (so they can move in tandem).
		Press again to repeat the cycle.
LEFT TRACKBALL BUTTON		See <i>Using the Trackball</i> on page 2-3 in the following section.
RIGHT TRACKBALL BUTTON		See Using the Trackball on page 2-3 in the following section.

 Table 2.1
 Keyboard Functions (Continued)

## **USING THE TRACKBALL**

### Introduction

The trackball is a pointing device located on the right side of the keyboard. It consists of a motion-sensing mechanism (operating off the ball itself) and two buttons (left and right) situated around the trackball. (See *Figure 2.2*).



By using the trackball to move the cursor to contact points on the screen and then clicking or double-clicking on the contact, commands can be executed. Examples are: starting software tasks, selecting commands from menus, entering data into the computer.

- 1. Use a gentle rolling motion of the trackball to move the cursor across the monitor screen.
- 2. Use one of the following actions with the left trackball button, as detailed in *Table 2.2*, to accomplish the required function.

-	
Action	Description
<b>Click –</b> To select an item or cancel a pending operation.	Press and release the left trackball button.
<b>Double-click –</b> To start an item.	Press and release the left trackball button twice in rapid succession.
<b>Click and drag</b> – To move an item from one location to another, or to select an item from a drop-down menu, or to select a section of text for editing, or to move scroll bars.	Press and hold the left trackball button while rolling the trackball. Release the trackball button when the desired function is complete.

Table 2.2 Using the Left Trackball Button

## **POWERING UP THE PROFILER**

### Introduction

When powered up, the system proceeds to start Windows and Profiler applications, and initializes the Profiler equipment.

### **Power Up Procedure**

- 1. Press the **ON/OFF** button on the monitor to activate the monitor.
- 2. Press the **ON/OFF** button on the Computer.

The Computer starts, Windows is initiated, and the Program Manager is displayed.

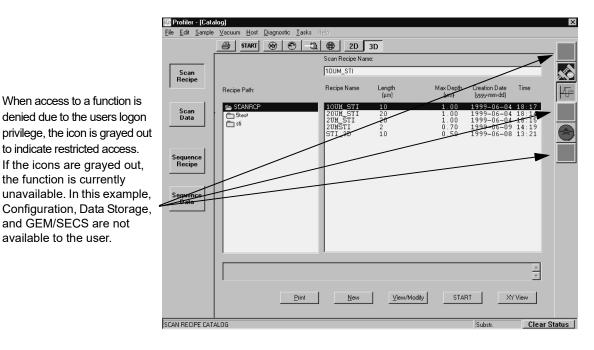
## SECURITY LOG ON

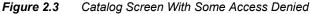
### Introduction

The Windows system running the Profiler is designed to operate with a security log on procedure that limits access to various system function. This feature allows the system administrator to control access to system functions based on a log on password. Each user is assigned a log on word and a password that determines which functions are available to that user. In this way, the system is protected from users accidentally changing key parameters or accidentally erasing key data. the function is currently

and GEM/SECS are not available to the user.

A user with limited access encounters system icons that are grayed out. (See *Figure 2.3*). This indicates that the functions represented by the icon are not available to that user. In other screens and windows, certain function buttons are grayed out. This means that the affected function is not available at that point in the procedure or that the user does not have access to that feature. Examples of button procedures with user access restrictions are some calibrations, data export, data import, and data manipulation.





## Log On Procedure

A dialog box appears after the system is fully booted up. Use the following procedure to log on:

- 1. Press CTRL-ALT-DEL on the keyboard to display the Log on dialog box.
- 2. The cursor should be blinking in the Log on ID field. Enter the Log On word. DO NOT CLICK OK.
- 3. TAB to the Password field.
- 4. The cursor should be blinking in the **Password** field. Enter the Password.
- 5. Press the Enter key or click OK.

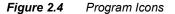
## STARTING THE WINDOWS PROFILER APPLICATION

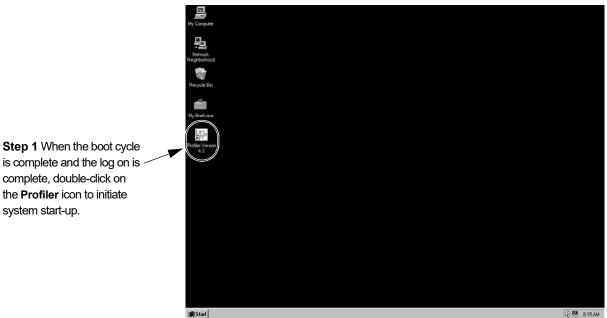
### Introduction

The Windows Profiler application is the interface with the P-15 system from which the scan functions are performed and viewed.

## **Profiler Start-Up Procedure**

1. Use the trackball to locate the Profiler icon with the screen cursor. Double-click on the Profiler icon to initiate startup of the P-15 system (See Figure 2.4).

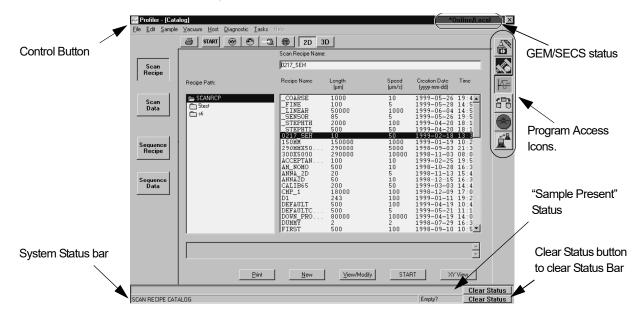




is complete and the log on is complete, double-click on the Profiler icon to initiate system start-up.

> 2. The system goes through its initiation at the end of which the Profiler Catalog screen appears. (See Figure 2.5)

Profiler Catalog Screen Figure 2.5



This is the starting point for operating the instrument. In this screen, scan and sequence recipes can be accessed for system operation. This screen is also the entrance point for the other applications in the system. Each icon along the right side of the screen opens another application that contains the parameters or controls for a specific type of task. (See *Table 2.3.*)

Table 2.3Profiler Program Access Icons

lcon	Description	lcon	Description
	<b>Configuration</b> Displays the Profiler Configuration screen. This screen provides access various configuration windows.		Database File Manager Displays the screen that provides access to files for export/import and delete.
	<b>Calibration</b> Displays the Profiler Calibration screen. This screen provides access to system calibration windows used for accessing various calibration procedures.		<b>Stress</b> Displays the Profiler Stress catalog screen. This screen contains access to the recipe and data file screens.
- The second sec	<b>Scan</b> Displays the Profiler Catalog screen. This screen provides access to the Scan recipes, Sequence recipes, and data files.		<b>GEM/SECS</b> Displays the GEM/SECS screen. This screen is used to configure the system relationship with its host.

## NAVIGATING BETWEEN PROGRAM LEVEL SCREENS

### Introduction

The program level Profiler screens all have the program icons along the right border of the screen. These icons can be used to navigate between the various other program screens contained in the Profiler software.

### **Navigation Procedure**

Use the following procedure to navigate between screens:

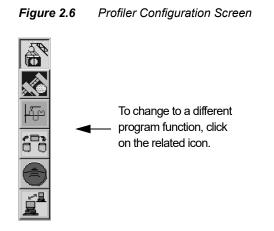
• Click on the icon of the required program screen. (See *Figure 2.6.*)

This *closes* the current program screen and accesses the chosen one. This could generate a message box that inquires if changes to settings, or data are to be saved or discarded. Choose the required answer and follow any instruction.

• Functions performed in some screens automatically access other screens. **EXAMPLE:** 

Performing a scan in the XY View screen generates the scan screen then the Analysis screen.

The above screens do not contain the program icons. To change or exit, click **File** in the Menu Bar and choose **Exit** from the drop-down menu. In some cases it is necessary to click the control button at the top left corner of the screen and choose **Close** from its drop-down menu. This closes the current screen and displays the program screen from which the procedure was entered.



### **EXITING THE WINDOWS PROFILER APPLICATION**

### Introduction

This procedure is used to close the Profiler and Windows applications.

### **Profiler Exit Procedure**

- 1. Close all screens up to a program screen (program level screens are represented by one of the program icons at the right side of the screen). (See *Figure 2.7*.)
- 2. Click on the control button at the top left of the screen to display the menu. (See *Figure 2.7.*)
- 3. Choose Close from the drop-down menu. (See Figure 2.7.)

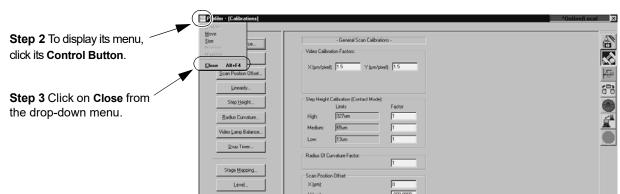
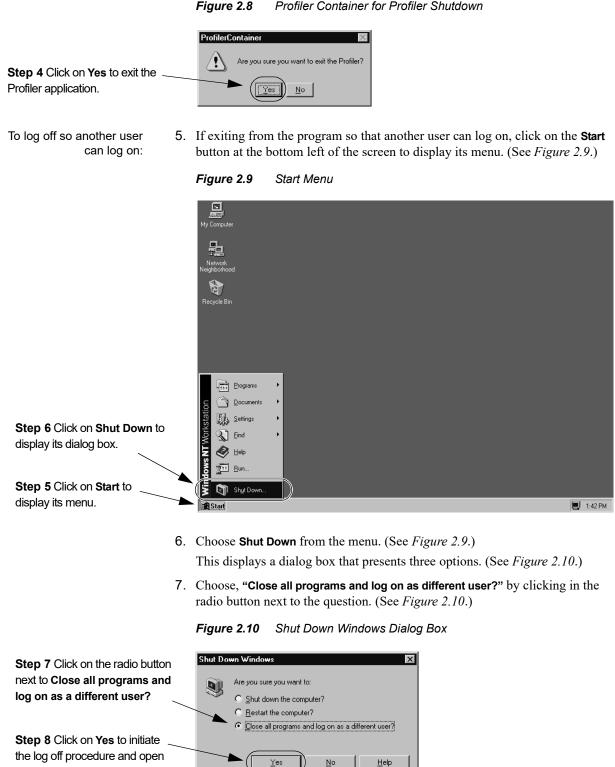


Figure 2.7Closing the Profiler Application Using the Control Button

4. A Profiler Container (message box) appears asking, "Are you sure you want to exit the Profiler?" Click on **Yes** to exit. (See *Figure 2.8.*)



the new log on.

8. Click Yes to log off and set up for another user to log on. (See *Figure 2.10*.)

### **POWERING DOWN THE PROFILER**

#### Introduction

This procedure is used to power down the P-15 system.

This procedure is used any time the P-15 system must be completely shut down. (For example: for maintenance, repair, relocation of the instrument, or when system use is suspended for an extended period of time.)

### **Power Down Procedure**

Figure 2.11

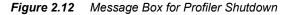
- 1. Close all screens up to a program screen (program level screens are represented by one of the program icons at the right side of the screen). (See *Figure 2.11*.)
- 2. Click on the control button at the top left of the screen to display it menu. (See *Figure 2.11.*)

Closing the Profiler Application Using the Control Button

3. Choose Close from the drop-down menu. (See Figure 2.11.)

Pofiler - [Ca × Step 2 To display its menu, General Scan Calibratio no Eactor click its Control Button. Close Alt+F4 st: 1.5 Y (µm/pixel): 1 Step 3 Click on Close from Step Heigh the drop-down menu. Badius Curvature /ideo Lamp Balanc 12. Drop Time Stage Mapping Level

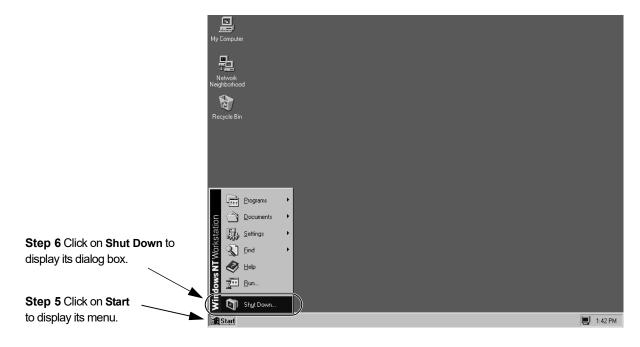
4. A Profiler Container (message box) appears asking, "Are you sure you want to exit the Profiler?" Click on **Yes** to exit. (See *Figure 2.12*.)





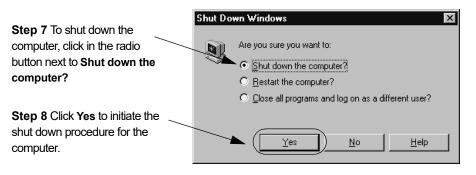
- To Log Off and Shut Down the System
- 5. If exiting from the program so that another user can log on, click on the **Start** button at the bottom left of the screen to display its menu. (See *Figure 2.13*.)

Figure 2.13 Start Menu



6. Choose **Shut Down** from the menu. (See *Figure 2.13*.) This displays a dialog box that presents three options. (See *Figure 2.14*.)





- 7. Choose, "Shut down the computer?" (See Figure 2.14.)
- 8. After the computer has closed all applications and written information to the system drive, it displays a message box that says, "It is now safe to shut down your computer."

This message box has a button at the bottom of it that says "Reboot?"

9. If rebooting the system (without powering down the system) click on Reboot?



**CAUTION:** When the instrument is powered up or reset, the stage moves the Z axis all the way up, then X and Y to the 0,0 position.

- 10. If powering down the Profiler:
  - a. Press the On/OFF button on the Profiler computer.
  - b. Press the **ON/OFF** button on the monitor to turn off the monitor.

### PERFORMING AN EMERGENCY SHUTDOWN

The P-15 Profiler is powered up and shut down from the computer On/Off switch. In case of an emergency, turn off the computer and this shuts down the entire system.

## **CLEARING A DIAGNOSTIC MESSAGE**

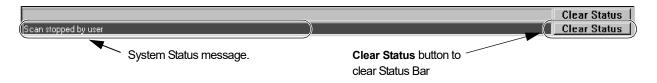
#### Introduction

Diagnostic messages appear in the status bar at the bottom of the window when an action or circumstances create the potential for instrument malfunction, such as occurs with a motion error. The system status bar also presents messages that guide the user through many of the system procedures. When a diagnostic message appears, the status bar at the bottom of the screen becomes red and the status bar must be cleared before it can display any new messages.

### **Clearing a Diagnostic Message Procedure**

After reading the message in the status bar at the bottom left of the screen, click the **Clear Status** button on bottom right of the status bar to proceed. See *Figure 2.12*.

#### Figure 2.15 Clearing the Status Diagnostic Messages



## **PROTECTING THE STYLUS ARM ASSEMBLY**

## **System Provisions for Stylus Protection**

The P-15 profiler incorporate several design features that protect the stylus from damage. (See *Table 2.4.*)

Protection Name	Stylus Arm Protective Measure	Description of Result
Data Point Saturation	During an ascending scan, the scan is terminated when the stylus reaches its upper limit of travel (when it has pivoted up as high as it can go)	The stylus automatically retracts and the scan is terminated. In the Scan window, the trace ascends and flat lines at the top of its range.
Lowest Elevator Position	As a safety factor, the elevator can be programmed to lower only to a preset limit.	With the <b>Lowest Elevator Position</b> properly set, when the measurement head is lowered, it only goes as far as the setting allows, thus protecting the stylus and sample from damage. This setting is also used to trigger the head descent slow down point which occurs 1000 $\mu$ m (set in the system registry) above the Lowest Elevator Position.
Proximity Sensor	The Proximity Sensor is designed to detect the sample as the head lowers and slow the descent.	With the Proximity Sensor <b>ON</b> , the head slows and stops as it nears the sample surface. If the Proximity Sensor is turned <b>OFF</b> , then the head descent slows when it reaches 1000 $\mu$ m above the Lowest Elevator Position. The system then depends on the stylus contact with the sample surface to stop the head descent. If the stylus is coming down in a hole or off the edge of the sample, the system or the sample could be damaged by contact with the sensor assembly.

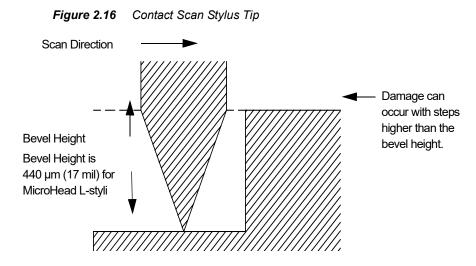
 Table 2.4
 Stylus Arm Assembly Protection

## **Potential Stylus Damage During Scans**

Despite precautionary features, there are still circumstances where damage can occur.

- Damage occurs whenever the stylus is down and a vertical wall that is fixed to the stage moves against the stylus shaft.
- The stylus can be damaged whenever it encounters an obstacle higher than the bevel height of the stylus tip (higher than 440 µm (17 mils) for the MicroHead L-style stylus. (See *Figure 2.16*.)

• The stylus can be damaged by a shorter object if it has sharp corners or burrs that bite into the stylus tip.



• If the stylus is lowered or a scan is started when the sample is not directly under the stylus, damage to the stylus could occur.

This is most likely to happen when lowering the measurement head such that the stylus drops into the center hole of a hard disk or misses the edge of the sample. Then when the stage is moved, the stylus is damaged.



**CAUTION:** Do not move the stage unless the stylus is well above the sample surface.



**CAUTION:** Do not start a scan unless the stylus is directly over the sample or damage to the stylus or head could occur.

- If a sample or precision locator is changed without resetting the **Lowest Elevator Position**, the head can lower onto the locator if the stylus misses the locator surface.
- Damage could occur when **MAN LOAD** is clicked, causing the sample or locator to hit the stylus. The measurement head must be at least 6.4 mm (0.25 in.) above the top of the precision locator.



**NOTE:** The stylus tip is located about 4 mm (165 mils) below the measurement head.



**CAUTION:** If changing the sample or precision locator to a different height, reset the **Lowest Elevator Position.** Otherwise, damage to the stylus or the measurement head can occur.

When designing custom jigs or fixtures, consider the precautions noted in this section. For instance, when designing a custom hard disk locator, its center section must be flush with the top of the disk surface. Care must be exercised when nulling where there is a hole in a jig, a vacuum hole, or a groove in a surface.

For hard disks only, when measuring the disk, avoid nulling in the Disk Locator hole.



**NOTE:** The KLA-Tencor Warranty Policy does not cover damage to the stylus arm assembly or the pivot caused by operator error or carelessness.

## Adjusting the Video Image

#### Introduction

The Video Controls allow the view of a particular sample surface to be optimized. The brightness and contrast can be varied for the camera.



**NOTE:** Changing the focus can invalidate sequences that use pattern recognition because the sample image is less likely to match the stored image in the pattern recognition files.

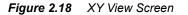
The purpose of adjusting the video image is to clarify the image resolution and contrast so it can be clearly viewed.

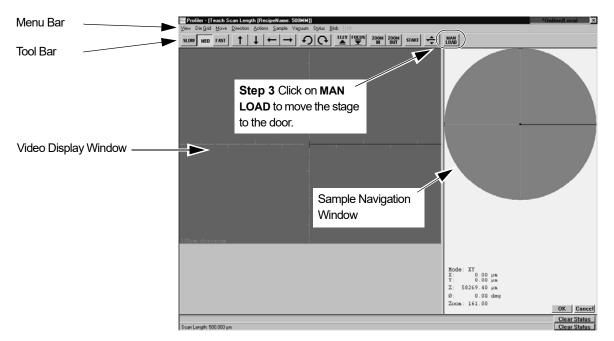
### Video Image Adjustment Procedure

- 1. Open the **Scan Recipe** window. (Click on the **Scan Recipe** button in the Catalog screen. See *Figure 2.17*.)
- 2. Once the Scan Recipe window is active, with a recipe highlighted, click the **XY View** button to display the XY View screen. (See *Figure 2.17*.)

Step 2 With a Scan Recipe	Profiler - [Catal	Vacuur Host Diagnostic Iasks Help						*Online/	Local X
highlighted, click on the XY icon	Teo For Torin		2D 3D						12
to display the <b>XY View</b> screen.			Scan Becipe Name:						
	Scan Recipe	(	Recipe Name	Leasth	Camelan	Cound	Creation Date	Time	
		Recipe Path:		Length (µm)	Sampling Rate (Hz)	Speed (µm/s)	(yyyy-mm-dd)		147
	Scan Data	SCANRCP	200MM 1500MM	200 500	200 200	100 100	2001-03-23 2001-03-23		66
Step 1 When the screen opens,								- 1	
click on the Scan Recipe button	Sequence Recipe								
to display the Scan Recipe list in	Hecipe								
the Information Display window.	Sequence Data								
the mornation Display window.	Data								
	· ·								
List window			I					_	
								*	
		1							
			Print	New	View/	Modily	START	XY View	
								CI	ear Status
									ear Status

Figure 2.17 Scan Recipe Window in the Catalog Screen





3. Click on MAN LOAD (see *Figure 2.18*) in the Tool Bar to move the stage to the door. (See *Figure 2.18*.)

The head rises to a taught height and the stage moves to the door (or the taught manual load position).

4. Open the door.



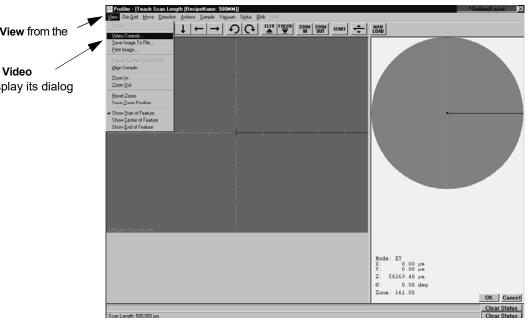
**CAUTION:** Do not open the door until the stage has completely stopped moving. All motors stop immediately when the door is opened. (Unless the interlock is disabled.)

- 5. Place the sample on the stage in the proper orientation.
- 6. Turn on the vacuum switch located on the left inside edge of the door.

The sample should now be securely in place on the stage.

- 7. Close the door.
- 8. Click on MAN LOAD to move the stage back under the system head.
- 9. Click the **FOCUS** button to null the stylus on the sample surface and focus at the chosen magnification. (See *Figure 2.18*.)
- 10. Click View in the Menu Bar to display its menu. (See Figure 2.19.)
- 11. Select Video Controls. (See Figure 2.19.)

Figure 2.19 XY View Screen – View Menu



**Step 10** Choose **View** from the Menu bar.

Step 11 Choose Video Controls... to display its dialog box. The Video Controls dialog box appears. (See Figure 2.20.)

Figure 2.20 Video Control Dialog Box

Step 12 Use the slide	Video Cont	rols		Step 13 When desired
bar or directly enter	Contrast.	•		results are achieved,
the value required.	Lamp Brightness:	•		click on <b>Apply</b> .
	olignutess.			、 、
				Step 14 Click on Exit.

- 12. Adjust contrast and brightness controls:
  - a. Click and drag the slide bars for contrast and lamp brightness to achieve desired effect.
  - b. If desired, type in the required values instead of dragging the slide bars.
  - c. Repeat if needed until desired results are obtained.
- 13. When values for Contrast and Lamp Brightness are set, click Apply.
- 14. When the adjustments are complete, click **Exit**

The settings are stored.

## **USING FILE NAME CONVENTIONS**

### Introduction

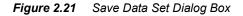
Scan and sequence recipes and data can be saved, as well as graphs and video images. In the Windows naming convention only the following special characters are allowed:

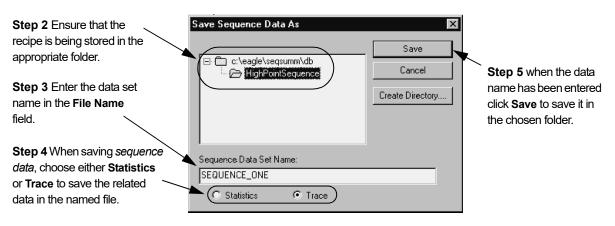
 Table 2.5
 Special Characters Allowed for Naming Purposes

• _ underscore	• - hyphen	• { left brace
• ! exclamation point	• & ampersand	• } right brace
• % percent sign	• (left parenthesis	• 'single quotation mark
• # number sign	• ) right parenthesis	• 'apostrophe
• \$ dollar sign	•	•

### Naming and Saving Files

When saving a file, click File to display its menu. Click the Save... button. A dialog box appears. The content and appearance differ slightly depending on what is being saved and the screen from which Save... was chosen. The one in *Figure 2.21* is for saving sequence data.





- 2. Choose the appropriate folder in which to store the item being saved. (See *Figure 2.21*.)
- **3**. Create a distinct file name for the item being saved. It is best to make the name representative of the content of the file if possible. The name can be up to 72 characters in length and should not contain empty spaces. Enter the file name in the file name field. (See *Figure 2.21*.)
- 4. Set any other necessary options required to properly store the information in the file. In *Figure 2.21* that would include setting the content format of the file to either **Statistics** or **Trace**, options only for sequence data. (See *Figure 2.21*.)
- 5. Click **Save** to save the data in the named file. (See *Figure 2.21*.)

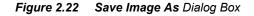
## SAVING VIDEO IMAGES

### Introduction

A video image can be captured in the XY View window and saved to a file. Many standard image output file formats are supported.

### Naming and Saving Video Images Procedure

1. Go to either the XY View or Theta View window, and click the View menu, then select Save Image to File to display the Save Image As dialog box. (See Figure 2.22).



Step 2 Choose a file to save	Save Image As 🔹 🖓 🗙	Step 2 New
the image in. Click on the menu-	Save in: Capture	folder. After
arrow, scroll until the directory or -		choosing a
folder is found and click on it.		directory for the
		file, click on this
Step 3 Name the file that the		icon and enter a
image is to be saved as.		name for the new folder.
Step 4 Choose a format to store		
the image as. Click on the menu $\_$	File <u>n</u> ame: 3dagain <u>S</u> ave	
arrow, scroll until the format	Save as type: Windows BMP 8 Cancel	
appears, click on the format.		

- 2. Choose the location in which the image is to be saved. To view the possible files, click on the menu-arrow next to Save in and click on the desired folder. To create another folder within a directory, click on the new folder icon and enter a name for the new folder.
- 3. Next to File name, enter a name for the image file that is to be created.
- 4. Set the format that the image is to be saved in:
  - a. Click on the menu-arrow next to Save as type:
  - b. Scroll until the desired format is visible.
  - c. Click on the desired format.
- 5. Click Save to save the video image.
- 6. To view the video image, import the file into an application.

## **EXPORTING DATA GRAPHS**

### Introduction

Data graphs are contained in the Scan Data catalog, Sequence Data catalog and in the Analysis screen when the scan data is being analyzed. 2D and 3D graphs can be exported directly from the Analysis screen during scan data analysis. 2D and 3D graphs from the Scan Data catalog can be exported in two ways: from the Analysis screen, and from the Database File Manager.

2D and 3D data graphs from the Sequence Data catalog can be exported only from the analysis screen because the file must be opened and the desired graph chosen and displayed before it can be exported.

The data graph is exported as a graphic image in one of the following file formats:

Bitmap format (*.bmp)	Encapsulated Post Script (*.eps)
TIFF format (*.tif)	JPEG format (*.jpg)
Word Metafile format (*.wmf)	GIF format (*.gif) (not supported)

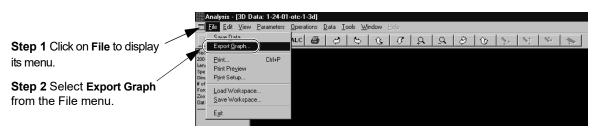
Figure 2.23 Export File Formats in Drop-Down Menu

File <u>n</u> ame:	1-24-01-otc-1-3d	<u>O</u> pen
Save as <u>t</u> ype:	BMP files (*.bmp) EPS files (*.eps) TIF files (*.eps) TIF files (*.th) WMF files (*.vmf) JPEG files (*.jpg) GIF files (*.jpf)	Cancel Help

## Exporting Data Graphs from the Analysis Screen

1. With the graph to be exported displayed in the Analysis screen, click **File** to display its menu. (See *Figure 2.24*.)

Figure 2.24	Analysis Screen – F	-ile Menu
-------------	---------------------	-----------



Opening the Export Graph

Dialog Box from the

Analysis Screen.

2. Select Export Graph... (See Figure 2.24.)

This displays the dialog box for graphic exports. (See Figure 2.25.)

Figure 2.25 Export Graph Dialog Box

This field contains any file tree that is directly under the folder in the Save In field above it.	Save in: scanexp	If a graph is saved, it is placed in the folder that is displayed in the Save In field.
<b>Step 3</b> Enter the file name in the <b>File name</b> field.	File name:     scan_4       Save as type:     BMP files (".bmp)       Cancel       Help	<b>Step 4</b> When the file has been named, click on <b>Save</b> to save the newly named file in the folder displayed in the <b>Save In</b> field.

**3**. Set the required variables in the **Save As** dialog box. See *Table 2.6* for an explanation of the variables to be set.

Variable	Description
Save In:	This drop-down menu provides a <i>browse</i> feature from which to search for the folder that the graphic is to be exported to or the application that is to analyze it. The location must be and displayed in the <b>Save In:</b> field.
Save In: file tree field	Select the <b>Directory</b> path.
File Name	Type the File Name, up to 68 -characters in length.
Save as Type	From the drop-down menu, select the <b>graphic</b> format: (BMP, TIFF, WMF, EPS, or JPEG).
Export Size (not visible from the Analysis screen)	The size options for the graph to be exported is not available in the Analysis screen because the operator can adjust the size of the image on the screen to the desired export size.

4. After all the information is entered, click **Save** to export the graph.

Exporting Graph from the

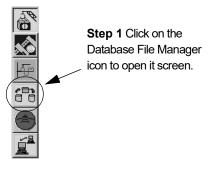
Database File Manager

## Exporting Graphs from the Scan Data Catalog

#### Exporting the Graph without Checking it in Analysis

1. Go to any top level screen containing the system icons and click on the **Database** File Manager icon. (See *Figure 2.26*)

Figure 2.26 Catalog Screen – Database File Manager Icon



2. In the Database Catalog screen, choose either the **2D** or **3D** button in the tool bar. Depending on the Catalog group chosen, this displays the 2D or 3D data or recipe sets. (See *Figure 2.27*.)

Figure 2.27	Data Catalog Screen for Export of Data or Recipes
-------------	---

Profiler - [Cata	alog]					*Online/Lo	cal ×
	nsfer Diagnostic Iasks Help						
Export	<u> </u>	/					12
Bitt.		Scan Data Name:					
Egit		1-24-01-0TC-1-30					- 20
	Scan Data Path:	Scan Data	Recipe ID	Length (µm)	Y Size (µm)	Creation Date (yyyy-mm-dd)	
Scan Data	SCAN DATA	1-24-01	200-3D	200	90	2001-03-24	60
Sequence Recipe							
Sequence Data							
Data							
	-						
	Drive:						
	Di	jete Thumphails	Review	Export	Import	Graph Export	

Step 2 Click on 3D to display 3D data or recipes.

- 3. Choose Scan Data from the Catalog buttons at the left of the screen.
- 4. Navigate to the folder containing the required graph.
- 5. If the file name is known and there is no need to see the graph, click on the file name of the graph, and click on **Export Graph...** at the bottom of the screen.

To Open the Export Dialog Box from the Database Screen This opens the export dialog box titled **Save As**. (See *Figure 2.28*).

Figure 2.28 Graphics Export Dialog Box

Save As		zip ? 🗙
Savejn:	🔄 3d-otc 🗾 🔳	
<b>₽</b> 3-24-01-		
File <u>n</u> ame:	1-24-01-otc-1-3d	<u>S</u> ave
Save as type:	BMP files (*.bmp)	Cancel
Export Size		Help
Original Formation	ormati 801 x 360 pixels	
C Resample	801 x 360 pixels	
🗖 Mainta	in Aspect Ratio	

6. Complete the information in the dialog box. See *Table 2.7* for more information.

 Table 2.7
 Graphics Export Dialog Features

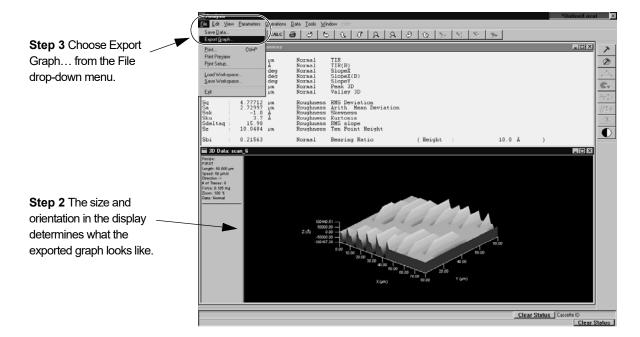
Feature	Description
Save In:	This drop-down menu provides a <i>browse</i> feature from which to search for the folder that the graphic is to be exported to, the application that is to analyze it, or the printer it is to be printed by. The location must be and displayed in the <b>Save In</b> : field.
Save In: file tree field	Select the <b>Directory</b> path.
File Name	Type the File Name, up to 68-characters in length.
Save as Type	Select the <b>graphic</b> format: ( <b>BMP</b> , <b>TIFF</b> , <b>WMF</b> , <b>EPS</b> , or <b>JPEG</b> ).
Export Size	Two options: Original Format and Resample
	Original Format – To export in the original format and size, click Original Format.
	<i>Resample</i> – To export in another size format, click <b>Resample</b> and use one of the following:
	• Enter the scale sizes in pixels to change the sample size. (Note that if the numbers do not maintain the aspect ratio of the original sample, the graph is distorted.) OR
	• To keep the same scale, enter the first size setting then click the Maintain Aspect Ratio checkbox. The system fills in the second number to keep the aspect ratio correct.

7. After all the information has been entered, click **Save** to complete the export.

To Open the Export Dialog Box from the Analysis Screen	1.	the Scan	-	ontaining the	e scan file	e, double-cli	porting it, after enter ock on the file. This	ring
	2.	If the cor	rect graph is c	displayed, re	esize or re	orient it as	required before expo	ort.

Exporting the Graph After Checking it in Analysis

*Figure 2.29* Scan Data Graph in the Analysis Screen



- 3. Choose **Export Graph**... from the **File** menu (see *Figure 2.29*) to open the Save As (export) dialog box.
- 4. Fill in the required information. (See field explanations in *Table 2.8.*)

 Table 2.8
 Graphics Export Dialog Features

Variable	Description
Save In:	This drop-down menu provides a <i>browse</i> feature from which to search for the folder that the graphic is to be exported to or the application that is to analyze it. The location must be and displayed in the <b>Save In:</b> field.
Save In: file tree field	Select the <b>Directory</b> path.
File Name	Type the File Name, up to 72-characters in length.
Save as Type	From the drop-down menu, select the <b>graphic</b> format: ( <b>BMP</b> , <b>TIFF</b> , <b>WMF</b> , <b>EPS</b> , or <b>JPEG</b> ).
Export Size (not visible from the Analysis screen)	The size options offered in the Database screen for resizing the graph to be exported is not available in the Analysis screen. In Analysis the operator can adjust the size and orientation of the image on the screen before it is exported.

5. After all the information has been entered, click Save to complete the export.

### Exporting Graphs from the Sequence Data Catalog

The sequence file graphs cannot be directly viewed through the Sequence Data screen. The operator must open the data file in the Analysis screen and choose a specific scan graph to be exported.

- 1. From the Database screen, click the Sequence Data button to open the Sequence Data window in the Database screen.
- 2. Navigate to the folder containing the sequence data set that has the graph(s) to be exported.
- **3**. To export a graph from a Sequence Data set, double-click on that sequence data set (see *Figure 2.30*) to open the Analysis screen with it displayed.

The Analysis screen opens with the first scan from the first slot displayed in the Analysis window. To find the required scan graph it might be necessary to open the Surface Parameters Data (statistics) window.

Figure 2.30 Choosing a Sequence Data Set

		Sequence Data:				
in ipe		PRELIM_IMAGE				
	Sequence Path:	Sequence Data Sets	Sequence ID	Number of Slots	Creation Date (yyyy-mm-dd)	Time
n a nce pe	≫ SEQUENCE ☐ HufPerinSequence ☐ min_scon	THEC-OVI PREAM TO REC-3 SEC_1 SEC_2 SECUENCE SUBJCAN1 TEST	INC-071 00125 537 DONINION CORE_530 CORE_550 CORE_550 CORE_550 CORE_550 CORE_550 CORE_550 CORE_550		1999-07-26 2001-02-18 1999-05-13 2000-10-26 2000-10-26 2000-10-26 2000-10-26 2000-10-27 2000-11-27 2000-10-27 2001-01-03	$\begin{array}{c} 10:34:54\\ 05:24:26\\ 15:20:32\\ 06:54:120\\ 08:08:06\\ 13:14:120\\ 08:08:06\\ 04:33:16\\ 02:29:40\\ \end{array}$
	Drive:	elete	The Review		Export	Import

4. If the Surface Parameter Data window is not open in the Analysis screen, click **STATS** to open it. (See *Figure 2.31*.) The Surface Parameters Data window can also be accessed by choosing **Surface Summary**... from the **View** menu.

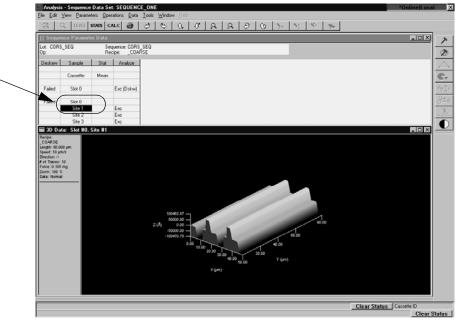
Figure 2.31 Opening the Statistics Window to View Scan List

Step 4 Click on STATS to open the Scan Parameters (Statistics) Window for viewing the list of scans in the sequence.



5. In the Surface Parameters Summary window, choose the required Slot and Site to display the scan that is to be exported. (See *Figure 2.32*.) The graph is displayed in the Analysis window.





6. Resize or reorient the graph if necessary before being exported.

**Step 5** Choose the Site to display the scan that is to be exported.

7. Choose **Export Graph...** from the **File** menu. This displays the **Save As** (export) dialog box. (See *Figure 2.33*.)

Figure 2.33 Save As (Export) Dialog Box

Save As			? ×
Save jn:	🔄 scanexp	• 🗈	
File <u>n</u> ame:	scan_4		<u>S</u> ave
Save as <u>t</u> ype:	BMP files (*.bmp)	•	Cancel
			<u>H</u> elp

8. Set the options for the Graphics Export features. See *Table 2.9* for an explanation of the variables to be set.

Variable	Description
Save In:	This drop-down menu provides a <i>browse</i> feature from which to search for the folder that the graphic is to be exported to or the application that is to analyze it. The location must be and displayed in the <b>Save In:</b> field.
Save In: file tree field	Select the <b>Directory</b> path.
File Name	Type the File Name, up to 68-characters in length.
Save as Type	From the drop-down menu, select the <b>graphic</b> format: (BMP, TIFF, WMF, EPS, or JPEG).
Export Size (not visible from the Analysis screen)	The size options offered in the Database screen for resizing the graph to be exported is not available in the Analysis screen. In Analysis the operator can adjust the size and orientation of the image on the screen before it is exported.

Table 2.9 Graphics Export Dialog Features

9. Click **Save** to export the graph.

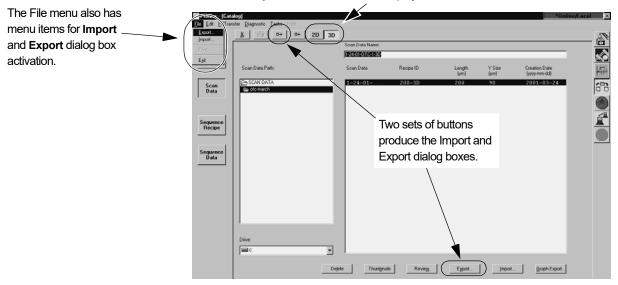
## EXPORTING DATA FROM THE DATABASE FILE MANAGER

Export of data files from the Database File Manager is performed the same way for both Scan Data and Sequence Data sets.

1. From the Database File Manager choose either 2D or 3D files.

2. Choose either the Scan Data or Sequence Data catalog button. This displays the related 2D or 3D data files in the chosen catalog.

*Figure 2.34* Data Catalog Screen for Export of Data or Recipes



**Step 1** Click on 2D or 3D to display related files.

3. Navigate to the required data set and click on it to highlight it.

There are three ways to access the **Export Sequence** (or **Scan**) **Data -- Select Export Directory** dialog box.

- The **Export**... button at the bottom of the screen
- The Export Data icon in the tool bar at the top of the screen
- The **Export**... menu item in the **File** menu
- 4. Select **Export**... from one of its access points.

This displays the **Export Sequence** (or **Scan**) **Data -- Select Export Directory** dialog box. (See *Figure 2.35*.)

Figure 2.35 Export Data Dialog Box

<b>Step 5</b> From the drop-down file manager, choose the directory► and file in which the data is to be stored.	Export Sequence Data Select Export Directory ? >  Export to: seqexp  So_1.bmp
Step 6 Choose an export format.	
The destination path and directory is displayed here.	Format     OK       C ASCII     C Binary       Export directory:     C:\EAGLE\SEQEXP

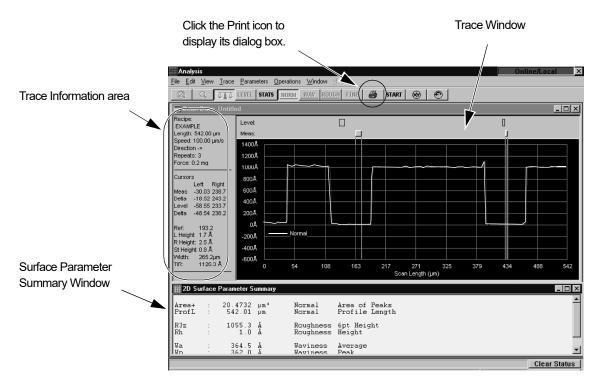
- 5. From the **Export to:** drop-down menu, choose the directory/folder that the data is to be exported to. The actual path and folder name are displayed at the bottom left of the dialog box. (See *Figure 2.35*.)
- 6. Choose an export format, either ASCI or Binary. (See Figure 2.35.)
- 7. Click **OK** to export the data to the destination folder.

### **PRINTING DATA**

### Introduction

When the scan is completed, the raw data is processed and displayed in the Analysis screen. (See *Figure 2.36*.) The Trace Information area, to the left of the trace, lists a summary of the trace data. Choosing **Surface Summary** from the **File** menu opens another window displaying calculated scan parameters, that can be pre-selected in the scan recipe.

#### Figure 2.36 Analysis Screen



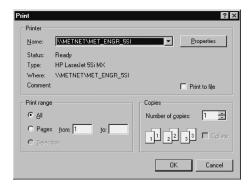
On the left side of the trace image is the Trace Information area.

- The Height text field displays the vertical distance between the trace intersections of the left and right measurement cursors.
- The Width text field displays the horizontal distance between the midpoints of the areas defined by the two cursors.
- Each cursor position and the stage position is displayed.

### **Print Procedure**

1. Go to the **Analysis** window, and click the **Print** icon to display the Print dialog box. (See *Figure 2.37*.)

Figure 2.37 Print Dialog Box



2. Set the options for the **PRINT** features. (See *Table 2.10*).

Table 2.10	Print Dialog Box Features
------------	---------------------------

Feature	Description
Print Range	Select the <b>Print Range</b> of pages ( <b>All, Selection, Pages From _ To _</b> ).
Properties	Select the <b>Print Quality</b> of text ( <b>Low, Medium, High</b> ).
Copies	Type the <b>Copies</b> number — to sort multiple copies, check the <b>Collate Copies</b> checkbox.

3. Click **OK** to print the data.

# SCAN RECIPES

### INTRODUCTION

The P-15 system performs scans of sample surfaces using recipes that set the parameters of each scan. Each recipe can be used alone or, if the system is capable of sequencing, in conjunction with other recipes in a sequence to gather necessary data from a given sample. Even some system calibrations use recipes to perform vital data gathering and analysis so the system can be calibrated for optimum performance.

The P-15 system is capable of high resolution scans in two or three dimensional formats. Both formats use trace data. The three dimensional scan uses a combination of parallel traces. The length of the traces, the distance between parallel traces, and the frequency of data point collection are all defined in the recipe. The two dimensional trace is a collection of data points made at a recipe specified frequency either as one trace, or a recipe specified number of traces over the same scan position, which are then averaged. The data is then presented in either a two or three dimensional graphical format for observation and analysis. Data storage and analysis are detailed in *Saving Scan Data* on page 8-47 and *Saving Scan Data* on page 9-45.

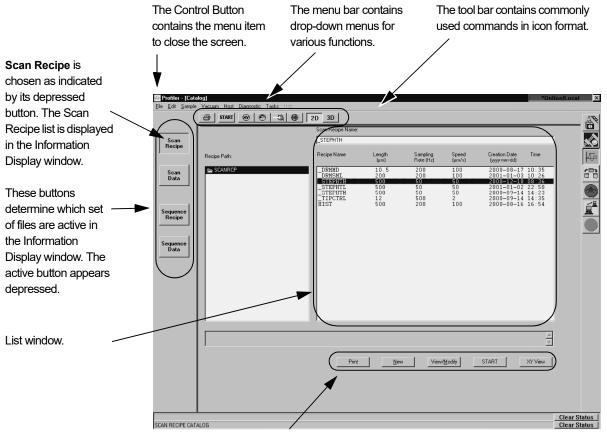
#### This chapter describes:

- Accessing the Scan Recipe Catalog Screen on page 3-2
- Scan Recipe Catalog Screen Components on page 3-3
- *List Window* on page 3-10
- Creating and Editing a Scan Recipe on page 3-13
- System Status Message on page 3-13
- Recipe Editor for 2D and 3D Scans on page 3-15
- Scan Parameter Definition Window on page 3-16
- Feature Detection (Only for 2D Scans) on page 3-43
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- Roughness and Waviness Parameters on page 3-70
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## ACCESSING THE SCAN RECIPE CATALOG SCREEN

The Catalog screen is the first screen to appear when the profiler application is opened. The functional areas in the screen are described in *Figure 3.1* and *Figure 3.2*.





These Command buttons present recipe interaction functions in a button format.

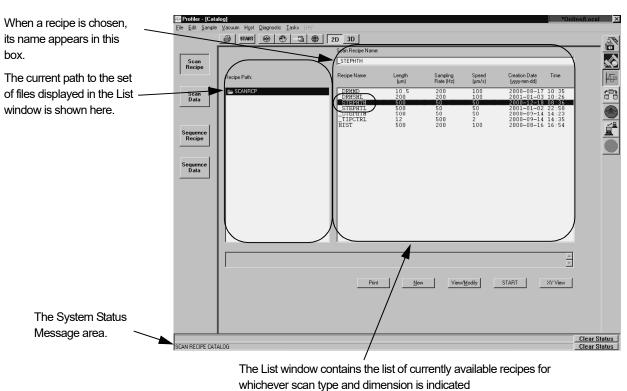


Figure 3.2 Catalog Sequence Recipe Screen

If the Scan Recipe button is not chosen, click on it. After the **Scan Recipe** button is clicked, the List window changes to the Scan Recipe list. The Scan Recipe screen is divided into functional **components**. Each is discussed in the following section, *Scan Recipe Catalog Screen Components* on page 3-3.

# SCAN RECIPE CATALOG SCREEN COMPONENTS

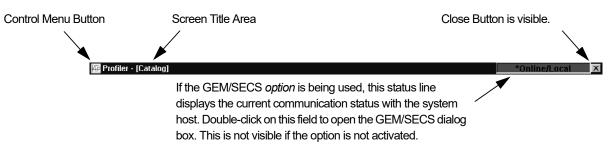
# **Screen Tools**

The Catalog Screen Tools section is divided into three parts: Title Bar, Menu Bar, and the Tool Bar. An additional tool bar is located below the List window and is discussed in *List Window* on page 3-10.

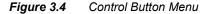
# **Title Bar**

The Title Bar contains the Control menu button, the Screen Title Bar, and the Close/Minimize icons or (See *Figure 3.3*) or the GEM Status for systems equipped with the GEM/SECS option.





• **Control Button**: This button is in the form of an icon that represents the currently displayed screen. (See *Figure 3.3*.) It is always in the same place but looks different depending on the screen currently displayed. Click on it to display its menu. (See *Figure 3.4*.)





The Control button menu contains the following options:

Table 3.1Control Button Menu

Menu Option	Description	When Active/Inactive
Restore	N/A	Disabled to prevent interference with other screen operations.
Move	N/A	Disabled to prevent interference with other screen operations.
Size	N/A	Disabled to prevent interference with other screen operations.
Minimize	N/A	Disabled to prevent interference with other screen operations.
Maximize	N/A	Disabled to prevent interference with other screen operations.
Close	Closes the current screen (window).	Active in all screens.

- Screen Title Area: This identifies the current active screen. (See *Figure 3.3.*) It is not interactive.
- Close: This button is used to close the application. It is part of the Windows formatting. Do not use this button. Instead; use the Menu Bar or Control Button functions. If the GEM Status is displayed, the Close Icon might be covered. (See *Figure 3.3.*)
- **GEM/SECS Status Display** (*for systems with the GEM option*): This area displays the current GEM status. To view the **GEM Status** dialog box double-click on the **GEM Status Display**. (See *Figure 3.3*.) Settings in the dialog box should only be changed by those with a thorough knowledge of GEM/SECS functions in the system.



**CAUTION:** Only system engineers familiar with the GEM operation should change any settings in the GEM Status dialog box. Changing these settings could disrupt processing.

The following table presents the possible GEM Status messages and the significance of each message.

Table 3.2GEM Status Display

GEM STATUS	Description		
Online/Local	Online -The P-15 system is in the operating mode. Local - In this state, the P-15 system is controlling its own activity.		
Online/Remote	Online -This P-15 system is in the operating mode. Remote - In this state, control of the P-15 system comes from the host.		
GEM Offline	This means that the GEM communication link is suspended.		
GEM Disabled	This means that the communication link is temporarily disabled for a user defined purpose.		

#### Menu Bar

The **Menu Bars** (See *Figure 3.2*) have various drop-down menus for operating some of the system options available with the *current screen*. Each screen has its own menu bar with its own options and variables. Some of the options in the Menu Bar are also represented by icons in the **Tool Bar** and the **Command buttons**. The following tables present the content of each drop-down menu in the **Menu Bar** for the **Scan Recipe Catalog** screen.



**NOTE:** ne or more of the menu options in a given drop-down menu might be grayed out. This can be due to the permission status of the operator currently logged onto the system, it being an option that is not currently available because it requires other system options to be enabled before use, or the option's unavailability at this stage in the procedure.

Figur	e 3.5	Menu Bar for Scan Recipe Screen				
<u>F</u> ile	<u>E</u> dit	<u>S</u> ample	<u>V</u> acuum	H <u>o</u> st	<u>D</u> iagnostic	<u>T</u> asks

The Menu Bar for the Catalog screen contains seven active menus. Help is currently unavailable. Each menu is discussed in its own table. The Menu Bar menus are contained in *Table 3.3* through *Table 3.8*.

 Table 3.3
 File Menu Options Description

File Menu	Description	Function Access
START	<b>START</b> Starts the currently highlighted scan procedure. The screen changes to the scan screen. In the screen depicted in <i>Figure 3.2</i> , it would start the <b>_STEPHTH</b> recipe scan.	Everyone has access.
Center Object Teach Die Grid	<b>Center Object</b> Displays the center object in the XY View Window.	Everyone has access.
XY View Erint Exit	<b>Teach Die Grid</b> Opens the Teach Die Grid procedure in the XY View Screen.	Access Restricted: Permission Required
	<b>XY view</b> Brings up the XY View screen, which is the typical scan screen.	Everyone has access
	Print Brings up the Print Manager for printing recipes.	Everyone has access
	<b>Exit</b> Exits the Scan screen. This sometimes prompts the display of dialog box asking if the current changes are to be saved.	Everyone has access

 Table 3.4
 Edit Menu Options Description

Edit Menu	Description	Function Access
<u>N</u> ew View/Modify	<b>New</b> This opens the Recipe Editor screen with an untitled recipe that is using the format of the highlighted recipe in the catalog screen. The recipe title is "UNTITLED" until the new recipe parameters are set and it is saved with a new name.	Access Restricted: Permission Required
✓ <u>2</u> D <u>3</u> D	<b>View/Modify</b> This opens the Recipe Editor screen displaying the parameters of the recipe that is highlighted on the <b>Scan Recipe</b> screen.	Access Restricted: Permission Required
	<b>2D</b> This displays the 2D list of Scan Recipes in the Catalog display area. (See <i>Figure 3.2.</i> )	Everyone has access.
	<b>3D</b> This displays the 3D list of Scan Recipes in the Catalog display area. (See <i>Figure 3.2.</i> )	Everyone has access.

Sample Menu	Description	Function Access
<u>M</u> anuał Load Load/Unioad	<b>Manual Load</b> This moves the sample stage to the Stage Door of the system (the manual load door) so a sample can be manually loaded onto the stage.	Everyone has access.
Initialize Handler	<b>Load/Unload</b> Not functional in systems without a handler.	N/A
Initialize SMIF <u>R</u> elease Cassette	<b>Initialize Handler</b> Not functional in systems without a handler.	N/A
	SMIF Load/Unload Not functional in systems without a handler.	N/A
	<b>Initialize SMIF</b> Not functional in systems without a handler.	N/A
	<b>Release Cassette</b> Not functional in systems without a handler.	N/A

 Table 3.5
 Sample Menu Options Description

#### Table 3.6 Vacuum Menu Options Description

Vacuum Menu	Description	Function Access
0"	<b>Off</b> This button is inactive in the P-15 because the Vacuum switch is manual.	N/A
0 <u>f</u> f ✔ 0 <u>n</u>	<b>On</b> This button is inactive in the P-15 because the Vacuum switch is manual.	N/A

Host Menu	Description	Function Access
<u>G</u> o Offline Attempt Online ✓ Local <u>R</u> emote	<b>Go Offline</b> This takes the P-15 system offline. This is used to prevent the system from responding to a host during a user defined operation.	Access Restricted: Permission Required
	Attempt Online This attempts contact with the host to open the system communication link. The system then operates according to its predetermined GEM parameters.	Access Restricted: Permission Required
	<b>Local</b> This is an Online state where there is communication with the Host but in which the P-15 system controls the system's operation.	Access Restricted: Permission Required
	<b>Remote</b> This is an Online state where there is communication with the Host and in which the host controls the P-15 system operation.	Access Restricted: Permission Required

Table 3.8	Diagnostics Menu Options Description
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Diagnostics Menu	Description	Function Access
Synthesize Data	Synthesize Data	Access Restricted: Permission Required

#### Table 3.9 Task Menu Options Description

Diagnostics Menu	Description	Function Access
Synthesize Data	Synthesize Data	Access Restricted: Permission Required

# **Tool Bar**

The Tool Bar has eight icons that work as short cuts to functions.

#### Figure 3.6 Tool Bar Icons



The function of each icon is described in *Table 3.10*.

 Table 3.10
 Tool Bar for the Scan Recipe Catalog Screen

Tool Bar Icon	Description	Function Access
<b>e</b>	Prints the currently highlighted recipe.	Everyone has access.

Tool Bar Icon	Description	Function Access
START	Starts a scan using the highlighted recipe in the List window.	Everyone has access.
8	Switches to XY View screen with the current recipe active, ready for a scan to be run.	Everyone has access.
$\odot$	Switches to the XY View screen with the stage rotation (theta) buttons active.	Everyone has access.
2D	<ul> <li>Displays the following in the List window:</li> <li>2D Scan Recipes, when in the Scan Recipe Catalog screen;</li> <li>2D Sequence Recipes, when in the Sequence Recipe Catalog screen</li> </ul>	Everyone has access.
3D	<ul> <li>Displays the following in the List window:</li> <li>3D Scan Recipes, when in the Catalog Scan Recipe screen;</li> <li>3D Sequence Recipes, when in the Catalog Sequence Recipe screen.</li> </ul>	Everyone has access.

 Table 3.10
 Tool Bar for the Scan Recipe Catalog Screen

# **Catalog Screen Access Buttons**

The Catalog screen presents access to four sets of information. The Scan Recipe and the Sequence Recipe screen, provide access to the currently defined recipes available for execution in the P-15 system. Two data screens provide access to saved Sequence and Scan data file information.

Tool Bar Icon	Description	Function Access
Scan Recipe	This button displays the list of currently available Scan Recipe folders, which when chosen, display their recipes in the Catalog screen's List window. (See <i>Figure 3.2</i> .)	Everyone has access.
Scan Data	This button displays the list of currently available Scan Data folders, which when chosen, display their data set in the Catalog screen's List window. (See <i>Figure 3.2</i> .)	Access Restricted: Permission Required
Sequence Recipe	<i>Optional</i> This button displays the list of currently available Sequence Recipe folders, which when chosen, present their recipes in the Catalog screen's List window. (See <i>Figure 3.2.</i> )	Everyone has access.
Sequence Data	<i>Optional</i> This button displays the list of currently available Sequence Data folders, which when chosen, present their data sets in the Catalog screen's List window. (See <i>Figure 3.2.</i> )	Access Restricted: Permission Required

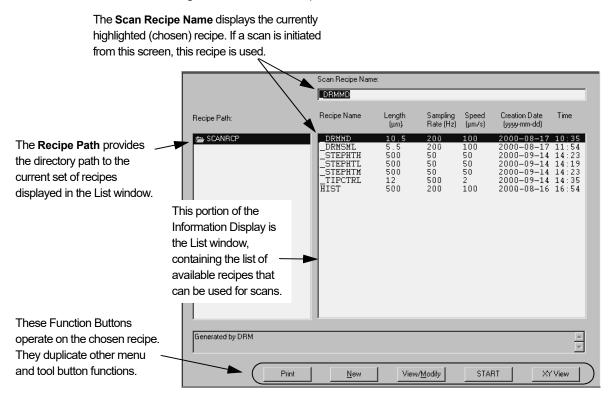
 Table 3.11
 Catalog Screen Access Buttons

# **List Window**

# List Window for Scan Recipe

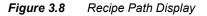
When the **Scan Recipe** button is clicked, the List Window displays the Scan Recipe information and associated function buttons. (See *Figure 3.7.*)

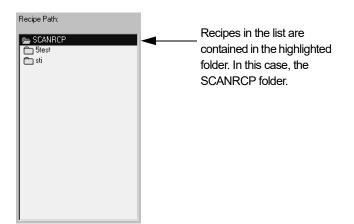
*Figure 3.7* Scan Recipe information in the List Window



## **Recipe Path Display**

This area is used for navigating to a particular folder of recipes in a directory. The recipes in the List window are contained in the highlighted folder in the Recipe Path display.



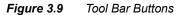


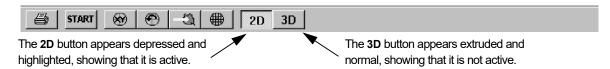
#### Scan Recipe Name Display

This field contains the name of the currently chosen scan recipe. The recipe is chosen by clicking on a recipe in the List window so that the recipe highlights. (See *Figure 3.7.*) The recipe in the **Scan Recipe Name** display is designated to be the *current* recipe. If the **START** button, at the bottom of the Information Display window (see *Figure 3.7*), or the **START** button in the Scan Recipe Catalog tool bar (see *Figure 3.6* and *Table 3.10*), is clicked, a scan is performed using the *current* recipe.

#### **Recipe List Window**

This area contains the list of scan recipes that have been created for the various types of scans used by the system. Scan Recipes are categorized into 2D Scan recipes and 3D Scan recipes. The recipes are accessible by clicking on either the 2D button or the 3D button in the tool bar at the top of the screen. (See *Figure 3.9.*) To determine which list is active, look at the 2D and 3D buttons. The active buttons appear to be depressed and highlighted. The inactive buttons appear extruded outward. (See *Figure 3.9.*)





When a recipe in the current list is clicked on, it highlights and its name appears in the **Scan Recipe Name** display box at the top of the Information Display Window. In this state, when the **START** button in the tool bar (see *Figure 3.9* and *Table 3.10.*) or the **START** button among the function buttons at the bottom of the Information Display window (see *Figure 3.7*) is activated, a scan is performed using that recipe. In addition, the current recipe is featured in the Scan Recipe Editor screen that appears when the **View/Modify** button (a function button under the Information Display window) is activated. (See *Figure 3.7*.)

#### Function Buttons - Scan Recipe List Window

The function buttons, located at the bottom of the Information Display window, operate on the recipes in the recipe List window. Each button is active if it is not grayed out. The **Print**, **START**, and **XY View** buttons all duplicate functions available in a tool bar menu, and the Tool Bar. (See *Figure 3.9.*) The **New** and **View/Modify** buttons are duplicates of **Edit** menu options. (See *Table 3.4.*) If the button is not accessible, it appears as a 2D object, not 3D, and it is grayed out. Buttons might be inaccessible because:

- The system is operating in a Security level that does not grant the current Log On access permission to perform the corresponding function, or
- Because a preceding (or set-up) activity is required before the function can be activated.

 Table 3.12
 Scan Recipe List Window Function Access Buttons

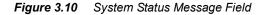
Function Icon	Description	Function Access
<u>P</u> rint	This prints the currently highlighted Recipe.	Everyone has access. This function is also performed by the <b>Printer icon</b> in the tool bar.
New	This opens the Recipe Editor for the creation of a New recipe. In the recipe editor, the title is "UNTITLED" until the recipe is named. The recipe content contains the default parameters.	Access Restricted: Permission Required. The same function is also found in the Edit menu under New.
[ <u>V</u> iew/Modify]	This opens the Recipe Editor allowing modification of the currently highlighted recipe.	Access Restricted: Permission Required. Same function is also found in the Edit menu under View/Modify.
START	This opens the XY View screen and begins the scan procedure associated with the currently highlighted scan recipe.	<b>Everyone has access.</b> This function is also performed by the <b>START</b> button in the Tool Bar at the top of the screen.
XY View	This opens the XY View screen with the currently highlighted recipe in place to perform a scan.	Everyone has access. This function is also performed by the XY Icon in the Tool Bar.

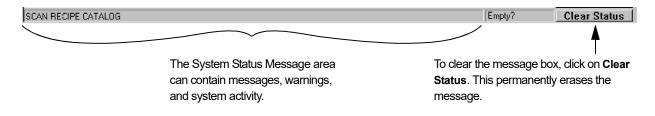
# System Status Message

This portion of the screen contains current system status messages. These messages can contain any of the following:

- Instructions to the user.
- Warnings or Cautions
- Current system activity.

It is important to check this field for system information if the system appears to be stalled or inactive. This message field can contain valuable information for system troubleshooting.





# **CREATING AND EDITING A SCAN RECIPE**

This section presents the procedure for creating a Scan Recipe. Included are:

- Accessing the Scan Recipe Editor where the recipe is created
- A description of the parameters required to create a recipe
- Naming the New Recipe
- Testing the New Recipe

# Accessing the Scan Recipe Editor

The actual creation of a scan recipe is performed in the Editor screen. This means that recipe creation and editing is restricted to those whose password permits access to the Recipe Editor. Use the following procedure to access the Recipe Editor screen:

1. Open the Profiler Catalog screen. (See Figure 3.13.)

2. Choose the Scan Recipe button to display the Scan Recipe catalog. (See *Figure 3.11.*)

	Figure 3.1	1 Scan R	lecipe Ca	talog Sci	reen					
Step 2 Click on Scan Recipe to display its contents in the Information Display window. The Scan Recipe button appears inset when its is chosen.	Scan Recipe	Vacuum Higt Diagn	<u>  ⊕ [-3 </u>   	2D 3     Connection Name      CRMMD      Recipe Name      DRMMD      STEPHTH      STEPHTH      TIPCTRL  HIST      New      New		50 50 500 200	Speed (µm/s) 100 50 50 2100 100	Creation Date (yyyy-mm-dd) 2000-08-17 2000-09-14 2000-09-14 2000-09-14 2000-09-14	11:54 14:23 14:19 14:23 14:35 16:54	Status Status

3. Choose 2D or 3D scan recipes by clicking on the appropriate icon. (See *Figure 3.12.*)



In the Scan Recipe list, a recipe is highlighted in the list. This has no effect on a New recipe. The new recipe is generated using default parameters. (See *Figure 3.13.*)

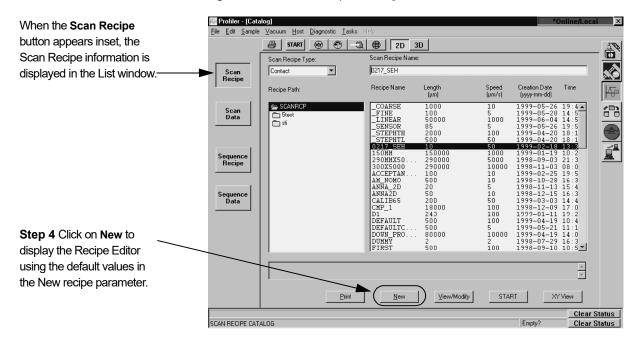


Figure 3.13 Scan Recipe Catalog Screen

Click on **New**, located among the function buttons at the bottom of the Information Display window. (See *Figure 3.13*.)

# **Recipe Editor for 2D and 3D Scans**

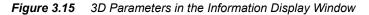
# Introduction

When **New** is clicked, the **Recipe Editor** appears with an UNTITLED recipe. (See *Figure 3.14*.) The UNTITLED recipe contains the default scan parameters. The **Recipe Editor** has eight windows for the 2D recipes and nine for the 3D recipes that, together, contain all the variable scan recipe parameters. Each of these windows is accessed through its own access button on the left side of the **Recipe Editor** Screen. (See *Figure 3.14*.) These windows are discussed one at a time, starting with the top button and working down, until all the parameters required for defining a recipe are explained.

The Title bar shows that the recipe name is currently UNTITLED and the screen is Recipe Editor.	Profiler - [Recipe Editor - **UNTITLED**]     ×       Becipe Dptions Help     20 Scan       Scan Parameter Definition     2D Scan       X Scan Size (µm):     13.000
Each Parameter button displays its parameters in the Information Display window.	Feature       Detection         Filters       Scan Speed (µm/s):       20 ▼         Cursors       Sampling Rate (Hz):       2003 ▼         General       Multi-Scan Average :       1 ▼         Roughness       Scan Direction:       Statt:       Center:         Bearing Ratio       Cutting Deth       Image: Content Conten Content Content Conten Content Content Co
The Information Display window contains the parameter set related to the currently activated Parameter button. The current Parameter button appears to be indented, as the <b>Scan</b> <b>Parameter Definition</b> does in this illustration.	High Spot Count       Scan Time:         Individual Trace (s):       0.7         Approx. Total (hr:max:s):       0;0:0.3         Setup       Stytus:         Analysis Tools       10.0         Sytus:       0.02         Vertical Ranging:       8:ange:/Recommended Maximum (mg):       0.05         Sytus:       0.02         Vertical Ranging:       6:5um/0.0039A         Profile Type :       *Lr         Substr.       Clear Status

Figure 3.14 Recipe Editor for a 2D UNTITLED Recipe

# **Scan Parameter Definition Window**



<b>3D Scan</b> contains scan characteristics. (The 2D version contains fewer	3D Scan X Scan Size (µm); 13.000 💌 Y Scan Size (µm); 13.000 💌
variables.)	Scan Speed (µm/s):         20         ▼         Traces:         50           Sampling Rate (Hz):         2000         ▼         Y Spacing (µm):         0.260
Scan Time category contains parameters that are results of above actions.	Scan Direction:
Stylus category contains	Scan Time:           Individual Trace (s):         0.7         Total Data Points:         65050           Approx. Total (hr:min:s):         0 : 1 : 7.7         Point Interval (μm):         0.016000
Stylus force and size parameters.	Stylus: Applied Force (mg): 1.00  Recommended Maximum (mg): 0.05
Vertical Ranging category contains vertical size (height, depth and scan profile of the scan.)	Stylus Radius (μm):       0.02         Vertical Ranging:

The Scan Parameter Definition button displays four categories of 2D or 3D scan parameters: 2D Scan or 3D Scan; Scan Time; Stylus; and Vertical Ranging.

### 2D Scan Category Parameters - Scan Parameters Definition

The parameters defined in this category deal with the actual mechanics of the 2D scan. Each is discussed in *Figure 3.16*.

Figure 3.16 2D Scan Category Parameters

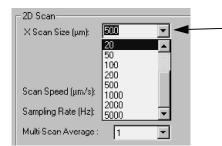
— 2D Scan — X Scan Size (μm): [	90		
Scan Speed (µm/s): Sampling Rate (Hz): Multi-Scan Average :	100 💌 200 💌 1		Show Position:
Scan Direction:		Ieach	Start: © Center: O End: O

- 1. **X Scan Size (μm)**. This variable sets the **length** of the actual scan. It is set in one of two ways:
  - Click on the menu arrow at the right of the X Scan Size field to display the drop-down menu. Click on the desired number in the menu. The number should appear in the field. The variables in the drop-down menu range, in various increments, from 1 5000 μm. (See *Figure 3.17.*) For the *standard* P-15, 80000 μm is the longest possible scan. The *long scan* P-15 can scan 200000 μm.
  - Alternative: Double-click in the X Scan Size field to highlight the current number. Enter the desired number in microns (µm). This variable is helpful when a specific scan length is required that is not in the drop-down menu.



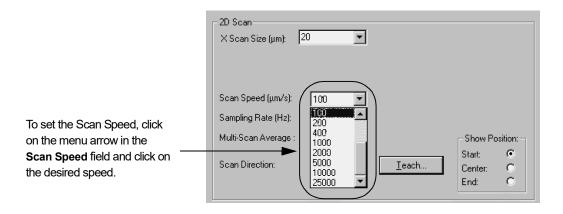
**NOTE:** The scan length can also be changed when using the Teach function. See Step *6. on page 3-22* for more details. See the Note.

Figure 3.17 X Scan Size (µm)



Step 1 Click on the menu arrow to display the drop-down menu. To choose the number of microns ( $\mu$ m) in the scan length, click on the appropriate number.

 Scan Speed (μm/s) - This parameter sets the speed at which the scan is performed. It has a range between 1 μm/s and 25000 μm/s, with numerous options within this range displayed in its drop-down menu. (See *Figure 3.18*.)



*Figure 3.18* Scan Speed Drop-down Menu

The Scan Speed should be determined in conjunction with the stylus tip size and the **Applied Force** setting. *Table 3.13* lists some recommended safe scan speeds for operation of the P-15 systems. Following the guidelines in the table should protect the stylus tip and the sample:

Table 3.13 Recommended Scan Speeds

Stylus Tip Size	Applied Force	Scan Speed	Related Condition
Submicron Tips	0.05 - 0.10 mg.	Not to exceed 10 $\mu$ m/s	Soft materials*
2 μm Tip	0.5 mg.	2.0 - 10 μm/s	Soft materials*
2 µm Tip	1 - 2 mg.	Not to exceed 200 $\mu\text{m/s}$	Normal scans

\*Soft Materials - such as copper, gold, aluminum, and photoresist

The following cautions are important in determining a safe scan speed.



**CAUTION:** When scanning soft material (e.g., copper, aluminum, and photoresist) follow the recommended applied force and scan speed for each listed stylus.



**CAUTION:** If the scan speed is set too fast when using a small applied force, features might be missed or inaccurately traced.

3. Sampling Rate (Hz) - is the frequency at which data points are collected. (It sets the number of data points that are collected per second during a scan.) Optimum data collection is determined by this number in conjunction with the scan speed, the length of the scan, and the size of the stylus tip. The Sampling Rate should be set so that each data point has meaning. In general, as the scan progresses, the Sampling Rate should not calculate out to be greater than 1/4 the radius of the

stylus tip. Any more than that reduces the significance of each data point. (See *Figure 3.21* and *Figure 3.22*.) Collecting more data points does not necessarily improve the accuracy of the scan results and can cause slower system calculations (as could be the case when using Multi-Scan averaging with an unnecessarily high Sampling Rate). (See the example below.)

**EXAMPLE**: The following demonstrates the relation between scan speed, scan length, and Sampling Rate:

- Scan Speed =  $10 \,\mu\text{m/s}$  Scan Length =  $100 \,\mu\text{m}$
- Sampling Rate = 20 Hz Stylus radius =  $2 \mu m$

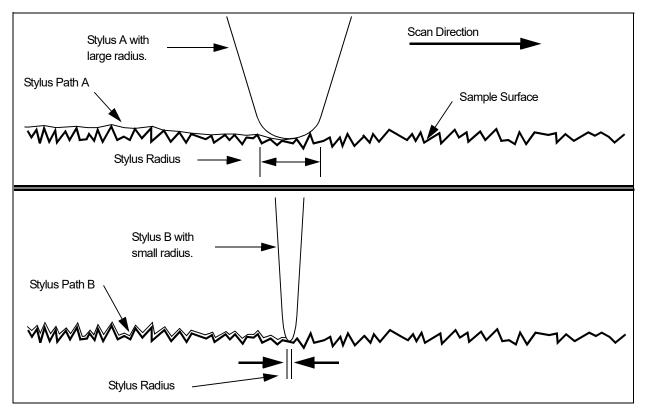
20 data points are collected each second during a 10 second scan (20 Hz.)

200 data points are collected during the total scan.

200 data points over a 100  $\mu$ m scan means that 2 data points were collected per micron during the scan.

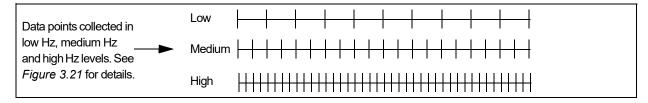
Figure 3.19 illustrates the impact of stylus radius in generating a scan trace.

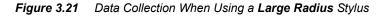
Figure 3.19 Scan Trace Comparison - Large vs. Small Stylus Radius

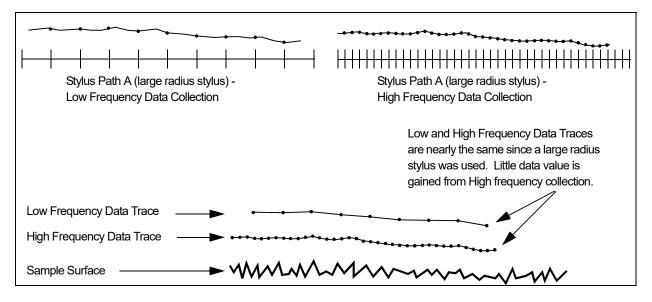


Comparing the Scan Path of the large radius stylus and the small radius stylus, assessment can be made regarding the validity of higher frequency data collection. In general, the larger radius styli do not detect the smallest features. They give traces that can resemble a statistical average. Little is gained by increasing the number of data points collected during a large radius stylus scan, if the stylus is not capable of capturing the smallest surface features. (See *Figure 3.19* and *Figure 3.21*.)









If the Stylus chosen is small enough to detect the features of interest in the scan, then a sampling rate should be chosen that accurately records the level of detail required from the scan. For a small stylus radius, as the Sampling Rate increases, assuming the speed is left the same, the number of data points collected forms a trace that comes closer to the actual scan path features. (See *Figure 3.22.*)

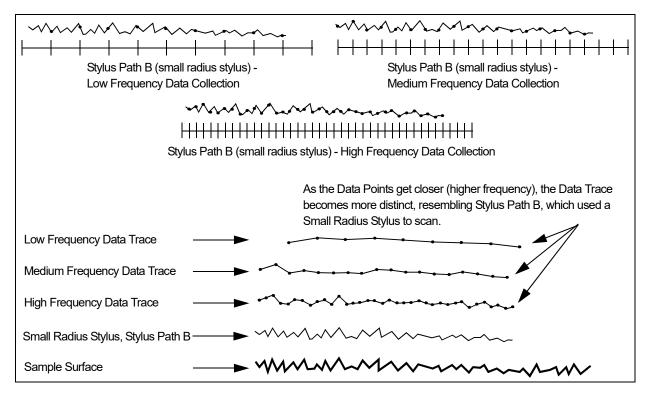
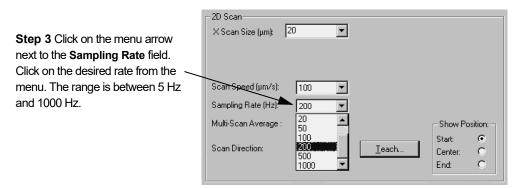


Figure 3.22 Data Collection When Using a Small Radius Stylus

Choose the desired Sampling Rate by clicking on the menu arrow next to Sampling Rate field. The recommended range is presented in the drop-down menu (5 Hz - 1000 Hz). Click on the desired rate from the menu.



*Figure 3.23* 2D Scan Options With Sampling Rate Menu

4. **Multi-Scan Average** - This is a 2D option that allows the user to repeat a single scan up to 10 times so that the scan data can be averaged by the number of scans performed. This feature provides an opportunity to level out the noise factors in a scan. The optimum Multi-Scan Average is between **3** and **5** times.

	X Scan Size (µm): 20
Step 4 Multi-Scan Average sets the number of times a scan is run before the data is averaged to present the scan for analysis. Click on the menu arrow next to the variable box and click on the desired number of scans.	Scan Speed (µm/s): 100 ▼ Sampling Rate (Hz): 200 ▼ Multi-Scan Average: 1 ▼ Scan Direction: 2 3 4 5 ↓ Leach C End: C
5	<ul> <li>Click on the menu arrow next to the Multi-Scan Average to display its menu. Click on the number of scans to be performed for averaging the data.</li> <li>Scan Direction - Arrow - This option dictates the direction of the scan, from left to right or from right to left or from right.</li> <li>Changing The Scan Direction: Click on the arrow to cause it to point the opposite direction.</li> </ul>
	NOTE: DO NOT use unless it is absolutely necessary. The recommended direction is left to right because it gives better repeatability, protects the stylus, and provides better data.

Figure 3.24 2D Scan Options With Multi-Scan Average Menu

Figure 3.25	2D Scan Options With Scan Direction Arrow
-------------	---

	-2D Scan			
	X Scan Size (µm):	10 🔽		
Step 5 The arrow dictates				
which direction the scan	Scan Speed (µm/s):	100 💌		
proceeds in. To change the	Sampling Rate (Hz):	200 💌		
scan direction, click on the	Multi-Scan Average :	1		Show Position:
arrow and it changes to				Start: 💿
indicate scan direction.	Scan Direction:	<b></b>	Ieach	Center: C End: C

6. Scan Direction - Teach - When the Teach button is clicked on, it displays the Teach Scan Length screen. This screen allows the user to set the starting, center, or end positions of a scan. The scan length is already set in the X Scan Size parameter. Use the following procedure to set the Teach... position:

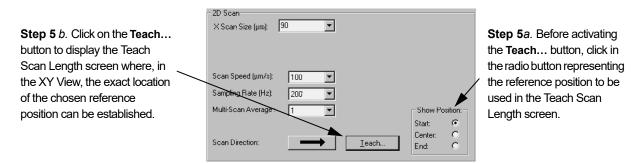


Figure 3.26 2D Scan Options - Show Position:

a. Before clicking the **Teach**... button, the desired **reference position** must be chosen. This is accomplished in the **Show Position** box, to the right of the **Teach**... button. Click in the radio button next to the desired reference position, **Start, Center**, or **End**, that is to be established with respect to the scan feature in the **Teach Scan Length** screen. (See *Figure 3.26*.)

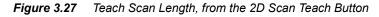
	Table 3.14	Show Position Options
--	------------	-----------------------

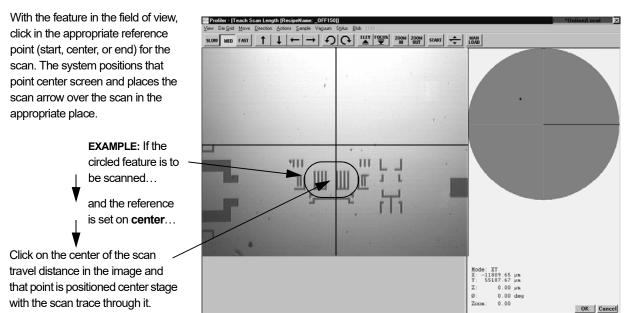
Option	Description	Graphic Representation
Start	The <b>Start</b> setting is used in the Video portion of the XY view screen to position the start of the scan at the intersection of the Video screen crosshairs. Wherever the user clicks in the video image, that position becomes the starting scan position, and appears at the center of the Video screen, with the scan distance presented as an arrow.	Click here to position Start
Center	The <b>Center</b> setting is used in the Video portion of the XY view screen to position the center of the scan at the intersection of the Video screen crosshairs. Wherever the user clicks in the video image, that position becomes the center of the scan, and appears at the center of the Video screen, with the scan distance presented as an arrow.	Click here to position Center Outcome
End	The <b>End</b> setting is used in the Video portion of the XY view screen to position the end of the scan at the intersection of the Video screen crosshairs. Wherever the user clicks in the video image, that position becomes the end of the scan, and appears at the center of the Video screen, with the scan distance presented as an arrow.	Click here to position End Outcome

b. Locate the desired feature in the XY View portion of the screen. Click on the reference position (start, center, or end). The screen then positions the scan length arrow over the scan feature according to the chosen position. The reference position is at the center of the video screen crosshairs. (See *Table 3.14.*)



**NOTE:** When in the **Teach Scan Length** (XY view) screen, it is possible to change the scan length by clicking on a position in the video screen and dragging the new length. If the scan is immediately started from the Teach Scan Length screen, it scans the newly defined (dragged) distance even though the original recipe scan length is different. However, if the new distance is not saved it does not appear on the original recipe. If it is saved by clicking OK or actually saving the changes from the menu, the recipe then reflects the newly dragged scan distance.





can Length: 200,000 i

Clear Status

# **3D Scan Category Parameters - Scan Parameters Definition**

The parameters discussed in this section are those that are **additions to** or **differ from** the 2D parameters already presented. For information on parameters that are identical for 2D and 3D scans, see the descriptions in the 2D recipe section. (See *Table 3.15* for identification of which parameter settings are 2D or 3D.)

Parameter Setting	2D, 3D or Both	Description and Location			
X Scan Size	Both	X direction scan length; Step 1. on page 3-17.			
Y Scan Size	3D	The length in the Y-direction through which the X-direction scans are mad at each <b>Y Spacing</b> interval.			
Scan Speed	Both	The speed at which the scan is performed.			
Sampling Rate	Both	The rate at which data points on the scan are recorded for analysis.			
Traces	3D	This is the number of scans that are made to encompass the Y-distance requirement.			
Multi-Scan Average	2D	The number of single identical scans which are performed and used to create a scan data set that represents the average of the scans.			
Spacing	3D	This is the distance between X scans performed across the Y direction of the 3D scan area.			
Scan Direction	Both	The direction in which the scan is performed.			
Teach	Both	Displays the <b>Teach Scan Length</b> screen that is used to determine the start, center or end of the scan. Can also be used to drag a new scan length.			
Show Position	Both	Displays the current position and provides an opportunity to set a new position at which the scan, of scan length set in <b>X Scan Size</b> , is started, is centered, or ends.			

Table 3.15 3D Scan Parameters Summary

#### Y Scan Size (µm)

This parameter defines the size, in the Y-direction, of the 3D area to be scanned. It is the area across which the number of scans defined in the parameter **Traces** are divided up. (See *Figure 3.29 on page 3-26.*)



**NOTE:** If the variable in the **Spacing** parameter is changed, the **Y Scan Size** changes to accommodate the number of **Traces** at the new **Spacing** distance.

Setting or Changing Y Scan Size - Use one of the following procedures:

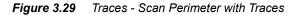
- Click the menu arrow to the right of the **Y** Scan Size field and click on the desired size.
- Highlight the current number and type in the new number. (See also **Automatic Parameter Adjustment**: in Step *on page 3-27*.)

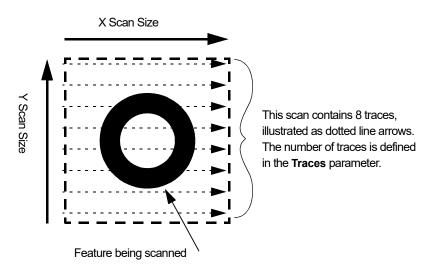
−3D Scan X Scan Size (μm):	13.000 💌 (	Υ Scan Size (μm);	50.000	Set the <b>Y Scan</b> <b>Size</b> by clicking on the menu arrow and
Scan Speed (µm/s): Sampling Rate (Hz):	20 <b>•</b> 2060 <b>•</b>	Traces: Υ Spacing (μm):	50 1.000 Show Position:	choosing the desired size, or by highlighting the current
Scan Direction:	$\longrightarrow$	Ieach	Start: O Center: © End: O	number and typing in the new number.

Figure 3.28 3D Scan Parameters

## Traces

This assigns the number of scans that are made in the X-direction across the **Y Scan** Size direction. In *Figure 3.29*, the number in the **Traces** variable box would be **8**.





If the **Y** Scan Size is set [Y Scan Size = (Traces -1) x Y Spacing], when the **Traces**: parameter is entered, the **Y** Spacing parameter automatically adjusts to reflect the appropriate spacing between scans.

Setting the Number of Traces: To change the number of Traces in a 3D scan, highlight the current Traces value and type in the new number of traces. (See also Automatic Parameter Adjustment: in *Y Spacing (mm)* on page 3-27.)

ì	20.0					
	- 3D Scan X Scan Size (μm):	13.000	Υ Scan Size (μm):	50.000	•	To set or change the number of
	Scan Speed (µm/s):	20 💌	Traces:	50		traces in a 3D scan, highlight the current <b>Traces</b>
	Sampling Rate (Hz):	2000 💌	Υ Spacing (μm):	1.000	sition: —	variable and type in the new
				Start: Center:	•	number.
	Scan Direction:		<u>T</u> each	End:	0	

Figure 3.30 3D Scan - Traces Parameter

# Y Spacing (µm)

This variable sets the distance in the Y-direction between X-direction scan traces in a 3D scan.

The spacing is very important to final 3D data collection set because, together with the stylus radius, it determines the essential resolution of the feature that is scanned. (See Step 3 on page -18.) Consider to following examples:

- If the distance between scans is too great with respect to the stylus radius, important variations in the scanned feature might be missed.
- Conversely, if using a larger stylus, and the distance between scans is very small, many of the data points are essentially redundant and, therefore, meaningless.

Automatic Parameter Adjustment: - In general, a connection exists in the software such that, when certain parameters are changed, other parameters are readjusted to accommodate the changes. The adjustments occur between the Y Scan Size, Traces, and Y Spacing parameters. Occasionally, after setting a parameter, the user might click on one of the other parameters and notice a minor adjustment to the parameter that had just been set. This happens to balance the numbers between Y Scan Size, Traces, and Y Spacing. (See *Table 3.16*.)

Change This Parameter	Adjusts These Parameter	Conditions Effecting Adjustment
Y Scan Size	Y Scan Size	Occasionally makes minor adjustments to the newly set number to accommodate the Y Spacing or Traces.
	Y Spacing	
	Traces	Occasionally makes minor adjustments (no more the $\pm$ 1) to the newly set number, to accommodate the Y Scan Size and Y Spacing. Usually only for scans less than 100 $\mu$ m.
Traces	Y Scan Size	This change is normally small, changing to accommodate the spacing required to perform the number of traces.
	Y Spacing	
	Traces	Occasionally makes minor adjustments (no more the $\pm$ 1) to the newly set number, to accommodate the Y Scan Size and Y Spacing. Usually only for scans less than 100 $\mu$ m.
Y Spacing	Traces	
	Y Scan Size	This change is normally small, changing to accommodate the spacing required to perform the number of traces.
	Y Spacing	Occasionally makes minor adjustment to the newly set number to accommodate the Y Scan Size or Traces.
Scan Speed	No Changes	
Sampling Rate	No Changes	

Table 3.16 Automatic Parameter Adjustments

1. **Show Position** - For 3D scans, the three options in this box are used for positioning the scan area parameters box, not to indicate the actual Start and End of the scan. One of these options must be chosen in conjunction with the **Teach**... position function button next to the **Show Position** box. (See *Table 3.17*.)

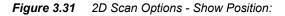
Selecting An Option: Click in the radio button of the desired position.

Show Position Option	Description	Graphic Representation
Start	The <b>Start</b> setting is used in the Video portion of the XY view screen to position the upper left corner of the scan area box in the Video screen crosshairs. Wherever the user clicks in the video image, that position becomes the upper left corner of the scan area box, and appears at the center of the Video screen. This is not the actual place where the scan starts. <b>Start</b> only defines the upper left corner of the scan area box. Literal START is near the lower left corner.	Click here to position Start
Center	The <b>Center</b> setting is used in the Video portion of the XY view screen to position the center of the scan area box in the center of the Video screen crosshairs. Wherever the user clicks in the video image, that position becomes the center of the scan area box, and appears at the center of the Video screen.	Click here to position Center Outcome Scan Feature
End	The <b>End</b> setting is used in the Video portion of the XY view screen to position the lower right corner of the scan area box in the center of the Video screen crosshairs. Wherever the user clicks in the video image, that position becomes the end of the scan area box, and appears at the center of the Video screen. This is not the actual place where the scan ends. <b>End</b> only defines the lower right corner of the scan area box. Literal END is near the upper right corner.	Click here to position End Outcome Scan Feature

 Table 3.17
 Show Position Options

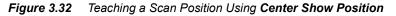
2. **Teach...** - This function takes the feature and positions it in the scan field according to the reference position option chosen in the **Show Position** box. (See also Step *1. on page 3-29.*)

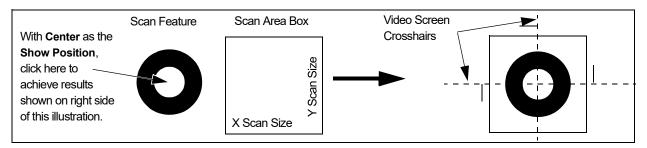
a. Before clicking the Teach... button, the desired reference position must be chosen. This is accomplished in the Show Position box, to the right of the Teach... button. Click in the radio button next to the desired reference position, Start, Center, or End, that is to be established with respect to the scan feature in the Teach Scan Length screen. (See *Figure 3.31*.)



<b>Step 2</b> Click on the <b>Teach</b> button to display the Teach	-3D Scan X Scan Size (μm):	90.000	Υ Scan Size (μm):	90.000	Step 1 Before activating the Teach button, click in the radio
Scan Length screen where, in the XY View, the exact location of the chosen reference position can be established.	Scan Speed (µm/s): Sampling Rate (Hz):	100 V 500 V	Traces: Spacing (μm):	10 9.000	button representing the reference position to be used in the Teach Scan
	Scan Direction:		Ieach	Start:  Center:  Cent	Length screen.

b. Locate the desired sample feature in the Video portion of the screen. Click on the position that corresponds to the reference position (Start, Center, or End), that is on or near the scan feature. The screen positions the scan area box over the scan feature according to the chosen position. The chosen position (Start, Center, or End) is at center screen, with the scan area box positioned accordingly. (See *Figure 3.32, Figure 3.33 & Figure 3.34.*)







**NOTE:** When in the **Teach Scan Length** screen, it is possible to change the scan area by clicking on a position in the video screen and dragging the box to form a new area. If the scan is immediately started from the **Teach Scan Length** screen, it scans the newly defined (dragged) area even though the original recipe scan area is different. However, if the new area parameters are not saved, they do not appear in the original recipe. If they are saved by clicking **OK** or actually saving the changes using the **File** menu, the recipe will reflect the newly dragged scan distance.

Assume that the features represented in the illustration were on the video screen.

- The feature with the dashed circle around it is the object of the scan,
- The white box represents the scan area defined by X Scan Size and Y Scan Size,
- Start is the Show Position.

Clicking here places the scan area box around the feature and sets this spot at the center of the view screen. (See results in *Figure 3.34*.)

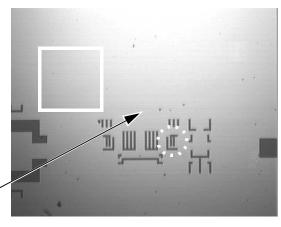
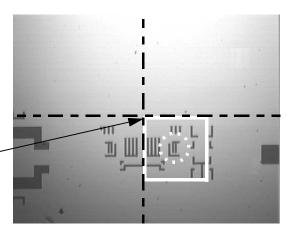


Figure 3.33

The preceding illustration demonstrates the use of the **Teach...** function from the 3D Scan parameters in the Recipe Editor. The illustration uses the **Start** option from the **Show Position** box. The results are demonstrated in *Figure 3.34*.

Teaching a Scan Position Using Start Show Position

Figure 3.34 Teaching a Scan Position Using Start Show Position



The scan area box aligns with the **Start** position at the point on the screen where the user clicks.



**NOTE:** The simplest way to set up a 3D scan is to choose **Center** as the **Show Position** and click directly in the center of the scan feature. This places the center of the feature in the center of the scan area box, and places the scan area box at the center of the screen crosshairs.

## Scan Time Parameters (2D and 3D) - Scan Parameters Definition

The **Scan Time** parameters box displays time and data point values, broken down into general components. (See *Figure 3.35*.) No values can be set or defined in this portion of the screen. These values are read only because they are determined by parameters set in other fields.



**NOTE:** These values are system generated from parameters set in other fields. This value **might be inaccurate up to 20%** of the actual value. Use these values only for casual reference.

Figure 3.35 Scan Time - Scan Parameters Definition

		−3D Scan- X Scan Size (μm): [	13.000 💌	Υ Scan Size (μm);	13.000 💌	
		Scan Speed (µm/s): Sampling Rate (Hz):	20 <b>•</b> 2000 <b>•</b>	Traces: Υ Spacing (μm):	50 0.260 Show Position: –	
The <b>Scan Time</b> parameters		Scan Direction:	$\rightarrow$	Ieach	Start: C Center: C End: C	
are display only.	-(	Scan Time: Individual Trace (s): Approx. Total (hr:min:s	0.7	Total Data Points: Point Interval (μm):	65050	
		Stylus: Applied Force (mg): Stylus Radius (μm):	1.00	Recommended Maxir	num (mg): 0.05	
		Vertical Ranging: Range/Resolution: Profile Type :	6.5um/0.0039A	•		

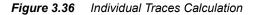
## Individual Traces (s)

This defines the number of seconds required to complete one scan. This time parameter divides **X** Scan Size ( $\mu$ m) by Scan speed ( $\mu$ m/s) and adds the result to the approximate move time. (See *Figure 3.36*.)



**CAUTION:** The following equation is not the actual equation used to produce the variables. The equation only takes into consideration the simplest and most general components used to produce the value displayed in the field. *Use generate values only for casual reference*.

For 2D and 3D [X Scan Size / Scan speed] + move time = Individual Traces (s)

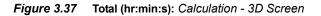


Individual Traces (s)	(	30. Scan X Scan Size (µm); 13.000 ▼ Y Scan Size (µm); 13.000 ▼	
parameter is calculated using			
the X Scan Size ( $\mu$ m) and the			
Scan Speed (μm/s) settings.	- (	Scan Speed (µm/s): 20 Traces: 50	
The calculated time is added to		Sampling Rate (Hz): 2000 ▼ Y Spacing (μm): 0.260	
the move time to give the total		- Show Position:	
Individual Traces (s) time.		Start: O	
		Scan Direction:	
	Ģ	└ Scan I me:	
	·	Individual Trace (s): 0.7 Total Data Points: 65059	
		Approx. Total (hr:min:s): 0 : 1 : 7.7 Point Interval (µm): 0.016000	

**Total (hr:min:s)** - This is the total time that it takes to complete the set of scans defined in the scan recipe section, **2D** or **3D Scan**.



**CAUTION:** Generating the value for the **Approx. Total (hr:min:s)** is very complicated. This variable can be inaccurate up to 20% in either direction. Use the generated time only for casual reference.



	- 3D Scan			
	X Scan Size (μm):	200.000 💌	Υ Scan Size (μm):	200.000 💌
	Scan Speed (µm/s):	50 💌	Traces:	10
	Sampling Rate (Hz):	100 💌	Υ Spacing (μm):	20.000
				Show Position:
Approx. Total (hr:min:s:).	Scan Direction:		Ieach	Start: © Center: C End: C
	-Scan Time:			
	Individual Trace (s);	4.0	Total Data Points:	4010
	Approx. Total (hr:min:	:\$): 0 : 1 : 59.1	) Point Interval (μm):	0.500000

**Number of Data Points:** - This is the total number of scan data points collected during the scan.

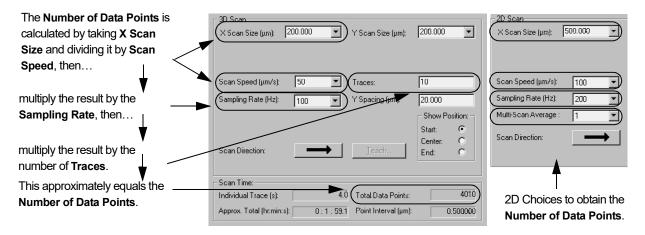


**CAUTION:** The following equation is not the actual equation used to produce the variables, it only approximates it. This equation only takes into consideration the simplest and most general components used to produce the value displayed in the field. *Use generate values only for casual reference.* 

For 3D	[(X Scan Size / Scan Speed) x Sampling Rate x Traces] + the number of traces = Number of Data Points
For 2D	[X Scan Size / Scan Speed] x Sampling Rate x Multi-Scan Average = Number of Data Points

The approximate value is seen in the following example





## **Point Interval**

Point Interval is the distance between data points in the X-direction of each trace.

For 2D and 3D

Scan Speed (µm) / Sampling Rate (Hz) = Point Interval:



<b>Point Interval</b> is the distance between data points in each	⊢3D Scan X Scan Size (μm):	500.000	Υ Scan Size (μm):	1001001
X-direction scan trace. It is defined as the	Scan Speed (µm/s): Sampling Rate (Hz):	100 <b>•</b> 200 <b>•</b>	))Traces: ))Spacing (µm):	10
Scan Speed divided by the Sampling Rate.	Scan Direction:		Ieach	Show Position: Start: © Center: O End: O
	Scan Time: Individual Trace (s): Total (hr:min:s):	0:1:7	Number of Data Point Point Interval (µm):	<u>s:</u> 10009 0.500

# Stylus Parameters (2D and 3D) - Scan Parameters Definition

The **Stylus** parameters box contains those variables that deal with the stylus operation. Only the Applied force variable is accessible for change in this screen.

Figure 3.40 Stylus Parameters (2D and 3D)

	3D Scan X Scan Size (µm): 13.000 💌 Y Scan Size (µm): 13.000 💌	
	Scan Speed (μm/s):         20         ▼         Traces:         50           Sampling Rate (Hz):         2000         ▼         Y Spacing (μm):         0.260	
Applied Force is the only parameter in <b>Stylus</b> that is adjustable. Click on the menu arrow to display the menu and	Scan Direction:	
choose the force.	Scan Time:           Individual Trace (s):         0.7           Total Data Points:         65050           Approx. Total (hr:min:s):         0 : 1 : 7.7           Point Interval (μm):         0.010000	
ĺ	Stylus: Applied Force (mg): 1.00 ▼ Recommended Maximum (mg): 0.05 Stylus Radius (µm): 0.02	
	Vertical Ranging: Range/Resolution: 6.5um/0.0039A Profile Type : -1	6.5 mm is the hi gain range.

## Applied Force (mg)

This is the force exerted by the stylus on the sample surface. With each different stylus radius there are recommended limits that should be taken into consideration when setting the Applied Force. The Applied Force should not exceed the recommended maximum force. (See Figure 3.41.)



Applied Force is the only adjustable parameter in the Stylus box.

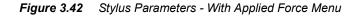


 Table 3.18
 Stylus Force Ranges for the Different Head Configurations

MH2If	MH2sr	MH2xr
0.05-50 mg in <i>hi gain</i> range (0.1 mg for medium and low ranges)	1-50 mg	0.5-50 mg

Changing the **Applied Force** setting:

- 1. Click on the menu arrow next to the variable box to display its menu.
- 2. Click on the desired force setting. (*Figure 3.42.*)



To change the Applied	☐ Stylus:
Force value, click on	Applied Force (mg):
the menu arrow to the	Stylus Radius (µm):
right of the variable box	Stylus Hadius (µm): 0.10
to display the menu.	Vertical Ranging: 0.50
Click on the desired	Range/Resolution: 2
force setting.	Profile Type :



**NOTE:** The force setting must be within the range of the head being used or a message is generated that requires the user to choose an appropriate setting.

#### Stylus Radius (µm)

Stylus Radius is the manufacturers stated radius of the stylus. The stylus radius cannot be changed in this screen.



**CAUTION:** Recommendations and limits are only correct if the "Stylus Change Procedure" was followed when the stylus was installed.

Use the Stylus Change Procedure to change the stylus radius setting. (See *Stylus Change Procedure* on page 4-1.)

#### Recommended Maximum (mg)

Each stylus type is associated with a maximum applied force setting. The maximum setting is deemed to be safe for the stylus and the sample while performing normal scans. This force should not be exceeded.



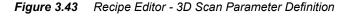
**CAUTION:** See *Table 3.13 on page 3-18* for special recommended force limitation when using any submicron tip on a soft sample. This number is set during the Stylus Change Procedure. If that procedure is not used when changing a stylus the recommended force could be incorrect. If a user sets the wrong Applied Force and exceeds the actual recommended force, stylus damage or potential damage of soft sample surfaces could occur.

## Vertical Ranging Parameters (2D and 3D) - Scan Parameters Definition

**Vertical Ranging** contains two parameters: **Range/Resolution** and **Profile Type**. These two parameters are used together to set up the system for:

- Range: The maximum feature measurement limit (theoretical), up or down, that is considered when scanning for a feature,
- Resolution: The theoretical vertical resolution of the scan of a feature.

Three set of ranges are available depending on the type of head the instrument uses. The primary differences between the ranges are in their resolution capabilities, and the ability in the 131  $\mu$ m, 327  $\mu$ m, and 1000  $\mu$ m range to set the direction in which the range is applied. The ranges are described below.



Profiler - [Recipe Edi Recipe Options Help	itor - 13X13]
Scan Parameter Definition	30 Scan X Scan Size (µm); 13.000 ▼ Y Scan Size (µm); 13.000 ▼
Feature Detection Filters Cursors General Parameters	Scan Speed (µm/s): 20 Traces: 50 Sampling Rate (Hz): 2000 Y Spacing (µm): 0.260 Show Position: - Start: C
Roughness Waviness Bearing Ratio Cutting Depth	Scan Direction:
High Spot Count Peak Count 3D Cursors	Scan Time:         Individual Trace (s):         0.7         Total Data Points:         65050           Approx. Total (hr.min:s):         0 : 1 : 7.7         Point Interval (µn):         0.010000
Setup Analysis Tools	Stylus:     Applied Force (mg):     1 00 •     Recommended Maximum (mg):     0.05       Stylus Radius (µm):     0.02
	Vertical Ranging: Range/Resolution: 6.5um/0.0039A  Profile Type :
	Substr. Clear Status

#### Range/Resolution

This parameter sets the maximum size limit of the features that can be scanned in each given range, and the minimum feature size that can be resolved (positively detected). Three ranges are available. (See *Table 3.19*.)

Table 3.19 Range and Resolution Scan Parameters for the MH2If Head

Vertical Range (µm)	Resolution (Å)
± 3.2 (6.5 total)	0.004
± 13 (26 total)	0.016
± 65 (131 total)	0.08

 Table 3.20
 Range and Resolution Scan Parameters for the MH2sr Head

Vertical Range (µm)	Resolution (Å)
± 6.5 (13 total)	0.008
± 32 (64 total)	0.04
± 173 (327 total)	0.2

# The VERTICAL RANGING parameters box defines:

**1.** Which vertical features are scanned; those in the up, down, or both up and down direction, from the scans starting level.

2. The maximum theoretical height, depth or both height and depth of features that are considered, along with the minimum feature size that, theoretically, can be clearly resolved.

Table 0.21 Range and Resolution Cean Faranciers for the miles frequences			
Vertical Range (μm)	Resolution (Å)		
± 6.5 (13 total)	0.008		
± 65 (131 total)	0.08		
± 500 (1000 total)	0.6		

 Table 3.21
 Range and Resolution Scan Parameters for the MH2xr Head



**NOTE:** The Resolution numbers in *Table 3.19*, *Table 3.20*, and *Table 3.21* are theoretical. Noise levels could greatly effect the resolution.

Figure 3.44 Vertical Ranging - Range/Resolution Menu

To choose the  $131 \,\mu\text{m}$  range, dick on the menu arrow next to the variable box to display the menu. Click on  $131 \,\mu\text{m}$ .

Vertical Ranging:	
Range/Resolution:	131um/0.357A
Profile Type :	131um/0.357A 26um/0.015625A 6.5um/0.0039A

131  $\mu$ m, 327  $\mu$ m, and 1000  $\mu$ m ranges - The largest features are scanned using these ranges. In this range, using the **Profile Type** menu (see *Figure 3.45* and *Table 3.22*), the user can specify which features are considered for analysis:

- Features that step UP a maximum of 131 µm from the scan's starting point;
- Features that step **DOWN** a maximum of 131 μm from the scan's starting point;
- Or features that step ±65 μm, **BOTH UP AND DOWN**, from the scan's starting point

### Choosing the 131 $\mu$ m, 327 $\mu$ m, or 1000 $\mu$ m range:

Click on the menu arrow to display the menu. Click on the desired option. (See *Figure 3.44*.)

Range Limitations for 131 µm (MH2lf head):

- The limit for a scan with the Profile Type  $-\Box$  is  $\pm 65 \,\mu m$ .
- The limit for a scan with the Profile Type  $\int$  is approximately  $65 \ \mu\text{m} + (1/2 \ \text{x} \ 65 \ \mu\text{m}) \approx 100 \ \mu\text{m}.$
- The limit for a scan with the Profile Type  $\_$  is approximately -65 µm + (1/2 x -65 µm)  $\approx$  -100 µm

Range Limitations for 327 µm (MH2sr head):

- The limit for a scan with the Profile Type  $-\int$  is ±163 µm.
- The limit for a scan with the Profile Type  $160 \ \mu\text{m} + (1/2 \ \text{x} \ 160 \ \mu\text{m}) \approx 240 \ \mu\text{m}.$  is approximately
- The limit for a scan with the Profile Type  $\_$  is approximately -160 µm + (1/2 x -160 µm)  $\approx$  -240 µm

Range Limitations for 1000 µm (MH2xr head):

- The limit for a scan with the Profile Type  $-\int_{-}^{-}$  is  $\pm 500 \ \mu m$ .
- The limit for a scan with the Profile Type  $\int$  is approximately  $500 \ \mu\text{m} + (1/2 \ \text{x} \ 500 \ \mu\text{m}) \approx 750 \ \mu\text{m}.$
- The limit for a scan with the Profile Type  $\_$  is approximately -500 µm + (1/2 x -500 µm)  $\approx$  -750 µm.



**NOTE:** The best results are obtained from the  $\neg$  profile.

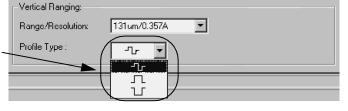
Saturated Data Points

If, in the course of a scan, the upper limit of any one of the ranges is reached and 50 data points are collected beyond the limit, the system aborts the scan and a message is issued reporting that there are too many saturation data points. The scan appears as complete, however, the end of the trace is only a continuation of the last data point, not actual scan data.



For the 131, 327, and 1000  $\mu$ m ranges, the three Profile Types allow the user to choose features that go up or down from the sample surface the full range, or split the difference between up and down features.

Saturated Data Points



**26** µm and **64** µm Ranges - These are the most common scan range for small scans. They offer the opportunity to scan features which are  $\pm 13$  µm or  $\pm 32$  µm from the scan starting point. These ranges do not offer the Up only or Down only option. (See *Table 3.22*.) If larger features are to be scanned, use the 131 µm, 327 µm, or 1000 µm range.

### Choosing the 26 $\mu$ m or 64 $\mu$ m range:

Click on the menu arrow to display the menu. Click on the 26 or 64  $\mu m$  range.

Range Limitations for 26 µm:

• The limits for a scan with the Profile Type  $\neg$  is  $\pm 13 \mu$ m

Range Limitations for 64 µm:

• The limits for a scan with the Profile Type  $\neg$  is  $\pm 32 \mu m$ .

If, in the course of a scan, the upper limit is reached and 50 data points are collected beyond the limit, the system aborts the scan and a message is issued reporting that there are too many saturation data points. The scan appears as complete, however, the end of the trace is only a continuation of the last data point, not actual scan data.

**6.5**  $\mu$ **m and 13**  $\mu$ **m Ranges** - These are the most sensitive scan range. It is for scans of features 3.2  $\mu$ m or smaller above or below the sample surface. This range does not offer the Up only or Down only option. (See *Table 3.22*.) If larger features are to be scanned, use either the medium range or the largest range.

### Choosing 6.5 $\mu$ m or 13 $\mu$ m range:

Click on the menu arrow to display the menu. Click on  $6.5 \mu m/0.015625 Å$ .

Range Limitations for 6.5 µm:

• The limits for a scan with the Profile Type  $\neg$  is  $\pm 3.2 \ \mu m$ 

Range Limitations for 13 µm:

• The limits for a scan with the Profile Type  $\neg \neg$  is  $\pm 6.5 \,\mu m$ .

3/05

If, in the course of a scan, the upper limit is reached and 50 data points are collected beyond the limit, the system aborts the scan and a message is issued reporting that there are too many saturation data points. The scan appears as complete, however, the end of the trace is only a continuation of the last data point, not actual scan data.

Profile Type	Range	Scan	Description
-1-	131 μm 327 μm 1000 μm	131 $\mu$ m scans features that are <b>65</b> $\mu$ m up or <b>down</b> from the scan's starting point.	During a scan using this profile type, if the scan goes out of range and stays out of range for 50 data points, the scan is aborted.
		327 μm scans features that are <b>160</b> μ <b>m up</b> or <b>down</b> from the scan's starting point.	When operating in this range, the sensor arm containing the stylus can be very near its vertical limit capacity.
		1000 $\mu$ m scans features that are <b>500</b> $\mu$ m up or down from the scan's starting point.	When it goes out of range for 50 data points on a <b>step up</b> , the scan is aborted. If the scan continued to go further out of range, at some point the sensor could be damaged.
			When it goes out of range for 50 data points on a <b>step down</b> , the scan is aborted. If the scan continued to go further out of range, the stylus would float out of contact with the sample.
- <u>1</u> -	64 μm	This scans features that are $32 \ \mu m$ up or down from the scan's starting point.	During a scan using this profile type, if the scan goes out of the $\pm 32 \ \mu m$ range and stay out of range for 50 data points, the scan is aborted.
			These limits are in the software. The system sends a saturation message when the scan is aborted.
- <u>1</u> -	26 µm	This scans features that are <b>13</b> μ <b>m</b> <b>up</b> or <b>down</b> from the scan's starting point.	During a scan using this profile type, if the scan goes out of the $\pm 13 \ \mu m$ range and stay out of range for 50 data points, the scan is aborted.
			These limits are in the software. The system sends a saturation message when the scan is aborted.
- <u></u>	13 μm	This scans features that are <b>6.5</b> $\mu$ <b>m up</b> or <b>down</b> from the scan's starting point.	During a scan using this profile type, if the scan goes out of the $\pm 6.5 \mu m$ range and stay out of range for 50 data points, the scan is aborted.
			These limits are in the software. The system sends a saturation message when the scan is aborted.
- <u></u>	6.5 μm	This scans features that are <b>3.2</b> $\mu$ <b>m up</b> or <b>down</b> from the scan's starting point.	During a scan using this profile type, if the scan goes out of the $\pm 3.2 \mu m$ range and stay out of range for 50 data points, the scan is aborted.
			These limits are in the software. The system sends a saturation message when the scan is aborted.

Table 3.22 Profile Types

Profile Type	Range	Scan	Description
	131 μm 327 μm 1000 μm	131 $\mu$ m scans features $\approx$ <b>100</b> $\mu$ m up from the scan's starting point.	During a scan using this profile type, if the scan goes out of range and stays out of range for 50 data points, the scan is aborted.
		327 μm scans features $≈$ <b>240</b> μm up from the scan's starting point.	When operating in this range, the sensor arm containing the stylus is actually very near its physical capacity.
		1000 μm scans features ≈ <b>750</b> μ <b>m</b> <b>up</b> from the scan's starting point.	When it goes out of range for 50 data points on a <b>step up</b> , the scan is aborted. If the scan continued to go further out of range, at some point the sensor could be damaged.
	131 μm 327 μm 1000 μm	131 $\mu$ m scans features $\approx$ <b>100</b> $\mu$ m down from the scan's starting point.	During a scan using this profile type, if the scan goes out of the range and stays out of range for 50 data points, the scan is aborted.
		327 $\mu$ m scans features $\approx$ <b>240</b> $\mu$ m	When operating in this range, the sensor arm is actually very near its physical capacity.
		<b>down</b> from the scan's starting point.	When it goes out of range for 50 data points on a <b>step down</b> , the scan is aborted. If the scan
		1000 $\mu$ m scans features $\approx$ <b>750</b> $\mu$ m down from the scan's starting point.	continued to go further out of range, the stylus would simply float out of contact with the sample.

Table 3.22 Profile Types (Continued)

# Feature Detection (Only for 2D Scans)

Feature Detection is used to enable automatic detection of some common classes of profile features (see *Figure 3.47* and *Figure 3.48*). Feature detection facilitates measurement throughput and consistency. It also makes it possible to automatically and reliably set the position of the measurement and leveling cursors relative to the rising and falling edge of a step-like feature or the apex of an arc-like feature.

In conjunction with feature detection, both the location of the edge (or the apex of an arc) and the step width can be calculated and displayed in the Analysis window.

## Accessing the Feature Detection parameters:

In the **Recipe Editor**, click on the **Feature Detection** button. (See *Figure 3.46*.) For information on how to display the **Recipe Editor**, see *Accessing the Scan Recipe Editor* on page 3-13.

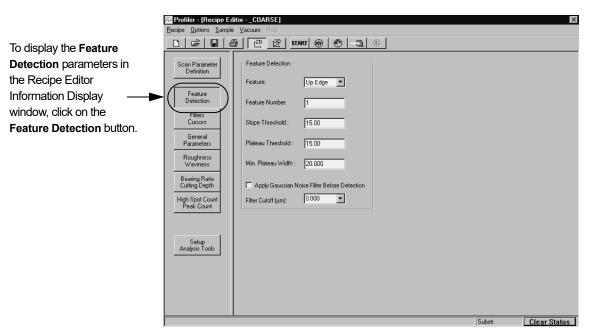
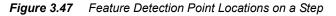


Figure 3.46 Feature Detection - Recipe Editor

## Feature

This parameter allows the user to choose between six different features that can be detected and identified during a scan.



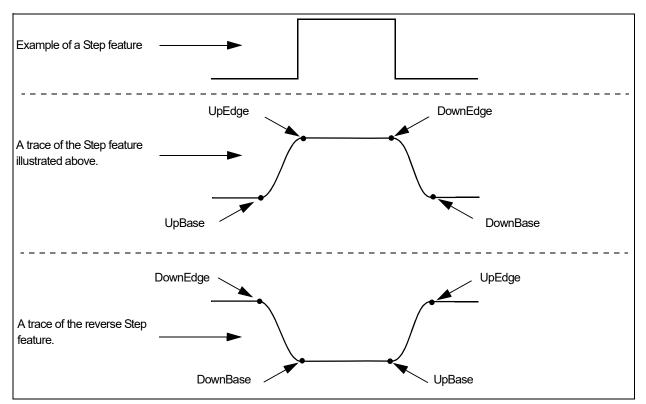
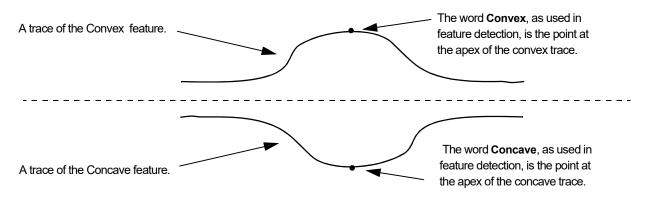


Figure 3.48 Feature Detection Point Locations for Convex and Concave



Feature	Description	
None	No feature detection is being used.	
UpEdge	At the trailing edge of a feature rise, it is the point at which the trace begins the plateau. (See <i>Figure 3.47</i> .)	
	<b>NOTE</b> : This point location can be modified by using <b>Distance to Edge</b> parameter in the <b>General Parameters</b> Window.	
UpBase	At the trailing edge of a plateau, it is the point at which the trace begins to turn upward. (See <i>Figure 3.47</i> .)	
DownEdge	At the trailing edge of a plateau, it is the point at which the trace begins to turn downward. (See <i>Figure 3.47</i> .)	
DownBase	At the trailing edge of a feature decline, it is the point at which the trace begins the plateau. (See <i>Figure 3.47</i> .)	
Convex	This is the point at the apex of a convex feature. (See <i>Figure 3.48</i> .)	
Concave	This is the point at the apex of a concave feature. (See <i>Figure 3.48</i> .)	

 Table 3.23
 Feature Detection Descriptions (See Figure 3.47 and Figure 3.48.)

Selecting a feature for detection:

- 1. Click on the menu arrow next to the variable box to display its menu.
- 2. Click on the desired feature to select it. If necessary, use the scroll bar to reveal other features. (See *Figure 3.49*.)

Figure 3.49 <u>F</u>	<u>-eature</u> - Fe	eature Detec	tion - Recipe	Editor
----------------------	---------------------	--------------	---------------	--------

	Feature Detection
	Feature:
Π	Feature Number: Up Base Down Edge Down Base
	Slope Threshold : 10.00
	Plateau Threshold : 10.00
	Min. Plateau Width : 10.000
	Apply Gaussian Noise Filter Before Detection
	Filter Cutoff (μm):

Feature Number

If there are multiple edges detected in the scan, **Feature Number** provides a way to select a specific edge for detection. (See *Figure 3.50*.)

Feature Detection allows the user to choose from six feature option (convex and concave not shown). Click on the menu arrow to display the menu. Click on the desired feature to choose it.

#### Changing the Feature Number:

Double-click in its variable box to highlight the current number and type in the new number. (Use a whole number. 1 is Default)

Figure 3.50 Detection Variables - Feature Detection - Recipe Editor

	Feature Detection	
Detection parameters are changed by clicking in the appropriate variable box to highlight the current number. Then type in the new number.	Feature: Feature Number: Slope Threshold : Plateau Threshold : Min. Plateau Width :	Up Edge
	Filter Cutoff (µm):	0.000 💌

Slope Threshold

This factor sets the value at which any rise or fall in a trace is considered to be a slope, not just part of the roughness or noise. This means that the Slope Threshold defines a point at which the system recognizes a trace line as following or preceding an edge, convex or concave point. (See Figure 3.50.)

#### Changing the Slope Threshold:

Double-click in its variable box to highlight the current number and type in the new number:

- Use values between 0 and 50.000
- Default is 10.000 for a step and 1.000 for an apex point. These values are sufficient for most scans above 200 Å in height.

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**NOTE:** For very noisy scans where the system is having difficulty detecting the feature, decrease the Slope Threshold. A value as low as 5.00 can work well.

## **Plateau Threshold**

This factor affects the precise horizontal location calculated for an edge or arc point. This parameter allows for the positional adjustment of the point to the left or right. (See Figure 3.50.)

#### Changing the Plateau Threshold:

Double-click in its variable box to highlight the current number and type in the new number:

- Use values between 0 and 50.000
- Default is 10.000 for a step and 0.000 for an apex point. These values are sufficient for most scans above 200 Å.



**NOTE:** When comparing data from scans of identical features, find a value that works and then use it consistently. Data is changed when differing **Plateau Threshold** numbers are used.

### Min. Plateau Width

Minimum Plateau Width defines the minimum horizontal distance between rising and falling edges (or falling and rising edges). This is used in feature detection to identify true features.

Changing the Min. Plateau Width:

Double-click in its variable box to highlight the current number and type in the new number:

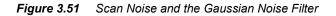
- Use values between 0.005 and 1000.00 μm (0.0002 to 39.3701 mil)
- Default is 10 μm.



**NOTE:** This is very dependent on which **Feature** is chosen for detection and which **Feature Number** is used.

### Apply Gaussian Noise Filter Before Detection

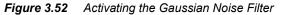
This is only used to filter out unwanted noise so the feature detection can more easily detect designated features. (See *Figure 3.51*.) *It does not apply the result to scan data*. For use of the **Gaussian Filter** with scan data, see *Filters* on page 3-50.



A Step scan with noise, before applying the Gaussian Noise Filter.
 A Step scan with noise, after applying the Gaussian Noise Filter.

To activate this feature

Click in the empty check box to put a  $\checkmark$  in it. (See *Figure 3.52*.) Then set the **Filter Cutoff** (µm) size.



	Feature Detection	
	Feature:	Up Edge 💌
	Feature Number:	1
To activate the Gaussian Noise	Slope Threshold :	10.00
Filter Before Detection feature,	Plateau Threshold :	10.00
click in its check box. A check $(\checkmark)$ indicates that it is chosen.	Min. Plateau Width :	10.000
	🔽 Apply Gaussian No	ise Filter Before Detection
	Filter Cutoff (µm):	0.45

## Filter Cutoff (µm)

This option is only activated when there is a check in the **Apply Gaussian Noise Filter Before Detection** check box. (See *Figure 3.52*.) The number to be entered is in microns. This determines the noise level that is filtered out.

For an in depth discussion on filters, see *Filters* on page 3-50.

Changing the Filter Cutoff

- 1. 1. Ensure that a Feature has been chosen.
- 2. 2. Click on the menu arrow to display its menu.
- **3**. 3. Click on the desired cutoff filter setting.

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L	7
	1

**NOTE:** A Feature must be chosen in order for the Gaussian Filter to become active. If **None** is showing in the **Feature** variable box, the Gaussian option is grayed out. To activate it, select a feature.

The Filter Cutoff range is from 0.25 through 800  $\mu$ m. Only established variables can be chosen.

Figure 3.53 Filter Cutoff Menu

Step 1 In order for the Apply Gaussian Noise Filter Before	Feature Detection
<b>Detection</b> , a Feature must be chosen. The filter is not available	Feature:
unless there is a feature chosen.	Feature Number: 1
	Slope Threshold : 10.00
	Plateau Threshold : 10.00
	Min. Plateau Width : 10.000
Step 2 After a Feature is chosen, —	Apply Gaussian Noise Filter Before Detection
put a check ( $\checkmark$ ) in the check box by clicking in it.	Filter Cutoff (µm):
	0.45 0.8
Step 3 Click on the menu arrow to	1.4
display its menu. Click on the	4.5
desired cutoff filter setting.	8

# Filters and Cursors (Only for 2D Scans)

## Filters

Two filters are available for removing noise from scan data, either as the scan is taking place, or after the scan occurs but before the data is saved. The oldest filter is the RC Filter. **RC** stands for Resister Capacitor Filter. The second, the **Gaussian Noise Filter**, is the best of the two and is generally chosen when a filter is required.

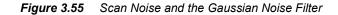
Click on the Filters/Cursors button to display the Filters/Cursors parameters.

Figure 3.54 Filters/Cursors Parameters - Recipe Editor

	ka Profiler - [Recipe Editor - 13×13]	×
The Filters/Cursors	Recipe Options Help	
parameters window is		
displayed by clicking on the	Scan Parameter Filters	
Cursors/Filters button in the	Definition Filter Option: Gaussian Filter	
Recipe Editor.	Feature Detection (Short Wavelength Cutoff): 0.25µm	
-	Filters         Waviness Filter           Cursors         Urg Wavelength Cutoff;	
	General Parameters X1 X2	
	Roughness Left Measurement: 0.024 0.024	
	Bearing Ratio Cutting Depth Right Measurement. 0.024 0.024	
	High Spot Count Left Level: 0.024 0.024	
	Right Level: 0.024 0.024	
	Setup	
	Analysis Tools	
	Substr. Clear State	IS

### **Gaussian Filter**

This option is used to filter noise out of a scan. Application of this filter can be made to the scan data as it is being generated (during the scan) or after the scan is complete but *before the data is saved*.



boforo ar	scan with noise, pplying the In Noise Filter.
•	scan with noise, olying the Gaussian ilter.

The illustration in *Figure 3.55* shows the effect of applying the **Gaussian Noise Filter** to a scan. This filter can be set to filter out noise from 0.25 to 800  $\mu$ m, as is evident in the available wavelength values in the **Noise Filter** drop-down menu.

To select the Gaussian Filter: (See Figure 3.56.)

- 1. Click on the Filter Option menu arrow to display its menu.
- 2. Click on Gaussian Filter.

Filters		, Two
Eller Online	Gaussian Filter 💌	use
Filter Option:	( Gaussian Filter	new
	RC Filter	Filte
<ul> <li>Noise Filter</li> <li>(Short Wavelength Cutoff):</li> </ul>	Default	desi
(onoix in oroionigin caloin).		com
Waviness Filter	Off	were
(Long Wavelength Cutoff):		prof

Figure 3.56 Filters Parameters - Filter Option Menu

Two Filter options are available for use in filtering out noise. The newest and best is the **Gaussian Filter**. The **RC Filter** might be desirable if scanned data is to be compared with older scans that were made on Tencor DOS based profilers using the **RC Filter**.

#### **RC** Filter

This is an older version noise filter. It was used with Tencor profilers before the Gaussian Noise Filter was introduced. If the scans performed using this recipe are going to be compared to scan performed by other *Tencor DOS based profilers* using the **RC Filter**, then the use of the **RC Filter** helps in scan to scan correlation.

Selecting the RC Filter: (See *Figure 3.56*.)

- 1. Click on the menu arrow next to the variable box to display its menu.
- 2. Click on RC Filter.

#### Noise Filter

The **Noise Filter** is a *Short Wavelength Cutoff* filter. This is an adjustable software filter used to reject short wavelength components of scan data. When used with the **Waviness Filter** (*Long Wavelength Cutoff*), it also isolates band passes for wavelengths. See *Setting the Short-Wave Filter Cutoff Values* on page 8-35 for more information about using the cutoff filters in surface analysis.

Selecting the Short Wavelength Cutoff: (See Figure 3.57.)

- 1. Click on the Noise Filter menu arrow to display its menu.
- 2. Click on the desired Shortwave Cutoff.



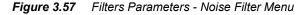
**NOTE:** The availability of cutoffs is dependent on the scan speed. A short wavelength cutoff cannot be entered if it is longer than the currently selected long wavelength cutoff, or shorter than the value of the analog cutoff.

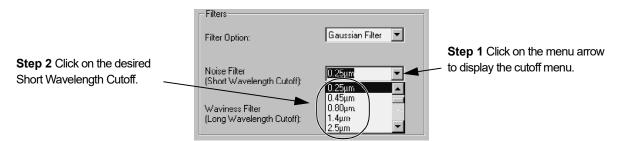
Short wavelength cutoff  $\leq$  Long wavelength cutoff

Short wavelength cutoff  $\geq$  Analog cutoff



**NOTE:** For scan speeds greater than 5  $\mu$ m/s, the shortest short wavelength cutoff selection turns the short wavelength filter completely off. If subsequent changes to the scan speed or scan length cause the short wavelength cutoff setting to become invalid, the cutoff is automatically changed to the nearest available valid value (possibly the default).





### Waviness Filter

The **Waviness Filter** is the *Long Wavelength Cutoff* filter. It is an adjustable software filter to separate long wavelength components of scan data. When used with the Short Wavelength Cutoff, it also isolates band passes for wavelengths.

Two types of Long Wavelength Cutoff filters are used:

- Gaussian, the best filter for use with Windows based systems.
- RC, used on older DOS based Tencor systems. Use this filter when comparing new data with data obtained using the RC filter on a DOS based system. This provides uniformity for comparison basis

To Select the Long Wavelength Cutoff: (See Figure 3.58.)

- 1. Click on the Waviness Filter menu arrow next to display its menu.
- 2. Click on the desired Long Wavelength Cutoff value.

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**NOTE:** The availability of cutoffs is dependent on the scan speed. The systems prevents the accidental entry of a long wavelength cutoff that is shorter than the currently selected short wavelength cutoff or the value of the analog cutoff.

If subsequent changes to the scan speed or scan length cause the long wavelength cutoff setting to become invalid, the cutoff is automatically changed to the nearest available valid value.

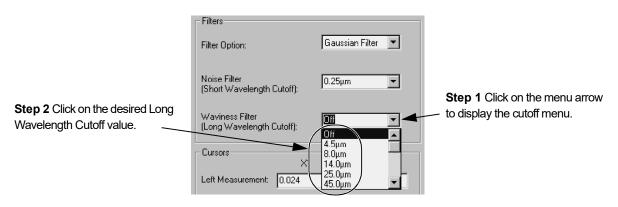


Figure 3.58 Filters Parameters - Waviness Filter Menu

### Cursors

Cursors are used for two general purposes:

- Measurement Cursors are used to gather data either between the two sets of cursors or within the boundaries of the cursor itself.
- Leveling Cursors are used to level the data points in the trace so the trace features fairly represent the actual scanned surface.



(	Cursors (	×1	×2 0.024	The limits of the cursor boundary — are displayed in the X1 and X2 columns for the various cursors.
)	Right Measurement:	0.024	0.024	
	Left Level:	0.024	0.024	
	Right Level:	0.024	0.024	Notice that the cursor parameters have not been set in the
	<ul> <li>✓ Relative to Feat</li> <li>✓ Fit and Level</li> </ul>	ure Detected		illustration. They are all at a single point on the trace.

Each cursor has limits that can be set. The limits of the cursor boundary are displayed in X1 and X2 in the **Cursors** parameters box. *The cursor limits are set relative to the starting point of the scan.* These values can be set in the window by clicking on the current value in the variable box and typing in the new value.

The easiest way is to set the cursors is in the analysis screen, after the scan, using the click and drag procedure. The procedure is described in the following discussion. (For more information on leveling cursors see *Leveling Cursors* on page 3-55.)

changed using the screen variable boxes by clicking in the appropriate variable box to highlight the current number. Then type in the new number.

Cursor parameters can be

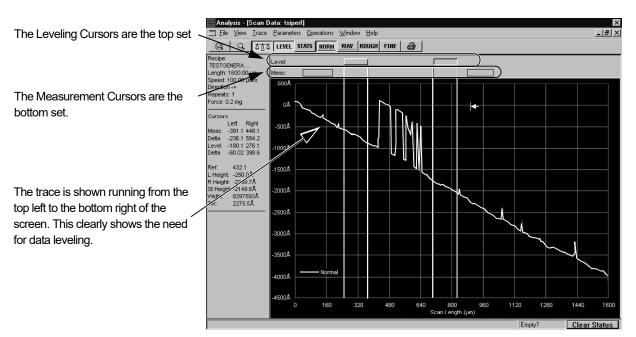


Figure 3.60 Analysis Screen with Trace in Need of Leveling

## Leveling Cursors

In general, the most effective way to set the **Leveling Cursors** is in the **Analysis** screen by clicking and dragging them into position. When they are in position, use the CALC procedure (see Step 4 on page -58) to enter the new **Cursors** variables. By visually positioning the cursors, the leveling positions are correct for the actual scan.

### Setting the Leveling Cursor positions:

- 1. After the scan is complete, the **Analysis** screen is displayed. Click on **LEVEL** to activate the Leveling Cursors. (See *Figure 3.61*.)
- 2. Reposition the leveling cursors using the following procedure.

Figure 3.61 Leveling Cursors

**Step 1** To reposition cursors, click on the **LEVEL** button in the tool bar to activate the Leveling Cursors.

**Step 2** When activated, click and hold in the gray area containing the cursor boundary box, an drag the cursors to the new position.

<u> </u>	Parameters Operations Window Help	_ 8 ×
	LEVEL STATS NORM WAV ROUGH FINE 🔿	
Recipe: 2D_SAMPLE Length: 150000.00 µm	Levet Heas:	
Speed: 1000.00 µm/s Direction -> Repeats: 1 Fore		
1 00 5. 0.2 mg	40002Å	

Notice the double arrow associates with the cursor that is active, the one that moves when drug.

a. Click on the LEVEL button in the tool bar. This activates the Leveling cursors. The active cursor header is displayed as a 3D rectangle. The cursor header being moved is indented while the other cursor is in relief. The Measurement cursor heads appear as 2D line boxes. (See *Figure 3.61*.)

b. As the track ball cursor approaches one of the active cursor heads, the cursor head changes appearance to indented and the track ball cursor appears as a double arrow as shown in *Figure 3.61*.

Click and hold on the cursor that is to be moved. Drag it to the desired position, using the track ball to move it. Release the mouse button when the cursor is in position.

- **3**. When the cursor is in position, set each cursor boundary using the following procedure:
  - a. Move the track ball cursor down into the black scan trace screen. The boundary that the arrow is pointing at is the one that is moves. (See *Figure 3.62.*)
  - b. Click and hold the mouse button while using the track ball to drag the boundary into position for leveling the scan. Release the mouse button when the boundary is correctly positioned.



**NOTE:** Both cursors should be positioned on the same X-plane. The cursor boundaries should be positioned on the same plain, avoiding noise peaks or valleys. This generally gives a flat scan trace.

- c. Repeat Step 1 and Step 3 for the remaining cursor.
- 4. Click on the **LEVEL** button to level the trace. (See *Figure 3.62*.) This cause the trace to be leveled and displays the trace with the Measurement Cursors active. (See *Figure 3.64* for a leveled trace.)



lysis - [Scan Data: tsip Window LEVEL STATS CALC NORM WAY ROUGH FINE 81 Recipe: TESTGENERA... Length: 1600.00 µm Speed: 100.00 µm/s Direction -> eve tepeats: 1 orce: 0.2 mg Left Right -343.1 799.2 -291.6 -196 -72, nnnå 432.1 15008 -250.4Å leight: R Height: -3263.9Å St Height: -3013.5Å 2060,4 11766177Å 3214.2Å วรกค∆ ะกกก 8 sonA 160 320 480 640 800 1120 1440 960 1280 . #h (µm) Clear Status

**Step 4** After Leveling cursors have been set, click on LEVEL to level the trace.

Step 3 When the Leveling Cursor is placed in the general area that it is to be used, move the track ball cursor down into the black trace screen to position the cursor boundaries.

A single arrow points at the cursor boundary that is to be adjusted.

Click and hold the mouse button and use the track ball to move the cursor boundary into place.

### Measurement Cursors

The Measurement cursors are used to measure various attributes of the scan. Some measurements are obtained between the cursors, while others are made within the boundary of a single cursor.

1. It is important to set the measurement cursors to accurately measure the desired feature. In Figure 3.63 the left cursor is set on the sample surface with the cursor borders positioned to measure a relatively flat trace segment. The right cursor is positioned to detect the height of the step being measured. (See Figure 3.63.)

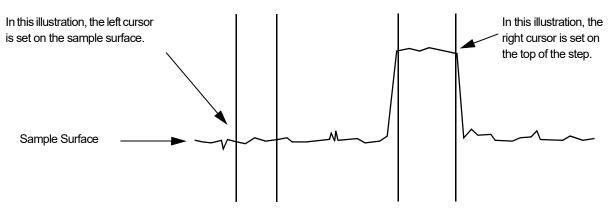
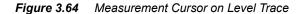


Figure 3.63 Setting Measurement Cursors

a. Click on the NORM button in the tool bar. This activates the Measurement cursors. The Measurement cursor header appears as a 3D rectangles. The Leveling cursors appear as 2D line boxes. (See *Figure 3.64*.)



usis - IScan Data: t X File View Trace Parame Help \_ 🖻 🗵 Step 1 The leveled trace appears Q Q DAD LEVEL STATS CALC NORM WAY ROUGH FINE 🗃 cipe: STGENERA.. evel: Length: 1600.00 µm Speed: 100.00 µm/s Direction -> 1400 epeats: 1 orce: 0.2 mg 1200Å Left Right -181.1 7.502 -56.02 -196.1 440.1 -72.52 551.7 800Å 432.1 1.7Å 1146.6Å :1145.0Å 1565489/ 1181.4Å 600Å 400Å 200Å оÅ -200,4 4008 lona. 1120 1440 320 640 800 800 april 1280 160 Clear Status

with the Measurement Cursors active. If the Measurement Cursors are not active. click on the NORM button in the tool bar.

Move the cursor into the graph area and position it next to the cursor boundary that is to be moved. It appears as an arrow. b. As the track ball cursor approaches one of the active cursors, the cursor header changes to appear indented and the track ball cursor appears as a double arrow as shown in *Figure 3.61*.

Click and hold on the cursor that is to be moved. Drag it to the desired position using the track ball to move it. Release the mouse button when the cursor is in position.

- 2. When the cursor is in position, set each cursor boundary using the following procedure:
  - a. Move the track ball cursor down into the black scan trace screen. The boundary that the cursor arrow is pointing at is the one that moves. (See *Figure 3.64.*)
  - b. Click and hold the mouse button while using the track ball to drag the boundary into position for its intended measurement in the scan. Release the mouse button when the boundary is correctly positioned.
  - c. Repeat Step 1 and Step 3 for the remaining cursor.
  - d. Click on the **LEVEL** button to level the trace.
- 3. When the trace has been leveled and the Measurement cursors have been placed, click on **Operations** to display its menu.
- 4. When the trace has been leveled and the Measurement cursors have been placed, click on the **CALC** button to cause the system to recalculate the data with new cursor positions. The new positions are saved as part of the recipe. (See *Figure 3.65.*)

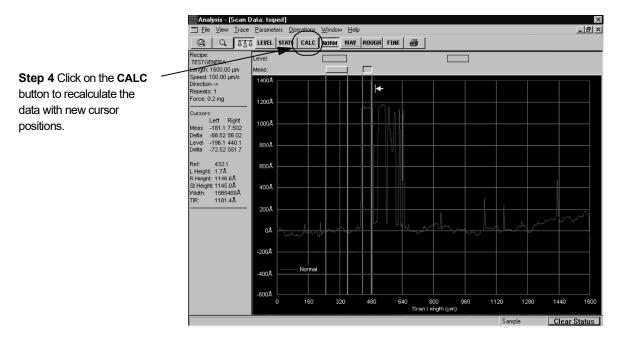


Figure 3.65 Analysis Screen CALC Button

The **Recalculation** process places the cursor **limits** in the **Cursors** window of the **Recipe Editor**. (See *Figure 3.66*.)



Cursor parameters (limits) are automatically changed when the **CALC** button is clicked in the **Analysis** screen (*before the data is saved*).

-	Left Measurement:	×1	×2	The limit
	Right Measurement:	450.000	490.000	columns
	Left Level:	10.000	50.000	When th
_	Right Level:	450.000	490.000	feature t and the
	☐ Relative to Featu ☐ Fit and Level	ure Detected		negative positive

The limits of the cursor boundary are displayed in the X1 and X2 columns for the various cursors.

When this box is checked, the feature takes on the "0" position and the cursors are set with negative numbers to the left and positive to the right.

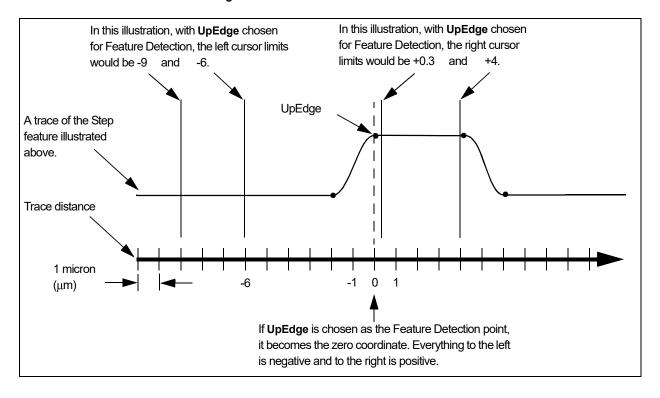
### **Relative to Feature Detected**

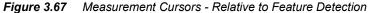
When there is a check ( $\checkmark$ ) in its checkbox, the cursor limits are set relative to the feature that is defined in the **Feature Detection** parameters window in the **Recipe Editor**. (See *Feature Detection (Only for 2D Scans)* on page 3-43.) The feature becomes the **0** point (the origin of the new coordinate system), with the points to the left being negative and those to the right being positive. (See *Figure 3.67.*)

The cursors are set in the same way described in Step 1 on page -55 through Step 3 on page -56. The system automatically places the measurement and leveling cursors relative to the actual feature instead of relative to the starting point of the scan.



**NOTE:** If **Relative to Feature Detected** is not checked, there should be no negative numbers in any cursor position because the start of the scan is the "0" point.





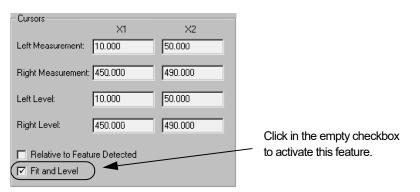
## Fit and Level

This option is designed to remove a secondary curvature from the overall trace of a curved surface. Features should then appear relative to a flat surface.

#### Selecting the Fit and Level option

• Click in the empty check box to put a check  $(\checkmark)$  in it.

Figure 3.68 Cursor Parameters - Recipe Editor

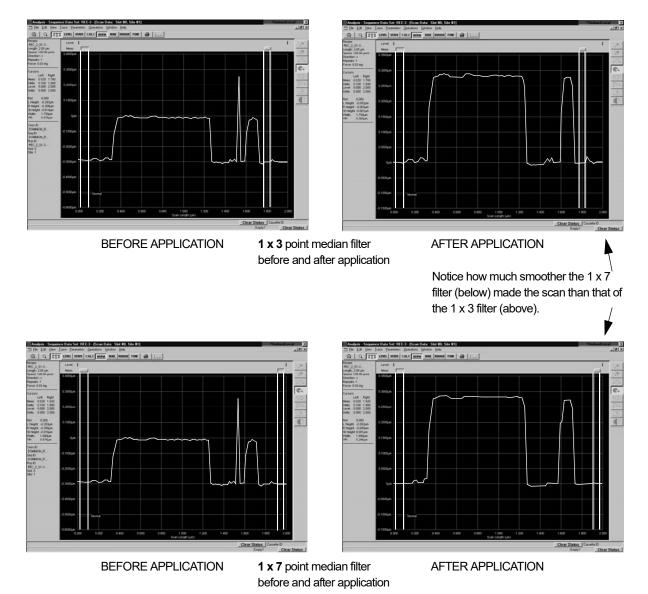


## Median Filter for 2D and 3D Data

This filter can be chosen as part of the recipe to help filter out spikes from environmental noise and particulate contamination. A median filter can be turned on before the scan, allowing the system to filter the data before the first viewing. It can also be used on saved data. With the data open in the Analysis screen, the saved data from single scans and sequences can be changed by opening the recipe used to create the scan from the Analysis screen, and changing the filter size in that recipe.

The median filter is used for both 2D and 3D data, with each type having its own menu of kernel sizes for the filters being applied to the data. When the filter is applied before the scan, the data is filtered and permanently changed.

The median filter works as a smoothing tool, taking out glitches and smoothing the trace surface in direct proportion to the size of the kernel. The median if found for the effected points in the kernel and is applied to data. The larger the kernel, the greater the smoothing effect on the data. In general, the smaller the kernel (i.e., the 1 x 3 for 2D and the 3 x 3 for 3D), the less the data is manipulated.



*Figure 3.69 Median Filter Application in Glitch Removal* 

The median filter is a major component of the Glitch Removal process used on data in the Analysis screen for both 2D and 3D data. (See 2D Glitch Removal on page 8-40, and Activate 3D Glitch Removal Tool. on page 9-17.)

The available filter sizes (kernels) for 2D data are: 1 x 3, 1 x 5, and 1 x 7 points.

Set or Change Median

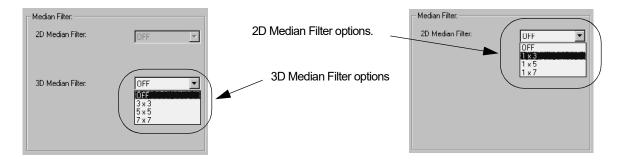
Filters for Saved Data

The available filter sizes (kernels) for 3D data are: 3 x 3, 5 x 5, and 7 x 7 points.

To add a filter or change the filter size on existing data, use the following procedure:

- 1. From the Catalog Screen, with either the Scan Data or Sequence Data catalog open, open the data set by double-clicking on it. The Analysis screen opens.
- 2. From the Analysis screen, click on **Edit** to display its menu.
- 3. Select Recipe. This opens the recipe used to generate the data.
- 4. Click on Filters/Cursors to display the Filters and Cursors parameters.
- 5. Click on the menu-arrow for either the 2D or 3D Median Filter to display the options. (See Sc*Figure 3.70.*)
- 6. Choose the required filter size for the 2D or 3D data.

Figure 3.70 2D and 3D Median Filter Options



7. Click on the Analysis screen icon in the tool bar to return to the Analysis screen for the affected data.

Setting Median Filter Prior to a Scan or Sequence To set the **median filter** for 2D or 3D scans, either single scan or for use in a sequence, prior to using the recipe, choose the required median filter while setting the other recipe parameters. If the recipe is already a part of a sequence, the recipe can also be opened from the sequence and the median filter added or changed prior to running the sequence.

For additional use of the median filter see 2D Glitch Removal on page 8-40, and Activate 3D Glitch Removal Tool. on page 9-17.

# **Unit Output**

Unit Output is designed to give the user an opportunity to determine units of output for the parameters calculated and to set automatic crossover values for unit changes. The options here let the user choose the units for the 2D graphical display through the recipe that is used to generate the scan. This option does not change the internal representation of data or the statistical parameters which continues to be in Angstroms. 1. Click on **Unit Output** in the Recipe screen window buttons to open the Unit Output parameters dialog box. (See *Figure 3.71*.) This dialog box is where units are chosen for statistical data and graphic presentation.

	Profiler - [Recipe EditorOFF150]		
	ipe <u>Q</u> ptions <u>S</u> ample <u>V</u> acuum Help		
	) 🕼 🖬 🖶 🗠 😰 START 🛞 🕙 – D. 🤅		
Click on Unit Output to open its dialog box.	Scan Parameter         Sto Scan         Y Scan Size (µm)         200.000         Y Scan Size (µm)           Peakedon         Scan Size (µm)         200.000         Y Scan Size (µm)         Traces:         Scan Size (µm)         Traces:         Scan Size (µm)         Traces:         Scan Size (µm)         <	e (um) \$0.000 • • Sence 10 um): 10.000 At Option for Penameters and Data Display ES ly mode ly mode	
		Empty? Clear Status	

*Figure 3.71* Recipe Screen with Unit Output Dialog Box

- 2. Choose the desired units for statistical data reporting and graphic presentation by clicking to place a dot in the radio button. (See *Figure 3.72*.)
- **3**. If one of the bottom two choices are made, the crossover value must be entered in the variable field. (See *Figure 3.72*.)

	Select Unit Output Option for Parameters and Data Display	×	
Choose the desired unit of output for graphics and calculated parameters. Make sure to enter the crossover values if either of the late two options are chosen.			To accept changes, click <b>OK</b> . To reject changes and retain current values, click <b>Cancel</b> .

Figure 3.72 Unit Output Dialog Box

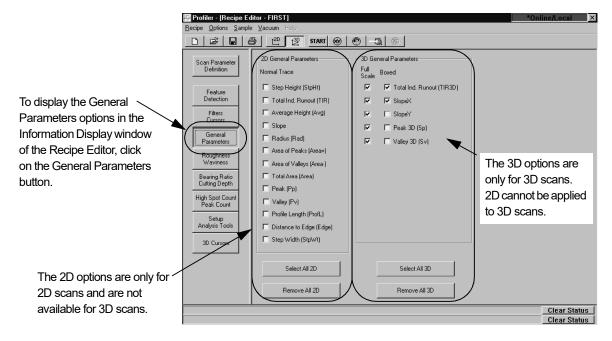
4. Click **OK** when all changes are complete, to accept the new values.

## **General Parameters**

The **General Parameters** window contains a variety of surface analysis calculations which are performed on the scan data when the options are chosen before the scan, or if they are applied to the scan data after the original data has been saved.

For each surface analysis option chosen, a post scan calculation is performed and displayed on the Analysis screen.





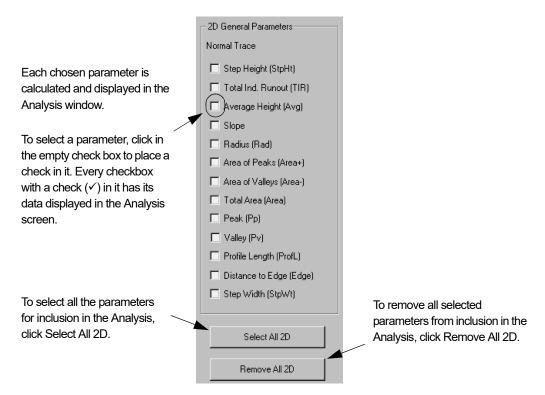
To access the **General Parameters** window, click on the **General Parameters** button in the **Recipe Editor** screen. (See *Figure 3.73.*)

## **2D** General Parameters (Normal Trace)

These parameters represent calculations that are performed using the data from a scan. If the options are chosen before the scan is performed, and are part of the *scan recipe*, the calculations are automatically performed by the software and displayed in the Analysis screen upon completion of the scan. Parameters from the 2D General Parameters are for single trace analysis, and as such, are not available for 3D scan data analysis. (See *Analyzing 2D Scan Data* on page 8-1.)

Each parameter is discussed below. (See *Figure 3.73.*)

Figure 3.74 2D General Parameters



### Adding 2D General Parameters to the Analysis

- In the 2D General Parameters options box, click in the checkbox of any option (see *Figure 3.79*) to include them in the current recipe and display each data value in the Analysis screen. A check (✓) in the checkbox activates the parameter.
- Add all the 2D General Parameters to the Analysis by clicking Select All 2D at the bottom of the list. This puts a check (✓) in the checkbox of all parameters.
- Remove all checked parameters from the 2D General Parameters by clicking Remove All 2D at the bottom of the list. This removes all checks from any chosen parameters

Parameter	Description	
Step Height (StpHt)	The difference in height between the left and right measurement cursors positions. Each cursor position is an average of the area between the cursor boundaries. The difference is between these averages.	
Total Indicator Runout (TIR)	The difference between the highest and lowest points in the scan.	
Average Height (Ave)	The average height of all data points between the measurement cursors relative to the leveled baseline. (ANSI)	
Slope	The ratio of the difference in vertical positions to the difference in horizontal positions of the measurement cursors. The slope is reported as an angle in degrees.	
	<b>NOTE:</b> The position of each cursor is taken to be the horizontal midpoint of each delta cursor band, and the data value at this location is the average of the vertical values within these bands. (ANSI)	
Radius	The distance from the center of curvature of the profile arc (assuming a circular profile within the sampling length) to the profile. The measurement cursors define two points of a circular arc. A <i>least squares</i> calculation is performed on the points between the cursors. The normal trace should not be leveled unless definite level reference points exist.	
Area of Peaks (Area+)	The total area bounded by the leveled baseline and the profile where it rises <i>above</i> the baseline. (ANSI)	
Area of Valleys (Area-)	The total area bounded by the leveled baseline and the profile where it descends <i>below</i> the baseline. (ANSI)	
Total Area (Area)	The sum of <b>Area of Peaks</b> and <b>Area of Valleys</b> . The delta cursors are not used. (ANSI)	

 Table 3.24
 2D General Parameters

Parameter	Description	
Peak (Pp)	Maximum Z value, measured relative to the leveled reference line, between the left and right measurement cursors.	
Valley (Pv)	Minimum Z value, measured relative to the leveled reference line, between the left and right measurement cursors.	
Profile Length (ProfL)	The length that would be obtained from drawing out the profile in a straight line. (ANSI)	
Distance to Edge (Edge)	<ul> <li>a straight line. (ANSI)</li> <li>Depending on the parameters settings in Feature Detection, this distance is either: <ul> <li>The distance between the beginning of the scan and the first rising or falling edge of a profile feature; or</li> <li>The distance between the beginning of the scan and the first concave or convex arc of a profile feature.</li> </ul> </li> <li>NOTE: This parameter is independent of the cursor positions. It is based on the feature detection parameters.</li> </ul>	
Step Width (StpWt)	The distance between the first rising edge of an upward step and the falling edge that follows, or the first falling edge of a downward step and the rising edge that follows. This value is meaningless for a convex or concave arc.	

Table 3.242D General Parameters (Continued)

## **3D General Parameters**

These parameters represent calculations that are performed using the data from a scan. Only three General Parameters exist for 3D scans. (See *Figure 3.75.*) If the options are chosen before the scan is performed, and are part of the *scan recipe*, the calculations are automatically performed by the software and displayed in the Analysis screen upon completion of the scan. Parameters from the 2D General Parameters are for single trace analysis and as such are not available for 3D scan data analysis. The options can be applied to live or saved data.

Each parameter option can be calculated in two different ways:

- **Full Scale:** With this checkbox selected, the parameter are calculated using data from the entire scan.
- **Boxed:** With this checkbox selected, the parameter are calculated using data from within the box that is defined in the 3D Cursors parameters window of the Recipe Editor. (See *Figure 3.73.*)

Either one or both calculation options can be used. If both are used, two sets of calculations are performed and presented in the Analysis screen.

Each parameter is discussed below. Figure 3.75 3D General Parameters 3D General Parameters Full Boxed Scale Total Ind. Runout (TIR3D) E SlopeX To select a parameter for 🔲 SlopeY inclusion in the Analysis, click Π 🔲 Peak 3D (Sp) Full Scale for data from entire Π □ Valley 3D (Sv) scan or **Boxed** for only data from enclosed cursors, or both can be chosen. To select all the parameters for inclusion in the Analysis, click Select All 3D. To remove all selected parameters from inclusion in the Analysis, click Select All 3D Remove All 3D. Remove All 3D

## Adding 3D General Parameters to the Analysis

- In the 3D General Parameters options box, click in the checkbox of any option (see *Figure 3.75*) to include them in the current recipe and display each data value in the Analysis screen. A check (✓) in the checkbox activates the parameter.
- Add all the 3D General Parameters to the Analysis by clicking Select All 3D at the bottom of the list. This puts a check (✓) in the checkbox of all parameters. (See *Figure 3.75*)
- Remove all checked parameters from the **3D General Parameters** by clicking **Remove All 3D** at the bottom of the list. This removes all checks from any chosen parameters. (See *Figure 3.75*)

Parameter	Description
Total Ind. Runout (TIR3D)	This is the 3D Total Indicator Runout. <b>TIR3D</b> is the difference between the highest and lowest points in the scan.
SlopeX	SlopeX refers to the slopes for lines in the plane: The SlopeX is the slope along the X-direction For the data set in any rectangular area (either a box or the entire area), a plane can be established using the <i>least squares</i> method.
SlopeY	SlopeY refers to the slopes for lines in the plane: The SlopeY is the slope along the Y-direction For the data set in any rectangular area (either a box or the entire area), a plane can be established using the <i>least squares</i> method.
Peak 3D (Sp)	Maximum Z value, measured relative to the leveled reference plane.
Valley 3D (Sv)	Minimum Z value, measured relative to the leveled reference plane.

 Table 3.25
 3D General Parameters

## **Roughness and Waviness Parameters**

### Introduction

Roughness and Waviness are defined by the Long Wavelength Cutoff setting. In general, when a long wavelength cutoff is set, the wavelengths greater than the cutoff are defined as **Roughness** and those less than the cutoff are defined as **Waviness**. (See *Figure 3.76*.) The long wavelength cutoff setting is generally determined by the specific application for which it is to be used.

A filter is used to remove aspects of the data so other aspects can be more carefully analyzed. As an example, the roughness could be filtered out so the waviness could be better analyzed. (See *Figure 3.77.*)

For applications where the user is unsure of a specific long wavelength cutoff, use the general rule of 1/5 the scan length. This means that for a scan of 50  $\mu$ m, the cutoff would be 10  $\mu$ m.

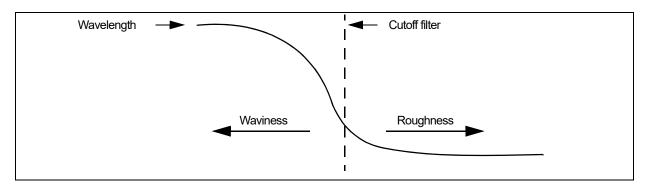
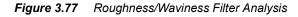
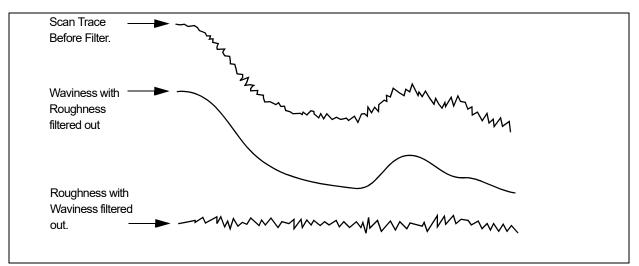


Figure 3.76 Waviness vs. Roughness





*Figure 3.78* shows the Recipe Editor with the Roughness and Waviness parameters in the Information Display window.

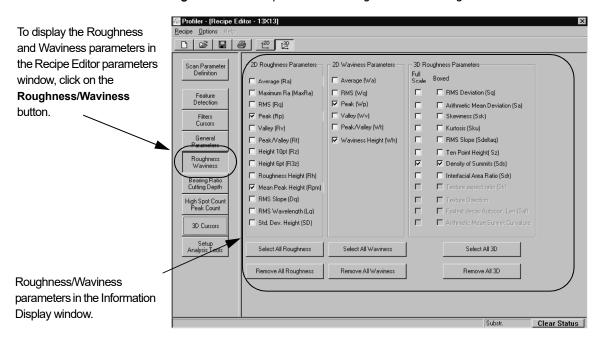
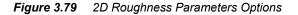
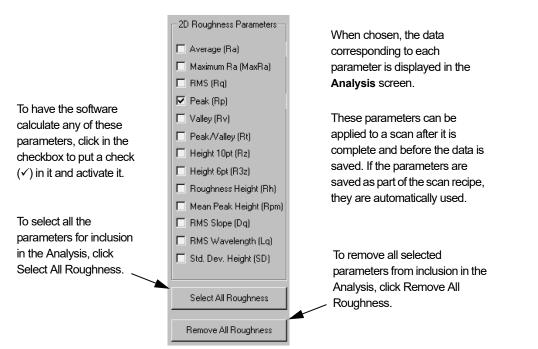


Figure 3.78 Recipe Editor Showing 2D and 3D Roughness/Waviness Parameters

## **2D Roughness Parameters**





Each of the roughness parameters available in the **2D Roughness Parameters** option box are described in *Table 3.26 on page 3-74*. (For more information Roughness, see the *Introduction* to *Roughness and Waviness Parameters on page 3-70*.)

### Adding 2D Roughness Parameters to the Analysis

- In the 2D Roughness Parameters options box, click in the checkbox of any option (see *Figure 3.79*) to include them in the current recipe and display each data value in the Analysis screen. A check (✓) in the checkbox activates the parameter.
- Add all the 2D Roughness Parameters to the Analysis by clicking Select All Roughness at the bottom of the list. This puts a check (✓) in the checkbox of all parameters.
- Remove all checked parameters from the **2D Roughness Parameters** by clicking **Remove All Roughness** at the bottom of the list. This removes all checks from any chosen parameters.

## 2D Roughness Parameters Table

 Table 3.26
 2D Roughness Parameters

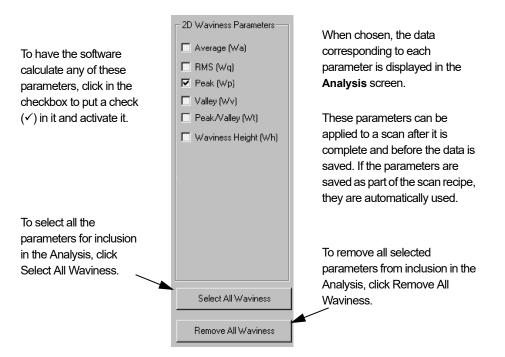
Parameter	Description
Average (R <sub>a</sub> )	This is the arithmetic average deviation of the absolute values of the roughness profile from the mean line or centerline. Also known as <i>centerline average roughness</i> . The centerline divides profiles such that all areas above it are equal to all areas below it. (ANSI)
Maximum $R_a$ (Max $R_a$ )	The trace within the cursors is divided into nineteen overlapping sections. Each section is one-tenth of the sampling length. The $R_a$ of each section is calculated, and the maximum is displayed. (ANSI)
RMS (R <sub>q</sub> )	The Root-Mean-Square (RMS) or geometric average deviation of the roughness profile from the mean line measured in the sampling length. (ANSI)
Peak (R <sub>p</sub> )	The distance between the mean line and the highest peak within the sampling length. (ANSI)
Valley ( $R_v$ )	The distance between the mean line and the lowest valley within the sampling length. (ANSI)
Peak/Valley (R <sub>t</sub> )	The vertical distance between the highest peak and the lowest valley in the sampling length leveled on the mean line. (Also known as $R_{max}$ , $R_{y}$ , Maximum Peak-to-Valley Roughness.) (ANSI)
Height 10pt (R <sub>z</sub> )	The average height difference between the five highest peaks and the five deepest valleys within the cursors measured from a line parallel to the mean line. (ANSI)
Height 6pt ( $R_{3z}$ )	The average height difference between the three highest peaks and the three deepest valleys in the sampling length measured from a line parallel to the mean line and not crossing the profile. (ANSI)

Parameter	Description
Roughness Height ( $R_h$ )	The difference in height in the roughness profile between the left and right cursor positions. Analogous to the Height data that always appears in the Summary box of the Analysis window. (ANSI)
Mean Peak Height ( $R_{pm}$ )	The mean value of the local peak heights relative to the mean line of the roughness trace within the sampling length.
RMS Slope ( $D_q$ )	The root mean square (RMS) value of the roughness trace slope. The Delta cursors are not used.
RMS Wavelength (L <sub>q</sub> )	$2\pi$ times the ratio of the root mean square (RMS) deviation of the profile (R <sub>q</sub> ) to the root mean square slope of the profile (D <sub>q</sub> ). L <sub>q</sub> is a measure of the spacing of local peaks and local valleys, taking into account their relative amplitudes and individual spatial frequencies. (ISO International Standards Organization)
Std. Dev. Height (SD)	The standard deviation of the local peak heights about the mean peak height relative to the mean line within the sampling length.

Table 3.26 2D Roughness Parameters (Continued)

### **2D Waviness Parameters**

Figure 3.80 2D Waviness Parameters



Each of the waviness parameters available in the 2D Waviness Parameters option box

is described in *Table 3.27 on page 3-76*. (For more information Waviness, see the *Introduction* to *Roughness and Waviness Parameters on page 3-70*.)

#### Adding 2D Waviness Parameters to the Analysis

- In the 2D Waviness Parameters options box, click in the checkbox of any option (see *Figure 3.80*) to include them in the current recipe and display each data value in the Analysis screen. A check (✓) in the checkbox activates the parameter.
- Add all the 2D Waviness Parameters to the Analysis by clicking Select All Waviness at the bottom of the list. This puts a check (✓) in the checkbox of all parameters.
- Remove all checked parameters from the **2D Waviness Parameters** by clicking **Remove All Waviness** at the bottom of the list. This removes all checks from any chosen parameters.

### 2D Waviness Parameters Description

Table 3.27 2D Waviness Parameters

Parameter	Description
Average (W <sub>a</sub> )	This is the arithmetic average deviation of the absolute values of the waviness profile from the mean line or centerline also known as centerline average waviness). The centerline divides profiles such that all areas above it are equal to all areas below it. (ANSI)
RMS (W <sub>q</sub> )	The Root-Mean-Square (RMS) or geometric average deviation of the waviness profile from the mean line measured in the sampling length. (ANSI)
Peak (W <sub>p</sub> )	The distance between the mean line and the highest peak within the sampling length. (ANSI)
Valley ( $W_v$ )	The distance between the mean line and the lowest valley within the sampling length. (ANSI)
Peak/Valley (W <sub>t</sub> )	The vertical distance between the highest peak and the lowest valley in the sampling length leveled on the mean line. Also known as $W_{max}$ , $W_y$ , Maximum Peak-To-Valley Waviness. (ANSI)
Waviness Height ( $W_h$ )	The difference in height in the waviness profile between the left and right cursor positions. Analogous to the Height data that always appears in the Summary box of the Analysis window. (ANSI)

### **3D Roughness Parameters**

Each of the roughness parameters available in the 3D Roughness Parameters option box is described in *Table 3.28 on page 3-78*. (For more information Roughness, see the *Introduction* to *Roughness and Waviness Parameters* on page 3-70.) chosen. To have the

click Select All 3D.

#### Add 3D Roughness Parameters to Analysis

- In the **3D Roughness Parameters** options box, click in the checkbox of any option (see *Figure 3.81*) to include them in the current recipe and display each data value in the Analysis screen. A check ( $\checkmark$ ) in the checkbox activates the parameter.
- Add all the **3D Roughness Parameters** to the Analysis by clicking **Select All 3D** at the bottom of the list. This puts a check ( $\checkmark$ ) in the checkbox of all parameters.
- Remove all checked parameters from the **3D Roughness Parameters** by clicking Remove All 3D at the bottom of the list. This removes all checks from any chosen parameters.

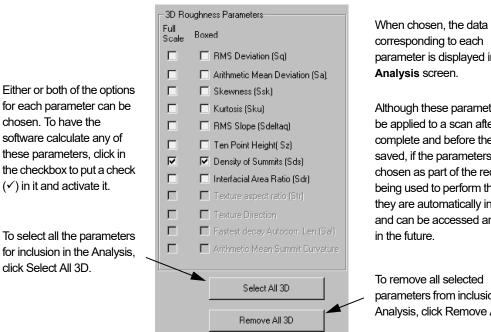


Figure 3.81 3D Roughness Parameters

corresponding to each parameter is displayed in the Analysis screen. Although these parameters can be applied to a scan after it is complete and before the data is saved, if the parameters are

chosen as part of the recipe being used to perform the scan, they are automatically included and can be accessed any time in the future.

To remove all selected parameters from inclusion in the Analysis, click Remove All 3D.

Each parameter option can be calculated in two different ways:

- Full Scale: With this checkbox selected, the parameter are calculated using data from the entire scan.
- Boxed: With this checkbox selected, the parameter are calculated using data from within the box that is defined in the 3D Cursors parameters window in the Recipe Editor. (See *Figure 3.73*.)

Parameter	Description
RMS Deviation ( $S_q$ )	Root-Mean-Square Deviation of the Surface. The root-mean-square value of the surface departures within the sampling area.
Arithmetic Mean Deviation ( $S_a$ )	Arithmetic Mean Deviation of the Surface. The arithmetic mean of the absolute values of the surface departures above and below the mean plane within the sampling area.
Skewness ( $S_{sk}$ )	The measure of asymmetry of surface deviations about the mean plane. It effectively describes the shape of the surface height distribution.
Kurtosis (S <sub>ku</sub> )	A measure of the peakedness or sharpness of the surface height distribution. It characterizes the spread of the height distribution.
RMS Slope $(S_{delta q})$	The root-mean-square value of the surface slope within the sampling area. RMS slope is sensitive to sampling rate.
Ten Point Height $(S_z)$	The average value of the absolute heights of the five highest peaks and the depths of the five deepest pits or valleys within the sampling area.
Density of Summit $(S_{ds})$	The number of summits of a unit sampling area.
Interfacial Area Ratio (S <sub>dr</sub> )	The ratio of the increment of the interfacial area of a surface over the sampling area. The Interfacial Area Ratio reflects the hybrid property of surface.

Table 3.283D Roughness Parameters

## **Bearing Ratio and Cutting Depth**

Access the Bearing Ratio and Cutting Depth Information Display window by clicking the Bearing Ration/Cutting Depth button in the Recipe Editor. (See *Figure 3.82*.)

Figure 3.82 Bearing Ration and Cutting Depth Parameters

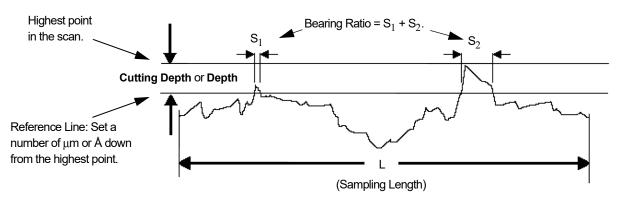
	🐺 Profiler - [Recipe Ed	itor - 13X13]
	<u>Recipe</u> Options Help	
To display the Bearing Ration and Cutting Depth parameters, click on the <b>Bearing Ratio/Cutting Depth</b> button.	Scan Parameter Definition Feature Detection Filters Cursors General Parameters Roughness Waviness Waviness Bearing Ratio Cutting Depth High Spot Count Peak Count Beating Ratio Cutting Depth High Spot Count Setup Analysis Tools	2D Bearing Ratio (tp)       3D Bearing Ratio (Sb)         Depth       Units         Scale       Boxed         Depth       Units         Depth       Depth         Units       Depth         Depth       Depth         Depth       Depth         Units       Depth         Depth       Depth         Boxed       Height         Depth       Depth         Depth       Depth         Depth       Depth         Subtr       Depth
		Substr Clear Status

Bearing Ratio (t<sub>p</sub>)

Bearing Ratio is also know as Bearing Length Ratio  $(t_p)$ . ANSI defines it as:

**Bearing Length Ratio**  $(t_p)$  and Others. A reference line is drawn parallel to the mean line and at a preselected or predetermined distance from it to intersect the profile in one or more subtended lengths. The bearing length ratio is the ratio of the sum of these subtended lengths to the length of the mean line.

Figure 3.83 Bearing Ratio



The Bearing Ratio is determined according to the following formula:

$$t_p = \ \frac{S1+S2}{L}$$

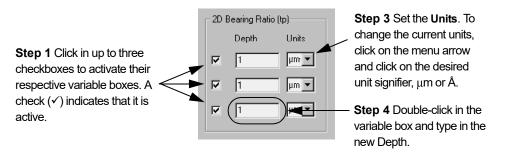
The **bearing length** is the sum of the subtended lengths (S1 and S2 in *Figure 3.83*). The **bearing ratio** is the ratio of the bearing length to the sampling length (L in *Figure 3.83*) as shown in the above formula.

### Setting the 2D Bearing Ratio

Use the following procedure to set the 2D Bearing Ratio variables.

 The option exists to create three 2D bearing ratio parameters. Click in up to three empty checkboxes to put a check (✓) in them and activate their variable boxes. (See *Figure 3.84*.)

Figure 3.84 2D Bearing Ratio



- 2. The depth is set down from the highest peak in the scan. It can be set in either microns (µm) or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- 3. Click on the desired unit signifier,  $\mu \mathbf{m}$  or  $\mathbf{A}$ .
- 4. **Depth** is the distance down from the top of the highest point in the scan. To set or change the **Depth**, double-click on the current **Depth** variable and type in the new depth. (See *Figure 3.85.*)

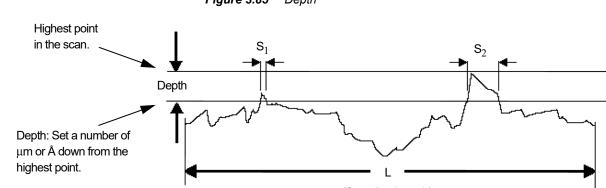
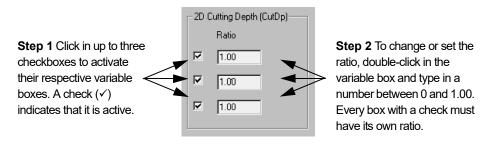


Figure 3.85 Depth

### 2D Cutting Depth (CutDp)

**Cutting Depth** is related to Bearing Ratio in that Bearing Ratio uses an operator set depth from the top peak in the scan, adding up the points between the top peak and the set depth, while **Cutting Depth** uses an operator set *ratio of data points* in the scan that are below the highest peak in the scan, causing the system to determine the depth. (See the definition of **Bearing Length Ratio** in *Bearing Ratio* (*tp*) on page 3-79.)





Use the following procedure to set the 2D Cutting Depth variables.

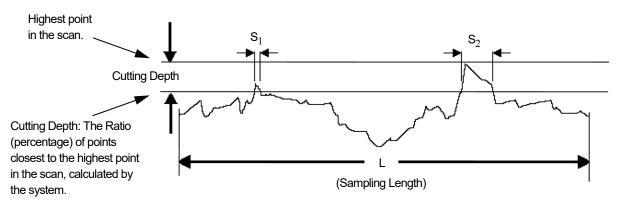
- The option exists to create three 2D cutting depth parameters. Click in up to three empty checkboxes to put a check (✓) in them and activate their variable boxes. (See *Figure 3.86*.)
- 2. The Cutting Depth is a ratio of points below the highest peak in the scan. The operator chooses the ratio and the software automatically takes the that ratio of data points in the scan that are the closest to the highest peak and calculates the Cutting Depth (CutDp) variable, displaying the results in the Analysis screen.

#### EXAMPLE:

If the user want to calculate a set of parameters comparing 20%, 30%, and 40% cutting depth, all three check boxes are checked and the respective variable boxes have: **0.20**, **0.30**, and **0.40** in them.

**To set or change one or more of the Cutting Depth variables**, double-click on the number in the variable field so that it highlights, and type in the new ratio. (See *Figure 3.86*.)

Figure 3.87 Cutting Depth



### **3D Bearing Ratio (Sbi)**

The 3D Bearing Ratio is a 3D version of the 2D Bearing Ratio in that it uses a distance down from the highest point in the scan to compute a bearing ratio with respect to a plane instead of area with respect to a single line trace.

In addition, two options are available for each of three parameter settings for calculating the 3D Bearing Ratio. The scope of the calculation is set by clicking in *one or both* of the range boxes: **Full Scale** and **Boxed**. The depth can then be set.

**Full Scale** - This option performs a calculation of the 3D Bearing Ratio over the entire scan.

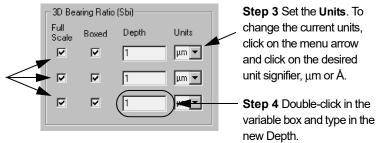
**Boxed** - This option performs a calculation of the 3D Bearing Ratio over the portion of the scan within the box that is defined in the 3D cursors parameters window. (See *Figure 3.88*.)

Use the following procedure to set the 3D Bearing Ratio variables.

1. To chose the scope of the 3D Bearing Ratio calculation, click in the empty checkbox to activate the variable field and place it in the recipe. **Either or both** options can be chosen.

Choose up to three sets of calculations with different depths. If all boxes are checked, two calculations are performed for each of the three variable depths.

Figure 3.88 3D Bearing Ratio (Sbi)



- The depth is set down from the highest peak in the scan. It can be set in either microns (μm) or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- 3. Click on the desired unit signifier,  $\mu \mathbf{m}$  or  $\mathbf{A}$ .
- 4. The **Depth** is the distance down from the top of the highest point in the scan. To set or change the **Depth**, double-click on the current **Depth** variable and type in the new depth.

### 3D Material Volume (Vm)

The 3D Material Volume is a 3D version of the 2D Cutting Depth Ratio. It is set by using a ratio (percentage) of the overall data points below the highest peak in the scan to compute a material volume (Vm) with respect to a plane instead of area with respect to a single line trace.

Step 1 The 3D Bearing Ratio variables become active when there is a check in one or both of the calculation scope check boxes. If both are checked, two calculations are made for each established depth. In addition, two options are available for each of three parameter settings for calculating the 3D Material Volume. The scope of the calculation is set by clicking in *one or both* of the range boxes: **Full Scale** and **Boxed**. The depth can then be set.

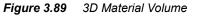
**Full Scale** - This option performs a calculation of the 3D Bearing Ratio over the entire scan.

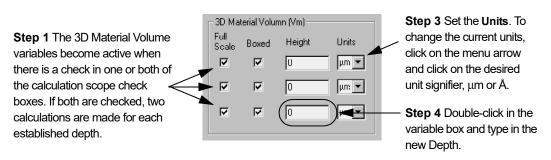
**Boxed** - This option performs a calculation of the 3D Bearing Ratio over the portion of the scan within the box that is defined in the 3D cursors parameters window. (See *Figure 3.89*)

Use the following procedure to set the 3D Material Volume variables.

1. To choose the scope of the 3D Material Volume calculation, click in the empty checkbox to activate the variable field and place it in the recipe. **Either or both** options can be chosen.

Choose up to three sets of calculations with different depths. If all boxes are checked, two calculations are performed for each of the three variable depths.





- The depth is set down from the highest peak in the scan. It can be set in either microns (μm) or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- **3**. Click on the desired unit signifier,  $\mu$ **m** or **A**.
- 4. The **Depth** is the distance down from the top of the highest point in the scan. To set or change the **Depth**, double-click on the current **Depth** variable and type in the new depth.

## **High Spot Count and Peak Count**

Access the High Spot Count and Peak Count Display Window by clicking the **High Spot Count/Peak Count** button in the Recipe Editor. (See *Figure 3.90*.)

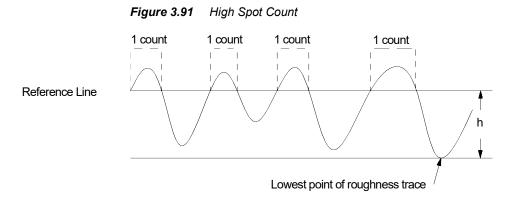
To display the High Spot Count and Peak Count parameters, click on the <b>High</b> <b>Spot Count/Peak Count</b>	Profiler - (Recipe Ed Recipe Options HEP      Scan Parameter Definition      Feature Detection      Filters Cursors      General Parameters Wavness      Wavness      Wavness	
	High Spot Count Peak Count 3D Cursors Setup Analysis Tools	

Figure 3.90 Bearing Ratio and Cutting Depth Parameters

### **High Spot Count (HSC)**

High Spot Count is the number of profile peaks per unit of length projecting through a reference line parallel to and at a given height above, a line drawn parallel to the mean line through the lowest point of the roughness trace. (See *Figure 3.91*).

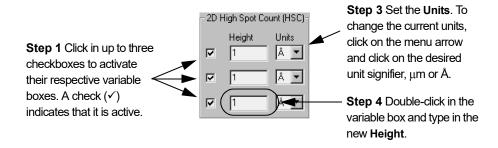
The mean line is the line at the mean height of all data. Another line is drawn through the lowest point in the trace, parallel to the mean line. The reference line is at a user specified height above the lowest point line. Projecting through means that the profile curve first climbs above the reference line and then falls below it. Thus, if the profile rises above the reference line, descends without falling below it, then rises again, multiple peaks are not identified.



Use the following procedure to set the 2D High Spot Count variables.

 The option exists to create three 2D High Spot Count parameters. Click in up to three empty checkboxes to put a check (✓) in them and activate their variable boxes. (See *Figure 3.92*.)

Figure 3.92 2D High Spot Count (HSC)



- The height can be set in either microns (μm) or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- 3. Click on the desired unit signifier,  $\mu \mathbf{m}$  or  $\mathbf{A}$ .
- 4. The Height is the distance up from the lowest point of the roughness trace.

**To set or change the Height**, double-click on the current **Height** variable and type in the new height. (See *Figure 3.92*.)

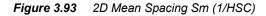
### 2D Mean Spacing Sm (1/HSC)

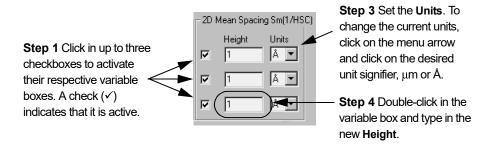
Mean Peak spacing is the mean value of the local peak spacing of the profile within the sampling length. The peaks for High Spot Count are defined by the Height parameter from the High Spot Count window. *Spacing* is the inverse of the count.

It is important to note that the 2D High Spot Count (HSC) and the 2D Mean Spacing Sm (1/HSC) are related. If running a scan in which these values are to be compared, the *height* of both must be identical for the data to have direct correlation.

Use the following procedure to set the 2D Mean Spacing Sm variables.

The option exists to create three 2D Mean Spacing Sm parameters. Click in up to three empty checkboxes to put a check (✓) in them and activate their variable boxes. (See *Figure 3.93*.)





- The height can be set in either microns (μm) or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- 3. Click on the desired unit signifier,  $\mu m$  or **Å**.
- 4. The **Height** is the distance **up** from the lowest point of the roughness trace. In most scans, this value is compared to High Spot Count (HSC) so this height must be identical to the **Height** in **High Spot Count (HSC)**.

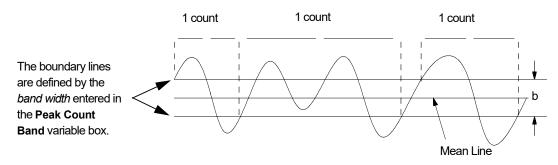
To set or change the Height, double-click on the current Height variable and type in the new height. (See *Figure 3.93*.)

### 2D Peak Count (PC)

Peak Count is the number of peak and valley pairs per unit length projecting through a band of width **b** centered about the mean line. (See *Figure 3.94*.)

The Mean line is the line at the mean height of all data. The band is the area bounded by two lines running parallel to the mean line, at an equal distance from the mean line.

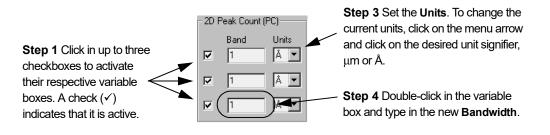
#### Figure 3.94 Peak Count



Use the following procedure to set the 2D Peak Count variables.

The option exists to create three 2D Peak Count bandwidth settings. Click in up to three empty checkboxes to put a check (✓) in them and activate their variable boxes. (See *Figure 3.95.*)

Figure 3.95 2D Peak Count (PC)



- 2. The bandwidth can be set in either microns  $(\mu m)$  or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- 3. Click on the desired unit signifier,  $\mu \mathbf{m}$  or  $\mathbf{A}$ .
- 4. The Band is the bandwidth surrounding the mean line. (See Figure 3.94.)

To set or change the Band, double-click on the current Band variable and type in the new bandwidth. (See *Figure 3.95*.)

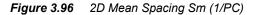
#### 2D Mean Spacing Sm (1/PC)

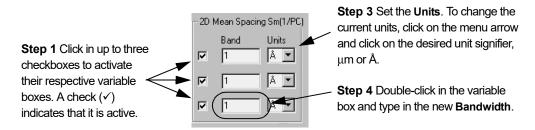
Mean Peak spacing is the mean value of the local peak spacing of the profile within the sampling length. The peaks for Peak Count are defined by the **Band** (bandwidth) parameter from the Peak Count (PC) window. *Spacing* is the inverse of the count. (See *Figure 3.94*.)

It is important to note that the **2D Peak Count (PC)** and the **2D Mean Spacing Sm (1/PC)** are related. If running a scan in which these values are to be compared, the *bandwidth* **of both must be identical** for the data to have direct correlation.

Use the following procedure to set the 2D Mean Spacing Sm

 The option exists to create three 2D High Spot Count parameters. Click in up to three empty checkboxes to put a check (✓) in them and activate their variable boxes. (See *Figure 3.96*.)





- 2. The bandwidth can be set in either microns  $(\mu m)$  or angstroms (Å). Determine which units are going to be used and, if a change is necessary, click on the menu arrow under units to display its menu.
- 3. Click on the desired unit signifier,  $\mu \mathbf{m}$  or  $\mathbf{A}$ .
- 4. The **Band** is the bandwidth bordered equidistant above and below the mean line of the scan. In most scans, this value is compared to **Peak Count (PC)** so this **Band** (bandwidth) must be identical to the **Band** in **Peak Count (PC)**.

To set or change the Band, double-click on the current Band variable and type in the new bandwidth. (See *Figure 3.96*.)

# **3D Cursors Parameters**

### Introduction

The 3D Cursors screen is designed to allow the user to view the cursor coordinates, and manipulate the cursor position and boundaries by coordinate. (See *Figure 3.97*.) Those who frequently use 3D cursors have found it more accurate to drag and drop the cursor boundaries rather than attempt to pin point them using the 3D Cursors window.

If necessary, it is possible to drag the cursor boundaries and then go into the 3D Cursors screen and fine tune the boundary settings. Fine tuning is, however, seldom done. In general, the 3D Cursors screen is only used as a reference screen.

## X Start Level

This option is used to level the 3D scan with respect to the X starting position of the<br/>scan. It assumes that the entire X=0 length of the scan is on the same plane, having no<br/>holes or steps. If this box is checked, the other options are not used in the leveling<br/>process. This option only levels in one direction, with respect to the X=0 plane.Initializing X Start LevelTo activate the X Start Level option, click in the empty checkbox next to X Start Level.<br/>(See Figure 3.97.)

Leveling Criteria The 3D scan progresses with each initial trace data point being used for the scan leveling in the Y direction (using the X=0 point of each scan trace).

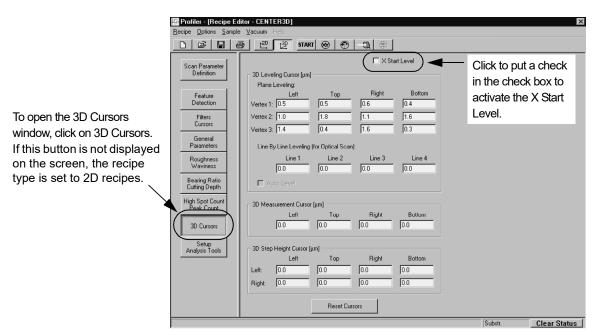


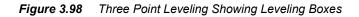
Figure 3.97 Recipe Editor - Choosing 3D Cursors

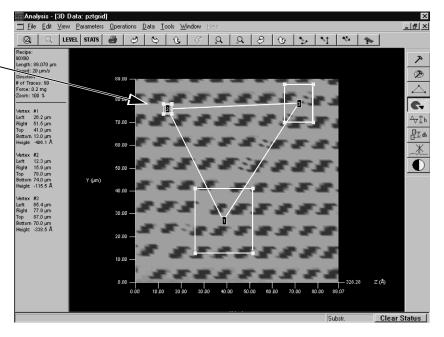
### 3D Leveling Cursor (µm)

The 3D Leveling Cursor field presents the option to define the three boxes that are used in the three-point leveling procedure. (See *Figure 3.98*.) This option is used by the system for leveling if neither the **X Start Level** nor the **Auto Level** checkboxes are checked. Each horizontal row of coordinates, called a vertex (after the old single point procedure that was used in the past), actually defines a box surrounding a set of data points. To be accurately used in the data leveling procedure, each box must contain only data points on the same plane. All three boxes must be located on the same plane to accurately level the data.

### Setting the Cursors: Click-and-Drag

Click-and-Drag Cursor Positioning If the tool bar's **Activate Leveling Tool** button icon  $\checkmark$  was used to place the leveling cursors on the scan image, then it is possible to click-and-drag the boxes to the best positions for leveling purposes. After being positioned, they can be sized to include only the proper data. It is essential that each box contain data from only one plane, no steps or holes. All three boxes must contain data from the same plane. (See *Figure 3.98*.)





After the boxes are positioned properly, with the content in all three boxes being on the same plane, leveling can take place. When the leveling is complete and saved, the coordinates of each one are recorded in the **Plane Leveling** boxes. (See *Figure 3.98.*) Each set of coordinates correspond to a box and are labeled with Box 1 being represented by Vertex 1, and so on with Boxes 2 and 3. (For more information on 3D leveling, see *Activate Leveling Tool on page 9-15* in the 3D Analysis chapter.)

Notice that leveling on one plane is difficult for the illustrated sample. Only one box contains data residing on only one plane.

The other two boxes would require adjustment in size so only the level represented by the lighter color is included in their boundaries. The coordinates are as follows: (See Figure 3.99.)

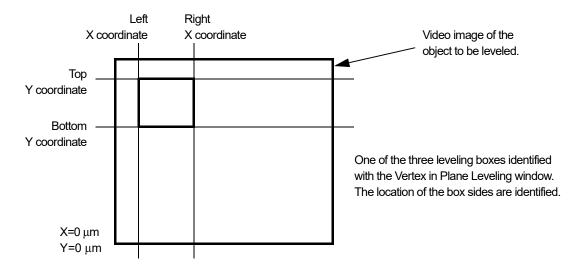
**Left** – This corresponds to the left side of the cursor box and is the X coordinate of that location. (See *Figure 3.98*.)

**Right** – This corresponds to the right side of the cursor box and is the X coordinate of that location. (See *Figure 3.98*.)

**Top** – This corresponds to the top of the cursor box and is the Y coordinate of that location. (See *Figure 3.98*.)

**Bottom** – This corresponds to the bottom of the cursor box and is the Y coordinate of that location. (See *Figure 3.98*.)





#### Setting the Cursors: Enter Coordinates in 3D Cursor Window

Cursor Positioning by Manually Setting the Coordinates It is possible, for certain types of 3D production scans, to preset the 3D cursors for repetitive scans by entering the coordinates in the respective boxes. This works better with scans where most of the scan surface is on the same plane and the features being scanned are located far enough away from other features to allow preset leveling. Use the X and Y screen coordinates, with X=0, Y=0 being the bottom left corner of the scan area. (See *Figure 3.99*.) Enter the number for each coordinate in the corresponding Vertex variable box. (See *Figure 3.100*.)



**NOTE:** It is difficult to place these exactly by simply entering a number. It might require entering the number and observing the results several times to correctly position the cursor.

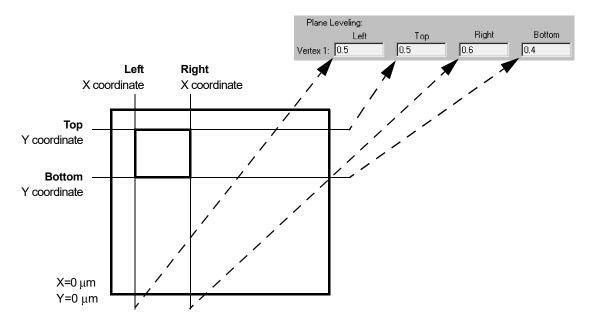
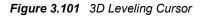


Figure 3.100 Matching Leveling Box and Cursor Locations

### Line by Line Leveling

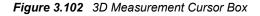
Line by line leveling was a feature for optical scans only. It is not available in the current systems.

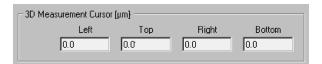


	– 3D Leveling C Plane Level				
The Line By Line Leveling is not available	Vertex 1: 0.5 Vertex 2: 1.0 Vertex 3: 1.4	Left	Top 0.5 1.8 0.4	Right 0.6 1.1 1.6	Bottom 0.4 1.6 0.3
in the current systems.	Line By Line	E Leveling (for Line 1	Optical Scan): Line 2 3.3	Line 3	Line 4

### **3D** Measurement Cursor

The 3D measurement cursor is used to isolate an area of the scan, from which the measurements designated in the recipe for inclusion in the Analysis data (such as some of the parameters in General Parameters on page 65 and Roughness and Waviness Parameters on page 70), can be reported. If no numbers are entered in the 3D Measurement Cursor variable boxes to define the measurement area, the data is compiled for the entire scan area.





#### Setting the Cursors: Click and Drag

The 3D Measurement Cursor box is associated with the Activate Height Tool button

in the Analysis screen tool bar. In the Analysis screen, if the Activate Height Tool button is clicked on, a box appears that can be resized and moved using the click-and-drag method. As the box is drug around the scan image, the height of all data points in the box is averaged with respect to sample plane and reported under **Height** in the analysis statistics at the left side of the screen.

After the box is sized and positioned, its position can be entered in the 3D Measurement Cursor variable boxes.

- 1. Click on the CALC icon in the toolbar or click on Operations in the menu bar
- 2. Choose **Recalc**, to recalculate the parameters and place the cursor locations in the 3D Measurement Cursor variable boxes.

#### Setting the Cursors: Manually Entering Coordinates

Manually setting the cursors is accomplished by entering the coordinate position of the intended measurement box (Active Height Tool) directly into the **3D Measurement Cursors** variable boxes. The coordinates work as follows:

**Left** – This corresponds to the left side of the cursor box and is the X coordinate of that location. (See *Figure 3.103.*)

**Right** – This corresponds to the right side of the cursor box and is the X coordinate of that location. (See *Figure 3.103*.)

**Top** – This corresponds to the top of the cursor box and is the Y coordinate of that location. (See *Figure 3.103*.)

**Bottom** – This corresponds to the bottom of the cursor box and is the Y coordinate of that location. (See *Figure 3.103*.)

Cursor Positioning Using Click-and-Drag

Set the Box Position in the 3D Measurement Cursor Variable Boxes

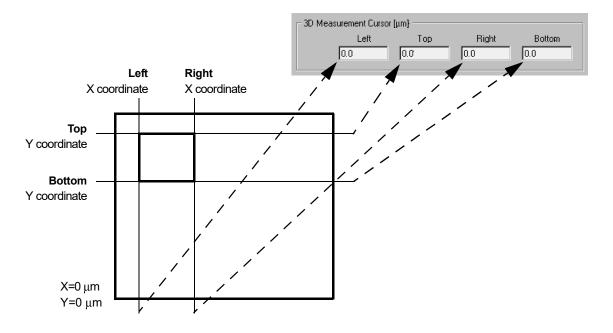


Figure 3.103 Matching Measurement Cursor Position to Measurement Box

#### **3D Step Height Cursors**

The 3D Step Height Cursors are two variable boxes that are designed to capture data on two planes and calculate the average difference in the height between them. For accurate results, all of the data in a cursor box should be on the same plane. In this way, the difference between the data in the two boxes is the average difference between the height of the two planes being measured.

Figure 3.104 3D Step Height Cursor Parameters

_ 3D Ste	p Height Cursor [	μm]		
	Left	Тор	Right	Bottom
Left	0.0	0.0	0.0	0.0
Right	0.0	0.0	0.0	0.0

#### Setting the Cursors: Click and Drag

Cursor Positioning Using Click-and-Drag The **3D Step Height Cursor** boxes are associated with the **Activate Step Height Tool** button in the Analysis screen tool bar. In the Analysis screen, if the Activate Step Height Tool button is clicked on, two boxes appear that can be resized and moved using the click-and-drag method. As the boxes are drug around the scan image, the height of all data points in the box is averaged with respect to sample plane and reported under one of the height measurements (depending on which cursor box

is being moved) in the analysis statistics at the left side of the screen.

- 1. If the view of the sample surface is not from the top, click **View** in the menu bar to display it menu.
- 2. Choose **Top** from the View menu.

\*

3. To determine the step height in the Analysis screen, the system subtracts the Z value of **Box 1** from the Z value of **Box 2**. The **Left** box, in the **3D Cursors** window, correlates to **Box 1** in the Analysis screen. This box should be placed on the lowest plane. Click in the center of **Box 1** and drag it to the base plane.

**NOTE:** If Box 1 is placed on the step plane instead of the base plane, the height reading is given as a negative number.

- 4. Resize the box to the proper dimensions to avoid artifacts and keep it separate from other planes.
- 5. Click in the center of Box 2 and drag it to the step plane.
- 6. Resize the box to the proper dimensions to avoid artifacts and keep it separate from other planes (like step edges or slopes).

After the box is sized and positioned, its position can be entered in the 3D Measurement Cursor variable boxes (see *Figure 3.104*) using the following procedure.

- 1. Click on the **CALC** icon in the tool bar, or to use the menu option on **Operations** in the menu bar to display its menu.
- 2. From the Operations menu, choose **Recalc**.

Both methods recalculate the parameters and place the cursor locations in the 3D Measurement Cursor variable boxes.

### SETUP ANALYSIS TOOLS

This tool has two purposes that are used in the Analysis of the gathered data.

- First, the leveling of the data is accomplished based on a choice of data to be used as a leveling basis.
- Second, the data is compiled as a histogram for comparison of feature depth in the scan.

The parameters available in this window work on already accumulated data. Therefore, the parameters can be adjusted and recalculated over and over again on the same data to help analyze the scan results.

Both the leveling and the depth analysis histogram are discussed in this section.

Set the Box Position in the 3D Step Height Cursors Variable Boxes

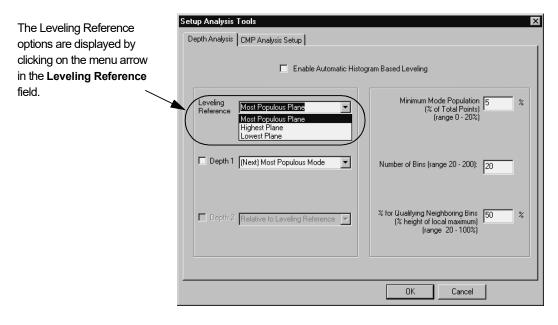
### **Leveling Reference**

The system offers three data planes to choose from for leveling the scan data. (See *Figure 3.105.*) The three options are:

- Most Populous Plane
- Highest Plane
- Lowest Plane

The leveling takes place based upon the data points identified in one of the three data distribution planes identified above. The planes are associated with modes that are defined as a bin or group of bins that hold a significant number of data points. The total Z-axis distance of the scanned object is divided up into equal Z-axis portions called bins.





The data bins form a histogram generated by the scan data. The contents of the bins are set using the parameters displayed directly below the Leveling Reference variable box in the **Setup Analysis Tools** dialog box. The parameters are:

- Number of Bins
- % for qualifying neighboring bins

### Number of Bins

Bins are actually ranges in the Z scan height. The total Z scan height is divided by the number of **Bins** chosen. Each bin presents the number of data points collected in its range, as compiled from data collected across the entire scan length.

### Percentage (%) for Qualifying Neighboring Bins

While it is possible to set up the bin distribution so that the points are clearly distributed in single bins, not spread over several bins, it is more likely that neighboring bins contain data points that, when taken together, constitute a mode. (See *Figure 3.106*.)

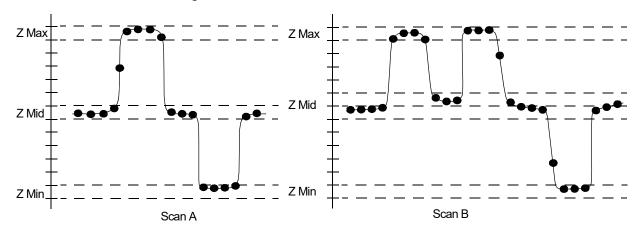


Figure 3.106 Data Point Distribution in Bins

In *Figure 3.106*, Scan A shows that the major distribution of points lie clearly in Z Min, Z Mid, and Z Max. The histogram of this distribution would be clearly presented in three ranges. However, in Scan B, the distribution for the Z Mid is between two bins. One bin near the center has 9 data points while its neighbor has 5 points. The user might want this distribution of points to be considered together as a mode. This is where the **Percentage for Qualifying Neighboring Bins** is used.

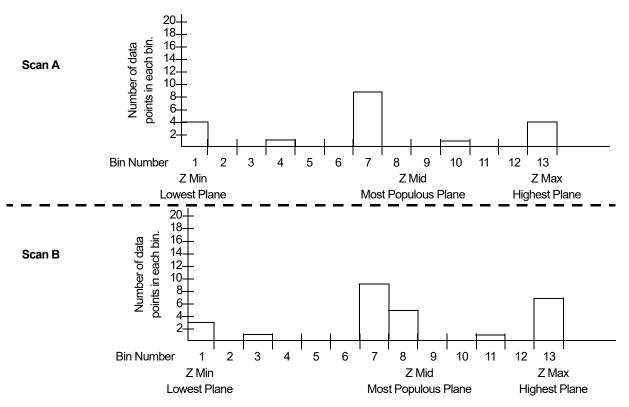
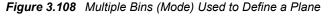


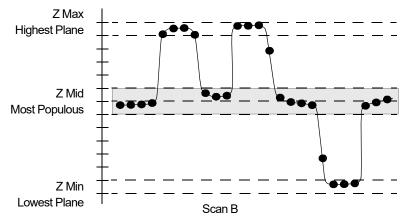
Figure 3.107 Histograms of Scans A and B

The user can set a percentage factor such that, if the bin containing the most data points (reference bin) has a neighboring bin that contains the user set percentage of the number of data points in the reference bin, it is also considered as part of the same mode and used in the leveling procedure.

#### **EXAMPLE:**

Using *Figure 3.106*, Scan B, if the user chose **Most Populous Plane** as the reference, and selected 50% as the **Percentage for Qualifying Neighboring Bins**, the system would check each mode in the scan data to determine which contains the highest number of data points. The modes would be comprised of bins or sets of bins, where a bin with a significant number of data points has one or more neighbors that contain at least 50% of the data points that it has. The mode with the highest number of data points is then considered to be the Most Populous Plane and is used in the leveling process. (See the shaded area in *Figure 3.108*, Scan B.)



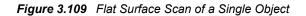


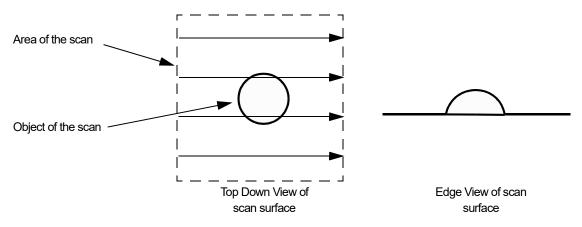
#### Leveling Reference

Three reference planes exist, from which one must be chosen to level the scan. Two of the planes are easy to understand and use; the Highest Plane and Lowest Plane.

- Highest Plane Referring to *Figure 3.108*, the Highest Plane corresponds to the data set in the Z Max range (or mode if looking at the histogram).
- Lowest Plane In the same illustration, the Lowest Plane corresponds to the data set in the Z Min range.

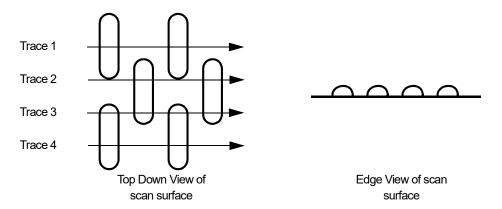
The third plane, Most Populous Plane, is more difficult to deal with and, depending on the topography of the sample, could lead to inconsistent results. The following illustrations describe the most common scan situations and the possible difficulties associated with using the Most Populous Plane for leveling and data analysis. The Scan illustrated in *Figure 3.109* would be an acceptable candidate for Most Populous Plane. This scan is of a single attribute with a relatively large surface area surrounding it. No matter which scan trace is used, the sample surface level, in this case the Lowest Plane, would also be the Most Populous Plane. Either the Lowest Plane or the Most Populous plane could be used for leveling.





The scan illustrated in *Figure 3.110* would not be an acceptable candidate for Most Populous Plane. This scan has four traces that would give different data sets depending on which trace was used to level the scan. If Most Populous Plane was chosen as the leveling reference, traces 1, 2, and 4 would level the trace on the Lowest Plane of the scan. Trace 3 would level the trace on the Highest Plane of the scan. This would change the way the data is analyzed. The depths calculated from either of its two neighboring scans would be very different.

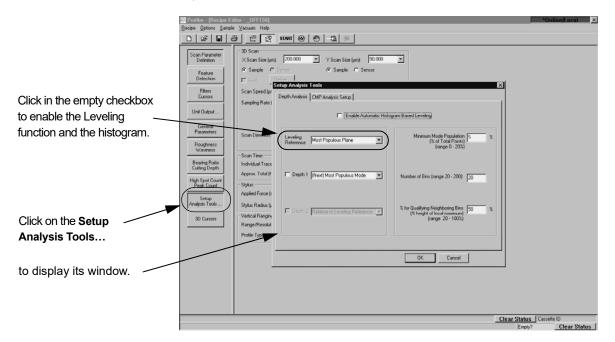
Figure 3.110 Most Populous Plane Trace Variation



### **Opening the Setup Analysis Tools Dialog Box**

From the Recipe Editor, click on the Setup analysis tools button to open the Setup Analysis Tools dialog box. (See *Figure 3.111*.)

Figure 3.111 Setup Analysis Tools Dialog Box



#### Setup Analysis Tools - Leveling

The Setup Analysis Tool's Leveling function and the histogram are both enabled by clicking in the empty checkbox next to Enable Automated Depth Analysis. (See *Figure 3.111*.)

To activate them, use the following procedure.

1. From the Recipe Editor, click on **Setup Analysis Tools** to display the **Setup Analysis Tools** dialog box. (See *Figure 3.111*.)

To enable the leveling and depth analysis functions, click in the empty checkbox —	Setup Analysis Tools     Image: Comparison of the setup o
and the variable fields become active.	Leveling Reference Most Populous Plane (% of Total Points) (range 0 - 20%) (range 0 - 20%)
	Depth 1 (Next) Most Populous Mode     Number of Bins (range 20 - 200): 20
	Depth 2 Relative to Leveling Reference      (% height of local maximum)     (% height of local maximum)     (range 20 - 100%)
	OK Cancel

Figure 3.112 Enable Automatic Depth Analysis

2. In the Setup Analysis Tools dialog box, click in the empty **Enable Automated Depth Analysis** checkbox. (See *Figure 3.112*.)

Change Leveling Reference

- 3. The Leveling Reference The leveling attribute must be tied to the available data set. The leveling algorithms are set up to operate on one of three data sets (planes), Most Populous Plane, Highest Plane, and Lowest Plane.
  - a. To select a data plane, click on the menu arrow next to Leveling Reference. (See *Figure 3.113.*)

b. Select the required data plane by clicking on it in the **Leveling Reference** drop-down menu. (See *Figure 3.113*.)

To change the leveling attribute, click on the menu arrow next tot the <b>Leveling</b> <b>Reference</b> and choose the required attribute from the	Setup Analysis Tools         Depth Analysis       CMP Analysis Setup         Enable Automatic Histogram Based Leveling	×
required attribute from the menu.	Leveling Reference Most Populous Plane Highest Plane Lowest Plane	
	Depth 1 [(Next) Most Populous Mode     Number of Bins (range 20 - 200): 20	
	Depth 2 Relative to Leveling Reference     (% height of local maximum)     (% height of local maximum)     (range 20 - 100%)	
	OK Cancel	

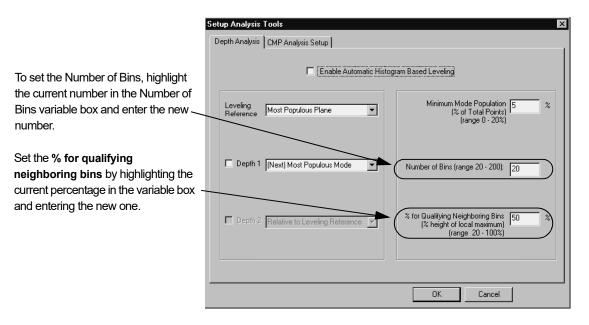
#### Figure 3.113 Setup Analysis Tools – Leveling Reference

#### Change Number of Bins

4. The Number of Bins – highlight the current number in the Number of Bins variable box and enter the new number of bins to be used. (See *Figure 3.114.*) Remember, the more bins, the fewer number of data points each bin might contain. Be sure to carefully evaluate the distribution of data points in the bins so that the % for Qualifying Neighboring Bins can ensure that the proper number of points are included in the calculated modes for the leveling procedure.



**NOTE:** The available range for the number of bins is 20 - 200.





Change % qualifying neighboring bins 5. % for qualifying neighboring bins – Highlight the current percentage, in the % for qualifying neighboring bins variable box, and enter the new percentage. (See *Figure 3.114.*)

Remember, the number of bins is divided up in equal spacing increments across the entire depth of the scan. The more bins, the more significant the **% for qualifying neighboring bins** becomes. This number, as well as the other attributes in this window can be adjusted after the scan data is collected; so assessing the data might help adjust the percentage to include all necessary data points.

In the illustration presented in *Figure 3.114*, the bins in the mid range, bins 7-10, all contain data points. To isolate the data points that are to be considered as part of the mode, a percentage must be entered that only accumulates the desired data points. If Most Populous Plane was chosen as the reference, the system accumulates the total of all adjacent bins, in data point clusters, matching the percentage set in % for qualifying neighboring bins, and uses the totals to determine which bins constitute the Most Populous Plane. If 50% was set as the % for qualifying neighboring bins, the system would key in on bin #8 and include the contents of bin #9 because its contents were greater than 50% of the number of data points in bin #8. The data points in bins #7 and 10 would not be included because they were less than the required 50%. The combination of data points would show that this is the Most Populous Plane in the scan and perform the leveling and depth calculations from this data.

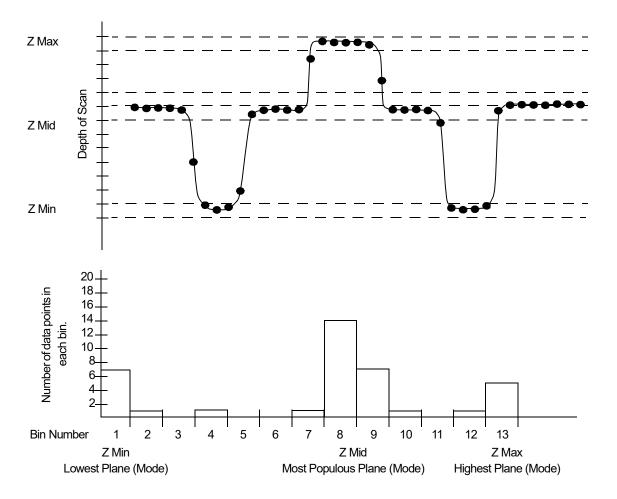


Figure 3.115 Histogram of a Scan

In the Histograms, the different planes (modes) are color coded for easy reference and identification. The Histogram is displayed in green. The major modes, when displayed, appear in red.

6. After all adjustments are complete, click **OK** to save the changes, or **Cancel** to discard the changes.

# **Diagnostic Options**

This dialog box presents options that can be used to run diagnostic scans such as **No Motion** and **No Nulling** scans.



**NOTE:** Scans using these options should only be used by KLA–Tencor service personnel or applications engineers for diagnostic purposes only.

1. To display the **Diagnostic Options** dialog box:

- a. Click on **Recipe** in the menu bar to display its menu,
- b. Click on **Diagnostic...** from the drop-down menu. (See *Figure 3.116.*)

Step 1 <i>a</i> . To access the Diagnostic Options dialog box, click on <b>Recipe</b> in the Menu Bar to display its menu. Step 1 <i>b</i> . Then click on Diagnostic button.	Profiler - [Recipe E di Scite Qptions Help. New Crit-N Gere Crit-O Save As Diagnostic Crit-D Save As Diagnostic Crit-I Egit Recipe Editor Corroos Corroos Corroos Corroos Corroos Corroos Recal Parameters Roughness Waviness Waviness Waviness Cuting Depth High Spot Count Peak Count Solution Solut	N 120 122 D Scan KScan Size (µm): 180000 Y Y Scan Size (µm): 13.000 Y
=		Substr. Clear Status

Figure 3.116 Recipe Editor - Recipe Menu

This displays the Diagnostic Options dialog box. (See *Figure 3.117.*)
 To chose an option for a diagnostic scan, click in the empty checkbox next to the desired option. A check (✓) in the checkbox indicates that the option is chosen.

Each **Option** is discussed below.



**CAUTION:** Each of the options is active for the recipe in which it is saved. If the recipe is used as a template to create other recipes, the option will remain intact unless turned off. This could create numerous scan data deviations from the expected scan results.

3. Click **OK** when all required options have been chosen. (See *Figure 3.117.*)

**Step 2** Click in the check box of the option that is to be used in the diagnostic. A check ( $\checkmark$ ) in the box means the option is chosen.

agnostic Options	×	_	Step 3 Click on OK when the
High Resolution Camera Only: —— No Motion Scan: Do Not Null Before Scan:			desired options have been chosen.
Scan Options:			
Do Not Back Scan Before Scan:			
Do Not Filter Noise:			
Do Not Level:			
No Linearity Correction:			
Linearity Calibration Only:			
Use Raw Data:			
No Stylus Arc Correction:	Help		

Figure 3.117 Diagnostic Options Dialog Box

Dia

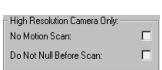
### High Resolution Camera Only-Diagnostic Options

The diagnostic options presented here are used by the P-15 camera. In some systems supported by this software, more than one camera is used. In those systems, this set of options would only apply to the high magnification camera.

Table 3.29 High Resolution Camera Only - Diagnostic Opt
---

Option	Description
No Motion Scan	During the scan, data is collected but the stage does not move. (See <i>Figure 3.118</i> .) <b>NOTE:</b> This scan is only available in 2D.
Do Not Null Before Scan	No movement of the elevator (for nulling) occurs before the scan is performed and the data collected. (See <i>Figure 3.118.</i> )

Figure 3.118 High Resolution Camera Only: Diagnostic Options



## **Scan Options**

This is a set of miscellaneous scan related options.

Figure 3.119 Scan Options: Diagnostic Options

– Scan Options: ––––––	
Do Not Back Scan Before Scan:	
Do Not Filter Noise:	
Do Not Level:	Γ
No Linearity Correction:	

 Table 3.30
 Standard - Diagnostic Options

Option	Description	
No Back Scan Before Scan	Back Scan is a technique where, immediately prior to the scan, the stage moves the scan start position back and begins the scan nulling and movement. The mechanical portion of the system has an opportunity to settle before actually reaching the beginning of the data collection.	
	This option prevents the Back Scan positioning from taking place. (See <i>Figure 3.119</i> .)	
No Noise Filter	This prevents postprocessing of the scan data with cutoff filters. (See <i>Figure 3.119</i> .)	
No Leveling	This prevents postprocessing data leveling of scan data. (See <i>Figure 3.119</i> .)	
No Linearity Correction	Only used during the Linearity Calibration. (See <i>Figure 3.119.</i> )	

### Linearity Calibration Only – Diagnostic Options

Option	Description
Use Raw Data	Raw data from the scan is presented with no postprocessing; without scaling to the measurement range.
	<b>NOTE:</b> This option has no useful application apart from the Linearity Calibration.
No Stylus Arc Correction	Data from the scan is presented with no postprocessing arcal correction.
	<b>NOTE:</b> This option has no useful application apart from the Linearity Calibration.

 Table 3.31
 Linearity Calibration Only – Diagnostic Options

#### Figure 3.120 Linearity Calibration Only

- Linearity Calibration Only:	
Use Raw Data:	
No Stylus Arc Correction:	

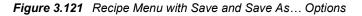
# **Saving Scan Recipes**

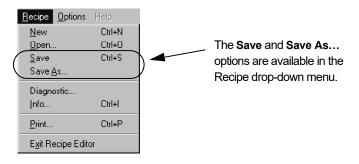
#### **Options for Saving Scan Recipes**

The recipes that are created using the **Recipe Editor** must be saved to capture the new or modified parameters. Two options available for saving a recipe are accessed in the **Recipe** drop-down menu are:

- Save, is used to either save changes to a current recipe, or to save the content of New recipe.
- Save As, is used when changes have been made to an existing recipe and the user wishes to preserve both the new recipe and the original one.

The two options are explained in detail later in this section. (See *Figure 3.121* and also *Figure 3.116 on page 3-106*.)





#### **Recipe Naming Convention**

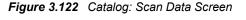
The P-15 system's software allows for Scan and Sequence Recipe names that are 79 characters long. This allows the user adequate space to make names that describe the content of the recipes being named.

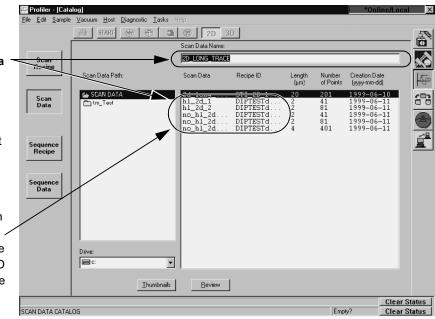
While the longer names provide greater flexibility for descriptive naming, several software display locations exist where the recipe names are displayed in truncated form. This could present difficulties when attempting to identify which recipe is actually represented by the truncated recipe name.

If a long name is to be used, make the first eight characters in the name reflect the recipe difference so its truncated version can be easily recognized in other screens.

#### EXAMPLE:

If the first 8 or more characters of several Scan Recipes are identical, the following problem could arise when attempting to identify which recipe was used to create the scan data. (See *Figure 3.122*.)





In *Figure 3.122* both the Scan Data name and the Scan Recipe name are truncated down to eight characters in the Scan Data file list. When the Scan Data file is clicked on, it highlights and the Scan Data file name is totally displayed (up to 74 of the 79 characters) in the Scan Data Name reference box. The Scan Recipe name is not displayed in total any place on this screen.

If the user attempts to discover the actual recipe name by opening the Scan Data File, the Analysis screen is opened and displays the Scan Data information. The Scan Data file name is completely displayed in the title bar but the Scan Recipe name is still truncated to 10 characters.

When a Scan Data file is chosen (clicked on) it highlights and the **Scan Data** file name is totally displayed in the **Scan Data Name** display box. The Scan Recipe is not totally displayed, only the first eight characters of the name.

In the Recipe display portion of the **Catalog: Scan Data** screen, both the name of the Scan Data and the Recipe ID name are truncated. (See the note above.)

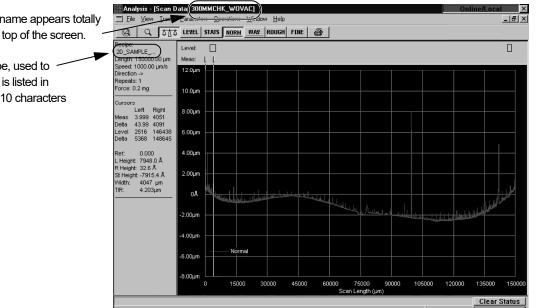


Figure 3.123 Analysis Screen

The Scan Data name appears totally displayed at the top of the screen.

The Scan Recipe, used to gather the data, is listed in truncated form (10 characters only).

> If the scan recipes used to gather data have the same first 8 or 10 characters, it could be very difficult to tell which actual recipe was used to gather the data presented in the Scan Data file.

#### END OF EXAMPLE

Use the following procedure to name a Recipe.

- Use file names that contain different characters in the first 8 characters. (See EXAMPLE above.)
- Be sure to connect all words in the file name together. Use an underline "\_" to ٠ separate the words.

If the words are not connected as in Figure 3.124, a warning is generated. (See Figure 3.125.)

Figure 3.124 Save Recipe As - Improper Name Format

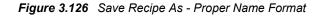
Save Recipe As	×
Name: GREAT NEW RECIPE	
OK / Cancel	Help

Notice the spaces between the words. This generates a system message. (See Figure 3.125.)



Recipe
Recipe name can not be empty OR contain spaces or punctuation characters.

The words need to be set together or separated by an underline "\_" character. (See *Figure 3.126.*)



Notice that the spaces are	Save Recipe As	×
filled in using the underline "_" character.	Name: GREAT_NEW_RECIPE	
	OK Cancel Help	

1. From the Recipe Editor screen, click on **Recipe** in the Menu bar to display its menu. (See *Figure 3.127*.)

2. Click on:

- a. **Save** to save the changes to the current recipe. This immediately saves recipe with no further operator requirement.
- b. **Save As** to preserve the original recipe unchanged and to save the changes as a new recipe. (See *Figure 3.127*.)



Figure 3.127 Recipe Editor

Step 1 Click on Recipe in the		Dambie V
• •	<u>N</u> ew	Ctrl+N
Menu Bar.	Open	Ctrl+O
Step 2 Click on either Save to save changes in the current recipe, or Save As to preserve the current recipe unchanged and the changes in a new recipe.	Save Save As XY-View Ineta View Denter Object Teach Die Grid Start Scan Analysis	Ctrl+S
	Diagnostic Info Print	Ctrl+l Ctrl+P
	E <u>x</u> it Recipe Edito	or

3. If Save As is clicked, the Save Recipe As dialog box appears. (See *Figure 3.127*.)

4. Type in the new recipe name, making sure there are no spaces between words. (See *Figure 3.128*.)

Figure 3.128 Save Recipe As Dialog Box

**Step 5** Enter the new recipe name and click on **OK** to enter the Recipe name into the Recipe file.

Э	Save Recipe As		1	×
е	Name: GREAT_	NEW_RECIPE		
	ОК	Cancel	Help	

5. Click on **OK** to form the new recipe. (See *Figure 3.128.*)

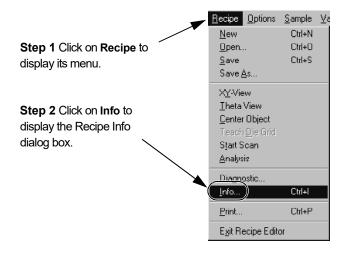
## **Entering Comments**

## Introduction

This feature is designed for recording important comments about the recipe. The only field that is active for user input is the Comments: field. The other fields are automatically set by the system to reflect the specific recipe.

## Procedure

1. Click on **Recipe** in the menu bar of the **Recipe Editor**.



#### Figure 3.129 Recipe Editor

2. The Recipe menu is displayed. Click on Info to display the Recipe Information dialog box. (ALTERNATIVE: Press Ctrl + 1.)

**3**. Click in the **Comments** text field and enter the information that is to accompany the recipe.

	Recipe Information	x
Step 3 The cursor should be	Name:OFF150 User:	
blinking in this field. Enter any required comments in the field.	Comments:	×
Step 4 After comments have been added, click on OK to save them and close the dialog box.	OK Cancel	Y

Figure 3.130 Recipe Information Dialog Box

4. When the information is entered, click on **OK** to save it and close the dialog box.

# STYLUS CHANGE PROCEDURE

# INTRODUCTION

Styli are available in various sizes for a variety of different scanning requirements. Each stylus is a delicate tool and requires careful handling.

Styli are color-coded to indicate radius. Check the color band on the stylus arm against the following table for the stylus radius.

Color Code Band	Stylus Radius (μm)	Cone Angle (Deg.)
Red	12.5	60
Yellow	5.0	60
Green	2.0	60
Orange	2.0	45
Black <sup>a</sup>	0.3–0.8	85
Black <sup>a</sup>	0.1–0.2	85
Dual Black (Not recommended for the P-15)	0.03-0.05 (DuraSharp)	40

 Table 4.1
 Available L-Stylus Radius

a. For radius values, refer to the SEM documents provided with the stylus.

## This chapter describes:

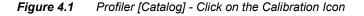
- Proximity Sensor Activation on page 4-2
- Stylus Removal and Replacement on page 4-4
- Scan Position Offset Calibration on page 4-11

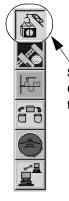
# **PROXIMITY SENSOR ACTIVATION**

Before beginning the procedure and subsequent calibrations, it is important that the Proximity Sensor settings be adjusted in order to ensure optimum system performance and to protect the sensor and stylus.

1. Ensure that the Proximity Sensor is being used during the following calibrations.

Defining parameters used by the proximity sensor are set in the Proximity Sensor Configuration dialog box. To access it from the **Profiler – [Catalog]** screen, click on the **Configuration** icon. (See *Figure 4.1.*)





Step 1 Click on the Configuration icon to display the Configuration screen.

2. In the Configuration screen, click Proximity Sensor... to display the Proximity Sensor Configuration dialog box. (See *Figure 4.3*.)

*Figure 4.2* Configuration Screen

	File Tasks Help		*Online/Local ×
Step 2 Click on the Proximity Sensor button to open the Proximity Sensor Configuration dialog box.	Ele Tasks Hepp	System Geometry -     Handler Load Position:     X (µm):     O     Y (µm):     O     Y (µm):     O     Theta (deg):     D     Elevator (µm):     O     Stage Configuration:     Theta (deg):     O     Levator (µm):     O     Elevator Position (µm):     C     Elevator Position (µm):     Elevator Sole Position (µm):     Elevat	• Stylus Details:         Current Stylus Details:         Property       Value         Tip Radux 5 000 µm         Incl Angle 60.00 deg.         Color Band Single Yellow         Scan Type Contact         Current ID:       1-5-567         5 µm Stylus       ▼         Eeplace Stylus       ↓         Ip History       ↓
	CONFIGURATION		Clear Status

3. In the **Proximity Sensor Configuration** dialog box, click in the empty checkbox next to **Use Proximity Sensor**. (See *Figure 4.3.*) The ✓ in the checkbox enables the option so the system uses the **Proximity Sensor** to stop the head from contacting the sample during the null on a sample surface, thus helping prevent damage to the sample or the stylus.

	Proximity Sensor Configuration Options: Pole Tip Recession Nulling: Use Proximity Sensor:	□K       □K       □Cancel	Step 6 After all changes are complete, click OK.
<b>Optional:</b> Click in the empty checkbox next to <b>Autofocus</b> <b>After Move</b> to enable this option. A check ( $\checkmark$ ) in the box indicates that it is enabled.	Enable Proximity Sensor Offset: Autofocus After Move: Proximity Sensor to Camera Offsets: × (µm): 0 Y (µm): 8250 Autofocus/Surface Track Thresholds: × (µm): 10000 Y (µm): 10000 Theta (deg): 15 Autofocus/Surface Track Disable Threshold: Elevator (µm): 1500		Step 3 Click in the empty checkbox next to Use Proximity Sensor and (Step 4) Enable Proximity Sensor Offset to enable these options. A check (✓) in the box indicates that they are enabled.

*Figure 4.3 Proximity Sensor Configuration Dialog Box* 

4. The **Enable Proximity Sensor Offset** option is very important when measuring small artifacts that are on elevated surfaces or near the edge of the sample. This ensures that the null and autofocus are taking place at the same Z level as detected by the proximity sensor. In addition, it protects the sensor and head from damage, especially near the wafer edge.

Click in the empty checkbox to put a  $\checkmark$  in it. This enables the Proximity Sensor Offset option. (See *Figure 4.3*.)

5. The **Autofocus After Move** option is designed null and focus on the sample in the XY view screen. It does require time to perform this function, so it can be turned off for running sequences and other procedures where the user does not need to see the image.

Click in the empty checkbox to put a  $\checkmark$  in it. This enables the Autofocus After Move option. (See *Figure 4.3*.)

- 6. Click OK to close the Proximity Sensor Configuration dialog box.
- 7. To save the changes made in the **Configuration** screen, click on **File** from the tool bar at the top of the screen to display the **File** menu.
- 8. Click on **Save** from the **File** menu.
- 9. Exit the **Configuration** screen by clicking on the small icon in the top left corner of the screen (to the left of the word Configuration), then from the drop-down menu click on **Close**.

## STYLUS REMOVAL AND REPLACEMENT

The following discussion contains procedures for changing the stylus in the sensor assembly of the P15 system.

Stylus replacement in the P-15 system is relatively simple. *Important:* 

Use only an approved stylus from KLA-Tencor.

Do not modify the measurement head in any way. If, while using the prescribed procedure, there is difficulty in mounting the stylus, call KLA-Tencor Customer Service.

Know the stylus type and radius for input later in the procedure.

Follow the instructions as presented in this section to avoid omitting steps.



**CAUTION:** The stylus tip is very fragile! When removing the stylus from its shipping container, use stainless tweezers (422320) to hold the arm while gently peeling back the foam. Grasp the arm in the center section and lift the stylus out tip first. To place the stylus back in its shipping container, place the rounded end into the round end of the holder and slowly rotate the tip end down. Release the tip only when it is properly positioned in the grove.

The procedure consists of six parts:

- Stylus removal procedure
- Stylus replacement procedure
- Scan Position Offset Calibration.

## **Stylus Removal**

1. From the **Profiler [Catalog]** screen click on the **Configuration** icon to display the **Configuration** screen. (See *Figure 4.4.*)

	nline/Local ×
File Edit Sample Vacuum Host Diagnostic Iasks Help	$\frown$
START ④ ① _	
Scan Recipe Name:	
Scan DRMMD Recipe	
Recipe Path: Recipe Name Length Sampling Speed Creation Date (µm) Rate (Hz) (µm/s) (yyyy-mm-dd)	Time Step 1 Click on the
Scan SCANRCP DRMND 10.5 200 100 2000-08-17	
Data	14:23
	14:23 alsplay the configuration
TIPCTRL 12 500 2 2000-09-14 HIST 500 200 100 2000-08-16	14:35         screen.
Sequence Recipe	<u> </u>
Sequence Data	
Generated by DRM	
Print New View/Modify START XY	View
	Clear Status

Figure 4.4 Profiler [Catalog] - Click on the Calibration Icon

2. From the **Configuration** screen click on the menu arrow to the right of the stylus type variable box to display its menu. (See *Figure 4.5*.)

Profiler - [Configuration]  Ele Tasks Help  System  Sample  Machine History Becorder  Mew Options  Export Path Defaults  Eattern Recognition Options  Seguence Execution Options  Intels Soft Home Position  Lowest Elevator Position  Manual Load Position  Progimity Sensor	- System Geometry -         Handler Load Position:         X (µm):       0         Y (µm):       0         Theta (deg):       0         Elevator (µm):       0         Stage Configuration:       0         Theta Soft Home Position (deg):       0         Levelor Diffset (deg):       0         Lowest Elevator Position (µm):       50000         Elevator Focus Speed (µm/s):       150         Move Elevator to Safe Position Before Moving Stage:       1         Elevator Safe Position (µm):       0	Current ID: 316:25 Current ID:	ar	
	Safety Interlock On:		sty	<b>Pep 3</b> Click on the ylus type of the stylus at is to be mounted.

Figure 4.5 Stylus Force Calibration Button

- 3. Click on the stylus type that will replace the current stylus. (See *Figure 4.5.*)
- 4. Click on **Replace Stylus** to display its dialog box. (See *Figure 4.6.*)

Marual Load Position       Lowest Elevator Position (µm):       23.96         Progimity Sensor       Elevator Position (µm):       1000         Progimity Sensor       Elevator Soure Speed (µm/s):       1000         Elevator Soure Speed (µm/s):       50       Ip History         Move Elevator Safe Position (µm):       0       Ip History         Step 4 To begin the stylus replacement procedure, click Replace Stylus to       Step 2 To begin the stylus to	Jasks Help     System     Sample Machine History Becorder     New Optiona     Export Path Defaults Pattern Recognition Options Seguence Execution Options Inets Soft Home Position Lowest Elevator Position	-System Geometry -           Handler Load Position:           X (µm):         0           Y (µm):         0           Theta (deg):         0           Elevator (µm):         0           Stage Configuration:         1           Theta Soft Home Position (deg):         0           Leveling Offset (deg):         0	Stylus Details:     Current Stylus Details:     Property Nature     Name Jum 456 Stylus     Tore Advance 2000 µm     Tore Angle 45 00 deg.     Codo Band Single Diange     Scan Type Contact      Current ID: 17-5567     Zym-45d Stylus	
	Signal Tower	Elevator Focus Speed (µm/s) 1000 Elevator Slow Focus Speed (µm/s) 50 Move Elevator to Safe Position Before Moving Stage 🔽 Elevator Safe Position (µm) 0	Replace Stylus	procedure, click

Figure 4.6 Configuration Screen

5. To make it easier to track stylus performance, the system provides an opportunity to name the stylus. The type of stylus has already been set before moving to this screen (see Step 3.), and is identified in the **Type** variable box. This variable cannot be changed in this dialog box, only in the Configuration screen. The name identifies the specific stylus of the Type referred to in the **Type** variable box.

The **Stylus ID** dialog box is displayed. (See *Figure 4.7.*) It contains the name of the stylus and a list of previously identified styli of the Type referenced in the **Type** variable box.

*To identify a new stylus:* When using a new stylus, double-click in the ID variable box and enter the new name.

*To enter the name of previous stylus*: When mounting a previously used stylus, click on the name of the stylus from the **Previous ID's** list. The name should appear in the **ID** box.

	Stylus ID 🛛 🗙	1
Step 5 To enter a new stylus name, double-click to highlight the old name in the ID box and enter the new name.	Please verify the selected Stylus type. To choose a different type press Cancel. Select / type an ID number or leave the field empty. To proceed, press OK. New Stylus Type: [25 µm Stylus] ID: [3:16-26] Previous IDs:	The Type of stylus being mounted in the system should be reflected in the Type box.
If a previously used stylus is being mounted, click on the name given to that stylus.		
Step 6 When the stylus name has been successfully entered, click OK to save it and close the dialog box.	Current Stylus Type: 25 μm Stylus ID: 3-16-25	

### Figure 4.7 Stylus ID Dialog Box

- 6. When the new name is entered, click **OK** to save it and exit the dialog box. (See *Figure 4.7.*)
- 7. The profiler message box is displayed inquiring if the name displayed is the correct stylus name. Click **Yes** to affirm the name or **No** if the name is incorrect and needs to be changed.

When **Yes** is clicked, the system head is automatically raised to the manual load height for easy access to the stylus.

(If No is clicked, it is necessary to name the stylus again.)

## *Figure 4.8 Message Box for Stylus Name Affirmation*

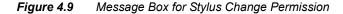
**Step 7** Click **Yes** if the name reflected next to ID is the name of the stylus just entered in the Stylus ID dialog box.



8. After **Yes** is chosen, another message box is displayed. (See *Figure 4.9*.) This box states that the stylus can be changed.

Notice that the message box contains a caution telling the user to "ensure the sensor is unlocked." Disregard this part of the message, it is not for the MicroHead II sensor assembly.

DO NOT CLICK OK UNTIL THE STYLUS HAS BEEN CHANGED.





9. Open the Stage door.



**CAUTION:** Do not operate the stage or any motor driven component with the door open or the system will have to be rebooted.

- 10. Loosen the thumbscrew holding the stylus wrench to the side of the head and slide the wrench out of its holder.
- 11. The head of the stylus clamp screw is visible from the front of the instrument. Place a finger under the Stylus Mount to support it while the screw is being loosened. Loosen the screw by inserting the stylus wrench and turning the wrench counterclockwise 1/2 turn. Be careful to apply turning torque only. Do not push against the screw head any harder than is necessary to seat the wrench. (See *Figure 4.10* and *Figure 4.11*.) Do not remove the screw.

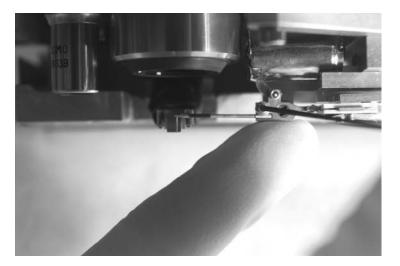


Figure 4.10 Supporting Stylus Mount During Stylus Change

12. With the stylus clamp screw loose, take hold of the stylus with tweezers and pull gently straight to the left until the stylus comes free. (See *Figure 4.11*.)

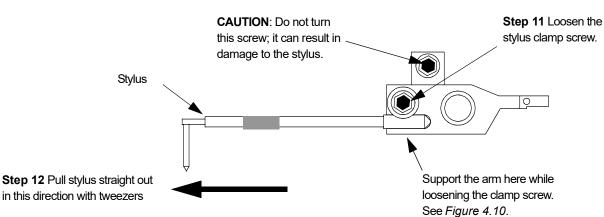
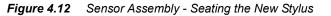


Figure 4.11 Sensor Assembly - Loosening Stylus Clamp Screw

## **Stylus Replacement**

1. Using tweezers, take hold of the new stylus with the tip pointing downward toward the stage. Insert the long arm of the stylus into the support groove in the stylus arm. Gently maneuver it into the slot. Once in the slot, move it up and down gently to ensure that it reaches the end of the slot and seats properly. (See *Figure 4.12.*)





2. Support the **stylus mount (arm) and stylus** with a finger to protect it from damage while tightening the mounting screw. (See *Figure 4.13*.)

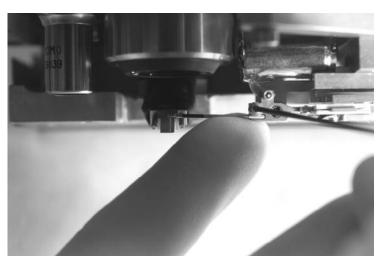
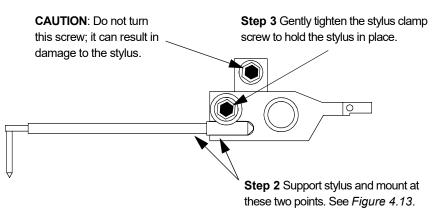


Figure 4.13 Supporting Stylus and Mount During Tightening Procedure

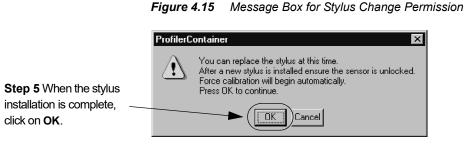
**3**. While supporting the stylus and the stylus arm, gently tighten the clamp screw to hold the stylus in place. Do not over tighten or damage can occur to the stylus arm pivot. (See *Figure 4.13* and *Figure 4.14*.)

Figure 4.14 Sensor Assembly - Seating the New Stylus



4. Remove the wrench from the clamp screw and replace it in its mount. Tighten the thumbscrew to hold the wrench in place.

5. When the stylus installation is complete, click **OK**. (See *Figure 4.15*.)



6. The system performs an Applied Force calibration.

## Scan Position Offset Calibration

#### Introduction

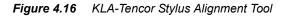
As soon as the Applied Force calibration is complete, the Scan Position Offset procedure is initiated. The Scan Position Offset Calibration procedure scans for data that it then uses to calculate the X-, Y-axis offsets from the optics and stylus, for positioning the sample stage.

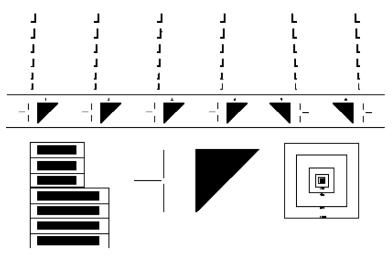
For the standard styli this procedure is performed in the following order:

- 1. 150 µm (standard) calibration
- 2. If the 150  $\mu$ m scan fails to locate the triangle, then the 500  $\mu$ m (backup) calibration is performed.
- 3. If the 500  $\mu$ m was performed successfully, the 150  $\mu$ m calibration must be performed again.

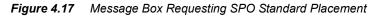
## **Calibration Procedure**

Use the Stylus Alignment Tool (KLA-Tencor Part Number 219517 – see *Figure 4.16*) to perform the Scan Position Offset Calibration and determine the distance that the stylus tip is offset from the crosshair overlay in the XY View window.





1. A message box is displayed requesting the user to place the Scan Position Offset tool on the stage. (See *Figure 4.17*.)





2. Open the stage door.

Step 10 After loading the Stylus Alignment Tool, click

the stage back under the

stylus.

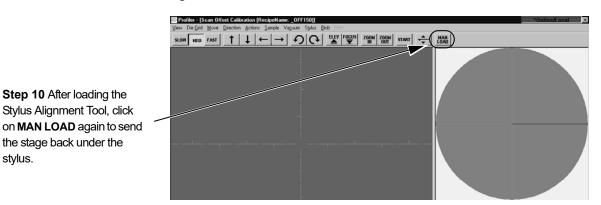
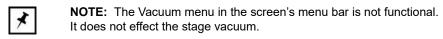


Figure 4.18 Manual Load from the Scan Offset Calibration Window

- 3. Place the Stylus Alignment Tool precisely in the center of the stage, squarely positioned with respect to the XY axis.
- 4. Turn the vacuum ON using the switch on the upper left inside door frame.



- 5. Close the stage door.
- 6. Click OK in the message box. (See *Figure 4.17.*)

The Scan Offset Calibration Option dialog box is displayed (see Figure 4.19) on top of the Calibration screen.

Two columns present the two options used to set up the Scan Offset Calibration. The first column is the Size column. It is used to determine the length of the step that is to be scanned and, therefore, which triangle the scan is to be performed on. If the step is 150  $\mu$ m, the system uses the 300  $\mu$ m triangle. If the step is 500  $\mu$ m, the system uses the 1000  $\mu$ m (1 mm) triangle.

7. Choose 150  $\mu$ m (standard) to continue with the calibration. (See Figure 4.19)

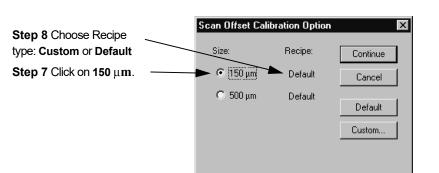


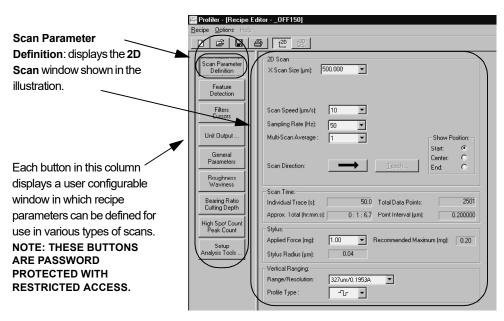
Figure 4.19 Scan Position Offset Calibration Options dialog box

8. Use the Default recipe unless there is a very good reason not to.

**RECIPE TYPES.** Two calibration options exist in the **Scan Offset Calibration Option** dialog box. Each option provides the user with the opportunity to choose between using a default recipe or to create/use a custom recipe. Default and Custom recipes are explained below:

- **Default**: This recipe is designed to operate with a scan speed and stylus force setting that is safe for the stylus. The default settings are the KLA-Tencor recommended recipe settings for all the calibrations.
- **Custom**: This recipe type offers the user the option to customize recipe parameters to meet specific scan requirements. In the Recipe Editor there are seven windows, each with configurable parameters. (See *Figure 4.20*.) For the **Scan Position Offset Calibration**, the only **Recipe Editor** window necessary is the **Scan Parameter Definition** that appears when the editor is first opened (see *Figure 4.23*). When chosen, the **Scan Parameter Definition** button (in the top left corner of the screen, circled in *Figure 4.20*) appears to be indented.

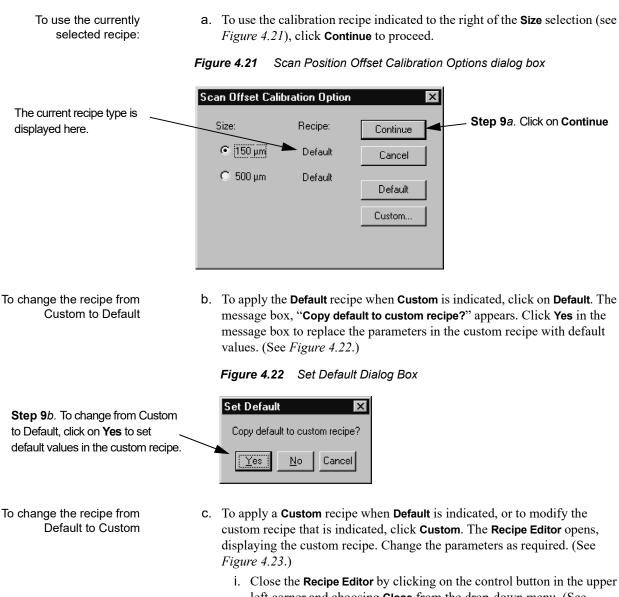




9. The recipes are set as follows:



**CAUTION:** KLA-Tencor recommends using the Default recipes unless there is a very good reason for creating a custom recipe.



i. Close the **Recipe Editor** by clicking on the control button in the upper left corner and choosing **Close** from the drop-down menu. (See *Figure 4.23.*) ii. If the new parameter values were not already saved, a dialog box requires the user to choose between the save options before exiting the Recipe Editor. Choose Save Changes to set the changes to the Custom recipe so they are used in the scan.

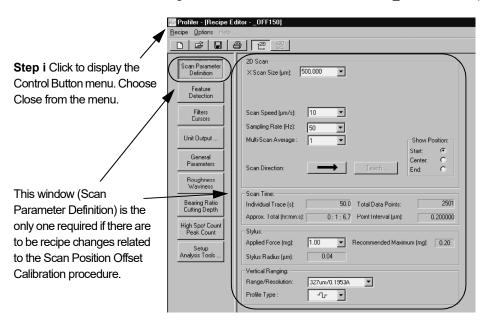
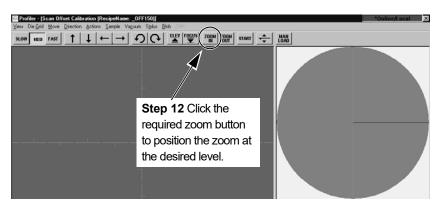


Figure 4.23 Scan Parameter Definition - \_OFF150 - Recipe Editor

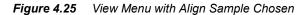
10. From the **Scan Offset Calibration** screen, click **MAN LOAD** in the tool bar to move the stage back beneath the stylus. (See *Figure 4.18*.)

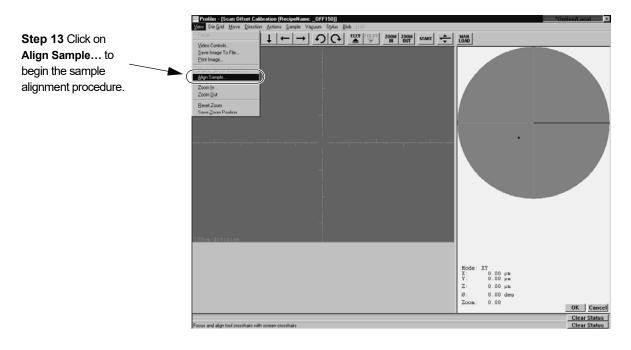
Figure 4.24 ZOOM IN - Scan Offset Calibration



11. (BEFORE CONTINUING see CAUTION below.) Click FOCUS in the tool bar. The Stylus Alignment Tool's surface image comes into focus. (See *Figure 4.24*.)

	L	<b>CAUTION:</b> As the stylus lowers toward the Stylus Alignment tool, watch carefully to ensure that both the proximity sensor and the stylus come down on the tools measurement surface. With the Proximity Sensor Offset option chosen in the Proximity Sensor Configuration box, the proximity sensor is coming down directly on the position where the measurement is to be made. If the stylus and the sensor are not descending directly onto the stylus alignment tool's measurement area, press the Space Bar on the computer keyboard or a mouse click, to stop the stylus descent. Manually relocate the tool under the stylus. Click on <b>FOCUS</b> again to resume the procedure.
	12.	The zoom setting should be the same as that at which the scans are performed. KLA-Tencor recommends that the optics be zoomed all the way out (set at 0), or that the desired zoom setting be locked. (See <i>Saving the Current Zoom Position</i> on page 5-12.)
		To zoom in or zoom out, click and hold the correct button until the optics are at the required zoom setting. (See <i>Figure 4.24</i> .)
BEGIN Align Sample 13 Procedure		The Stylus Alignment Tool must be aligned with respect to the X-, Y-axis in order for the calibration to be as accurate as possible. Click on <b>View</b> in the menu bar to display its menu. (See <i>Figure 4.25</i> .)
	14.	Choose Align Sample from the menu. (See Figure 4.25.)
		This displays the Alignment Angle Dialog Box. (See Figure 4.26.)





15. In the Alignment Angle dialog box, leave the setting at the default, "0" and click **OK** to accept the alignment angel of  $0^{\circ}$ . (See *Figure 4.26*.)

Figure 4.26 Alignment Angle Dialog Box

Alignment Angle	;	X
Alignment Angle:	I	Degrees
ОК	Cancel	Help

The prompt at the bottom of the screen now says,.

#### Click the left mouse button to teach the first point

- 16. Use the arrow buttons to locate the border line between the  $300 \,\mu\text{m}$  triangles and the  $1000 \,\mu\text{m}$  triangle. Still using the arrow buttons, follow the line to the left side of the tool. (See *Figure 4.27*.)
- 17. Move the cursor to the line and click precisely on the line.

The prompt at the bottom of the screen now says,

Press OK to accept the first alignment location

Click **OK** at the bottom right corner of the screen.
 The prompt at the bottom of the screen now says,

Click the left mouse button to teach the second point

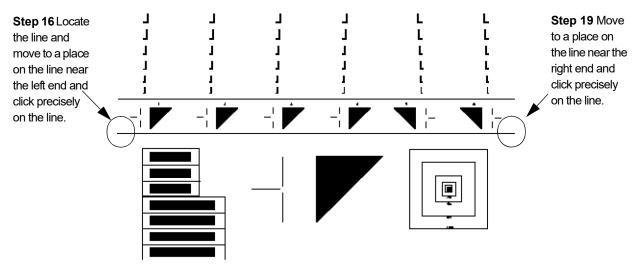


Figure 4.27 KLA-Tencor Stylus Alignment Tool

19. Use the left arrow button follow the dividing line to the right until it reaches the end of the line. (See *Figure 4.27*.)

**END Align Sample** 

Procedure

20. Move the cursor directly over the line and click precisely on the line.

The system adjusts the theta alignment so the Stylus alignment tool is lined up with the X- and Y-axis. The prompt at the bottom of the screen now says,

#### Press OK to accept the second alignment location

21. Click **OK** at the bottom right of the screen to accept the stage alignment of the Stylus Alignment Tool.

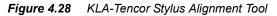
The prompt at the bottom of the screen now says,

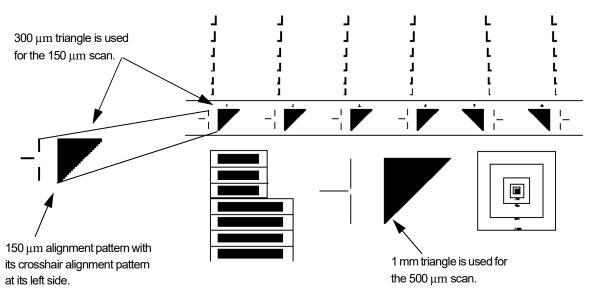
## Focus and align tool crosshairs with screen crosshairs

There are two different alignment patterns that can be used in the Scan Position Offset Calibration. Each scan is conducted at the midpoint of the triangle where the step distance is one half the length of both right angle triangle sides. The first and primary alignment pattern is the 300  $\mu$ m triangle which is called the 150  $\mu$ m alignment pattern. It has this name because the scan traverses the triangle at it midpoint where the distance is 150  $\mu$ m. The second is the 1000  $\mu$ m (1 mm) triangle which is called the 500  $\mu$ m alignment pattern because its midpoint scan distance is 500  $\mu$ m. It is used when the 150  $\mu$ m scan fails to locate the 300  $\mu$ m triangle.

When making this calibration, first use the 300  $\mu$ m triangle to complete the 150  $\mu$ m scan. If the stylus offset is too great, the scan misses the triangle. If this happens, try the 1000  $\mu$ m (1 mm) triangle to complete the 500  $\mu$ m scan. If that is successful, retry the 300  $\mu$ m triangle.

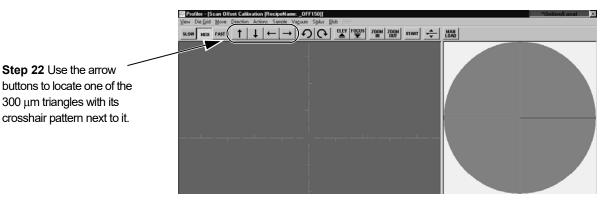
If the 500  $\mu$ m scan missed the 1000  $\mu$ m triangle, the stylus needs to be physically realigned by an authorized KLA-Tencor service representative.



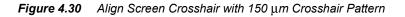


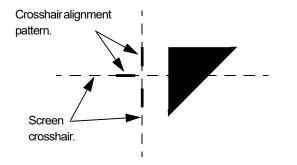
22. Use the linear movement arrow buttons (see *Figure 4.29*.) to locate one of the 150  $\mu$ m alignment patterns with its crosshair alignment pattern at its left side. (See *Figure 4.28*.)

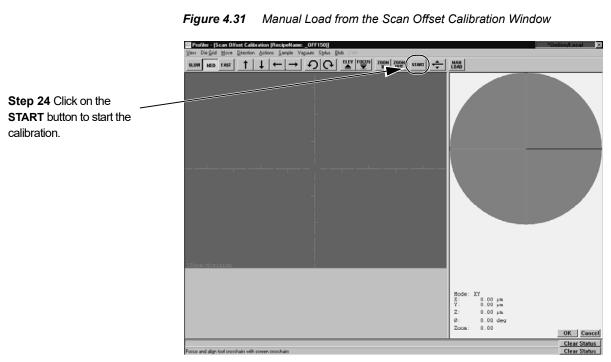




**23**. Click at the center of the Crosshair Pattern to align it with the screen crosshair. (See *Figure 4.30*.) The crosshair pattern should align precisely with the screen crosshair.







24. Click the **START** button located in the screen tool bar. (See *Figure 4.31*.)

The video image changes to side view as the stage moves to position the start of the scan on the beginning of the start pattern near the calibration triangle.

When the stylus has reached the beginning of the 150  $\mu$ m scan trace, the screen changes to the **Scan: \_OFF150** window. The scan automatically begins.

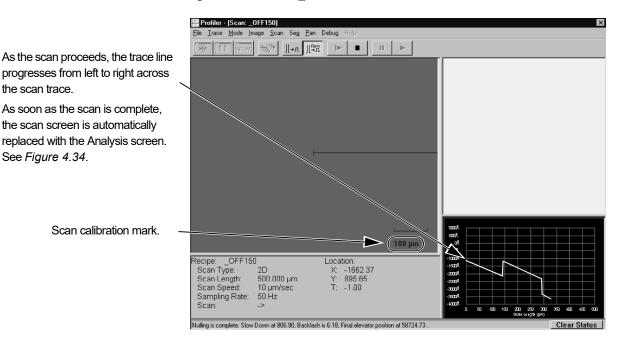
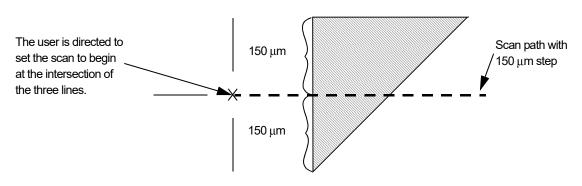


Figure 4.32 Scan: \_OFF150 Window

The scan can be viewed at the bottom right of the **Scan: \_OFF150** screen as it progresses from left to right across the scan trace window, forming a linear image of the scanned surface. The Start pattern next to triangle is set up to direct the scan through the middle of the triangle using the **\_OFF150** recipe. In a perfectly calibrated system, the scan trace goes directly through the center of the 300  $\mu$ m triangle creating a 150  $\mu$ m trace step. However, this is not a common occurrence for a system that has not yet been calibrated after a stylus change.

The system uses the step and the distance across the triangle to determine where the trace was performed and then automatically calculates the offsets.

Figure 4.33 Trace Path Through Upper Triangle



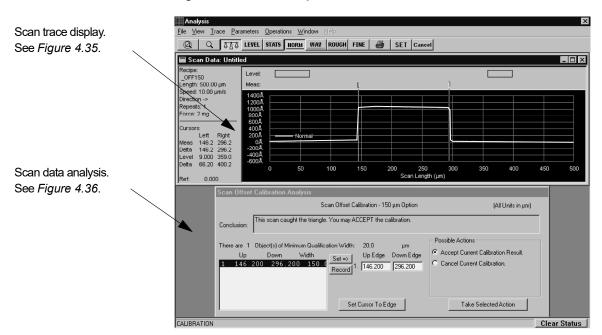


Figure 4.34 Data Analysis Window.

When the scan is complete, the **Data Analysis** window automatically replaces the **Scan: \_OFF150** screen. The window contains a scan data trace as shown in *Figure 4.35*. If the scan was successful, the system detected the triangle and set cursors at the edges of the triangle for visual inspection. It is possible to observe the scan and determine, visually, where the trace is running through the triangle.

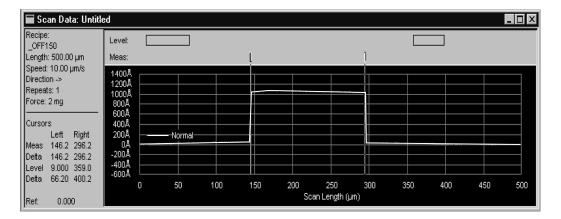
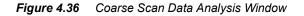


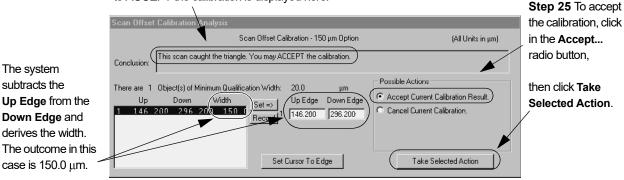
Figure 4.35 Scan Data Portion of the Analysis Window

In the bottom half of the window, the **Scan Offset Calibration Analysis** appears. In *Figure 4.36* the system has subtracted the Up Edge from the Down Edge and calculated the result to be 150.0  $\mu$ m. Using this analysis of the scan, the system makes a recommendation based upon its recognition of the **Stylus Alignment Tool** triangle pattern.

25. To accept the recommendation, ensure that Accept Current Calibration Result is chosen, then click on Take Selected Action. (See *Figure 4.36*.)



If the scan was recognized by the system, a recommendation to ACCEPT the calibration is displayed here.



If the trace misses the triangle or is unable to identify it, one of several messages can be displayed. If the message reads, "Unknown situation..." or is otherwise uncertain, perform the entire scan procedure again, this time using the 1000  $\mu$ m (1 mm) triangle and replacing the 150  $\mu$ m scan recipe with the 500  $\mu$ m scan recipe, \_OFF500. If the 500  $\mu$ m scan is acceptable, perform the 150  $\mu$ m scan again. The results should be acceptable.

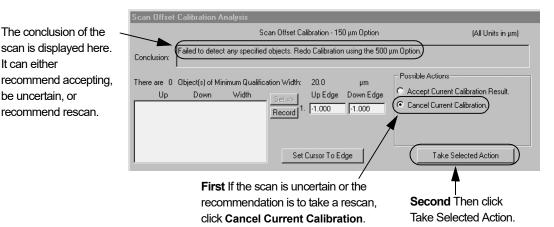
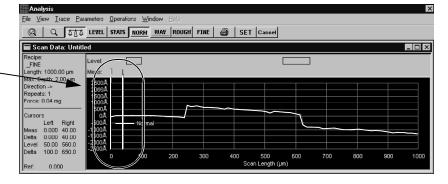


Figure 4.37 "Unknown Situation" Corrective Action

When the Triangle is Present, But System Does Not Find It. The message could also say that the scan might have caught the triangle and ask the user to choose either to accept it, change the location, or reject it. If the **Conclusion** box informs the user that the system either didn't find the triangle for sure or asks the user to check the trace for the presence of the triangle, it might be necessary to reset the measurement cursors. (See *Figure 4.38.*)



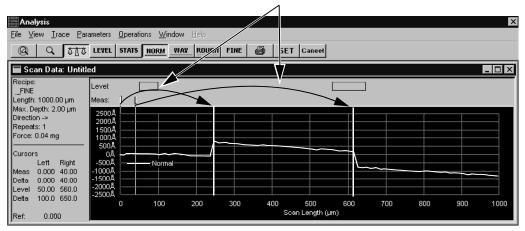
In this case, the system placed the identification cursors at the left edge of the trace, missing the triangle that is obviously displayed mid trace. (See *Figure 4.39* for resolution.)



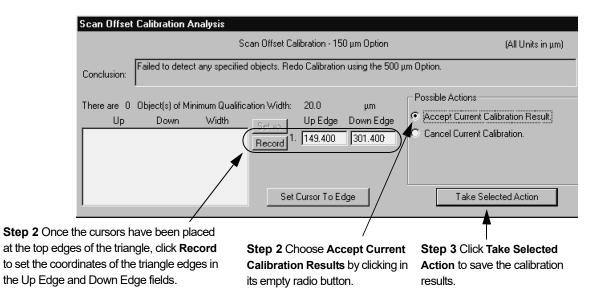
1. If the triangle is obvious, reset the measurement cursors to the top edges of the triangle. To reset the measurement cursors, look in the top area over the graph, click and hold on the right cursor, then drag it to the top right corner of the step in the trace. Repeat for the left cursor, dropping it on the top left corner. (See *Figure 4.39.*)

Figure 4.39 Analysis Screen with Cursors Manually Placed

Click, hold and drag each cursor to the top edges of the step.



2. Once the measurement cursors are in position, click **Record** in the Scan Offset Calibration Analysis section of the screen. (See *Figure 4.40*.)





- **3.** When the edges of the triangle have been recorded, choose **Accept Current Calibration Result** in the **Possible Actions box**. (See *Figure 4.40*.)
- 4. Click Take Selected Action. (See *Figure 4.40*.)

On rare occasions the system fails to recognize the triangle even though it is in the data set. The system might also make a determination that one of a number of detected features is the correct one. To determine if the triangle is in a given data set, review the scan data set of detected features at the bottom left of the Scan Offset Calibration Analysis portion of the screen. If the triangle is present then the scan calibration can be reset.

- 1. Click on the scan feature data set that represents the triangle so that it highlights. In *Figure 4.41* the system choose feature number 1 and set its parameters in the Up Edge and Down Edge fields. (See *Figure 4.41*.) However, feature number 2 is 151.71  $\mu$ m which is very near the expected scan distance of 150  $\mu$ m. In this example the user would click on that feature to highlight it.
- 2. With the feature highlighted, click on **Set** to choose that feature as the triangle. The Up and Down parameters of the data set are recorded in the Up Edge and Down Edge fields. (See *Figure 4.41*.)

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When More Than One

Possibility is Displayed

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	There are 0	Object(s) of Minimum Qua	lification Width: 20.0	μm	Possible Actions
	Up	Down Width 25 251.025 1.0 88 901.890 151	Set => Up Edg	e Down Edge	<ul> <li>Accept Current Calibration Result.</li> <li>Cancel Current Calibration.</li> </ul>
First: Click on the	(2 /50.1	.88 901.890 151.			
feature that represents					
the triangle.			Set Cursor To	Edge	Take Selected Action

Figure 4.41 Hand Selecting the Triangle Data in Analysis Screen

- 1. Once the feature is chosen, choose Accept Current Calibration Result. (See *Figure 4.42.*)
- 2. Click Take Selected Action. (See Figure 4.42.)

Scan Offset Calibration Analysis Scan Offset Calibration - 150 µm Option (Ali Units in µm) This scan may have caught the triangle. You may ACCEPT the calibration or, if the triangle was not caught, you may RESCAN using the second computed offset Conclusion: Possible Actions There are 0 Object(s) of Minimum Qualification Width: 20.0 μm Accept Current Calibration Result. Up Down Width Up Edge Down Edge Set => 
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Figure 4.42 Accepting Adjusted Scan Results

**3**. After the scan calibration has been accepted, the **Calibrations** screen returns. Close the Calibration screen.

# **XY VIEW SCREEN**

## INTRODUCTION

The name XY View comes from the function of the screen itself, which is for viewing the sample surface, and positioning a scan. The XY View screen also provides other tools required to set up and perform a scan.

The appearance of the video image depends on the zoom setting being used to view the sample surface and the current accuracy of the focus.

The P-15 has a zoom capability that allows the operator to zoom in and out to view the sample surface at different magnification levels.

This chapter describes:

- Starting the XY View Application on page 5-2
- Setting the Magnification on page 5-11
- Focusing the View on page 5-13
- Positioning the Scan Site on page 5-16
- Using Die Grid Navigation on page 5-19
- Using Blob Analysis (Center Object Search) on page 5-32
- *Aligning the Sample* on page 5-35

# STARTING THE XY VIEW APPLICATION

## Procedure

1. When the **Catalog** screen is first displayed, the **Sequence Recipe** list is in the Information Display window. To change to the **Scan Recipe** list, click on the **Scan Recipe** button. (See *Figure 5.1.*)

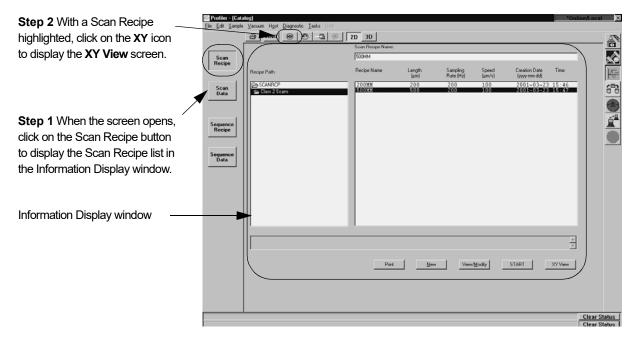
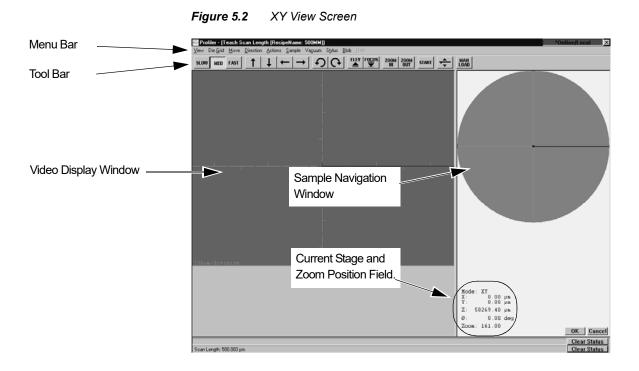


Figure 5.1 Scan Recipe Window in the Catalog Screen

2. Once the Scan Recipe window is active, ensure that the desired scan recipe is highlighted by clicking on it. With the recipe highlighted, click the **XY** button to display the XY View screen. (See *Figure 5.1*.)

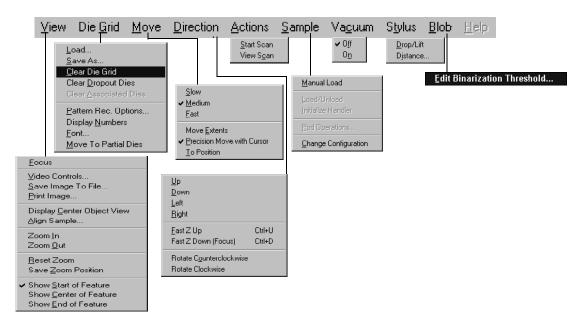


## **XY View Window Features**

## XY View Menu Bar

The Menu Bar contains the majority of the available screen function commands. Each function is explained in detail in this section.

Figure 5.3 XY View Screen Menu Bar



## View Menu

 Table 5.1
 View Menu Description

View Menu	Description
	<b>Focus</b> Using the current magnification setting, this button causes the system to focus on the sample that is on the stage at the same time that the stylus is nulled on the sample surface.
	<b>Video Controls</b> Displays the Video Display Dialog Box.
Eocus	Save Image to File Displays the dialog box which set up the location of the file where the image is to be saved.
⊻ideo Controls <u>S</u> ave Image To File <u>P</u> rint Image	<b>Print Image</b> Displays the dialog box for printing the image in the video portion of the screen.
Display <u>C</u> enter Object View <u>A</u> lign Sample Zoom <u>I</u> n	<b>Display Center Object View</b> This puts the center of the object being scanned at the screen crosshair.
Zoom <u>O</u> ut <u>R</u> eset Zoom Save Zoom Position ✓ Show <u>S</u> tart of Feature Show <u>C</u> enter of Feature Show <u>E</u> nd of Feature	Align Sample Displays the dialog box used for setting up the angular rotation of the sample on the sample stage and initiates the automated procedure for aligning the sample to the video display.
	<b>Zoom In</b> Causes the optics to zoom in to a higher magnification.
	<b>Zoom Out</b> Causes the optics to zoom out to a lower magnification.
	<b>Reset Zoom</b> Resets the zoom position to "0" when the Zoom is active (position not saved).
	<b>Save Zoom Position</b> Displays a dialog box where the zoom position is set and locked so that it cannot be changed by the Zoom In and Zoom Out buttons.
	<b>Show Start of Feature</b> Displays, at the crosshair of the video display, the starting point of the scan.
	Show Center of Feature Displays, at the crosshair of the video display, the center of the scan on the sample surface.
	<b>Show End of Feature</b> Displays, at the crosshair of the video display, the end of the scan on the sample surface.

## Die Grid Menu

Table 5.2	Die Grid Menu
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Die Grid Menu	Description
	<b>Load</b> Displays the dialog box used to load a die grid pattern.
	<b>Save As</b> Saves the die grid pattern.
	<b>Clear Die Grid</b> Removes any die grid pattern on the video display window. [See <i>Clearing a Die Grid (Turn OFF Die</i> <i>Grid Navigation)</i> on page 5-30.]
Load Save As Clear Die Grid Clear Dropout Dies Clear Associated Dies	Clear Dropout Dies Blocks the dies from being scanned when a mouse cursor is placed over the die on the Sample Positioning Window and the SHIFT+LEFT MOUSE BUTTON is pressed.
<u>Pattern Rec. Options</u> Display <u>N</u> umbers <u>F</u> ont <u>M</u> ove To Partial Dies	<b>Clear Associated Dies</b> Removes dies which were previously <b>associated</b> in a sequence recipe.
	Pattern Rec. Options This displays the Load Die Grid dialog box. [See Loading a Die Grid (Turning ON Die Grid Navigation) for a Single Scan on page 5-28.]
	<b>Display Numbers</b> Displays the numbers on the Sample Positioning Window.
	<b>Font</b> Displays the font dialog box used to change the screen fonts.
	Move To Partial Dies Scans the partial die at the edge of the wafer perimeter, only when this feature is enabled.
	Normally, these partial dies cannot be scanned because of the circular wafer edge, but this feature allows them to be scanned.

#### Move Menu

Table 5.3Move Menu	
Move Menu	Description
	<b>Slow</b> – Sets the XY stage to move in the slowest, or smallest increment, speed as defined in the <b>Move Extents</b> .
Slow ✓ Medium East	<b>Medium</b> – Sets the XY stage to move in medium, or intermediate increment, speed as defined in the <b>Move Extents</b> .
Move <u>E</u> xtents ✓ <u>P</u> recision Move with Cursor <u>T</u> o Position	<b>Fast</b> – Set the XY stage to move in fast, or largest increment, speed as defined in the <b>Move Extents</b> .
	<b>Move Extents</b> – Sets the increment (Slow, Medium, Fast) for the stage movement. Enter the $\mu$ m per click distance in each field for X/Y movement and the degrees in the Theta fields.
	Figure 5.4 Move Extents Dialog Box
	Move Extent       X / Y       Theta         Slow Move Extent:       I       μm       1       degr.       OK         Medium Move Extent:       100       μm       2       degr.       Cancel         Fast Move Extent:       300       μm       5       degr.
	<b>EXAMPLE For the X and Y movement:</b> If <b>Fast</b> speed is selected (with the Fast value set to 300 microns), then the stage moves by 300 microns each time an arrow button is clicked.
	<b>EXAMPLE for Theta Rotation:</b> For the theta (rotational) movement. Sets the rotational increment (Slow, Medium, Fast) in degrees, for the stage movement with each button or key click. If <b>Fast</b> speed is selected (with <b>Fast</b> set to $5^{\circ}$ ), then with each click the stage rotates $5^{\circ}$ .
	Precision Move – Takes out any backlash in the lead screws.
	<b>To Position</b> – This displays the <b>Move To Position</b> dialog box. Enter the coordinates the stage is to move to. If a rotational move is used to reorient a feature already in view so it can be scanned in a different direction, also choose <b>Rotate About Camera Position</b> . Click <b>OK</b> to make the move.
	<i>Figure 5.5</i> Move To Position Dialog Box
	Move To Position

## **Direction Menu**

Direction Menu	Description
	<b>Up</b> -Moves the stage in the +Y direction away from the front door by one increment (as defined in <b>Move Speeds</b> for the set speed) per button click. Click and hold the button for continuous movement.
Up Down Left	<b>Down</b> – Moves the stage in the -Y direction toward the front door by one increment (as defined in <b>Move Speeds</b> for the set speed) per button click. Click and hold the button for continuous movement.
Bight       East Z Up     Ctrl+L       Fast Z Down (Focus)     Ctrl+E       Botate Counterclockwice	
Rotate C <u>o</u> ockwise Rotate C <u>l</u> ockwise	<b>Right</b> – Moves the stage in the +X direction toward the right by one increment (as defined in <b>Move Speeds</b> for the set speed) per button click. Click and hold the button for continuous movement.
	<b>Fast Z Up</b> – Raises the measurement head away from the stage by one increment per button click. Click and hold the button for continuous movement. This is the same as clicking the <b>Elev</b> button.
	<b>Fast Z Down (Focus)</b> – Lowers the measurement head and sensor to the null position, and focuses the video image. The measurement head automatically lowers to the correct distance from the sample for real-time video. This is the same as clicking the <b>Focus</b> button
	<b>Rotate Counterclockwise</b> – Rotates the stage in the theta counterclockwise direction by one increment (as defined in <b>Move Speeds</b> for the se speed) per button click. Click and hold the button for continuous movement.
	<b>Rotate Clockwise</b> – Rotates the stage in the theta clockwise direction by one increment per button click. Click and hold the button for continuous movement.

#### Actions Menu

Actions Menu	Description
Start Scan	<b>Start Scan</b> Starts the scan process.
View S <u>c</u> an	View Scan Changes to the View Scan window.

#### Sample Menu

Table 5.6Sample Menu

Sample Menu	Description
	<b>Manual Load</b> Moves the stage towards the front door. This is used for loading wafers.
Manual Load	<b>Load/Unload</b> Not applicable for the P-15 system.
Load/Unload Initialize Handler	<b>Initialize Handler</b> Not applicable for the P-15 system.
Eod Operations Change Configuration	<b>Pod Operations</b> Not applicable for the P-15 system.
	<b>Change Configuration</b> This brings up the <b>Safe Area</b> configuration box.

#### Vacuum Menu

## Table 5.7 Vacuum Menu

Vacuum Menu	Description
✓ O <u>f</u> f O <u>n</u>	<b>Off</b> Not applicable for P-15 systems. The vacuum status is set using a manual switch next to the door.
	<b>On</b> Not applicable for P-15 systems. The vacuum status is set using a manual switch next to the door.

## Stylus Menu

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Table 5.8Stylus Menu
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Stylus Menu	Description
<u>D</u> rop/Lift Distance	<b>Drop/Lift</b> Causes the stylus to pivot up. A check mark is visible while it is in the UP position. Click on it to release it back to its normal scanning position
	<b>Distance</b> Displays the <b>Distance From Sample</b> dialog box. This is the distance from the stylus to the sample surface during scan positioning. Set the number in $\mu$ m and click <b>OK</b> . The distance remains in effect until changed by the user. <b>Figure 5.6</b> Distance Dialog Box
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#### Blob Menu

	Table 5.9	Blob Menu
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Blob Menu	Description
Edit Binarization Threshold	Edit Binarization Threshold Activates the Blob Analysis capability when the Display Center Object View feature is selected from the View menu.
	This allows the user to draw a box around an object visible in the video image, and the stage moves to the center of that object using the image contrast to locate the object. The contrast value can be set from 0 to 255 with a typical range of 60 to 100.
	<b>EXAMPLE</b> : if selecting a dark object, set the threshold to a high value so that greater contrast is used to help distinguish the object from the surrounding area. [See <i>Using Blob Analysis (Center Object Search)</i> on page 5-32.]

## Tool Bar Buttons

 Table 5.10
 XY View window Tool Bar Buttons

Button	Description
SLOW	Sets the XY stage to move in small increments as set in <b>Move Extents</b> .
MED	Sets the XY stage to move in moderate increments as set in <b>Move Extents</b> .
FAST	Sets the XY stage to move in large increments as set in <b>Move Extents</b> .
1	Moves the stage in the +Y direction (away from the front door) by one increment (as set in <b>Move Extents</b> ) per button click. Click and hold the button for continuous movement.
↓	Moves the stage in the -Y direction (toward the front door) by one increment (as set in <b>Move Extents</b> ) per button click. Click and hold the button for continuous movement.
←	Moves the stage in the -X direction (toward the left) by one increment (as set in <b>Move Extents</b> ) per button click. Click and hold the button for continuous movement.
$\rightarrow$	Moves the stage in the +X direction (toward the right) by one increment (as set in <b>Move Extents</b> ) per button click. Click and hold the button for continuous movement.
り	Rotates the stage in the theta counterclockwise direction by one increment (as set in <b>Move Extents</b> ) per button click. Click and hold the button for continuous movement.
<b>(</b>	Rotates the stage in the theta clockwise direction by one increment (as set in <b>Move Extents</b> ) per button click. Click and hold the button for continuous movement.
ELEV	Raises the measurement head away from the stage by one increment per button click. Click and hold the button for continuous movement.
FOCUS	Lowers the measurement head containing the sensor assembly to the null position, with the stylus just above the surface, and focuses the video image.
ZOOM IN	Changes to a higher magnification with each click.
ZOOM OUT	Changes to a lower magnification with each click.
START	Starts the scan process.

Button	Description
* <u>*</u>	A toggle that lifts and drops the stylus.
MAN LOAD	Toggle button that moves the stage to and away from the Manual Load position. Before each movement, the measurement head moves to the set Z-height to protect the sensor assembly from accidental contact.

 Table 5.10
 XY View window Tool Bar Buttons (Continued)

# SETTING THE MAGNIFICATION

## Introduction

The system has an optical zoom function that allows the operator to view the sample surface at different magnifications for feature identification and scan placement.

If the system has Pattern Recognition operating, zooming in and out could prevent the system from performing accurately because the recognition function also takes into consideration the size of the image as well as its shape.

# **Changing the Magnification**

Click the **ZOOM IN** or **ZOOM OUT** to change the magnification. Each click changes the magnification level in or out by a small amount.

#### (Alternative:

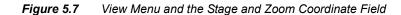
In the Menu bar click on **View** to display its menu. From the **View** menu, select either **Zoom In** or **Zoom Out** to change the magnification. Each click changes the magnification level in or out by an amount a little more than twice the size of the button icons.)

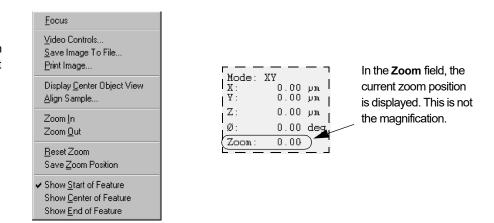
For systems using the Pattern Recognition option, the zoom function can greatly effect those system's ability to perform the recognition function. If the Zoom position is set and left at a particular zoom level, the system is dependable using the Pattern Recognition option.

# Resetting the Zoom to "0.00"

If the zoom function has been used, it might be necessary to use the **Reset Zoom** to return the zoom magnification to exactly "**0.00**" in the Zoom field at the bottom right of the screen.

Click on **Reset Zoom** and the system automatically zooms out to the furthest position and sets the Zoom field to **0.00**.





# Saving the Current Zoom Position

For systems operating with the Pattern Recognition option, it is extremely important that the Zoom position be *locked* so the system can perform the pattern recognition function properly. Saving the current zoom position is also called "zoom lock." This function relies on both shape and size for the recognition process to be effective. The most reliable way to secure the zoom position is to use the **Save Zoom Position** dialog box to set and lock the desired position.

Another reliable way is to leave the zoom feature at 0.00, then pattern recognition should work well. In this case, it is very important that, before the pattern recognition process is used, the operator remember to reset the zoom to 0.00.

- Check to ensure that the current Zoom position, displayed in the Zoom field at the bottom left of the screen, is the position that the zoomed magnification is to be frozen at. If so, proceed to the next step. If not, adjust the zoom (magnification) to the required level using the zoom icons or menu items.
- 2. To save the current zoom position, click on **Save Zoom Position** in the **View** menu. This opens the Save Zoom Position dialog box. (See *Figure 5.8*.)

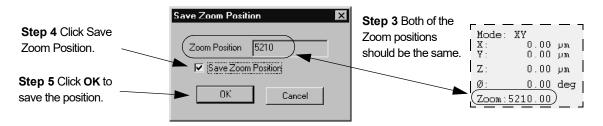
Figure 5.8 View Menu in XY Vies Screen



Click **Reset Zoom** from the View menu to reset the **Zoom** to exactly **0.00**. The Save Zoom Position dialog opens with the current zoom position in the Zoom field.

- 3. Ensure that the zoom position in the dialog box **Zoom** field agrees with the **Zoom Position** in the screen display. (See *Figure 5.9*.)
- 4. Put a check in the Save Zoom Position check box. (See Figure 5.9.)

Figure 5.9 Save Zoom Position Dialog Box



5. Click **OK** to save the position and disable the zoom icons in the tool bar and the zoom menu items in the View menu. (See *Figure 5.9.*)

# FOCUSING THE VIEW

## Introduction

Focusing on the sample surface is controlled by a combination of the nulling process and the system focus knobs.

## Nulling

#### Fast Approach

In the first phase of the nulling descent, the measurement head lowers the stylus at a higher speed until it reaches a preset level above the sample surface. The default level set in the registry is  $1000 \,\mu\text{m}$  above the Lowest Elevator Position. If the stylus touches the surface during the fast approach phase of the descent, an error is generated. The error is not speed dependant.

If the proximity sensor and the proximity sensor offset is used during the descent, the stage moves to position the proximity sensor over the same location at which the stylus eventually touches the surface.

If the proximity sensor is enabled, the Fast Approach ends when either the proximity sensor indicates the approaching surface. If the proximity sensor is disabled, the Fast Approach ends when the head reaches 1000  $\mu$ m above the Lowest Elevator Position. The descent slows at this point and, if the Proximity Sensor Offset is applied, the system moves the stylus back over the contact point on the sample surface.

#### Slow Approach

This is the phase of the nulling descent in which the stylus contacts the sample surface. Even though this phase is called the Slow Approach, it is possible for the descent speed to be set to the same rate as the Fast Approach.

The Slow Approach ends when the stylus hits a surface and the stylus is pushed up above the horizontal position.

#### Final Adjustment

During the last phase of the nulling operation, the head moves upward very slowly until the stylus drops just barely below the horizontal position and slightly above the surface.

#### Focus

After the final adjustment to the head and stylus position, the system focusses on the surface.

After the null and focus procedure, if the sample surface is not in focus, the focus knobs can be used to bring the surface into focus. (This should only be required after stylus change.)

The purpose of focusing the view is to sharpen the image in the video window. If the focus is clear the first time, and the sample is flat, focus should be maintained each time the stage moves to another location on the same sample surface.

#### **Proximity Sensor**

The proximity sensor can be used in the transition between the Fast Approach and Slow Approach phases of the nulling procedure. The following restrictions apply to proximity sensor use:

- The proximity sensor works on optical principles and is therefore not for use with transparent surfaces. For transparent surfaces teach the Lowest Elevator Position and turn the proximity sensor off.
- The system accommodates the physical offset between the stylus and the proximity sensor by adjusting the stage position at the appropriated time before the scan procedure. The accommodation cannot be performed for measurements 15 mm or closer to the right hand side of the chuck. If measurements are to be taken at X-coordinate values that might fall within that restricted range, the Proximity Sensor Offset must be disabled. The proximity sensor can still be used, provided the sample is flat and not transparent.
- For small samples that are not transparent, the proximity sensor can be used in the nulling procedure provided that the offset has been correctly taught. The original offset was taught at the factory and should not be changed unless there is very good reason. Using the proximity sensor is especially convenient for sample with widely varying thickness between measurements, to avoid focussing errors, and to avoid repeated teaching of the Lowest Elevator Position.
- For samples having the same thickness (i.e., within ± 200 mm), disable the proximity sensor and rely on the Lowest Elevator Position. Since these samples have the same thickness, the Lowest Elevator Position does not need to be reset.

# Focus the Optics – Top- or Side-View

1. Raise the measurement head.



**CAUTION:** Before lowering the head, be sure that the sample is under the center of the optics, that the stage is not significantly out of level, and that there are no physical obstacles.

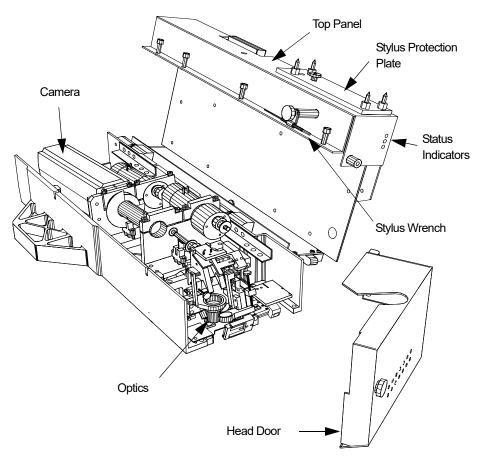
2. Use the **Focus** button to null the stylus on the sample (use a patterned sample with easily defined features).



**NOTE:** If the Proximity Sensor is not enabled, the elevator is designed to slow its rate of descent to 10  $\mu$ m/sec when it reaches 1000  $\mu$ m above the **Lowest Elevator Position**.

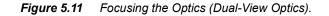
3. Open the measurement chamber door and then the head door. (See *Figure 5.10*.)

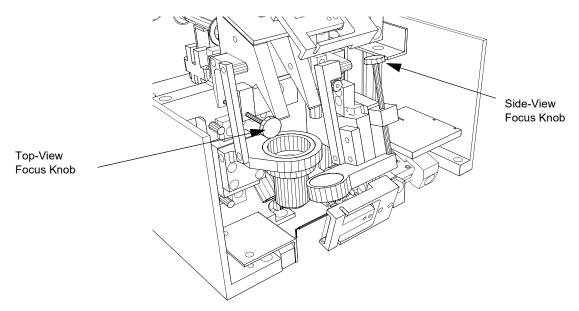
Figure 5.10 MicroHead Measurement Head.



- 4. If the initial view requires focusing, turn the **Top-View Focus** knob to focus the top view. (See *Figure 5.11*)
- 5. Click the Stylus Drop-Lift icon to lower the stylus onto the sample surface.

6. If the side view requires focusing, use the **Side-View Focus** knob to focus the side view. (See *Figure 5.11*)





7. Test the Video Calibration after any mechanical refocusing event by clicking on a clearly definable feature and see if it lines up exactly with the screen crosshair. If not, perform the Video Calibration.

# **POSITIONING THE SCAN SITE**

## Introduction

The stage can be moved in the X, Y, and theta direction to orient an object image for scan positioning. The stage can be moved to reach any point on the sample surface within the Safe Area limits. (See *Safe Area Configuration* on page 11-21)

The stage moves incrementally in the following directions:

- The X direction moves the stage left and right
- The Y direction moves the stage forward and backward
- The theta direction rotates the stage clockwise and counterclockwise.

A common way to move the stage is to click on the arrow button that points in the direction that the stage is to move. Notice that the arrow points in the direction the stage moves and not in the direction that the image moves in the field of view.



**NOTE:** When using the toolbar arrow buttons, the image appears to wiggle as it stops. This is a normal part of the procedure designed to eliminate the slight mechanical backlash in the stage movement that could make precise positioning difficult.

*Figure 5.12* shows the stage coordinate system (SEMI Standard M20-92) used by the Profiler. The X and Y coordinates relative to the center of the measurement area are displayed in the current stage coordinate area of the XY View window. The travel area of the stage is limited to a circle 210 mm (8.2 in.) in diameter. (See *Figure 5.12*).

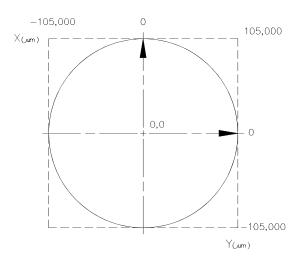


Figure 5.12 Coordinate System of the KLA-Tencor Profiler Stage

#### **Scan Site Positioning Procedure**

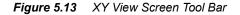
- 1. After the sample is loaded on the stage and the stage returned to the scan position under the stylus, click **FOCUS**.
- 2. Use one or more of the following methods to locate a scan site. (See Table 5.11.)

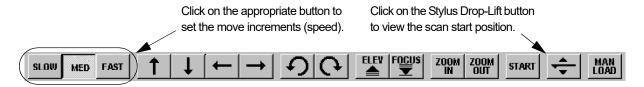
Table 5.11 Locating a Scan Site

Movement Required	Movement Method
To make a large move across the sample surface, use the <b>Sample</b> <b>Navigation Window</b> (See <i>Figure 5.14</i> .)	<b>Sample Navigation Window</b> – The navigation circle represents the stage area. Click the location on the Sample Navigation Window to move to the corresponding location on the sample. (See <i>Figure 5.14.</i> )
Move to a different site in the current <b>Video Display</b>	Video Display Window – Click the desired site in video display window. (See <i>Figure 5.14</i> .)
Window (See Figure 5.14.)	The site moves so that the video crosshair are centered on the chosen location.

Movement Required	Movement Method				
Move in increments across the sample using the <b>Video Display</b>	Arrow Buttons Positioning – Click the Fast, Medium, or Slow buttons (move extents) to change the stage movement increments. (See <i>Figure 5.13</i> .)				
Window to locate a feature or scan site.	With the cursor over the arrow button, click for one move of the distance defined by the move extents setting. Click and hold to start and continue the stage movement in increments defined by the move extents. Release to stop the stage movement.Image: Image: I				
	menu. The <b>Move Extent</b> dialog box appears in which the new speeds for each button can be entered.				
Precision positioning using the Stylus Drop-Lift	<b>Stylus Drop-Lift Positioning</b> – After the null is complete, click the <b>Stylus Drop-Lift</b> button. This changes the optics to side-view with the stylus in the down position. Click on the scan site beginning point. Repeat if necessary until the stylus is at the desired starting point of the scan.				

Table 5.11Locating a Scan Site





Video Display Window

# USING DIE GRID NAVIGATION

## Introduction

scan position.

When scanning a wafer, the *die grid navigation features* can be used to teach scan and sequence sites by die location rather than by stage coordinates.

3. Click the Stylus Drop-Lift button to null the stylus on the sample and confirm the

Die grid navigation is composed of two components: Die Grid Navigation Window; and Die Window.

The Die Grid Navigation Window presents a representation of the die positions on the wafer surface. (See the Die Grid Navigation Window in *Figure 5.15.*) The small highlighted rectangle, in the upper right quadrant of the die matrix, represents the die currently being scanned. Each time a new die is chosen, the scan is performed on the same position in that die. (See Die Window in *Figure 5.15.*)

The Die Window is designed to pinpoint the location of the feature to be scanned on each die. (See the Die Window in *Figure 5.15.*) The cursor in the rectangle represents the location on the die where the feature to be scanned resides. To move to another scan position in the die, click on the new position in the Die Window box.

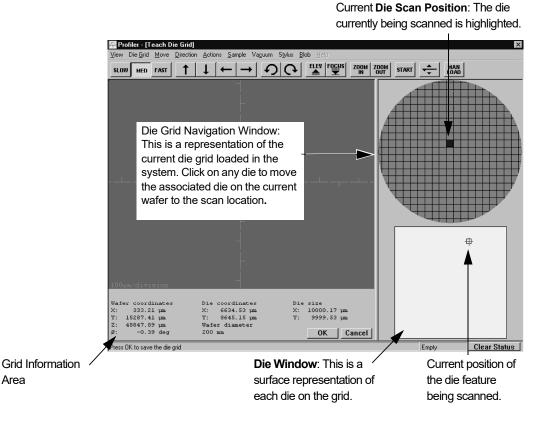


Figure 5.15 Teach Die Grid Screen with Loaded Die Grid

Once a die grid pattern is loaded, the Die Grid Navigation Window appears in the Teach Scan screen (except in calibration procedures), Teach Sequence Site screen, and Teach Blob Analysis screen.

Die Grid windows (see *Figure 5.15*) differ from standard Teach windows in three aspects:

- **Die Grid Navigation Window**—replaces the Sample Navigation Window. (See *Figure 5.2.*) Click in the desired die grid to quickly move the corresponding die into the field of view in the Video Display Window.
- **Die Window**—for positioning a feature in the field of vision within the die itself. Click in the desired region to quickly move that area of the die into the field of view.
- Grid information area—contains wafer and current die coordinates, wafer diameter, and die size.

In making it more convenient to position scans on a wafer, Die Grid Navigation provides the following options:

- Mask out the dies that are not to be measured. Masked dies appear blacked out on the Die Grid Navigation Window, providing visual reference points.
- Display the die coordinates on the Die Grid Navigation window and even change the font and size of the numbers.
- Show the partial dies on the edge of the wafer.

# **Creating a Die Grid**

#### Introduction

To use a die grid, one must be created using a sample with clearly defined identical dies, equally spaced. Once created, it can be used whenever measurements are being made on samples which are identical to the one used to make the die grid. Numerous die grids can be created, stored, and loaded as they are needed.

Wafer alignment on the sample stage is critical to the systems ability to consistently locate dies on the wafer. It must be precisely placed with it X- Y- orientation identical to that of the die grid. This can be accomplished by using a precision locator on the sample stage. The loaded die grid pattern is accurate only as long as the wafer is not moved after the initial die grid alignment procedure. This means that the vacuum must be turned on when the wafer is loaded and not turned off until the wafer is unloaded. If the wafer is moved, the die grid must be reloaded, a procedure which realigns the wafer dies with the die grid.

The die grid is created by establishing its size and position on a wafer, and identifying a unique and distinguishable feature which the system can use to locate the same position on any die.

## Teach a Die Grid

Creating a die grid is a user friendly procedure. Once the Teach Die Grid procedure is initiated, each step is prompted by a message at the bottom of the screen or next to the graphic.

1. Click on the **Scan Recipe** button at the top of the option list located at the left of the Catalog screen. (See *Figure 5.16.*)

	Ele Edit Sample	e <u>V</u> acuum Host <u>D</u> iagnostic	<u> </u>					*Onl	line/Local X
Step 1 Click on the Scan			Scan Recipe Name:						
<b>Recipe</b> button to open the list	Scan Recipe		200MM					_	×3
of available scan recipes.	( note	Recipe Path:	Recipe Name	Length (um)	Sampling Rate (Hz)	Speed (µm/s)	Creation Date (yyyy-mm-dd)	Time	450
	Scan Data	Class 2 Scans	OFF150 OFF500 STEPHTH STEPHTM 200MM	500 1600 500 500 200	50 50 50 50 200	10 50 50 50 100	2001-04-06 2001-04-06 2001-04-06 2001-04-06 2001-04-06 2001-03-24	14:16 13:38 13:40	676
	Sequence Recipe Sequence Data		SOOMM	500	200	100	2001-03-23		
			Pirel	New	v View.	/Modity	START	× v View	
	SCAN RECIPE CAT	TALOG							Clear Status Clear Status

Figure 5.16 Scan Catalog Screen

2. Click on the **Die Grid** button in the tool bar, or select **Teach Die Grid** from the **File** menu. (See *Figure 5.16.*)

The **Teach Die Grid** window appears with a warning about the automatic null feature of the Teach Die Grid procedure. (See *Figure 5.17*.)

Figure 5.17 Warning – Automatic Null



- Step 3 Click OK to continue.
  - 3. Click **OK** to continue with the procedure. (See *Figure 5.17*.)

4. In the **Teach Die Grid** screen, the procedure is prompted from the message display area at the bottom left of the screen. (See *Figure 5.18*.)

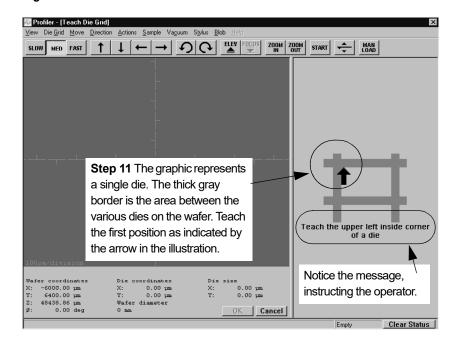
Figure 5.18 Teach Die Grid Screen

View Die Grid Move [	≥irection Actions §ample Vagi	uum Stylus Blob Help		
SLOW HED FAST	$\uparrow  \downarrow  \leftarrow  \rightarrow $	<b>り ( ) ( ) ( )</b>	N OUT START	LOAD
i i				
100um/division				
Wafer coordinates	Die coordinates	Die size		
X: 0.00 128 Y: 0.00 128	X: 0.00 1m Y: 0.00 1m	X: 0.00 12m Y: 0.00 12m		
2: 0.00 µm	Wafer diameter 0 mm		OK Cancel	
g: 0.00 deg				

**Step 4** The message prompt, here under the graphic, informs the operator of procedures as they occur and operator requirements.

Notice in *Figure 5.18* that the message prompt tells the operator to place a specific sized wafer on the stage and then click on OK. The system is configured to run a specific sized wafer. It is important that only that size wafer be used.

- 5. Obtain the wafer to be used in the teach die grid procedure
- 6. Click MAN LOAD to move the stage to the door.
- 7. Open the door and load the wafer onto the precision locator. (If there is no precision locator, have one installed before continuing with this procedure.)
- 8. Turn **ON** the vacuum using the switch located at the left inside edge of the door.
- 9. Close the door and click **MAN LOAD** to send the stage back under the measurement head.



10. Click on **OK** when all variables are correct.

Figure 5.19 Teach Die Grid - Teach First Position

- 11. Teach the upper left inside corner of the die: (follow the instructions on the screen)
  - Position the die image using the arrow buttons so that the upper left corner of the die is in the field of view.
  - Position the mouse cursor at the left inside corner of the die, as indicated in the *Figure 5.19* illustration, and click.

Step 12 Use the arrow buttons to locate a distinct feature. Use the

small or too large.

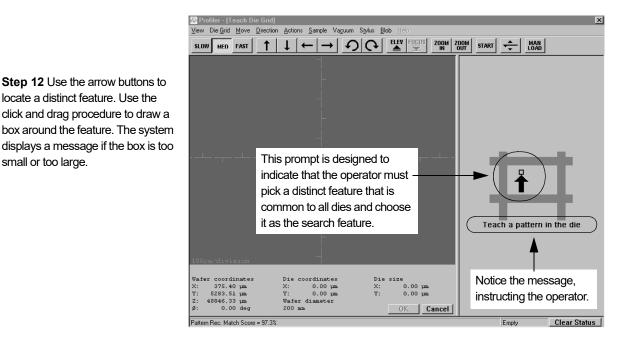
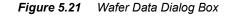


Figure 5.20 Teach Die Grid - Teach Feature

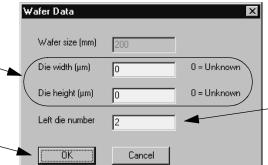
- 12. Teach a pattern in the die:
  - Using the arrow buttons, locate a feature that is present in every die. The pattern should be distinct from other nearby features.
  - Click and drag to draw a box around the feature. Start at the upper left corner and drag across the feature so that it is centered in the box when the mouse button is released.

The instrument centers the pattern in the image crosshairs twice. The Wafer Data dialog box appears. (See Figure 5.21):



Step 13 If the exact die size is known, highlight the variable box for each dimension and enter the value. Leave it 0 if the system is required to determine the size.

Step 14 When all variables have been set, click OK to continue.



This number represents the distance from the left wafer edge that the dies start. The distance is measured in full die widths, in this case, 2.

- 13. Verify and correct the wafer data and type in die width and height if known.
  - To *teach* the die size, leave **Die width** and **Die height** at **0**.
  - Left die number tells the instrument how far from the left edge to set its reference point. The value indicates the reference distance in the number of full die widths from the edge.
- 14. After making any required adjustments, click OK.

If the die width and height were not entered, the instrument continues to the third position in the Teach Die Grid sequence:

 Figure 5.22
 Teach Die Grid - Lower Right Corner

Teach Die Grid iew Die Grid Move I	<u>D</u> irection <u>A</u> ctions <u>S</u> ample Va <u>c</u> uum Stylus <u>B</u> lob <u>H</u> elp	*Online/Local
SLOW MED FAST		MAN LOAD
	-	
		in the second second
	Step 45 Line the arrow buttons	
	Step 15 Use the arrow buttons to move the field of view to the	
	lower right corner of the die and	h the lower right outside
	click on the outside corner.	corner of a die
afer coordinates 282.81 µm	Die coordinates Die size X: 0.00 µm X: 0.00 µm Notice	e the message,
: 2556.24 µm : 46340.73 µm : 0.00 deg	1: 0.00 µma 1: 0.00 µma	cting the operator.
		Clear State

- 15. Use the arrow buttons to move the die image so the lower right outside corner of the die is visible. Move the mouse cursor to the lower right outside corner of the die and click on it to teach the position.
  - The stage moves to various dies on the wafer, locating the pattern taught in **Step 12** The taught image appears in the navigation window with a comment underneath it that advises the operator which die is being checked. (See *Figure 5.23*.)

두 Pro	filer - [T	each D	ie Grid]															×
⊻iew	Die <u>G</u> rid	<u>M</u> ove	<u>D</u> irection	Action	ıs <u>S</u> am	nple Va	i <u>c</u> uum 9	6 <u>t</u> ylus <u>B</u>	lob <u>H</u> el	p								
SLOW	MED	FAST	1	1 [	←	<b>→</b>	Ð	G	ELEY	FOCUS	ZOOM IN	ZOOM OUT	START	* *	MAN			
		-	]		50	),	1		-			мо	Ci	omput	ing the patterr adjace	e die n loc	e size cation i	
												ll tł	ne na	aviga	re app ation w text e	win	dow,	g
	coord:			Die - X:		.nates 00 µm		Die X:	size 9976	5.37 <u>um</u>		tł	ne cu	irren	t syst	em	ı	
Y:	5287.8	вµш		Υ:		00 µm		Y:		5.55 µm		a	ctivit	y.				
Ø:		9 deg		200 1					01		ancel							
To abor	rt nulling p	ress <ap< td=""><td>acebar&gt; or</td><td>click m</td><td>ouse bu</td><th>itton!</th><td></td><td></td><td></td><td></td><td></td><td></td><td></td><td>Empty</td><td>,</td><td></td><td>Clear St</td><td>atus</td></ap<>	acebar> or	click m	ouse bu	itton!								Empty	,		Clear St	atus

Figure 5.23 Teach Die Grid - With Feature in Navigation Window

16. When the system completes its check, the die grid is applied. The Teach Die Grid screen changes its die grid navigation window to reflect the current die grid configuration on the wafer. (See *Figure 5.24*.) The taught die appears in dark blue. The operator is prompted to click **OK** to save the die grid.

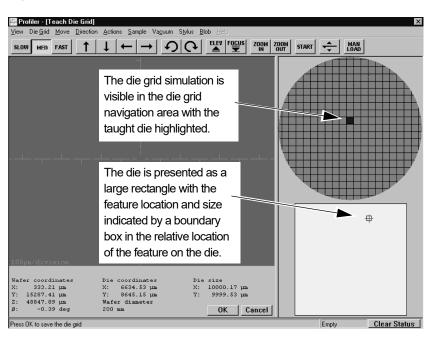


Figure 5.24 Teach Die Grid - Die Grid Simulation in Navigation Window

At the bottom of the die grid navigation window is a representation of the die grid, which appears as a bounded white rectangle. The taught feature is pictured a small bounded box appearing in its relative position in the die. This makes it easier for the operator to locate the feature if a visual search is necessary.

17. Click **OK** (bottom center of the screen) to save the die grid.

A save dialog box appears. (See *Figure 5.25*.)

Figure 5.25 Save Die Grid As Dialog Box

Save Die Grid As ? X - 🗈 💣 🚟 🏢 Save in: 🗟 diegrid 🔊 N-H-Ld.die 🔊 amat.die 🔊 diegrid. die 🔊 stagemap.die Step 21 After 🔊 INTC-Resist.die 🔊 thinfilm.die completing Step 🔊 INTC-SiGe.die 🔊 INTC-W.die 18 - Step 20, 🔊 Marcus.die click on Save. File <u>name</u>: <u>S</u>ave Save as type: Data files (\*.die) • Cancel

- 18. Choose the drive and directory for storage of the die grid file. (See *Figure 5.25*.)
- **19**. Ensure that the proper file format is chosen for saving the die grid file. Click on the **Save As Type:** menu arrow to display its menu and choose the required format from the menu. (See *Figure 5.25*.)
- 20. Type a name for the die grid in the File name: variable box. (See Figure 5.25.)
- 21. Click on Save. (See Figure 5.25.)

The extension **\*.die** is supplied automatically. Die Grid Navigation is enabled with the new die grid applied. *Using Die Grid Navigation* on page 5-19 describes how to use Die Grid Navigation with sequences.

# Loading a Die Grid (Turning ON Die Grid Navigation) for a Single Scan

1. Ensure that the wafer is in place on the stage. It must have the same pattern as that of the die grid being loaded.



**CAUTION:** It is very important that the wafer is placed in the same orientation that the die grid was taught. If not, the system cannot find the dies. Use a precision locator to place the wafer in the proper orientation.

2. In the XY View, Scan Editor, or Sequence Editor windows, click on Die Grid from the menu bar. (See *Figure 5.26*.)

where the die grid is to be saved by clicking in the down arrow and selecting the appropriate directory.

Step 18 Choose the location

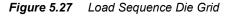
**Step 20** Type in the name of the new die grid.

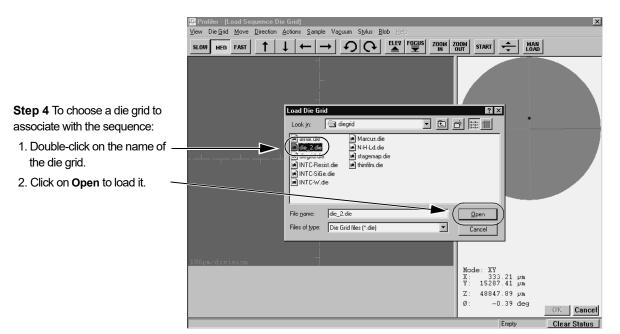
**Step 19** Choose the format for the die grid to be saved in by clicking the down arrow and choosing the appropriate format. It should be Data files (\*.die).

Step 2 Click on Die Grid	Profiles - (Sergence Editor - "UNTITI-Encel Segunce Editor - "UNTITI-Encel Segunce Edit - Serge Vacuum - Segs     Definit     provide Des.
to display its menu.	Son Recip Catalog December 1 Date Annual Catalog Catalog December 1 Date Annual Catalog Catalog December 1 Date X Y Theta X-Off Y-Off
Step 3 Click on Load to display the Load Die Grid dialog box.	Brownen     Add3>       Brownen     Add3>       Brownen     Darone Arg Le       Corresto     Corresto       Sonter     Darone Arg Le       Corresto     Corresto       Sonter     Corresto       Mode     Node       Mode     Corresto       Mode     Corresto <tr< td=""></tr<>
	Clear Status Clear Status

Figure 5.26 Sequence Editor with Die Grid Menu

- 3. Click on Load to display the Load Die Grid dialog box. (See *Figure 5.27*.)
- 4. In the Load Die Grid dialog box, double-click on the name of the die grid to be used. This displays die grid name in the File Name display box.





5. Click on **Open** to load the die grid.

The system nulls the stylus and begins to search for the pattern that is displayed on the right side of the screen. After it successfully locates the test pattern, the die grid is loaded.

Die Grid navigation is now active and the die grid selected is applied.

# Clearing a Die Grid (Turn OFF Die Grid Navigation)

- 1. Go to the Teach Scan window.
- 2. Click the Die Grid menu, and select Clear Die Grid. (See Figure 5.28.)

Figure 5.28 Die Grid Menu From the Menu Bar



Standard navigation is active again.

# Navigating Across the Wafer Using the Die Grid

- 1. Load a die grid using the procedure in *Loading a Die Grid (Turning ON Die Grid Navigation) for a Single Scan* on page 5-28)
- 2. Die Grid Navigation uses the representation of the sample that appears in the Sample Navigation Grid at the right of the XY View screen. To move the to a specific die, click on its location. The system moves the stage to that die and focuses on the feature. The feature's position is indicated in the die representation below the Sample Navigation Grid.

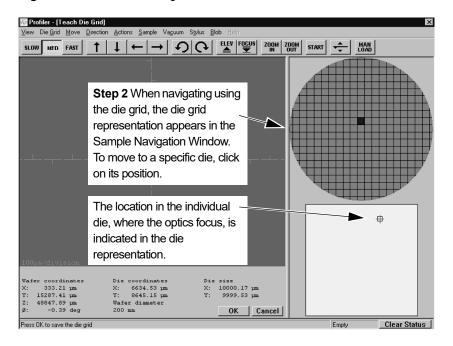


Figure 5.29 Die Grid Navigation

# **Enabling the Dropout Die Option**

Go to the **Teach Scan** window, and press the **SHIFT** key while clicking the dies in the Die Grid Navigation Window that are to be dropped out. These dies are not scanned.

The die is blacked out. To restore a dropped out die, click it again.

# **Clearing Dropout Dies From the Grid**

From the **Die Grid** menu, click on **Clear Drop Out Dies**. The dies are restored to availability for scan purposes.

## Moving to Partial Dies

- 1. From the Die Grid menu select Enable Partial Die to enable the Partial Die option.
- 2. Go to the **Teach** window, click on **Die Grid**, then click on **Move To Partial Dies**. (See *Figure 5.28*.)
- 3. In the Die Grid Navigation Window, click on the partial die to navigate to it.

# Displaying Grid Numbers in the Die Grid Navigation Window

From a **Teach Scan/Site** window, click on **Die Grid**, then click on **Display Numbers**. (See *Figure 5.28*.)

If the numbers are too small to see, increase the size of the Die Grid Navigation Window by clicking and dragging the window's vertical separator bar to the left.

# To Change the Font and Color of the Grid Numbers

- 1. Go to a **Teach Scan/Site** window, click on **Die Grid**, click on **Font**. A standard font dialog box appears.
- 2. Select the font attributes desired and click **OK**.

# USING BLOB ANALYSIS (CENTER OBJECT SEARCH)

## Introduction

Blob, or Center Object Search, locates features by their mass distribution (general shape), which might not be apparent from the two-dimensional video image. To use Center Object Search, first store the image of the object by teaching it. The instrument compares the stored image with features within its search area, looking for a similar mass distribution. When the instrument finds a similar object, it positions the scan, orienting the center of the scan line or scan area (3D) with the center of the object.

Center Object Search works best with features that are rounded or conical.

# **Starting Blob Analysis**

1. With the object in question displayed in the XY View video screen click on View to display its menu.

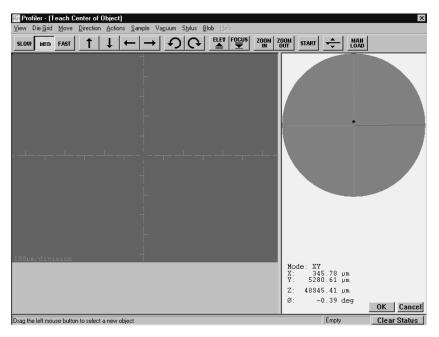
	· · · · · · · · · · · · · · · · · · ·	( .8 )
	Figure 5.30 XY View Screen – View Menu	
Step 1 Click on View to Display its Menu.	Or Profiler - (Teach Center of Object)       Yewn Die Grid Move Direction Actions Sample Vaguum Stylus Blob Hoto       Focus       Yideo Controls       Same Image To File       Profilera	*Online/Local X
Step 2 Choose Display Center Object View from the View menu.		
	Locator Taught X = 0.000µm. Y = 0.000µm	0.00 pm           Y:         0.00 pm           Z:         0.00 pm           Ø:         0.00 deg           Zoon:         0.00           OK         Cencel           Clear Status         Clear Status

2. Select Display Center Object View from the View menu. (See *Figure 5.31*)

The Teach Center Object window appears. (See Figure 5.31)

3. In the Video Display, locate the object to be scanned.

Figure 5.31 Teach Center Object Window



4. Click and drag the cursor box around the object, placing its center dot on the object's center of mass.

The instrument positions the object in the center of the video image.

The instrument uses pattern recognition to analyze the object. The object's pattern is stored with the recipe and made available each time the recipe is used with Display Center Object View checked.

If the instrument is having trouble finding the object, it might help to edit the binarization threshold, that is, change the level of contrast the instrument uses in recognizing the object. (See *Changing the Level of Contrast* on page 5-34.)

## **Changing the Level of Contrast**

1. Click the **Blob** menu and select **Edit Binarization Thresholds**. (See *Figure 5.32* and *Table 5.9 on page 5-9*.)

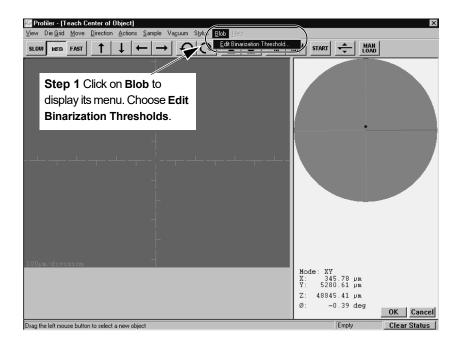


Figure 5.32 Teach Center of Object Screen

The Select Object Type dialog box appears. (See *Figure 5.33*):

Figure 5.33 Select Object Type Dialog Box

hoose Object Type	×
C Light Object	]
Threshold: 240	
O Dark Object	]
Threshold: 60	
OK Cancel	

• If **Dark Object** is selected, raise the threshold.

A threshold of **0** accepts only objects of very high contrast—black objects against a white background. The highest threshold, **256**, accepts a very low contrast object—gray object against a lighter background.

• If Light Object is selected, lower the threshold.

A threshold of **0** in this case recognizes very low contrast objects—gray objects against a darker background. A threshold of **256** recognizes high contrast objects—very bright objects against a very dark background.

2. Click **OK** to accept the settings and close the dialog box.

# ALIGNING THE SAMPLE

## Introduction

This procedure aligns the sample image with the X-axis of the view screen using a straight feature on the sample. Two methods for accomplishing this, each of which rotate the stage (theta movement) to accomplish the alignment, are detailed in the following sections. With the sample features aligned with the X-axis, more accurate scans can be taken and die grid navigation is more accurate.

## Procedure

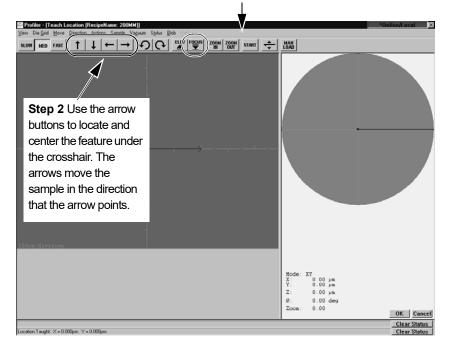
#### Aligning the Sample with the Instrument

This procedure assumes that the sample is already on the sample stage and ready for alignment. The sample must have a straight, easily discernible feature that can be used to aligned the sample features with the X-axis of the XY view screen.

1. Click on the **FOCUS** button in the tool bar. The stylus nulls on the sample surface and the sample image comes into focus.

Figure 5.34 Arrow Button Movement - Scan Offset Calibration

Step 1 Click on the FOCUS button to lower the head and focus on the sample.



2. Using the linear movement arrow buttons, locate the center of the feature to be used for alignment. (See *Figure 5.34*.)



**CAUTION:** It is very important that the chosen feature be such that it lies in a straight line across the X-axis of the sample. A thin line is best for use in the alignment procedure.

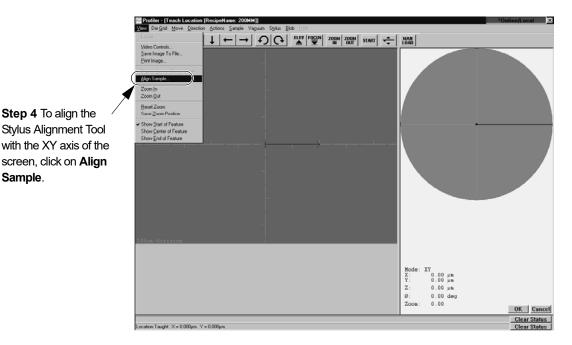


NOTE: The arrows move the stage not the optics.

**3**. Use the arrow buttons to approximately center the screen crosshair in the center of the feature. (Or, move the cursor to the center of the feature and click. This should move the crosshair to that location.)

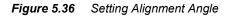
Sample.

4. Click on View in the tool bar to display its menu. In the menu, click on Align Sample. (See *Figure 5.35*.) This sets up the Alignment Sample procedure which aligns the XY axis of the screen with the chosen feature.



Align Sample Procedure - Scan Offset Calibration Figure 5.35

5. A dialog box appears requesting input of the intended alignment angle. The default is **0** which aligns the feature with the X-axis after the procedure is complete. Click on **OK** in the dialog box to accept the **0** value. (See *Figure 5.36*.)



Step 5 Click on OK to accept the "0" angle alignment.	Alignment Angle			
	Alignment Angle:	Degrees		
	ОК	Cancel Help		

- 6. Using the **right** arrow button  $(\rightarrow)$ , scroll across the feature to the left portion of the feature. Stay close to the feature, and stop when a reasonable distance has been covered (or at the end of the feature if it is small).
- 7. Place the crosshair cursor on a portion of the feature that is easily duplicated at its other end and click with the left mouse button. The system performs adjustments which align the screen crosshair to the feature at the point of contact.

- 8. The message prompt displays at the bottom left of the screen, "**Press OK to** accept the first alignment position." Click **OK**, at the bottom right of the screen, to accept the first alignment position.
- 9. Using the left arrow button (←), scroll across the center of the feature (starting point). Stay close to the feature, and stop when the sample has move a significant enough distance to give the software a long interval over which to align the sample with the X-axis. Place the crosshair cursor over the same portion of the feature that was used to set the first position and click with the left mouse button. The system performs final adjustments, aligning the feature with the XY axis.
- 10. The message prompt displays "**Press OK to accept the second alignment position**." Click **OK**, at the bottom right of the screen, to accept the second alignment position.
- 11. After the adjustments have been completed by the system, the message prompt at the bottom of the screen indicates that the **OK** button must be clicked to accept the new alignment adjustment. Click **OK** (bottom right of screen) to accept or click **Cancel** to run a new alignment angle calculation.

This completes the Align Sample procedure.

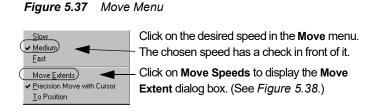
#### **Manual Alignment of the Sample**

The sample can be aligned manually using the XY view screen in conjunction with the theta (rotational) movement arrow buttons on the tool bar.

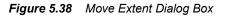
- 1. Follow Step 1 through Step 3 in Aligning the Sample with the Instrument.
- 2. Use the theta movement arrows in the tool bar (in conjunction with the other arrow buttons as necessary) to rotate the chosen feature until it aligns with the X-axis on the XY view screen.
  - a. Click the **D** button for counterclockwise rotation.
  - b. Click the 🖸 button for clockwise rotation.

The Theta movement buttons may rotate the image past the point required to align the sample features with the X-axis. If this happens, the following adjustments to the theta movement can be made:

 Check the Speed Setting in the Move menu. In the tool bar at the top of the XY view screen, click on MOVE to display the menu. (See *Figure 5.37.*) Three speeds (which are actually movement increments) are available: Slow, Medium and Fast. If the image always rotates past the X-axis, refine the movement by moving to the next slower movement. If the Slow setting still does not allow alignment, move to step *ii*.



ii. The amount of rotation in the theta arrow buttons is set in degrees in the **Move Extents** dialog box with each setting (**Slow, Medium,** or **Fast**) having its own rotation in degrees.



There are three movement				
speeds available in the <b>Move</b>				
menu. All three are defined in the				
Move Extents dialog box. For				
each 100 μm the stage moves 1°.	_			

EXAMPLE: In the **Fast Move Extent** box is set to 300. This means a 3° movement with each click on a theta arrow.

Move Extent			x
Slow Move Extent:	×/Υ <b>1</b> μm	Theta 1 degr.	OK
Medium Move Extent:	100 µm	2 degr.	Cancel
Fast Move Extent:	300 µm	5 degr.	

Check the **Slow Move Extent** box and set it as low as **0.01**. Click on **OK** to set the new speed.

iii. In the XY view screen, click on Move and choose Slow. (See *Figure 5.37.*) The theta movement should now be small enough for proper alignment.

# **VIEW SCAN WINDOW**

# INTRODUCTION

#### This chapter describes:

- 2D Screen Function on page 6-1
- 2D Screen Function on page 6-1
- *3D Screen Function* on page 6-10
- Show Measurement Site During Sequence Run on page 6-21
- *Aborting A Scan* on page 6-23

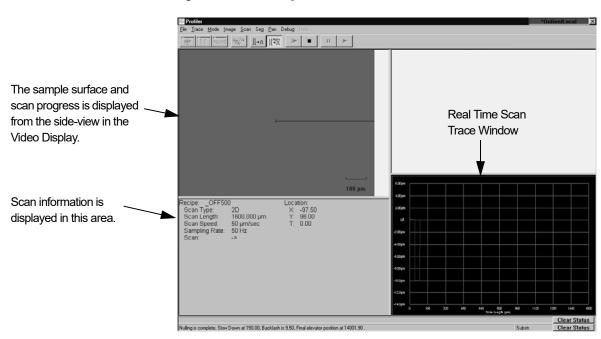
# **2D SCREEN FUNCTION**

The **View Scan Window** appears while a scan is being run. It allows the user to observe the progress of the scan and to adjust scan parameters in the various screens for optimum scan results. The scan can be started once the recipe has been chosen and the sample loaded onto the sample stage. The scan can be started from several places. The most common two starting points are:

- With the required recipe chosen, click on **START** in the Scan Recipe screen.
- From the Scan Recipe screen, click on the XY icon. From the XY screen click on **START**.

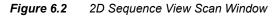
Click **START** to begin the scan. The View Scan screen appears. (See *Figure 6.1*.)

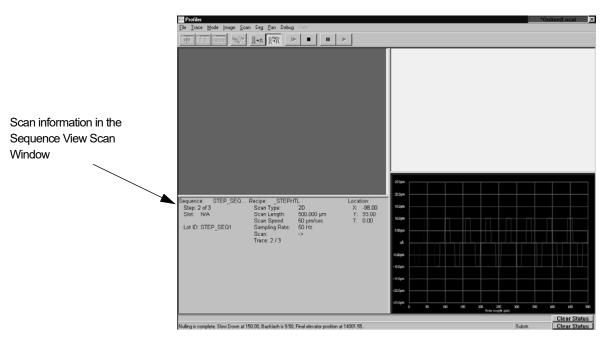
The head lowers bringing the stylus into contact with the sample at the start-of-scan position. The scan begins, first briefly traveling *opposite* the scan direction, then reversing. This allows the mechanical instruments to settle down and the stage to reach the programmed scan speed before data collection begins. The View Scan window appears and the scan begins. The video image freezes during the scan and the Real Time Scan view in the lower right corner displays the data in real time as it is collected. (See *Figure 6.1*). When the scan is finished, the data is automatically displayed in the **Analysis** window.



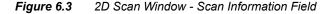
*Figure 6.1* 2D Single Scan View Scan Window

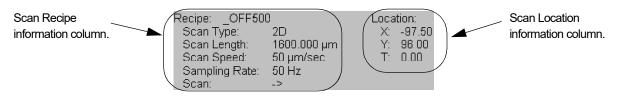
Two columns of information are presented in the lower left quadrant of the 2D scan screen (*Figure 6.1*) and three columns in the 2D sequence screen (*Figure 6.2*).





## 2D Scan Information Field





#### **2D Recipe Column**

The first column in the 2D Scan Information Field is the Recipe column. It contains the scan recipe name and some of the critical determining recipe parameters. *Table 6.1* presents a brief description of each parameter.

 Table 6.1
 Scan Screen - Recipe Information Column

Parameter	Description		
Recipe	Gives the name of the recipe being used to create the scan. If the name is followed by "" then it is truncated.		
Scan Type	The type of scan being produced, 2D or 3D.		
Scan Length	The length of the scan on the X-axis direction.		
Scan Speed	How fast the stage moves during the data gathering portion of the scan.		
Sampling Rate	The number of data points being collected per second during the scan.		
Scan	The direction in which the scan is being performed> is in the positive direction, and <- is in the negative direction.		

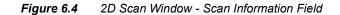
#### Scan Information Field - 2D Location Column

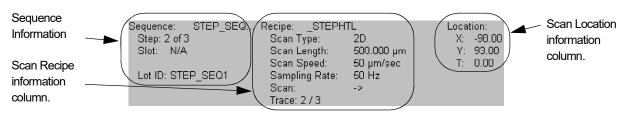
The second column in the Scan Information field is the Location column. It contains the coordinates and orientation of the scan starting point. *Table 6.2* presents a brief description of each parameter.

 Table 6.2
 View Scan Screen - 2D Location Information Column

Parameter	Description		
Х	The X coordinate of the scan origination point		
Υ	The Y coordinate of the scan origination point		
Т	The rotational value of the sample at the scan origination point.		

## Scan Information Field - 2D Sequence Recipe Column





#### **2D Sequence Column**

The first column in the Scan Information field is the **Sequence** column. It contains the information regarding the sequence being used in the scan. *Table 6.3* presents a brief description of each parameter.

Table 6.3	View Scan Screen - 2D Location Information Column

Parameter	Description
Sequence	The Sequence Recipe Name
Step	Shows which step of the total number of step the system is currently performing.
Slot	N/A – No handler for P-15.
Lot ID	The name of the sample lot. This is assigned by the operator or the system defaults to Recipe Name. (See <i>Table 7.7 on page 7-11.</i> )

### **2D Recipe Column**

The second column in the Scan Information Field is the **Recipe** column. It contains the scan recipe name and some of the critical determining recipe parameters. *Table 6.1* presents a brief description of each parameter.

 Table 6.4
 Scan Screen - Recipe Information Column

Parameter	Description
Recipe	Gives the name of the recipe being used to create the scan. If the name is followed by "" then it is truncated.
Scan Type	The type of scan being produced, 2D or 3D.

Parameter	Description
Scan Length	The length of the scan on the X-axis direction.
Scan Speed	How fast the stage moves during the data gathering portion of the scan.
Sampling Rate	The number of data points being collected per second during the scan.
Scan	The direction in which the scan is being performed> is in the positive direction, and <- is in the negative direction.
Trace	The current trace in the sequence.

 Table 6.4
 Scan Screen - Recipe Information Column

#### **2D** Location Column

The second column in the Scan Information field is the **Location** column. It contains the coordinates and orientation of the scan starting point. *Table 6.2* presents a brief description of each parameter.

 Table 6.5
 View Scan Screen - 2D Location Information Column

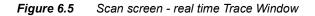
Parameter	Description
x	The X coordinate of the scan origination point for the current scan in the sequence.
Y	The Y coordinate of the scan origination point for the current scan in the sequence.
Т	The rotational value of the sample at the scan origination point for the current scan in the sequence.

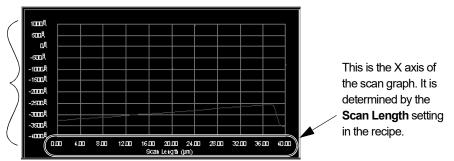
## Video Image

The upper left quadrant of the screen displays a side-view of the scan as it progresses across the sample surface. A trace arrow in the top-down view, visible with its origin at the crosshair of image, marks the course of the scan. (See *Figure 6.1 on page 6-2.*)

## **Real Time Scan Trace Window**

This window presents a real time trace of the scan. (See *Figure 6.5.*) A 2D scan can be set up for multi-scan averaging which causes the system to scan the same location as many times as the set parameter requires. Each subsequent scan's trace appears in a different color in the window using a four color rotation. At the end of the scan, the traces are averaged by the system and the result presented in the Analysis screen.





This is the Y axis of the scan graph. It is set by system to capture the height and depth of sample surface features.

In the Real Time trace window the height/depth of the features relative to the surface is presented as a trace across the graph. The graph's **Y** coordinates are set by the system and displayed in a scale that is appropriate for displaying scan features. The X-axis scale is determined by the scan length set in the scan recipe. (See *Figure 6.5.*)

## 2D View Scan Screen Tool Bar

The tool bar buttons are provided for convenience. Many of their functions are duplicated from other screen menu items in the menu bar. *Table 6.6* presents a brief description of the function of each button.

Use the buttons to customize the appearance of the Real Time view. Note that while the scan is still **Live** (not saved), the XY view, Analysis Window, Recipe Editor and Scan View screen can all be toggled between so parameters can be readjusted to improve the scan. The first buttons in the following table open the various screens. All the buttons are located in the tool bar at the top of the View Screen. (See *Figure 6.8* and *Table 6.1*.)



**NOTE:** During the scan, the buttons are grayed out and cannot be accessed until the scan is complete. Only the **STOP** icon is active.

Button	Description
	XY View Screen Icon – Changes to view the XY View screen.
	Analysis Screen Icon – Changes screens to view the Analysis screen.
RECIPE	<b>Recipe Editor Screen Icon</b> – Changes screens to view the Recipe Editor Screen
∭→л	<b>Manual Scaling</b> – Resizes the trace to fit in the graph. Requires operator initiation.
][ <sup>Auto</sup>  →Л	Auto Scaling – Automatically resizes the trace after each scan.
	<b>START SCAN</b> – Starts a stopped scan. The scan that was stopped begins again from the start, the prior partial scan is not retained.
•	<b>STOP SCAN</b> – Stops a scan that is in process. A stopped scan cannot be started again from the place in the scan where it stopped. The scan begins again from the beginning.
Ш	<b>PAUSE SEQUENCE</b> – N/A for single scans.
•	START/RESUME SEQUENCE – N/A for single scans.

 Table 6.6
 2D View Scan Window Tool Bar Buttons

## 2D View Scan Screen Menu Bar

The menu bar contains those functions that are related to the activities required in the View Scan Screen. Some of the functions are duplicated in the tool bar. (See *Figure 6.6.*) Each menu is discussed in its own table.

File	Trace	Mode	Image	Scan	Sea	Pan	Debug
<u>_ nv</u>	T.900	10000	Junaão	200			- obag

File Menu	Description of Menu Items		
	Oscilloscope – Not available with P-series systems.		
Eile Oscilloscope XY View Analysis Edit Recipe Exit Scan	XY View – Returns to the XY View screen. If the scan was stopped in the View Scan screen, and the File/XY View menu item was used to toggle to the XY view screen, the scan start position can be adjusted. The user then toggles back to the View Scan screen from the Actions/View Scan menu item in the XY View screen, and the scan can be run again in the new location.		
	<ul> <li>Analysis – Returns to the Analysis screen with the current data displayed.</li> <li>If the scan is stopped by the user, the user can toggle to the Analysis screen by using the File/Analysis menu item.</li> <li>If the user returns to the View Scan screen from the Analysis screen to start a stopped scan, when the scan is complete, the screen does not automatically return to the Analysis screen. To return to the Analysis screen, use the File/Analysis menu item.</li> </ul>		
	<ul> <li>Edit Recipe – Opens the Recipe screen for the current scan.</li> <li>If the user stops a scan and wants to edit the scan recipe, the Recipe Editor can be opened using the File/Edit Recipe menu item.</li> </ul>		
	Exit Scan – Closes the current screen.		

 Table 6.7
 2D View Scan Screen - File Menu

 Table 6.8
 2D View Scan Screen - Trace Menu

Trace Menu	Description of Menu Items	
<u>I</u> race Rescale	<b>Rescale</b> – Resizes the trace to fit in the graph. Requires operator initiation.	
✓ Auto Scale	Auto Scale – Scales the trace as it is being created.	
AC/DC	AC/DC – Grayed out - Not available.	

Table 6.9 2D View Scan Screen - Mode Menu

Mode Menu	Description of Menu Items
<u>M</u> ode ✓ <u>B</u> ackground Subtraction	<b>Background Subtraction</b> – appears active but is not available for use with the P-15 system.

Image Menu	Description of Menu Items
Image	<b>Zoom In</b> – Not available in the P-series systems.
Zoom In	Center Anchor – Not available for single 2D scans.
Center Anchor     Corner Anchor     Edit Scan Parameters	Corner Anchor – Not available for single 2D scans.
	Edit Scan Parameters – Use the File/Recipe menu item for this function.

 Table 6.10
 2D View Scan Screen - Image Menu

 Table 6.11
 2D View Scan Screen - Scan Menu

Scan Menu	Description of Menu Items
Scan Start St <u>o</u> p	<b>Start</b> – Starts the scan after it has been stopped mid process. This is the same as the START button in the tool bar. The grayed out option is the currently active one. In the illustration, the scan has been started, only stopping can be performed.
	<b>Stop</b> – Stops the scan during a scan without canceling the procedure. The scan can be started all over again, but not from the point in the scan where it was halted.

 Table 6.12
 2D View Scan Screen - Sequence Menu

Sequence Menu	Description of Menu Items
Seg	Pause – Used in Scan Sequences only.
Pause	Resume – Used in Scan Sequences only.
<u>R</u> esume	

Pan Menu	Description of Menu Items
<u>P</u> an Slow	<b>Slow</b> – Small size stage movement increments. The Slow movement is defined in the Move Speeds dialog box.
✓ <u>M</u> edium <u>F</u> ast Move Speeds	<b>Medium</b> – Medium size stage movement increments. The Medium movement is defined in the Move Speeds dialog box.
Left Right	<b>Fast</b> – Large size stage movement increments. The Fast movement is defined in the Move Speeds dialog box.
Up Down	<b>Move Speeds</b> – Opens the Dialog box to define the stage movement increments.
	Left – Not Available in the P-Series systems.
	Right – Not Available in the P-Series systems.
	<b>Up</b> – Not Available in the P-Series systems.
	<b>Down</b> – Not Available in the P-Series systems.

 Table 6.13
 2D View Scan Screen - Pan Menu

 Table 6.14
 2D View Scan Screen - Debug Menu

Debug Menu	Description of Menu Items
Debug	Switch to 2D – unavailable for this application
Switch To 2D	Switch to 3D – unavailable for this application
Switch to 3D Turn on Square Tool	Turn on Square Tool – unavailable for this application

# **3D SCREEN FUNCTION**

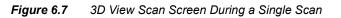
The function of the 3D View Scan screen is similar to that of the 2D screen. Some additions to the screen are made to facilitate 3D analysis and operator monitoring of the scan process. Some menu items from the Menu bar are not accessible when operating 3D sequences.

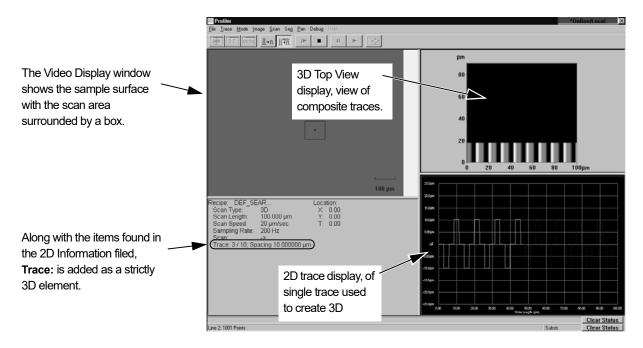
The **View Scan Window** for 3D scans appears while a scan is being run. It allows the user to observe the progress of the scan and to adjust scan parameters in the various screens for optimum scan results. The scan can be started once the recipe has been chosen and the sample loaded onto the sample stage. The scan can be started from several places. The most common two starting points are:

- With the required recipe chosen, if the user believes that the scan starting point is already set to the desired point, click on **START** in the Scan Recipe screen.
- To view the sample and align the starting point of the scan, from the Scan Recipe screen, click the XY icon. After the necessary adjustments are made to the start position in the XY View screen, click **START**.

Click START to begin the scan. The View Scan screen appears. (See Figure 6.7.)

The head lowers bringing the stylus into contact with the sample at the start-of-scan position. The scan begins, first briefly traveling *opposite* the scan direction, then reversing. This allows the mechanical instruments to settle down and the stage to reach the programmed scan speed before data collection begins. The View Scan window appears, switches to side view optics, and the scan begins. The video image shows the stylus in contact with the sample surface during the scan from the side-view perspective. The Real Time Scan graph in the lower right quadrant displays the data in a real time trace as it is collected. (See *Figure 6.7*). After each trace, the data is presented in the 3D Top View window, with each successive trace being added to the others until all traces are viewed in the window. When the scan is finished, the system performs calculations on the data and automatically displays it in the **Analysis** window.





Two columns of information are presented in the lower left quadrant of the 3D *scan* screen (*Figure 6.7*) and three columns in the 3D *sequence* screen (*Figure 6.8*).

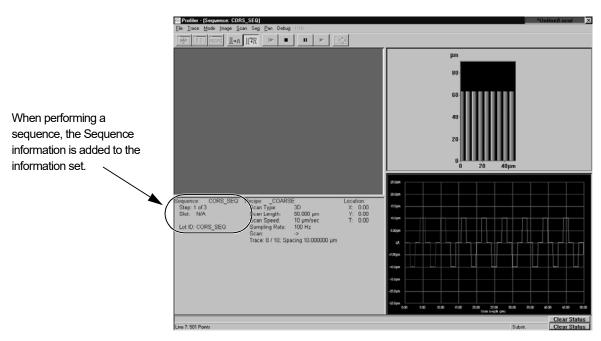
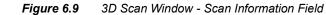


Figure 6.8 3D View Scan Screen During a Scan Sequence

## **3D Scan Information Field**



	Recipe: DEF_SE Scan Type:	AR 3D	Location: X: 0.00
The only parameter in this field that is different from the 2D field is <b>Trace:</b>	<u>Scan:</u>	100.000 μm 20 μm/sec 200 Hz >	Y: 0.00 T: 0.00
7	(Trace: 3 / 10; Sp	acing 10.000000 µr	n)

0104396-000 AA 3/05

#### **3D Scan Recipe Column**

The first column in the Scan Information Field is the scan Recipe column. It contains the scan recipe name and some of the critical determining recipe parameters. *Table 6.15* presents a brief description of each parameter. The 3D column adds **Trace** to information presented in a 2D parameter set.

 Table 6.15
 Scan Screen - Recipe Information Column

Parameter	Description
Recipe	Gives the name of the recipe being used to create the scan. If the name is followed by "" then it is truncated.
Scan Type	The type of scan being produced, 2D or 3D.
Scan Length	The length of the scan in the X direction.
Scan Speed	How fast the stage moves during the data gathering portion of the scan.
Sampling Rate	The number of data points being collected per second during the scan.
Scan	The direction in which the scan is being performed> is in the positive direction, and <- is in the negative direction.
Trace	Presents: 1) The current scan number out of the total number of scans to be completed. (2) Spacing between traces through the scan area in both proportion (showing how many traces are being made) and size.

#### **3D** Location Column

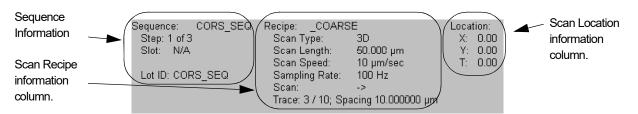
The second column in the Scan Information field is the Location column. It contains the coordinates and orientation of the scan starting point. *Table 6.16* presents a brief description of each parameter. This information is identical with that for 2D scans.

Parameter	Description
Х	The X coordinate of the scan origination point
Υ	The Y coordinate of the scan origination point
Т	The rotational value of the sample at the scan origination point.

 Table 6.16
 View Scan Screen - 3D Location Information Column

## Scan Information Field - 3D Sequence Recipe Column

Figure 6.10 3D Scan Window - Scan Information Field



#### **3D Sequence Column**

The first column in the Scan Information field is the **Sequence** column. It contains the information regarding the sequence being used in the scan. *Table 6.17* presents a brief description of each parameter.

Table 6.17 View Scan Screen - 3D Location Information Col	umn
---	-----

Parameter	Description
Sequence	The Sequence Recipe Name
Step	Shows which step out of the total number of steps the system is currently performing.
Slot	N/A – No handler for P-15.
Lot ID	The name of the sample lot. This is assigned by the operator or the system defaults to Recipe Name. (See <i>Table 7.7 on page 7-11.</i> )

#### **3D Recipe Column**

The second column in the Scan Information Field is the **Recipe** column. It contains the scan recipe name and some of the critical determining recipe parameters. *Table 6.18* presents a brief description of each parameter.

 Table 6.18
 Scan Screen - Recipe Information Column

Parameter	Description
Recipe	Gives the name of the recipe being used to create the scan. If the name is followed by "" then it is truncated.
Scan Type	The type of scan being produced, 2D or 3D.

Parameter	Description
Scan Length	The length of the scan on the X-axis direction.
Scan Speed	How fast the stage moves during the data gathering portion of the scan.
Sampling Rate	The number of data points being collected per second during the scan.
Scan	The direction in which the scan is being performed> is in the positive direction, and <- is in the negative direction.
Trace	For the current 3D scan it presents: 1) The current scan number out of the total number of scans to be completed. (2) Spacing between traces through the scan area in both proportion (showing how many traces are being made) and size.

Table 6.18 Scan Screen - Recipe Information Column

#### **3D Location Column**

The second column in the Scan Information field is the **Location** column. It contains the coordinates and orientation of the scan starting point. *Table 6.19* presents a brief description of each parameter.

Table 6.19 View Scan Screen - 2D Location Information Column

Parameter	Description
X	The X coordinate of the scan origination point for the current scan in the sequence.
Y	The Y coordinate of the scan origination point for the current scan in the sequence.
Т	The rotational value of the sample at the scan origination point for the current scan in the sequence.

## 3D View Scan Screen Tool Bar

The tool bar buttons are provided for convenience. Many of their functions are duplicated from other screen menu items in the menu bar. *Table 6.20* presents a brief description of the function of each button.

In 3D sequences most of the buttons are not active. Note that while the scan is still under way and when a sequence scan is paused, the XY view, Analysis Window, Recipe Editor and Scan View screen icons are all disabled. All the buttons are located in the tool bar at the top of the View Screen. (See *Figure 6.8* and *Table 6.20*.)



**NOTE:** During the scan, the buttons are grayed out and cannot be accessed.

Button	Description
	XY View Screen Icon – Disabled for this process.
	Analysis Screen Icon – Disabled for this process.
RECIPE	Recipe Editor Screen Icon – Disabled for this process.
][→л	<b>Manual Scaling</b> – Resizes the trace to fit in the graph. Requires operator initiation.
][→Ω	Auto Scaling – Automatically resizes the trace after each scan.
	START SCAN – Sequences: Once the STOP SCAN icon is clicked, the sequence is terminated and there is no opportunity to use this button. Not used in sequences.
	<b>Single Scans</b> : In a single 3D scan, this initiates the scan from the View Scan window. If the STOP SCAN icon is clicked, the scan is terminated an this icon is not used to restart a stopped scan.
•	<ul> <li>STOP SCAN –</li> <li>Sequences: Stops a scan sequence that is in process and returns to the Scan Catalog screen.</li> <li>Single Scans: Stop a scan that is in progress and returns to the Scan Catalog screen.</li> </ul>
н	<b>PAUSE SEQUENCE</b> – Stops a sequence that is in process. If a scan is in process when the sequence is paused, that scan is repeated when the sequence is resumed.
<b>F</b>	<b>START/RESUME SEQUENCE</b> – Starts a sequence or resumes a paused sequence. Resuming a sequence starts it from the beginning of the interrupted scan.
	<b>PAN AND ZOOM</b> – This icon is not applicable for the P-15 system.

Table 6.203D View Scan Window Tool Bar Buttons

## 3D View Scan Screen Menu Bar

The menu bar contains those functions that are related to the activities required in the View Scan Screen. Some of the functions are duplicated in the tool bar. (See *Figure 6.11.*) Each menu is discussed in its own table.

Figure 6.11	View Scan Screen Menu Bar
-------------	---------------------------

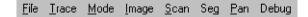


 Table 6.21
 3D View Scan Screen - File Menu

File Menu	Description of Menu Items
	<b>Oscilloscope</b> – Not available with P-series systems.
<u>File</u>	XY View – Disabled for 3D scans
<u> </u>	Analysis – Disabled for 3D scans
	Edit Recipe – Disabled for 3D scans
	Exit Scan – Disabled for 3D scans

 Table 6.22
 3D View Scan Screen - Trace Menu

Trace Menu	Description of Menu Items
<u>Irace</u> <u>R</u> escale ✓ <u>A</u> uto Scale AC/DC	<b>Rescale</b> – Resizes the trace to fit in the graph. Requires operator initiation.
	Auto Scale – Scales the trace as it is being created.
	AC/DC – Disabled.

 Table 6.23
 3D View Scan Screen - Mode Menu

Mode Menu	Description of Menu Items
<u>Mode</u> ✓ <u>B</u> ackground Subtraction	<b>Background Subtraction</b> – appears active but is not available for use with the P-15 system.

Image Menu	Description of Menu Items
Image	Zoom In – Not available in P-15 systems.
Zoom_In	Center Anchor – Not available in P-15 systems.
✓ Center Anchor	Corner Anchor – Not available in P-15 systems.
Corner Anchor	Edit Scan Parameters – Use the File/Edit Recipe menu
<u>E</u> dit Scan Parameters	items to perform this function.

 Table 6.24
 3D View Scan Screen - Image Menu

 Table 6.25
 3D View Scan Screen - Scan Menu

Scan Menu	Description of Menu Items
Scan Start Stop	Start – Sequences: The sequence is terminated when the STOP button is clicked. There is no opportunity to use this menu item.
	<b>Single Scans</b> : Starts a 3D scan from the View Scan window. Operates the same as the Start Scan icon.
	Stop –
	Sequences: Stops the sequence during a scan, canceling the sequence and returning to the Sequence Catalog screen.
	Single Scans: Stops the scan and returns to the Scan Catalog screen.

 Table 6.26
 3D View Scan Screen - Sequence Menu

Sequence Menu	Description of Menu Items
Seg Bause Besume	<b>Pause</b> – Pauses the scan sequence. The current scan is abandoned and will be started over when the Resume icon or menu item is clicked.
	<b>Resume</b> – Resumes the sequence again, initiating it at the beginning of the scan that was interrupted.

Pan Menu	Description of Menu Items
<u>P</u> an	Slow – Might appear active but is non functional.
Slow	Medium – Might appear active but is non functional.
✓ Medium Fast	Fast – Might appear active but is non functional.
 Move Speeds	<b>Move Speeds</b> – Might appear active but is non functional.
Left <u>Rig</u> ht	Left – Not Available in the P-Series systems.
Up Down	Right – Not Available in the P-Series systems.
	Up – Not Available in the P-Series systems.
	<b>Down</b> – Not Available in the P-Series systems.

 Table 6.27
 3D View Scan Screen - Pan Menu

 Table 6.28
 3D View Scan Screen - Debug Menu

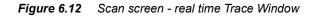
Debug Menu	Description of Menu Items
Debug	Switch to 2D – unavailable for this application
Switch To 2D	Switch to 3D – unavailable for this application
Switch to 3D Turn on Square Tool	Turn on Square Tool – unavailable for this application

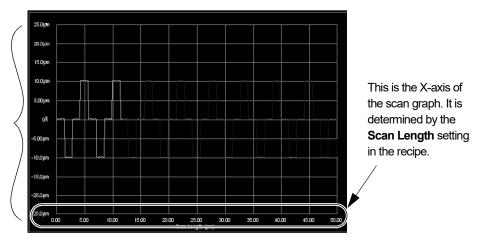
## Video Image

The upper left section of the screen displays scan image on the sample surface. (See *Figure 6.8.*) Prior to the scan, a scan boundary box surrounds the scan area in the image.

## **Real Time Scan Window**

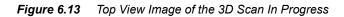
This window presents a real time trace of the scan. (See *Figure 6.12*.) In the Real Time trace window the height/depth of the features relative to the surface is presented as a trace across the graph. The graph's **Yaxis** scale is set by the system and displayed in a scale that is appropriate for the scan features. The X coordinates are determined by the scan length set in the scan recipe.



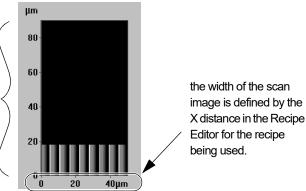


This is the Y-axis of the scan graph. It is set by system to capture the height and depth of sample surface features.

In a 3D scan each subsequent scan's trace is presented in the 3D Top View display. (See *Figure 6.13*.) At the end of the scan the system presents the results in the 3D Analysis screen.



The height of the scan image is defined by the Y distance in the Recipe Editor for the recipe being used.



# SHOW MEASUREMENT SITE DURING SEQUENCE RUN

### Introduction

During a sequence scan procedure, the user can toggle between a view of the current scan site (actually, the image contains as much of the scan site as allowed by the current magnification) on the Video screen and the Die Measurement Site Map. (See *Figure 6.14.*) To toggle between the views, use the following procedure:

- 1. In the Sequence Scan Screen, click View in the menu bar.
- 2. Choose **Toggle Video or Wafer View** to toggle between the scan site (Video) and the wafer die map (Wafer View).

When the **Show Measurement Site** is enabled, the video screen presents a frozen image of the scan start position. The **Die Measurement Site Map** contains the location(s) of the scan sites or die in which the scans take place.

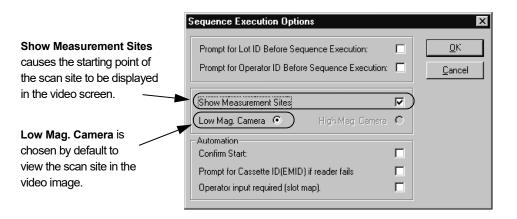
Figure 6.14 View Menu (Sequence Scan Screen)



# Configuration

The Configuration screen provides the user with the option to set the system so the video display can toggle between the measurement site image and to the video image of the scan site. This dialog box is entered through the Configuration screen button, **Sequence Execution Options**.

Figure 6.15 Sequence Execution Options



#### **Show Measurement Sites**

To activate the Show Measurement Sites option,

- 1. From the Configuration Screen, click Sequence Execution Options...
- 2. Click to put a check in the **Show Measurement Sites** checkbox. The default for this feature is that it is disabled.

When this is clicked, the Low Magnification is automatically chosen and cannot be disabled; it is the default setting. If the Show Measurement Sites is enabled, the system allows the user to toggle between the display of the measurement sites on a scan site sample image (like a wafer map), and the actual video view of the scan site.

3. Click **OK** to save the settings and close the dialog box.

#### **Camera Settings**

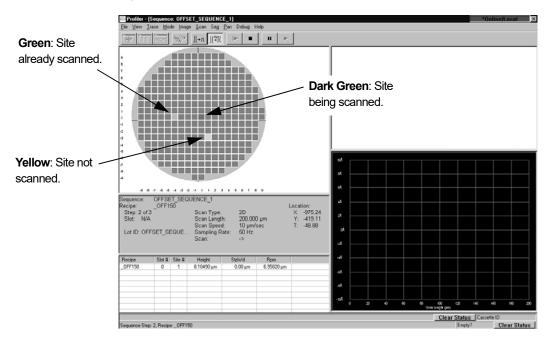
The camera setting for the P-15 system is set to low magnification by default. The view of the scan site is presented in low magnification. The view is limited by the magnification and might or might not contain the entire scan area.

## Wafer Image Display

If the Wafer Map is chosen, all of the sites that are to be scanned are visible on the wafer image. If the wafer has a die grid and the die is loaded, the wafer map looks like the die map and the entire die containing the scan site(s) is highlighted in a color. The die is color coded to represent its scan status. The colors are as follows:

- Yellow: Site waiting to be scanned
- Dark Green: Site being scanned
- Green: Site already scanned.

If the wafer is not characterized by a die grid, or the die map is not loaded, the scan sites appear as colored dots at the scan location. The color code is the same as that of the wafer having a die grid map.



*Figure 6.16* Sequence Scan Screen with Die Measurement Site Map

#### Scan Site Image Display

As the sequence progresses through each scan site, the image of the current scan site is displayed in the video screen. This is the view that alternates with the **Die Measurement Site Map** (see *Figure 6.16*) as the **View** menu options are toggled between (see *Figure 6.14*). This image is not live, but is a snap shot of the scan site start position as it appears before the scan.

# ABORTING A SCAN

Click the **Stop** button at any time to abort the scan. The scan can be started all over again, but not from where it stopped. All data from the aborted scan is lost. If a sequence is halted using the **Pause** button, and the sequence is resumed, the Analysis screen might not be displayed at the end. Click **File/Analysis** to open Analysis.

# **SEQUENCE RECIPE AND DATA (OPTIONAL)**

## INTRODUCTION

The Sequence Recipe and Data application is a system option. It must be purchased. The Pattern Recognition, which can be used with the Sequence option, must also be purchased. The Sequence application uses sequences that contain multiple scan recipes combined into one file for automatic sequence scanning. This saves time when repeatedly scanning the same location(s) on multiple samples. The Sequence Recipe and Data application consists of two parts:

- Sequence Recipe Editor to load, create, edit, and save Sequence Recipes for scanning.
- Sequence Database to load, collect, manipulate, and save data obtained from scanning.

Sequences can be created using any combination of 2D and 3D recipes. The Sequence Recipe contains information that directs the system to precisely position the sample beneath the measurement head for each measurement in the sequence of scans. Each measurement location in a sequence is called a site. The information for how to scan each site is contained in the Scan Recipe that is connected with the site in the Sequence Recipe. See *Chapter 3* for more information on creating and editing Scan Recipes.

The Sequencing feature provides the following capabilities:

- Combine a 600 sites and Scan recipes
- Set reference points for correcting translational and rotational variations between substrates (deskew)
- Re-scan portions of a long scan, using the long scan as a data reference for the subscans so their measurements correlate with each other
- Set Deskew manually or automatically using Pattern Recognition
- Set Pattern Recognition options to search locally for a match when a match is not found in the camera's field of view at deskew sites, and carry out user-selected instructions if the search fails
- Set pattern recognition to reference sites using site-by-site Pattern Recognition
- In Multi Analysis mode, apply different Scan recipes to a single scan
- Automatically display, print, export, and save statistics and trace data for all sites
- Teach scan sites and alignment reference points interactively, with or without theta
- Export the data from each wafer immediately following the wafer processing
- Choose the number of times the Sequence Recipe is run and allow the data to be saved for each run

#### This chapter describes:

- Starting the Sequence Editor Application on page 7-2
- Sequence Editor Window Features on page 7-3
- Editing the Options Field in the Sequence Editor on page 7-7
- Creating a Sequence Recipe on page 7-13
- *Running a Sequence* on page 7-29
- Correlation Scans on page 7-29
- Viewing Saved Sequence Data on page 7-31
- Using Multi Analysis In Sequence on page 7-32
- Viewing Sequence Data with the Corresponding Trace, Site-by-Site on page 7-35
- Sequencing with Manual Deskew on page 7-36
- Deskewing Twice To Align Theta on page 7-38
- Sequencing with Pattern Recognition Deskew (Pattern Recognition Option Only) on page 7-38
- Using Groping with Pattern Recognition on page 7-44
- Sequencing with Site-by-Site Pattern Recognition on page 7-48
- Saving Sequences on page 7-49
- *Saving the Sequence Data* on page 7-50
- Sequence Transportability on page 7-51
- Handler... Button Options Window For Sequencing on page 7-58
- on page 7-63

# STARTING THE SEQUENCE EDITOR APPLICATION

- 1. In the Catalog screen, if it is not already active, click the **Sequence Recipe** button.
- 2. Select a Sequence recipe to be edited.

**3**. Click the **View/Modify** button. (It is also possible to double-click on the recipe to open the Sequence Editor.

The Sequence Editor screen appears. (See Figure 7.1).

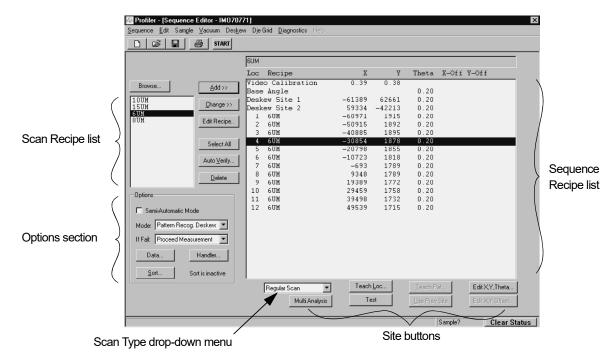


Figure 7.1 Sequence Editor Screen

## **SEQUENCE EDITOR WINDOW FEATURES**

The Sequence Editor window consists of the following elements:

- Scan recipe catalog for selecting from available Scan recipes
- Options section for setting sequence options
- Control buttons for sequence programming
- Sequence list, linking sites with Scan recipes

#### **Sequence Editor Menus**

The Sequence Editor menu bar provides access to commands through its menus. Click on the titles in the menu bar to view their menus.

## Sequence Editor Toolbar

The Sequence Editor toolbar contains buttons that provide an alternative way to access commonly used functions. (See *Table 7.1.*)

 Table 7.1
 Sequence Editor window buttons

Button	Description
	Creates a new default Sequence recipe.
Ê	Opens Sequence recipe editor for the currently chosen recipe in the sequence.
	Saves the current Sequence recipe; if the current Sequence recipe has never been saved, displays the <b>Save Sequence As</b> dialog box first.
<b>5</b>	Prints the selected Sequence recipe.
START	Starts a scan using the current Sequence recipe.

Table 7.2Sequence List Buttons

Button	Description
<u>A</u> dd >>	Adds the selected Scan recipe into the sequence.
<u>C</u> hange >>	After highlighting an existing site in the Sequence list, clicking this button changes the Scan recipe for the site to whatever is highlighted in the catalog.
Edit Recipe	Displays the Scan Recipe Editor, open to the recipe selected in the Scan recipe Catalog (the field to the left of the <b>Edit Recipe</b> button.)
Select All	This selects all the recipes in the current Sequence Recipe.
Auto ⊻erify	This goes to the XY View screen and locates the current scan location in the video screen for verification.
<u>D</u> elete	Deletes the selected site from the sequence.

Button	Description
Data	Displays the Data Saving Options dialog box where sequence data can be automatically saved, exported, or printed.
<u>S</u> ort	Displays the dialog box for the sort software option.
Handler	Displays the <b>Handler</b> dialog box. The P-15 has no handler so the only option available is <b>Manual Load</b> .

Table 7.3Options Buttons

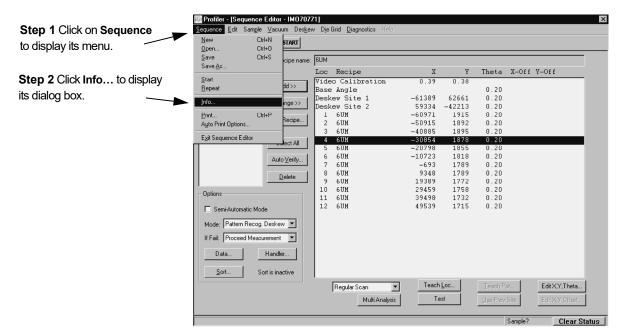
Table 7.4 Site Buttons

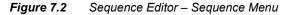
Button	Description
Teach <u>L</u> oc	Goes to the XY view so a measurement site can be chosen based on a location observed on the screen.
<u>T</u> each Pat	Goes to the XY view so a pattern can be taught for pattern recognition.
Edit X,Y,Theta	Defines a measurement site by allowing the manual entry of the X, Y, and Theta coordinates.
Multi Analysis	Defines the measurement site as a multi analysis site where analysis is performed on data from the last site with defined coordinates. Basically, uses the same raw data but with a different scan recipe.
Test	Runs only the highlighted site without running the whole sequence.
Use Prev Site	A measurement site can be set up to use the previous site's pattern for site-by-site pattern recognition.
Edit X,Y Offset	X and Y offset values can be manually entered from a pattern rec site to a measurement site.

## **Displaying the Sequence Information Dialog Box**

The Sequence Information dialog box displays the title, author, date and time of creation (or modification) of the sequence. It also provides a text box for annotations.

1. In the Sequence Editor, click the **Sequence** menu to display its menu. (See *Figure 7.2*).





2. From the Sequence Menu, select Info... (See Figure 7.2)

Figure 7.3 Sequence Information Dialog Box

	Sequence Information	×
Step 4 This field, the Comments: text box, can be used to record messages or information on the sequence listed in the dialog box heading.	Name: c:\eagle\seqrcp\CORS_SEQ User: Modified: November 21, 2000 04:51:21 PM Comments: Sequence run on sample, X-calib	
	OK Cancel	

The Sequence Information dialog box is displayed. The Name, User, and Modified fields cannot be edited.

- 3. Click in the **Comments** field, or press **TAB**← or **TAB**→ until the **Comments** text box is highlighted.
- 4. Enter the text of the information which needs to be passed from one operator to the other.

# **EDITING THE OPTIONS FIELD IN THE SEQUENCE EDITOR**

In the **Options** variable fields, sequence mode (deskew options) and data transfer options can be defined for the sequence displayed in the editor.

### Semi-Automatic

In the Sequence Editor, put a check in the **Semi-Automatic** check box to enable the mode. (See *Figure 7.4*)

For **2D** scans, the Semi-Automatic mode causes a sequence to display the trace data after each scan and pause before proceeding to the next step. Each step can be verified and, if needed, the scan sites can be adjusted and the scan performed again before proceeding to the next step.

For **3D** scans, the Semi-Automatic mode does not halt the sequence between steps.

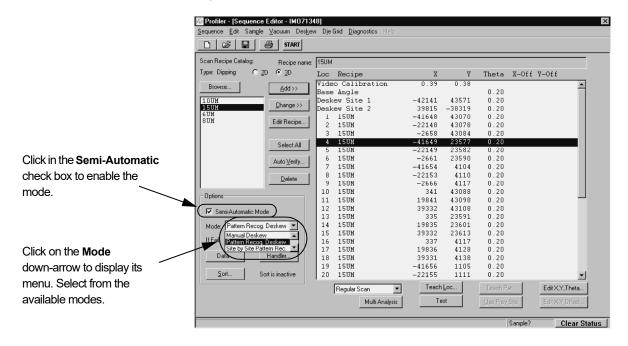


Figure 7.4 Sequence Editor – Mode Menu

## Set Deskew Mode

Click the **Mode** drop-down menu (see *Figure 7.4*), and select the from the following **Sequence** modes. (See *Table 7.5*)

 Table 7.5
 Mode Drop-down Menu Options

Mode	Description
No Deskew	The sequence contains no deskew points for alignment.
Manual Deskew	Deskew points are set and must be confirmed manually by the operator.
Pattern Rec. Deskew	Deskew points are set using the Pattern Recognition option.
Site-by-Site Pattern Recognition	Scan sites are set relative to a Pattern Recognition site and deskew is performed by pattern recognition.
Site-by-Site No Deskew	Each site is scanned without deskew.



**CAUTION:** It is important that when scanning with Pattern Recognition, use the same zoom setting for the scan that was used to capture the pattern. If zoom is used during the procedure, always zoom completely out before starting the scan. If a particular zoom setting is required, use the Zoom-lock feature to ensure that the zoom setting remains unchanged throughout the procedure.

Set Scan Status Option if Pattern Recognition Fails

1. Click the If Fail drop-down menu, and select the action to take if the pattern recognition fails to find a site. (See Table 7.6.)

F Profiler - [Sequence Editor - IM071348] X <u>S</u>equence <u>E</u>dit Sample <u>V</u>acuum Des<u>k</u>ew DjeGrid <u>D</u>iagnostics H 🗅 😂 🖬 🎒 START Recipe name: 15UM Loc Recipe Video Calibration X-Off Y-Off X Y Theta 0.39 0.38 ٠ Browse  $\underline{A}dd >>$ Base Angle Deskew Site 1 Deskew Site 2 1 15UM 2 15UM 0.20 0.20 10UM 15UM -42141 43571 <u>C</u>hange >> 39815 -41648 -22148 0.20 0.20 0.20 -38319 43070 43078 6UM 8UM Edit Recipe... 3 15UM -2658 43084 0.20 4 15UM -41649 23577 0.20 Select All 23582 23590 15UM 15UM -2214 0.20 -2661 0.20 6 Auto ⊻erify... -2661 -41654 -22153 -2666 341 19841 0.20 0.20 0.20 0.20 0.20 0.20 0.20 15UM 15UM 4104 8 9 4110 <u>D</u>elete 4117 43088 43098 15UM 15UM 10 Options 11 12 13 15UM 39332 335 19835 0.20 0.20 0.20 0.20 15UM 15UM 43108 23591 ☑ Semi-Automatic Mode Mode: Pattern Recog. Deskew 💌 14 15 15UM 23601 15UM 15UM 15UM 23613 4117 4128 0.20 0.20 0.20 0.20 39332 Proceed Measurement IF F 16 17 337 19836 Step 1 Click on the If Fail 18 19 20 15UM 15UM 39331 -41656 0.20 Skip, No Measurement Retry Pat. Rec. Manually 4138 ancel Sequence 1105 15IIM -22155 1111 0 20 • Teach <u>L</u>oc... Regular Scan • Edit X,Y,Theta... Multi Analysis Test Clear Status Sample

Sequence Editor – If Fail Menu Figure 7.5

Table 7.6	If Fail Drop-down Menu
-----------	------------------------

Feature	Description
Proceed Measurement	Continue with the next site as if the scan had worked.
Skip, No Measurement	Measurement of that wafer is suspended.
Retry Pat. Rec. Manually	Allows user to move the site into the field of view.
Find Site Manually without Pat. Rec.	Allows the user to click on the center of the pattern being used for pattern recognition and click <b>OK</b> to continue with scan without pattern recognition confirmation.
Cancel Sequence	Sequence is suspended. User must restart the sequence.

down-arrow to display its menu. Select from the available modes.

Begin: Set Data Options2. Click the Data button to choose options for data collection that automatically execute upon sequence completion.

Sequence Editor

Figure 7.6

	🔚 Profiler - [Sequence Editor - CORS_SEQ]
	Seguence Edit Sample Vacuum Deskew Die Grid Diagnostics Help
	Scan Recipe Catalog: Recipe name: COARSE
	Type: Contact C 2D C 3D Loc Recipe X Y Theta X-Off Y-Off
	Browse Add>> Video Calibration 1.50 1.50
	Base Angle NOT USED
	FIRST         Deskew Site 1         -2282         1757         0.00           COARSE         Deskew Site 2         -3046         2579         0.00
	Edit Recipe 2COARSE 0 0 0.00
	3 _COARSE 0 0 0.00 CLI-LAW 4 COARSE 0 0 0.00
	Select All 5 FIRST 0 0 0.00
	Auto Verify 6 FIRST 0 0 0.00
	Prove Tenty.
	Delete
Step 2 Click the Data	Dptions
•	Opuns
button to open the <b>Data</b>	Semi-Automatic Mode
Options dialog box.	Mode: Pattern Recog. Deskew
	If Fait Proceed Measurement
	Cata Handler
	Sort Sort is inactive
	Regular Scan 🔽 Teach Loc I each Pat Edit X/Y.Theta
	Multi Analysis Test Use Prev Site Edit X.Y Offset

The **Data Options** dialog box appears. (See *Figure 7.7.*) Once set, the Profiler automatically either exports, saves, or prints the file data.

Figure 7.7 Data Options

Print Options	×	
Save Options None Statistics only Trace Data and Statistics Use Lot ID Use Name: CORS_SEQ Path c:\eagle\seqsumm\db Use Operator ID Print Options Enable Auto Print Print: Details	Export Options None ASCII File Statistics Only Binary File Trace Data and Statistics Use Lot ID Use Name: CORS_SEQ and use lot ID for statistics name Use Operator ID OK Cancel	<b>Step 1</b> When the options have been chosen, click <b>OK</b> .

3. Choose an option from the Save, Export, and Print options. (See *Table 7.7.*)

Feature	Description
None	Saves or exports no data.
Statistics	Saves or exports only the statistics for the specified parameters, the recipe ID, part ID, and sequence ID.
	The results for each parameter at each measurement site are not printed, saved, or exported. Statistics are calculated for scans taken with the same recipe and are saved only if two or more scans are taken with that recipe.
Trace Data	Saves or exports everything, including the recipes used, the raw data points for each scan, parameter results, and the statistics.
Use Lot ID	Prompts the operator to enter the Lot ID before running the sequence, then saves or exports the data under the Lot ID name.
Use Name	Saves or exports the data under the sequence name or a user-specified name. The Path button opens a dialog box for designating the path of the desired file.
Use Operator ID	Prompts the operator to enter their ID before running the sequence. The data file contains the operator ID but is still saved under the Lot ID or the <b>Use Name</b> .

Table 7.7Save and Export Options

The Export Options also contain a choice of export file type. (See Table 7.8.)

#### Table 7.8 Export Options

Feature	Description
ASCII File	Data is exported in ASCII code.
Binary File	Data is exported in binary code.

The Print Option contain the following feature. (See Table 7.9.)

#### Table 7.9 Print Option

Feature	Description
Enable Auto Print	Automatically prints data at the end of the sequence.
	Click the <b>Details</b> button to open a standard print dialog box and set print options.

End: Set Data Options

4. Click **OK** to set the options.

## **Teaching the Base Angle**

The Base Angle is an offset angle relative to the orientation of the sample's pattern. It is used to align scans with the wafer geometry. It is to be used primarily for scan sequences using manual load in conjunction with the **No Automatic Load/Unload** handler option in the system. (See *No Automatic Load/Unload* on page 7-62.) The Base Angle is fixed for all scans in the sequence. Use the following procedure to program the Base Angle.

- 1. Double-click **Base Angle** in the sequence list. (See *Figure 7.8*)
- 2. A warning is displayed before the Teach Location screen appears. The warning says that deskew and measurement sites could be invalidated. Click **OK** to proceed or **Cancel** to abort the procedure.

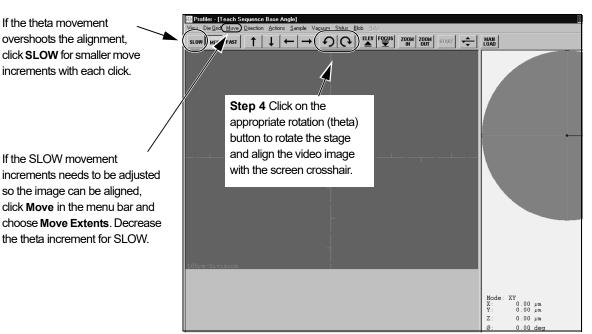
	4 Profiler - [Se	quence Ed	litor - CORS_S	GEQ]							
	Seguence <u>E</u> dit Sample <u>Vacuum</u> Des <u>k</u> ew Dje Grid <u>D</u> jagnostics Help										
			START								
	Scan Recipe Cat	alog:	Recipe name:						_		
	Type: Contact	⊙ <u>2</u> D	⊙ <u>3</u> D	Loc Recipe	X	Y	Theta	X-Off Y-Off			
	Browse	Г	A.44.1	Video Calibration	1.50	1.50			_		
			<u>A</u> dd >>	Base Angle	NOT USED						
	HIST DRMMD		Change >>	Deskew Site 1	-2282	1757	0.00				
Step 1 Double-click on	DRMSML		Europeur	Deskew Site 2 1 COARSE	-3046 0	2579 0	0.00				
Base America to onen the	STEPHTH		Edit Recipe	2 COARSE	0	0	0.00				
Base Angle to open the	_STEPHTL STEPHTM	-		3 _COARSE	Ō	ō	0.00				
Teach Location screen.	TIPCTRL		Select All	4 _COARSE	0	0	0.00				
		-		5 FIRST	0	0	0.00				
			Auto ⊻erify	6 FIRST	0	0	0.00				
Before the Teach		_	Delete								
	- Options			ProfilerContaine	r			$\mathbf{X}$			
Location screen opens, a											
warning is displayed.	Semi-Autor	natic Mode		Teachi	aching base angle may invalidate deskew and measurements sites.						
	Mode: Patter	n Recog. De	skew 💌		_						
	If Fail: Proceed Measurement			OK Cancel							
	IT Fail: Floceed Measurement							/			
	Data	Ha	andler								
	<u>S</u> ort	Sort i	s inactive								
				Regular Scan 💌	Teach L	0C	Teach Pa	at EditX,Y,Thet	a		
					Test			C2. EXV/00.			
				Multi Analysis	Tes		∐se Prev	Site Edit X,Y Offse	5		

*Figure 7.8* Sequence Editor

- **3**. The Teach Location window appears. (See *Figure 7.9*). Locate a line or other pattern to use for a reference.
- 4. Click the clockwise or counterclockwise **Rotation** buttons in the toolbar until the crosshair is aligned with the reference feature.



**NOTE:** As the range rotates, if necessary, move the stage to keep the reference feature in the field of view.



#### Figure 7.9 Teach Location Window

- 5. ALTERNATIVE to steps 3. and 4.: To align the current sample surface with the screen crosshair, use the principles described in *BEGIN Align Sample Procedure* on page 12-18. Use a horizontal feature on the sample surface in place of the dotted line on the Stylus Alignment Tool described in the procedure.
- 6. Click **OK** to return to the **Sequence Editor** window.

Notice that the Base Angle now has a value instead of the phrase Not Used.

When running a sequence with a non-zero Base Angle, the stage rotates to that position immediately before deskew (if applicable).

# **CREATING A SEQUENCE RECIPE**

A sequence allows the user to assemble a series of scans that can be performed on a single scan position or on multiple scan sites on a sample. In a production environment, the sequence can be set up to run multiple sites on multiple identical samples. The sequence recipe can be created for many different scenarios. The following procedure progresses through the creation of a sequence recipe that includes die grid navigation, a necessary ingredient for scanning multiple dies on a sample.

This procedure assumes that no wafer is currently present on the measurement chamber table/chuck.

Begin: Load Sample Procedure
 1. From the Catalog screen, click on the Sequence Recipe button to display scan recipes in the Information Display Window.

2. To load a sample, click on **Sample** in the menu bar at the top of the screen to display its menu. (See *Figure 7.10*.)

Figure 7.10	Sequence Recipe Catalog Screen
-------------	--------------------------------

Step 2 Click on Sample in	er - ILatalogj	l <u>o</u> st <u>D</u> iagnostic <u>T</u> asks <u>H</u> elp		
the menu bar to display its	<u>Manual Load</u>		3D	
menu.	Load/Unload Initialize Handler		equence Recipe Name:	 
Step 3 Click on Manual	а	C	ORS_SEQ	
Load to bring the stage to	Initialize SMIF	h:	Sequence	eation Date
the stage door.	<u>R</u> elease Cassette		ORS SEQ	,yy-mm-dd) )00 <b>–11–</b> 2
Sc. Da	an			 
Step 1 Click on the				
Sequence Recipe button to	ence ipe			
display the Scan Recipe				
Catalog screen.	ence			
Da	ta			

- **3**. Choose **Manual Load** from the Sample menu. The sample stage moves to the stage door.
- 4. *After the stage stops*, open the stage door.

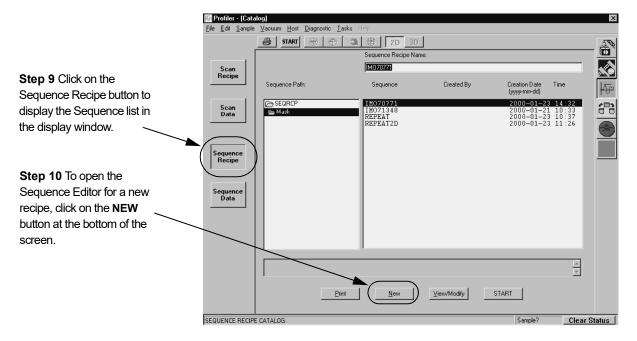


**CAUTION:** Wait until the stage has completely stopped moving before attempting to open the measurement chamber door. If it is open when the system is in movement, the profiler software does not operate because the interlock switch stops all the stage and elevator motors.

- 5. Place the patterned wafer on the stage paying close attention to the orientation of the wafer. The die grid should be as square with the stage X-Y-axis as possible. It is best to use a precision locator to place the wafer securely and squarely on the stage. Otherwise, if the system has to deskew the wafer very much, measurements and pattern recognition could fail later.
- 6. Turn the vacuum on using the switch on the upper left door frame.
- 7. Close the measurement chamber door.

End: OPTIONAL Manual Wafer Load Procedure 8. After the door is closed, click on **Sample** in the menu bar, then on **Manual Load**. The stage moves back under the measurement head.

Figure 7.11 Scan Sequence Catalog



- 9. Click on the **Sequence Recipe** button to change to the Sequence catalog list. (See *Figure 7.11.*)
- 10. From the **Sequence** catalog, open a new sequence by clicking on the **NEW** button at the bottom of the screen. (See *Figure 7.11*.)

The Sequence Editor opens, formatted to create a new sequence recipe. (See *Figure 7.12*.)

,	Profiler - [Sequence Editor - **UN	·			×
		s <u>k</u> ew DjeGrid <u>D</u> iagnostics Help			
	🗋 🛱 📓 🞒 START				
Step 11 Click on Sequence	Recipe na	me: c:\eagle\SCANRCP\intel mask\"	15UM2ED		
and then on Save or Save As to		Loc Recipe	X Y	Theta X-Off	Y-Off
	Browse Add >>	Video Calibration Base Angle	2.78 2.86	-0.57	
display the dialog box for saving	15UM2ED	Deskew Site 1	NOT VALID	-0.57	
and naming the sequence.		Deskew Site 2	NOT VALID		
	Edit Recipe.				
	Select All				
	Auto Verify	1			
	Delete				
	Options-				
	Semi-Automatic Mode				
	Mode: Pattern Recog. Deskew 💌				
	If Fail: Proceed Measurement 💌				
	Data				
	Sort Sort is inactive				
	Die Grid Enabled:mos13.die	Regular Scan 💌	Feach Loc	Ieach Pat	Edit X,Y,Theta
		Multi Analysis	Test	∐se Prev Site	Edit X,Y Offset
				Sample	Clear Status

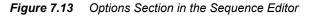
Figure 7.12 Sequence Editor for NEW Recipe with Pattern Recognition

- 11. Click on Sequence in the menu bar to display its menu. (See Figure 7.12.)
- 12. Click on Save or Save As to name and save the sequence.
- 13. The **Save Recipe** dialog box appears. Type in the name of the new sequence and click on **OK** to save it.

#### Linking a Die Grid with a Sequence

When linking a die grid with a sequence, it is better to link it while creating a new sequence recipe rather than to associate a die grid with an existing recipe that uses the same recipe sequence. Use the following procedure for linking a recipe as part of the creation of a new recipe.

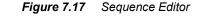
 To use a die grid, Pattern Recognition Deskew must be in place. To tie the deskew process to pattern recognition, use the following procedure. In the **Options** box located in the lower left corner of the Sequence Editor, click on the menu arrow next to the **Mode** field. 2. Click on Pattern Recog. Deskew... (See Figure 7.13.)

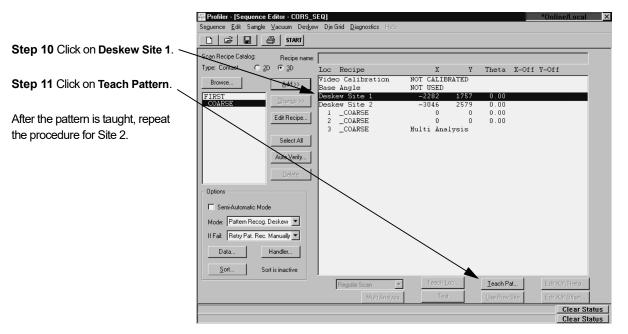


Step 1 Click on the menu arrow for its menu. Step 2 Choose Pattern Recog. Deskew.	Options         Semi-Automatic Mode         Mode:       No Deskew         If Fail:       No Deskew         Pattern Record Deskew         Data       Handler         Sort       Sort is inactive
Begin: Load Die Grid	<ul> <li>3. This sequence is being set up to work on a particular wafer with a set die grid that is to be measured. The sequences must be connected to the Die Grid for scanning and navigational purposes.</li> <li>Die Grid Navigation with single scans requires loading the die grid at the beginning of each scanning session. With sequences, a die grid can be associated with a sequence, so that it loads and aligns the wafer automatically when teaching sites for the sequence. The die grid can also be disassociated if the sequence no longer requires Die Grid Navigation.</li> <li>For additional information about the use of Die Grid Navigation, see Using Die Grid Navigation on page 5-19.</li> <li>MOTE: Whenever possible, load a die grid before teaching any sites; because it invalidates all currently taught positions.</li> <li>Ensure that the wafer on the stage has the same pattern as that of the die grid being loaded.</li> <li>MOTE: It is very important that each wafer is placed in the same orientation that the die grid was taught in. If not, the system cannot locate the dies. When placing the wafer in the proper orientation.</li> <li>4. In the menu bar, click on Die Grid to display its menu. (See Figure 7.14.) If Die Grid is grayed out in the menu bar, the Safe Area might be incorrect. Set the Safe Area in the Configuration screen to the size of the wafer being used. See Safe Area Configuration on page 11-21.</li> <li>Figure 7.14 Die Grid Menu</li> </ul>
<b>Step 4</b> Click on <b>Die Grid</b> in the menu bar to display its menu.	Die Grid       Step 5 Click on Load to display         Associate Dies       the Load Die Grid dialog box         Load       overlay on the XY View screen.         Liear       Info

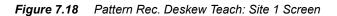
5. Click on Load... (See Figure 7.14.) Figure 7.15 Load Die Grid Dialog Box Load Die Grid Look jn: 🔄 diegrid 🔊 anna.die 🛋 seq\_tst.die Step 6 Double-click on 🔊 seq\_tst2.die Step 7 Click on Open to the name of the die grid open the die grid. to be used. File name seq\_tst.die Open Files of type: Die Grid files (\*.die) • Cancel This displays the XY view screen with the Load Die Grid dialog box overlay. (See *Figure 7.15* for dialog box.)) 6. In the Load Die Grid dialog box, double-click on the name of the die grid to be used. This displays the die grid name in the File Name display box. (See *Figure* 7.15.) 7. Click on **Open** to load the die grid. (See *Figure 7.15.*) The system nulls the stylus and begin to search for the pattern that is displayed in the sample navigation window. After it successfully locates the test pattern, the die grid is loaded. CAUTION: The die grid must match the die grid pattern on the wafer that has been loaded. If not, the die grid feature cannot be found and the die grid does not load. 8. A warning message box appears warning that adding the die grid to the recipe changes the base angle and can invalidate deskew and measurements sites. Since this is a new recipe and the site have yet to be determined, click on OK. (See Figure 7.16.) Figure 7.16 Sequence Editor Sequence Editor X Step 8 Read the The die grid will change the base angle, which may invalidate deskew and measurements warning and click OK sites. to close it. OK I Cancel End: Load Die Grid 9. In the Sequence Editor, save the Sequence Recipe by clicking on Sequence to display its menu, then on Save. Begin: Teach Global 10. This procedure is designed to set up the pattern recognition that allows the Pattern Recognition Sites system to recognize the current wafer as related to the die grid and to perform a deskew procedure on to align the wafer with the X-Y-axis. In the Sequence Recipe Catalog screen, click **Deskew Site 1.** (See *Figure 7.17.*)

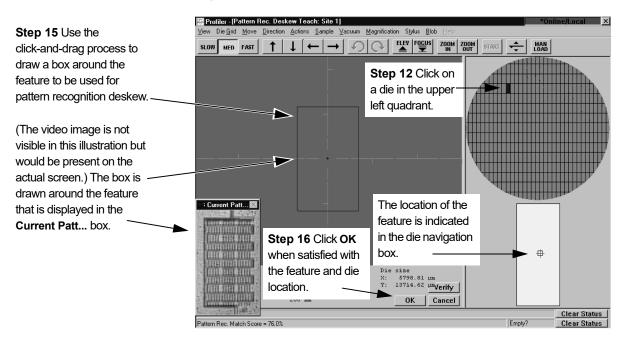
11. The **Teach Pattern** button at the bottom of the screen becomes active. (See *Figure 7.17.*) Click the button to begin the Teach Pattern procedure for Site #1.





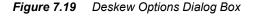
12. The **Pattern Rec. Deskew Teach: Site 1** screen is displayed. Click on a die in the upper left quadrant of the sample navigation grid. the dark (blue on the screen) rectangle has been chosen in *Figure 7.18*.

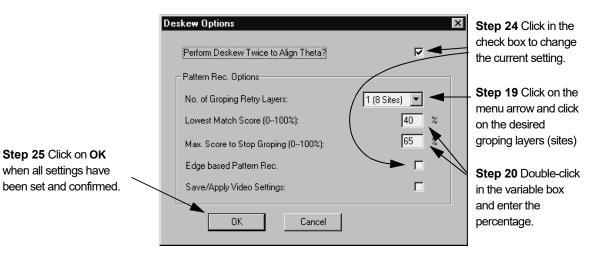




- 13. After the die in the upper left quadrant is clicked, the system moves that die into view in the video window. Click on **FOCUS** in the tool bar to bring the die into clear focus.
- 14. Use the arrow buttons in the tool bar to move the field of vision to a feature in that die that is used for centering the die and aligning the wafer. It is best to use the same feature that is used in the die grid. (See *Figure 7.18*.)
- 15. After locating the feature, use the click and drag procedure, starting from the upper left corner of the feature, to draw a rectangle around the feature. When the box is complete, the system centers it in the X-Y-grid and a replica of it is produced in a box on the screen. The die navigation box, under the die grid navigation grid, now contains a small blue box indicating the position of the feature with respect to the die boundaries. (See *Figure 7.18*.)
- 16. When satisfied with the die position and the feature, click on **OK**.
- 17. Repeat Step 10 through Step 16 for Site 2. For a location, choose the lower right quadrant, at approximately the opposite die position, at an approximate 45° angle through the center of the die grid from the first die.
- Deskew Options set the number of groping Layers, set the maximum and minimum percentage match for identification of a feature, and offer the ability to turn on or off Deskew Twice and Image Processing options. (See Using Groping with Pattern Recognition on page 7-44.)

Click on **Deskew** in the menu bar and then on **Options...** to display the dialog box. (See *Figure 7.19*.)





- 19. Set the No. of Groping Retry Layers by clicking on the down-arrow and then clicking on the desired number of layers and sites. (See *Using Groping with Pattern Recognition* on page 7-44 for more information on groping layers.)
- 20. Set the Lowest Match Score by double-clicking in the variable box and typing in the new percentage. (See *Figure 7.19*.)
- 21. Set the Max. Score to Stop Groping by double-clicking in the variable box and typing in the new percentage. (See *Figure 7.19*.)

- End: Teach Global Pattern Recognition Sites
  - Begin: Setting Deskew Options

End: Set Deskew Options

Begin: Set Data Options

- 22. To enable **Edge Based Pattern Rec**., click to put a check in the checkbox. (See "Edge Based Pattern Rec." in *Table 7.12 on page 7-46*.)
- 23. To enable **Save/Apply Video Settings**, click to put a check in the checkbox. (See "Save/Apply Video Settings" in *Table 7.12 on page 7-46*.)
- 24. If desired, click to put a check in the check box for **Perform Deskew Twice to Align Theta** to enable it. (See "Perform Deskew Twice to Align Theta" in *Table* 7.12 on page 7-46.)
- 25. Click on **OK** when all the parameters have been set.
- 26. Data Options are explained in detail beginning in Step 2. on page 7-10, in *Editing the Options Field in the Sequence Editor*.

Click on **Data**... in the Options section in the lower left corner of the Sequence Editor. This displays the **Data Options** dialog box.

The **Data Options** dialog box appears. (See *Figure 7.7.*) Once set, the Profiler automatically either exports, saves, or prints the file data.

Figure 7.20 Data Options

Print Options	×	
Save Options None Statistics only Trace Data and Statistics Use Lot ID Use Name: CORS_SEQ Path c:\eagle\seqsumm\db Use Operator ID Print Options Enable Auto Print Print:	Export Options None ASCII File Statistics Only Binary File Trace Data and Statistics Use Lot ID Use Name: CORS_SEQ and use lot ID for statistics name Use Operator ID OK Cancel	Step 28 When the options have been chosen, click OK.
Details		

- 27. Set the options according to the scan sequence requirements. (See Step 2 on page -10 through Step 4 on page -11, in *Editing the Options Field in the Sequence Editor*.)
- 28. Click on **OK** when options have be set.

End: Set Data Options

29. Save the Sequence by clicking on **Sequence** to display its menu, then on **Save**.

Figure 7.21 Sequence Editor Set Up for New Recipe

	暦 Profiler - [Sequenc	e Editor - **UNTI	[LED**]				*Online/Local	×
	<u>S</u> equence <u>E</u> dit Samp	ole <u>V</u> acuum Des <u>k</u> ø	w Dje Grid <u>D</u> iagnostics	Help				
		START START						
	Scan Recipe Catalog:	Recipe name	FIRST					
	● <u>2</u> D ● <u>3</u> D		Loc Recipe	X	Y	Theta X	-Off Y-Off	
	290MMX50 300X5000	Add >>	Video Calibrat: Base Angle	ion 1.16	1.15	-0.38		
(	ANNA2D ANNA2D2	nange >>	Deskew Site 1 Deskew Site 2	-41929	55988 <u>-400</u> 20	-0.38 -0.38		
(	FIRST	Edit Recipe	1 FIRST	NOT DEFI	NED	-0.38		
	PIEZO_60 PIEZO_90 SECOND		2 SECOND	NOT DEFI	NED			
The Sequence Editor comes up	TEST	Select All						
with no recipes listed. Use Step		Auto ⊻erify		$\checkmark$				
<b>30</b> to create a sequence of		Delete		When the red	cine is a	ndded it		
recipes:	r			appears in th				
	Options			••				
1. Highlight a scan recipe.	Semi-Automatic M			scan location	•			
2. Click on the Add button.	Mode: Pattern Reco			displayed as	NOT D	EFINED.		
	If Fail: Skip, No Mea	asurement 💌						
3. Repeat Steps 1 and 2 for	Data	Handler						
each additional recipe.	<u>S</u> ort	Sort is inactive						
	Die Grid Enabled:seg ts	st.die	Regular Scan	▼ Teach	Loc	Ieach Pat	Edit X,Y,Theta	
			Multi	Analysis Te	est	Use Prev Site	Edit X,Y Offset	
							Clear Statu	_
						Em	pty? Clear Statu	IS

Adding Scan Recipes

30. The Sequence Editor appears with no scan recipes in the Sequence list. Add the required recipes to the sequence using the following procedure: (See *Figure* 7.21.)

- a. In the scan recipe list, click on the first recipe to be included in the sequence. It highlights when selected.
- b. Click on the Add button to add the recipe to the sequence.
- c. Repeat this procedure for every scan recipe that is to be added to the sequence.

**Begin**: Teach Scan Location 31. In the **Sequence Editor**, click on the first scan recipe in the sequence. It highlights when chosen. (See *Figure 7.22*.)

	🜆 Profiler - [Sequence	e Editor - **UNTIT	'LED**]				*Online/L	ocal 🛛 🗙
	<u>S</u> equence <u>E</u> dit Sam <u>p</u> le	e <u>V</u> acuum Des <u>k</u> e	w DjeGrid <u>D</u> iagnostics Help					
		START 5						
	Scan Recipe Catalog:	Recipe name:	FIRST					
Stop 21 Click on the first Seen	<u>● 2</u> D ● <u>3</u> D	_	Loc Recipe	Х		Theta	X-Off Y-Off	
Step 31 Click on the first Scan	290MMX50 300X5000	<u>A</u> dd >>	Video Calibration Base Angle	1.16	1.15	-0.38		
Recipe so that it highlights.	ANNA2D ANNA2D2	Channen	Deskew Site 1	-41929	55988	-0.38		
	FIRST	<u>C</u> hange >>	Deskew Site 2 1 FIRST	39250 NOT DEF		-0.38		_
	JOETEST PIEZO_60	Edit Recipe	2 SECOND	NOT DEF				-
	PIEZO_90 SECOND							
	TEST	Select All						
		Auto ⊻erify			Step 3	<b>2</b> Wher	n the first	
		Delete			-			
	1						as been	
	Options				chosen	, click o	n the Teach	
	Semi-Automatic Mo	ode			Loc but	ton to b	egin the	
	Mode: Pattern Recog	9. Deskew 💌			Teach p	orocedu	re	
	If Fail: Skip, No Mea	surement 💌			, ,			
	Data	Handler						
					▶			
	Sort	Sort is inactive			<u> </u>			
	Die Grid Enabled:seg_tst	.die	Regular Scan 💌	( Tead	:h <u>L</u> oc )	Ieach Pat	Edit X,Y,TF	neta
	_		Multi Analysis		Fest	Use Prev S	ite Edit X,Y Of	fset
								ar Status
						E	motu? Cle	ar Status

Figure 7.22 Sequence Editor - Teach Scan Location

32. Click on the **Teach Loc** button at the bottom of the screen.

The XY view screen appears and the system proceeds to null on the sample surface. It then searches for the feature in the die. When it is found, the scan path indicator is displayed over the feature. (See *Figure 7.23*.)

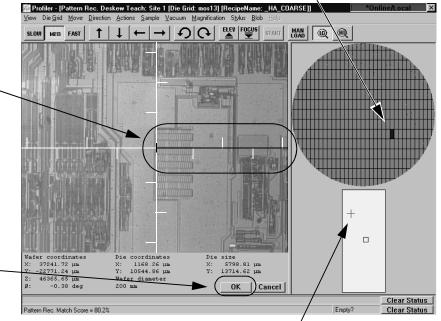
**33**. The die grid is visible in the sample navigation window with the die navigation box below it. During a scan sequence, the system uses the Pattern Recognition Deskew to situate the wafer. It begins with the top left die and moves to the bottom right die.

Choose a die that is close to the bottom right die. If there is a preset pattern for checking the dies, choose the die closest to the bottom right die. It becomes a starting point for the sequence following the Associate Dies procedure.

34. Find the feature in the die that is to be scanned using the first recipe. Click in the relative position in the die navigation box to move the feature close to the field of view. Use the arrow buttons to move the feature into view. Click in the relative position in the die navigation box



**Step 33** Choose a die close to the bottom right die used for Pattern Recognition Deskew. If there is a set die checking scheme, choose the one closest to the bottom right die as a starting point for the sequence.



**Step 34** The **Teach Location** screen displays the sample surface under low magnification. Position the scan path across the chosen feature.

Step 35 Position the scan path indicator over the portion of the die that is to be scanned by the recipe in the sequence. Use the arrow buttons to move the field of vision and locate the scan location.

**Step 36** Click **OK** when the scan path indicator is properly placed.

The die navigation box can be used to position the scan for the recipe. Click on the place in the die where the scan feature resides. The video image displays that position.

- **35**. After the feature is centered in the video window, position the scan path indicator over the feature in the die that is to be scanned using the first recipe in the sequence. (See *Figure 7.23*.)
- **36**. When the scan path indicator is correctly positioned, click on **OK**. (See *Figure 7.23*.) The screen changes back to the Sequence Recipe screen.

In the Sequence Recipe screen, there are now coordinates next to the scan recipe which describe the location of the scan path in the die for that recipe. (See *Figure 7.24.*)

🚟 Profiler - [Sequence Editor - VG_SEQ	]					*Online/Local	X
$\underline{S} equence  \underline{E} dit  Sample  \underline{V} acuum  Des \underline{k} ev$	• Die Grid <u>D</u> iagnostics Help						
🗅 🖙 🖬 🎒 START							
Scan Recipe Catalog: Recipe name;	бим						
● 2D O 3D	Loc Recipe	Х	Y	Theta	X-Off	W 066	
2904450	Video Calibration	1.16	1.15	Ineta	x-011	1-011	
300×5000 <u>A</u> dd >>	Base Angle	1.10	2.20	-0.38			
ANNA2D ANNA2D2 Change >>	Deskew Site 1	-41929	55988	-0.38			
FIRST JOETEST	Deskew Site 2 1 FIRST	39250	-40020 -22771	-0.38			
PIEZO_60 Edit Recipe	2 SECOND	40250	-30011	-0.38	)		
PIEZO_90 SECOND					/		
TEST Select All							
Auto <u>V</u> erify		7					
Delete		· .					
Options	This scan s	equence l	nas two				
options	recipes that	t it uses. E	Both				
Semi-Automatic Mode	have the so						
Mode: Pattern Recog. Deskew 💌	nave the sc	an localic	ons				
If Fail: Skip, No Measurement	taught as in	dicated b	y the X,				
	Y, and Thet	a coordin	atoc				
Data Handler			ales.				
Sort Sort is inactive							
	l						
Die Grid Enabled:seq_tst.die	Regular Scan	<ul> <li>Teach</li> </ul>	Loc	<u>T</u> each Pa	at	EditX,Y,Theta	
	Multi Analysis	; Te	st	Use Prev	Site	Edit X,Y Offset	
						Clear St	
					Empty?	Clear St	atus

Figure 7.24 Sequence Editor

37. Repeat Step 31 through Step 36 (Teach Scan Location) for each recipe in the sequence. Be sure to use the same die as that used to teach the first location.

#### Associating Dies with a Sequence Using Die Grids

After a die grid has been associated with the scans in a sequence, it is possible to associate other dies on the same sample with the scans using the die grid. This creates a longer sequence in which additional scan locations on the sample are scanned automatically, using validated scan locations.

Use the following procedure to associate dies with the sequence scans using die grids.

- 1. Ensure that the procedure in *Linking a Die Grid with a Sequence* on page 7-16 has been completed for the sequence being used.
- 2. From the Sequence Editor highlight the recipe that is to have additional dies associated with.
- 3. Click on **Die Grid** in the menu bar. (See *Figure 7.25*.)

4. Click on Associate Dies... (See *Figure 7.25*.)

Figure 7.25 Sequence Editor with Die Grid Menu

Step 3 Click on Die Grid in the	Re Profiler - [Sequence Editor - VG_SEQ]	*Online/Local ×
•	Sequence Edit Sample Vacuum Die Grid Diagnostics Help	
menu bar to display its menu. —	🗅 😂 🔚 🎒 START Associate Dies	1
	Load	
	Scan Recipe Catalog: Recipe name: F Align / Update Sequence	
		-Off Y-Off
	290MMX50 300X5000 Add>>> T Into 1.16 1.15 Base Angle -0.36	
	ANNA28 Deskew Site 141929 55988 _0.38	
Step 4 Click on Associate	Deskew Site 2 39250 -40020 -0.38	
. ,	JUETEST         1         FIRST         37241         -22771         -0.38           PIEZO_60         Edit Recipe         2         SECOND         40256         -30011         -0.38	
Dies to begin the process of	PIEZO_90	
choosing new scan sites.	SECOND TEST Select All	
choosing new courrence.		
	Auto ⊻enĭy	
	Delete	
	Options	
	Semi-Automatic Mode	
	Mode: Pattern Recog. Deskew	
	If Fait Skip, No Measurement	
	Data Handler	
	Sort Sort is inactive	
	Die Grid Enabled:seg. tst.die Regular Scan 💌 Teach Loc Ieach Pat	Edit X,Y,Theta
	Multi Analysis Test Use Prev Site	Edit X,Y Offset
		Clear Status
	Emp	oty? Clear Status

This displays XY screen titled "**Associate Dies With Sequence Scan Sites**," with a graphic display of the die grid configuration, visible to the right of the video display area. (See *Figure 7.27*.)

- 5. If the die grid comes up with the dies already chosen, click on **Die Grid** in the menu bar.
- 6. Choose **Clear**. This takes out all the old dies and leaves only the one that was used for teaching the current recipe locations. It has the number 1 in it.

Figure 7.26 Die Grid Menu



Step 6 Click on Clear to remove the unwanted dies from the die grid.

7. Each rectangle on the die grid configuration represents a single die. The green one with the number one (1) in it represents the original scan site designated for the chosen scan recipe. To add dies, simply click on the desired die where the additional scan is to be made. Each successive site turns green and contains a number.



**NOTE:** The scans are performed according to the die site numbers. To reduce sequence timing, choose the scan sites in a circular fashion for minimum time of travel between scan sites. (See *Figure 7.27*.)

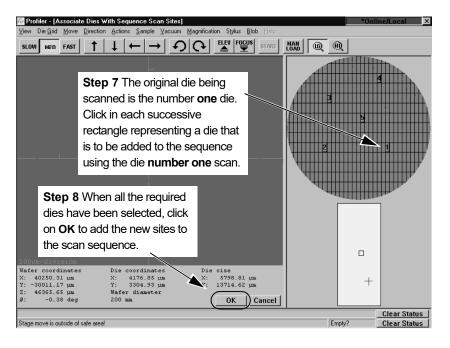


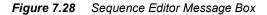
Figure 7.27 XY View with Sequence Scan Sites

×

**NOTE:** Dies can be selected or deselected by clicking or them.

- 8. After all the required dies have been selected, click on **OK** to add them to the sequence. (See *Figure 7.27.*)
- 9. The **Sequence Editor** message box appears with a message saying that the chosen sites will be added to the sequence, asking whether to proceed with the additions.

Click on  $\mathbf{OK}$  to continue or  $\mathbf{Cancel}$  to abort the addition of the sites to the sequence.





When **OK** is clicked, the Sequence Editor is displayed with the additional sites in the Sequence Recipe.

Notice that each new site has the coordinates of the scan location for that die. In the illustration *Figure 7.29*, two sets of new sites have been added, one for additional dies using the scan named FIRST, and one for dies using the scan named SECOND.



**CAUTION:** The coordinates presented for the scans in the new sites might not be exactly where they are needed. It is important to verify each of their locations.

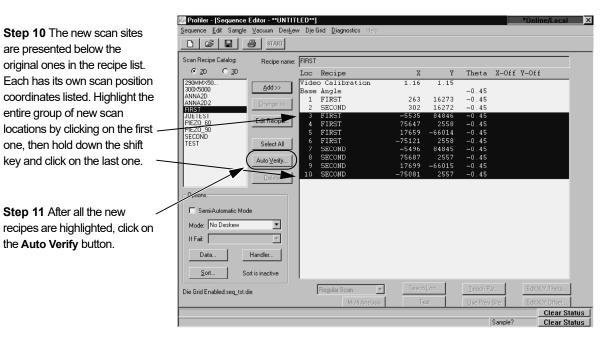


Figure 7.29 Sequence Editor with New Scan Sites

#### Begin: Auto Verify

- 10. Highlight the entire group of new scan sites by clicking on the first one, holding the shift key down and clicking on the last one.
- 11. Click on the **Auto Verify** button to begin the process of verifying each scan location.
- 12. The XY view screen is now displayed. The system moves the field of vision to each scan site and displays the site with the scan path positioned as it is during the actual scan. Adjust each site individually using the following procedures:
  - a. The feature being scanned should be visible in each site. If not, locate it.
  - b. Ensure that the scan path indicator is positioned correctly. If it is not, move the cursor to the exact location where the scan is to **begin** and click. The system should adjust the scan position on the screen.
  - c. When complete, click on **OK** to verify that location. The next site appears on the screen automatically.

End: Auto Verifyd. When the last site is verified, the screen reverts back to the Sequence Editor. Save the Sequence by clicking on File and Save or Save As.

e. A dialog box appears. Enter the name of the new sequence and click **OK** to save it.

#### Disassociating a Die Grid with a Sequence

- 1. Make sure the sequence is displayed in the Sequence Editor
- 2. Click on **Edit** to display its menu.
- 3. Select Clear Die Grid.

### **RUNNING A SEQUENCE**

- 1. Click the Start button, or click the Sequence menu, and select Start.
- 2. Perform manual deskew, if applicable. Also, refer to manual deskew section for explanation of how to do this.
- 3. Click the Stop button to stop the sequence before normal termination.

## **CORRELATION SCANS**

Scans are correlated when a long scan is performed first, then small scans are performed in the same general location. Correlation scanning combines local area scans with macroscopic scans so that discrete features can be related to global surface planarity.

From the scan data of a long scan, distinct features can be located which require a repeat scan at high resolution, then create a sequence that performs high resolution sub-scans along the length of the long scan. Data for each sub-scan is based on the long scan, providing a data reference for correlating the measurements of the sub-scans.

- 1. Open an existing Sequence recipe or create a new one in the Sequence Editor.
- 2. Select the recipe to use for the long scan (one that traverses the targeted feature).
- 3. Click the Scan Type arrow below the sequence to open the list.
- 4. Click the Correlation Long Scan button.

A message dialog box appears, warning that the recipe immediately following is designated a Correlation Sub-scan and if it is set up for multiple analysis, it resets to single scan. The Sub-scan is the short scan that is tied to the long scan. It provides the local, small-scale analysis. It is set up in step 7, next page.



**NOTE:** Multiple correlation scan sets can be established; each set is marked by the initial long scan in red lettering and its associated sub-scans immediately following in blue.

#### 5. Click **OK**.

The long scan recipe becomes red; the recipe immediately following becomes blue, indicating that it is a sub-scan to that long scan. Sub-scans always follow long scans in sequence. 6. Designate the other sub-scans (usually  $100 \ \mu m$  or less) as done for the long scan, using the Scan Type list to select Correlation Sub-scan.

*Figure 7.30* shows the Sequence Editor for a correlation scan where the parent long scan recipe is EXAMPLE, Loc is location 1. The sub-scans are EXAMPLE2, Loc are location 2, location 3, and location 4.

Figure 7.30 Correlation Scan Sequence

	Profiler - [Sequence Editor - EXAMPSEQ] Online/Local X									
	$\underline{S} equence  \underline{E} dit  S ample$	⊻acuum Des <u>k</u> e	w Djel	Grid <u>D</u> iagnostics Help						
The first recipe, the parent		START 5								
long scan, is in red.	Scan Recipe Catalog:	Recipe name:								
	<u>•</u> 2D ○ <u>3</u> D		Loc	Recipe	X	Y	Theta	X-Off	Y-Off	
	COARSE	Add >>		o Calibration	1.15	1.15				
	TEST5		Base	Angle	NOT USED	1070	0.01			
	TEST9	Change >>		EXAMPLE	-40	1372	0.81	、 、		
	TEST10 TEST14_A		15	EXAMPLE2 EXAMPLE2	-11 38	1373 1375	0.00	)		
	IESTI4_R	Edit Recipe	Ι ĭ	EXAMPLE2	262	1377	0.00	)		
The subscan recipes, the	TEST14_C		$\sim$	BINIE BBC	202	10//	0.00	/		
an malation as har and	TEST15 NANOEDGE	Select All								
correlation subscans, are	STEPHTM	Select All								
in blue.	STEPHTH	Auto ⊻erify								
IT BIGC.	EXAMPLE									
	EXAMPLE2	Delete								
	<b>•</b>									

- 7. Teach the long scan position.
  - a. Press the **Teach LOC** button.
  - b. Go to the location and click on it. To accept the location, click **OK** in the dialog box that appears.
- 8. Teach the sub-scan position.
  - a. Press the **Teach LOC** button.
  - b. Go to the location and click on it. To accept the location, click **OK** in the dialog box that appears.

The Teach Sub-Scan window appears.

**9**. If the current position of the sub-scan is not close enough to the position of the long scan for both to appear in the video image, a red arrow and the coordinates of the long scan appears on the video image.

Move the stage in the direction of the arrow to bring the long scan into view.

The long scan is represented in the window by a red scan line; the sub-scan by blue.

- 10. Position the sub-scan on the desired portion of the long scan line.
- 11. Click **OK**.

The Sequence Editor returns to view.

12. Repeat for all sub-scans.

#### Viewing the Correlation Scan Data

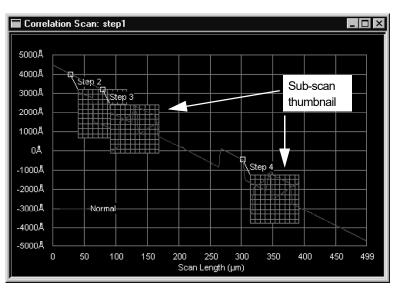
1. Run the correlation sequence. Save the recipe and click **Start**.

The Analysis window appears, showing the results of the first recipe in the sequence.

- 2. Click the File menu, and select Correlation Scan. The Correlation Scan dialog box appears.
- 3. Click the long scan
- 4. Click **OK** to display the **Correlation Scan** window.

The Correlation Scan window appears, showing the long scan trace and thumbnail callouts of each of its sub-scans positioned on the long scan (see *Figure 7.31*).

Figure 7.31 Correlation Sub-scan Window



- Double-click the thumbnail on the graph to view the sub-scan trace. The trace appears in its own analysis window. A Statistics window also appears for the long scan.
- 6. Click the **File** menu, and select **XXX** to view the correlation scan statistics. Multiple Analysis cannot be used with correlation scans.

# VIEWING SAVED SEQUENCE DATA

## Viewing Old Sequence Data

- Go to the Catalog window, and click the Sequence Data button. The Sequence Data Catalog window appears.
- 2. Select the data set from the list in the catalog, and click the **Review** button, or double-click the desired data set.

# **Recovering Sequence Data**

In the case of a system crash during a sequence execution, using this recovery tool, it is possible to go back to the screen that displayed the last data, including unsaved data.

- 1. Go to the Sequence Data catalog window.
- 2. Select a sequence.
- 3. Click the Recover button.

# **Calculating Combined Sequence Statistics (Option)**

Values from different sequence sets can be combined into one, and used to calculate the standard deviation, mean, and so forth. The computer accesses stored data from selected data sets in the Sequence Data catalog and recalculates them.

1. Click the Sequence Data command button in the Catalog screen.

The Sequence Data catalog window appears.

- 2. Highlight the data files to be combined.
- 3. Press CTRL while clicking to highlight multiple data files.
- 4. Click the **Combine** button.
- 5. Enter a name for the new combined data set.
- 6. Click **OK**.

A statistics summary with the new data appears after a short calculation interval.

# USING MULTI ANALYSIS IN SEQUENCE

Multiple data analyses can be obtained from a single scan by applying the data analysis settings of additional recipes to its raw data. The process is a modification of a sequence recipe in which the instrument uses the first scan recipe to scan and analyze in the usual manner, then takes settings from the subsequent recipes to reanalyze the first recipe's scan data.

It is important to note that the raw data for the scan be saved and therefore can be subjected to numerous different parameter adjustments. Each set of data that is obtained from applying the new parameters can be save under its own name. This means that after the scan is run and the results saved, the additional information can be retrieved at a later date, even calculated on a desktop version of the software if it has been purchased.

Time can be saved and throughput improved by using multiple analysis for:

- Measurements that require more than one cursor setting such as two different step heights on a single scan
- Measurements with different filter settings
- Measurements with different surface parameters enabled in the Scan recipe.
- 1. Go to the Sequence Recipe catalog window, and select a Sequence recipe.
- 2. Click the View/Modify button to open the Sequence Editor window.

3. Click the **New** button at the bottom of the screen or click the **Sequence** menu, and select **New**.

A blank sequence list appears.

- 4. Set up the scanning recipe to scan with its existing settings:
  - a. Click the name of the required recipe to be used for the scan.
  - b. Click Add to add the Scan recipe to the list.
- 5. To make changes to an existing Scan recipe.
  - a. Click its name in the list
  - b. Click **Edit** recipe to change any parameters and filter settings. Cursor positions can only be changed by entering them numerically.
  - c. Save the recipe.
  - d. To teach cursor positions later from the scan trace:
  - e. Click **Save As** to create a new recipe even if no changes were made to the recipe at this point.
  - f. Exit the Recipe Editor window to return to the Sequence Editor window.
  - g. Select the new recipe that was just created.
  - h. Click Add to add the Scan recipe to the list.
- 6. Set up the analyzing Scan recipes:
  - a. Go to the **Scan Recipe** catalog list, and click a Scan recipe containing the required analysis settings.

This recipe should have the same scan length, scan speed, sampling rate, stylus force, contact speed, and range as the scanning recipe.

b. Make changes to the Scan recipe as in Step 5b.

This step can also be performed before compiling the sequence list, using the Scan recipe to scan the sample and teach the cursor positions.

- c. Add the Scan recipe to the sequence list.
- d. While the Scan recipe is still highlighted, click the Multi Analysis button.

This instructs the instrument not to scan the sample again but to reanalyze the data according to the recipe's data analysis parameters. Note that the Multi Analysis button is not active (dimmed) for the first recipe in a sequence.

- e. Repeat the process as many times as needed.
- 7. Click the Sequence menu, and select Save As to save the sequence.

#### Viewing Multi Analysis Results

- 1. Tile the windows to display the Sequence Parameter Summary window and the Scan Trace simultaneously.
- 2. Go to the Sequence Parameter Summary window:
  - Site 1 shows data analyzed with the first Scan recipe in the sequence list.
  - Site 2 data corresponds to the second Scan recipe, and so on with each additional site.
- 3. To view each Scan recipe's data set in both Trace and Summary windows:

- a. Click the arrow in the Recipe drop-down menu on the tool bar.
- b. Select the Scan recipe.

# VIEWING SEQUENCE DATA

## **Viewing Wafer Summary Data**

The Sequence Parameter Data window displays the detailed results of each site scanned in the sequence.

1. Go to the File menu in the Analysis window, and select Surface Summary.

Figure 7.32 Sequence Parameter Data window

		<b>is - [Sequen</b> ∕iew <u>T</u> race		eter Data] <u>W</u> indow <u>H</u> e	lp				Online	Local
	EXAMP	LE						• 8		
	Lot: EXAM Op:	IPSEQ	Sec Re	quence: EXAMP cipe: EXAMP	'SEQ 'LE					
Recipe drop-down menu 🦯	Deskew	Sample	Stat	Analyze	Area+	ProfL	R3z	Bh	Wa	Wp
		Cassette	Mean		0.01342 μm²	499.51 μm	929.5 Å	712.6 Å	208.4 Å	669.4 Å
			S. D.		0 Ų	0.00 µm	0.0 Å	0.0 Å	0.0 Å	0.0 Å
			Min		0.01342 µm²	499.51 µm	929.5 Å	712.6 Å	208.4 Å	669.4 Å
			Max		0.01342 µm²	499.51 µm	929.5 Å	712.6 Å	208.4 Å	669.4 Å
			Range		0 Ų	0.00 µm	0.0 Å	0.0 Å	0.0 Å	0.0 Å
	None	Slot 10	Mean	Inc	0.01342 μm²	499.51 μm	929.5 Å	712.6 Å	208.4 Å	669.4 Å
		0.0110	S. D.		0 Å <sup>2</sup>	0.00 µm	0.0 Å	0.0 Å	0.0 Å	0.0 Å
			Min		0.01342 µm²	499.51 µm	929.5 Å	712.6 Å	208.4 Å	669.4 <i>i</i>
			Max		0.01342 µm²	499.51 μm	929.5 Å	712.6 Å	208.4 Å	669.4 <i>i</i>
			Range		0 Ų	0.00 µm	0.0 Å	0.0 Å	0.0 Å	0.0 Å
	None	Slot 10								
		Site 1		Inc	0.01342 μm²	499.51 μm	929.5 Å	712.6 Å	208.4 Å	669.4 Å
								(C.)		lear Status

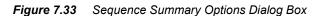
- 2. Maximize the Sequence Parameter Data window to view the entire Sequence Parameter Data screen from the Analysis window.
- **3**. Go to the **Sequence Parameter Data** window, and click on the **Recipe** drop-down menu on the left of the toolbar. (See the **Recipe** location at the top left of *Figure 7.32.*) This drop-down menu displays all Scan recipes that are included in the sequence.
- 4. Choose the desired recipe by clicking on it.

## **Sequence Summary Options**

The Sequence Summary Options dialog box specifies the information to be displayed in the Sequence Parameter Data window. The individual scans in any sequence can be viewed in the Analysis window by clicking the appropriate site number in the Sequence Parameter Data window.

1. Open the Analysis window.

2. Click the **Operations** menu, and select **Summary Display Options** to display the Sequence Summary Options dialog box. (See *Figure 7.33*.)



Step 3 Click in the checkbox to put a check in the option. That item get displayed in the summary screen.	Sequence Summary Options     X       Display Selections     Image: Cassette Summary       Image: Cassette Summary     Image: Cassette Summary       Image: Slot Summary     Image: Cassette Summary
<b>Step 4</b> Once all changes have been made, click <b>OK</b> to activate the changes.	Display Order  Cass. summary: Slot summary for all slots; Site list for all slots.  Cass. summary: Slot summary followed by Site list for each slot.  Cancel  Cancel

- **3**. Choose the items to be displayed in the summary screen. A check in the box indicates those that are displayed. (See *Figure 7.33*.)
- 4. Click **OK** to activate changes to the summary display items. (See *Figure 7.33*.)

# Viewing Sequence Data with the Corresponding Trace, Site-by-Site

The screen can be set up to display a site's parameter data along with the trace itself.

- 1. Open both the Analysis and the Sequence Parameter Data windows.
- 2. Go to the Windows menu, and select Tile Vertically.
- 3. Size the windows by clicking and dragging their frames.
- 4. Display the desired trace:
  - a. Go to the **Sequence Parameter Data** window, and click the numbered **Site** box of the trace desired.

The Analysis window displays the trace for that site.

- b. Repeat for other sites, displaying each trace in turn.
- 5. Save the workspace:
  - a. Click the File menu, and select **Save Workspace** to save this window orientation.
    - The dialog box appears.
  - b. Enter a name for the workspace.
  - c. Click **OK** to save.
- 6. To review both parameter data and the trace:
  - a. Click the File menu, and select Load Workspace to retrieve the workspace.
  - b. Highlight the workspace name in the drop-down menu.

c. Click **OK**. The screen reconfigures to the desired trace/data window orientation.

## SEQUENCING WITH MANUAL DESKEW

The reason for programming a sequence is to automate a repetitive series of measurements on multiple samples. The example contains all of the essential features of a sequence.

Even with a locator or some sort of fixture, the second and subsequent samples cannot reliably be placed on the stage in the exact same position, and with the same alignment, as the first. The new sequence can still be used, but each of the scan sites must be manually located and retaught before running the sequence.

Deskew enables and defines two points on a sample to be used as reference points prior to the start of a sequence. These points are then used to mathematically correct for translational (X, Y) and rotational (theta) error in sample positioning.

- 1. Create a new sequence.
- 2. When ready to set up manual deskew, proceed with the following steps.
- 3. Set the deskew mode to Manual Deskew.

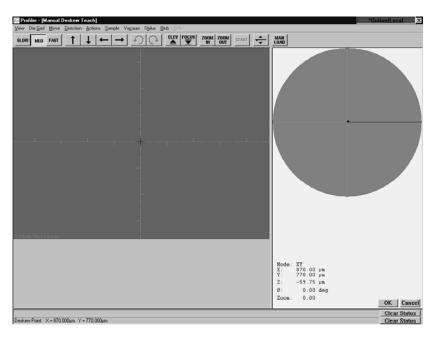
Note that two deskew steps now appear in the sequence list on the right side of the window.

4. Select the first deskew site by double-clicking anywhere on the **Deskew Site 1** line in the sequence list.

5. Click the **Teach Loc** button, or double-click the deskew site. The Manual Deskew Teach window appears. (See *Figure 7.34*).

The two deskew points should be in opposite quadrants, with each being at least half way to the edge of the substrate.

Figure 7.34 Manual Deskew Teach Window



6. Select the first deskew point. Select an obvious point, such as the corner of an easily and uniquely identifiable rectangle.

Click the chosen position.

The stage moves so that the crosshair are centered on the selected site.

7. Click **OK**.

The Sequence Editor window reappears, with the X and Y coordinates of the selected site entered in the deskew Site 1 step.

- 8. Select the second deskew point.
- 9. Repeat steps Step 5 through Step 7 for the second deskew site.
- **10.** Once the deskew sites have been successfully established, proceed to program the rest of the sequence steps.
- 11. Run the sequence.

After each deskew operation, the instrument pauses and requests acceptance of the deskew site.

- 12. If it is out of the field of view, use the arrow buttons to move the stage and search for the site. Click on the deskew site, moving it to the center of the crossmarks.
- 13. Click **OK** to accept the deskew site.

14. Repeat **Step 11** through **Step 13** for deskew site #2. The tool then proceeds with the measurement sites.

# **DESKEWING TWICE TO ALIGN THETA**

With a single deskew operation, there is no stage rotation to compensate for the small rotational error in sample placement. A second deskew can be performed to compensate for this error by enabling this option in the Pattern Recognition and Deskew Options dialog box. This allows accurate sample rotations within a sequence.

1. Go to the main **Configuration** window, and click the **Pattern Recognition Options...** button.

The Deskew Options dialog box appears (see Figure 7.35).

Figure 7.35 Deskew Options Dialog Box

ľ	Pattern Recognition and Deskew Options	×	Step 3 Click OK
I	Pattern Recognition Options:		when all choices
	Number of Groping Retry Layers:	I 18 Sites) ▼ Cancel	are complete.
	Minimum Match Score (%):	20	
	Minimum Score to Stop Groping (%):	25	
	Edge based Pattern Recognition:		Step 2 Click in the
	Save/Apply Video Settings:		checkbox to enable or disable the
	Deskew Option:		deskew twice option.
	Perform Deskew Twice to Align Theta:		

- 2. Click the **Perform Deskew Twice to Align Theta?** check box to enable or disable the second deskew.
- 3. Click **OK** to set the options and close the dialog box.

# SEQUENCING WITH PATTERN RECOGNITION DESKEW (PATTERN RECOGNITION OPTION ONLY)

The **Pattern Recognition** option minimizes operator intervention in sequence operation by automating the precise setting of deskew points at the beginning of a sequence.

Pattern Recognition deskew replaces and automates the manual deskew process. The same considerations of global deskew point placement that apply to manual deskew apply equally to pattern recognition deskew.



**NOTE:** To minimize positioning error, space the deskew points at least one-half the diameter of the sample. Do not set the deskew points parallel to the X-axis or Y-axis, but instead use two points on a diagonal line. If the deskew points are identical, the sequence aborts.



**NOTE:** Although a coordinate transformation is made, there is no stage rotation to compensate for the small rotational error in sample placement unless the deskew option is set to perform a second deskew. See *Deskewing Twice To Align Theta* on page 7-38 for more information.



**NOTE:** Note also that any rotational error is magnified when traversing a long distance across a large wafer. This might cause the deskew site to be outside the field of view when a wafer is loaded.

A pattern recognition deskew site is a unique pattern of wafer features visible within the instrument's field of view. The size and shape of the pattern must be uniquely different from other wafer features visible in the field of view to ensure that the instrument can locate the sites without ambiguity. (See *Table 7.10*).

Table 7.10 Pattern Examples

Pattern Example	Description
Good Patterns	Alphanumeric characters
	Circular or rectangular pads that appear singly
	Crosses
	Alignment marks
	<ul> <li>Other polygon shapes</li> </ul>
Bad Patterns	Sections of a repetitive grid
	• Circular pads or rectangular pads that repeat in or near the field of view

When choosing patterns, keep the following points in mind. (See *Table 7.11*).

Table 7.11 Pattern Search Criteria

Search Criteria	Description
Search time depends on pattern size.	The larger the pattern, the faster the system can recognize the pattern. However, larger patterns require more accurate initial positioning within the camera's field of view because the search area is reduced.
	Also, Pattern Recognition options can be set so that the system performs a pattern search if the pattern is not found within the field of view. See <i>Using Groping with Pattern Recognition</i> on page 7-44 for information.
When using rectangular pads, use the entire rectangle.	If only two corners are used, other rectangles in the field of view could confuse the pattern recognition system.
The pattern should be unique and as simple as possible.	However, uniqueness cannot be sacrificed for simplicity.
Select symmetric patterns.	They are less sensitive to image rotation. Circular patterns are rotationally symmetric and therefore are good patterns. Similarly, the best polygon patterns have the most sides.
High contrast features make pattern recognition matches easier.	When available, select high contrast features. Noise does not have as much effect on the pattern recognition match. The pattern colors are important because the pattern recognition system reads the black and white image, not the color image.
Avoid patterns with rough surfaces.	By using edge enhancement, the instrument computer emphasizes the fine features present on a rough surface. Because roughness is random, these features add noise to the system and make the pattern recognition system less reliable.



**NOTE:** It is generally a good idea to avoid fixed dust particles in the field of view as well. Avoid selecting wafer-specific defects or features as patterns, or the instrument computer could become confused. This includes dust particles, partially etched areas near the edge of the wafer, and so on.

To set up Pattern Recognition deskew:

- 1. Go to the **Sequence Editor** window.
- 2. Select the sequence recipe that is to have Pattern Recog. Deskew.
- 3. Select **Pattern Recog. Deskew** from the **Mode** drop-down menu. (See *Figure 7.36.*)

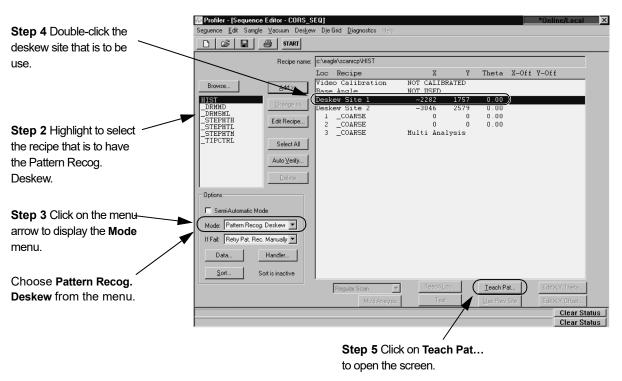


Figure 7.36 Profiler Sequence Editor Window

4. Double-click the **Deskew Site 1** entry near the top of the sequence list or highlight the **Deskew Site 1** entry. (See *Figure 7.36*.)

5. Click the **Teach Pat** button. (See *Figure 7.36.*)

The Pattern Rec. Deskew Teach window appears and the stylus automatically nulls on the sample surface.

Figure 7.37 Pattern Rec. Deskew Teach window

6. Select a pattern to use for pattern recognition.

As a rule of thumb, select something that is simple and easily recognizable, like an alphanumeric character or an alignment mark. (See *Table 7.10 on page 7-39* and *Table 7.11 on page 7-40*.) Something that looks much like another feature that is also within the field of view does not work reliably because the wrong site might be identified.

- 7. Define a rectangular area that encloses the chosen pattern as follows:
  - a. Press and hold the left trackball button at the top left corner of the desired rectangle.
  - b. Move the trackball toward the bottom right corner of the desired rectangle.A blue box appears that follows the trackball cursor as it moves.
  - c. When satisfied with the desired rectangular area, release the trackball button.

The system processes the image information defined by the rectangle.

- d. If the rectangle was too small or too large, a message dialog box appears indicating that the rectangle was too small or too large:
  - i. Click OK.
  - ii. Teach the pattern again.

8. The blue box remains on the window with a darker blue dot in the center. The stage moves until the selected feature is centered in the crosshair (*Figure 7.38 on page 7-43*).

Figure 7.38 Pattern Rec. Deskew Teach Window After Teach

- 9. Move the stage a small distance.
- 10. Click **Verify** to test whether the system can accurately find the taught feature. A box is drawn around the feature when it is found.
- 11. If recognition fails, select another pattern and retry.
- 12. Click **OK** to accept the new pattern.
- 13. Repeat Step 2 to Step 9 for Deskew Site 2 to establish the second deskew point.
- 14. Once the deskew sites have been successfully established, proceed to programming the rest of the sequence steps.

Due to the number of variables that affect pattern recognition, the computer might not always be successful in locating a deskew site. The instrument can be preset to do one of four things in the event of a failure:

- Continue scanning
- Stop scanning the wafer and proceed to the next scan site
- Repeat the pattern recognition
- Stop the entire sequence
- **15.** Choose a Pattern Recognition Failure Response from the **If Fail** drop-down menu. (See *Figure 7.39*.)

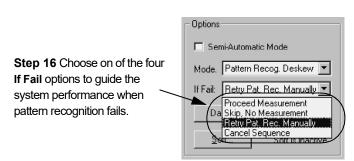


Figure 7.39 If Fail Menu in Options Portion of Sequence Recipe Screen

16. Run the sequence.

# **USING GROPING WITH PATTERN RECOGNITION**

#### Introduction

Deskew Options can be set so that the system performs a pattern search if the pattern is not found within the field of view when the sample is positioned at the deskew site. This search is called groping. Note that these same parameters (in a slightly different format and with slightly different wording for the Lowest Match Score parameter) are available in the Pattern Recognition and Deskew Options dialog box in the Configuration screen. (See *Pattern Recognition Options and Deskew* on page 11-29.) The parameters set in the Deskew Options dialog box take precedence over those from the Pattern Recognition and Deskew Options dialog box.

Access to the Pattern Recognition and Deskew Options dialog box is through the Configuration screen's **Pattern Recognition Options...** button. (See *Pattern Recognition Options and Deskew* on page 11-29.) Access to the Deskew Options dialog box is through the **Deskew** menu in the Sequence Recipe screen. Notice that, the parameter, "Minimum Match Score" in the Pattern Recognition dialog box, has not yet been changed to "Lowest Match Score" as it has in the Deskew Options dialog box. *The values set in the Deskew Options dialog box for each sequence recipe override those set in the Pattern Recognition Options dialog box.* 

The three groping parameters are described in *Table 7.12*.

## **Setup Procedure**

1. From the Sequence Editor, click **Deskew** in the menu bar to display its menu.

2. Click Options... to open the Deskew Options dialog box. (See Figure 7.40).

Figure 7.40 Pattern Recognition and Deskew Options Dialog Box

Deskew Options	x
Perform Deskew Twice to Align Theta?	V
Pattern Rec. Options	
No. of Groping Retry Layers:	1 (8 Sites) 💌
Lowest Match Score (0100%):	40 %
Max. Score to Stop Groping (0100%):	65 %
Edge based Pattern Rec.	
Save/Apply Video Settings:	
OK Cancel	

- **3**. Click on the **Number of Groping Layers** menu-arrow to display its menu. (See *Figure 7.40.*)
- 4. Choose the number of layers from the menu. (See *Figure 7.40*. For information on the groping layers see *Table 7.12*.)
- 5. Set the Lowest Match Score (%) by highlighting the current percentage and entering the new one. (See *Figure 7.40*. For information on match scores see *Table 7.12*.)
- 6. Set the Minimum Score to Stop Groping (%) by highlighting the current percentage and entering the new one. (See *Figure 7.40*. For information on match scores see *Table 7.12*.)

7. Edit the fields by using the parameters described in *Table 7.12*.

Table 7.12	Froping Parameters
------------	--------------------

Parameter	Description		
Number of Groping Retry Layers	This parameter controls how much of the area around the deskew site is searched for the pattern. Each layer consists of a square area constructed by evenly surrounding the deskew site with squares the size of the camera field of view. (See <i>Figure 7.41</i> ).		
	Figure 7.41 Groping Retry Layers		
	Groping 1st Retry Layer 2nd Retry Layer disabled searches for 8 searches for		
	searches only camera field of view		
	3rd Retry Layer searches for 48 more squares; 4th Retry Layer searches for 80 more squares. It stops after the 4th try.		
	Available choices are:		
	• None (the default)		
	• 1 (8 Sites)		
	• 2 (24 Sites)		
	• 3 (48 Sites)		
	• 4 (80 Sites)		
	NOTE: It takes 10 s to move the stage, null the stylus, and search one such area; 8 search sites (1 layer of retry) takes as long as 90 s; and 24 sites (2 layers) takes as long as 250 s, and so on.		
	First, the deskew site field of view is searched. If the pattern is not found, the stage moves to one corner of the next layer and searches the field of view there. This continues until the pattern is found or until all search sites have been examined. If the pattern is still not found, the stage moves to one corner of the next layer and continues.		

Parameter	Description
Lowest Match Score (Was changed from Minimum Match Score, which is still the term used in the Configuration screen version of this parameter.)	Lowest Match Score is used to compare all the groping positions in the given groping levels. Once the groping stops (assuming that the Minimum Score to Stop Groping is not found) the highest score achieved, among those scores that qualified for Lowest Match Score acceptance, is chosen as the search pattern (model). This number must be smaller than the Minimum Score to Stop Groping. Allowed values range between 20 to 100%; the default is 65%. This parameter allows adjustment of the threshold at which the pattern recognition system concludes that it has found a candidate for the desired deskew site.
Minimum Score To Stop Groping	Minimum Score to Stop Groping defines a value at which the system accepts the image as the model for which it is searching. Groping stops if this score is reached and the image corresponding to the score is considered to be the search pattern (model). EXPLANATION: If the pattern recognition system is groping to find the desired pattern, frequently the matching pattern is found with little ambiguity. If a score equal to or better than the Minimum Score to Stop Groping occurs, the searching process stops and the deskew site is placed. Allowed values range between 20 to 100%; the default is 70%. If no matches are found that are as good as this setting, the search continues until all retry layer areas are searched. The highest score above the Lowest Match Score setting determines the placement of the deskew site.
Edge Based Pattern Recognition	The <b>Edge Based Pattern Recognition</b> option is used for low contrast image recognition on a sample surface or where there is a large surface light variation. If this option is chosen (with a check in the check box), the normal image contrast grayscale processing takes place first, then a series of filters are applied that further contrast and sharpen edges for a better pattern recognition. The image data is stored before these filters are applied so the data is not effected by this option. It is strictly a tool used for pattern recognition where contrast is low or where light varies significantly. If the option is not chosen, only the image contrast grayscale processing is performed.

 Table 7.12
 Groping Parameters (Continued)

Parameter	Description
Save/Apply Video Settings	The lamp brightness setting is important in pattern recognition. If the lamp brightness is different from when the original sequence was established, the pattern recognition images could be difficult for the system to detect. A check in the <b>Save/Apply Video Settings</b> checkbox ensures that the lamp brightness is saved with each deskew site pattern so future scans have the same image view with the same light for pattern recognition.
Perform Deskew Twice to Align Theta	With a single deskew operation, there is no stage rotation to compensate for the small rotational error in sample placement. By enabling this option in the <b>Pattern Recognition and Deskew Options</b> dialog box, a second deskew is performed to compensate for this error. This allows accurate sample rotations within a sequence.

 Table 7.12
 Groping Parameters (Continued)

8. Click **OK** to set the options and close the dialog box.

# **Groping Analysis (Condensed)**

- 1. The first field of view is searched for the model. If the **Minimum Score to Stop Groping** is achieved, the image in the first field is chosen as the search pattern (model).
- 2. If the **Minimum Score to Stop Groping** is not achieved in the first field of view, the groping continues. Each position in every allowed groping level produces a score. If that score is greater than the Lowest Match Score, but less than the Minimum Score to Stop Groping, its score is saved for comparison with other scores in case the Minimum Score to Stop Groping is not achieved during the entire groping session.
- **3**. If at any time during the groping session the Minimum Score to Stop Groping is achieved, the image with that score is accepted as the search pattern (model) and the groping stops. Any residual Lowest Match Score values are discarded.
- 4. If the entire groping session produces only scores greater than the Lowest Match Score but less than the Minimum Score to Stop Groping, then the highest score among the Lowest Match Score candidates is chosen as the search pattern (model).
- 5. If no scores are obtained above the Lowest Match Score, then the groping session pattern recognition search failed.

# SEQUENCING WITH SITE-BY-SITE PATTERN RECOGNITION

Sometimes it is more effective to position a scan relative to a taught feature instead of as arbitrary stage coordinates. Site-by-Site Pattern Recognition stores an offset from a taught pattern for any scan in the sequence. The pattern must first be taught the "home" feature, then teach the scan. With Site-by-site Pattern Recognition enabled, the instrument stores the scan position as an offset from the taught feature.

- 1. In the **Options** section of the **Sequence Editor**, click the drop-down button of the **Mode** option. (See *Table 7.5 on page 7-8*.)
- 2. Click the Site-by-site Pattern Rec. option. (See Table 7.5 on page 7-8.)
- 3. Teach Pattern Recognition for the two initial deskew sites. (See Step 10 on page -18 through Step 16 on page -20.)
- 4. Insert Scan recipes for the measurement sites. (See STEP 30 ON PAGE -22.)
- 5. Click the site in the **Sequence** list to be taught.
- 6. Click the **Teach Pat** button, or click the **Use Previous Site** button to use the pattern from previous site.

The Pattern Rec. Deskew Teach Window appears.

- 7. Teach a **Pattern Rec**. feature near the intended scan location, following the guidelines in *Table 7.10* and *Table 7.11*.
- 8. Click **OK**.
- 9. With the site still highlighted, click the **Teach Loc** button.
- 10. Teach the location for the actual measurement. This position is recorded as an offset from the **Pattern Rec.** site.
- 11. Click **OK**.
- 12. Repeat for all sequence sites.

# SAVING SEQUENCES

Sequences can be saved on the hard drive or network drive



**NOTE:** For SEMI compliance, both scan recipes and sequences share the same directory. This means that a sequence cannot have the same name as an existing recipe.



**CAUTION:** Do not attempt to save directly to the Jaz drive. Save in the file first then transfer to the Jaz drive.

- 1. Click the Sequence menu, and select:
  - Save to save the current recipe, or
  - Save As to save the current recipe under a different name.

2. Type a sequence name in the Name field.

The name can be upper or lower case. If using special characters, only the following are allowed:

~ tilde	( left parenthesis
! exclamation point	) right parenthesis
(a) at sign	_ underscore
# number sign	- hyphen
<b>\$</b> dollar sign	{ left brace
% percent sign	} right brace
^ caret	' single quotation mark
& ampersand	' apostrophe

3. Click OK.

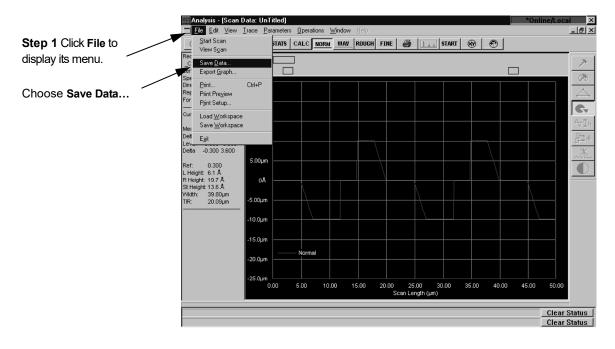
# SAVING THE SEQUENCE DATA

The Scan and Sequence Data sets can be saved and retrieved for future review and additional reanalysis using different scan recipe parameters.

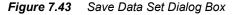
If a scan is completed without being interrupted, the Analysis screen automatically appears after the scan is complete.

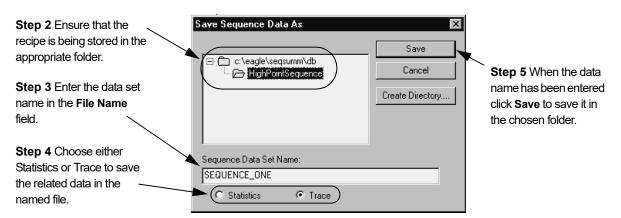
1. Click File, and select Save Data. The dialog box appears. (See Figure 7.43.)

Figure 7.42 Analysis Screen with File Menu



- 2. Ensure that the data is being saved into the correct folder. (See Figure 7.43.)
- Type a name (up to 72-alphanumeric characters) in the File Name field. The name can be upper or lower case. If using special characters, refer to Using File Name Conventions on page 2-19. (See Figure 7.43.)





4. Choose either Statistics or Trace. If both require saving, perform the save function two times, one for each option, giving names to each different data set.

**Trace** creates a scan data set containing the actual trace data. This can then be used to display the trace in the Analysis screen for further analysis or recalculation with new parameters. The system also uses this data to create the Thumbnail trace for comparison.

**Statistics** creates a file of the scan data parameters that were set in the scan recipe used to create the different scans. This data can also be displayed in the Sequence summary screen and analyzed or recalculated with different scan parameters.

 Click Save. Once a data set has been saved, it is added to the Sequence Data catalog. The Sequence Data catalog window allows for the selection of individual data sets for reviewing. Unwanted data sets can also be deleted.

# SEQUENCE TRANSPORTABILITY

## Introduction

This feature is designed to facilitate the use of a sequence recipe on a system that receives the recipe from another identical system. This is accomplished by using the center of the wafer as a reference instead of using the stage center. To accomplish this, the Wafer Center Calibration must be run on the sending and receiving systems, preferably using the same wafer. Both systems must already have all calibrations current, including Center of Rotation and Stage Mapping. As a result, there is no need to reteach locations or die grid models when transporting a sequence recipe to another system.

Another benefit of the Wafer Center Calibration is that, after service or maintenance where a component was replaced, running the calibration ensures that sequences do not need to be retaught.

In order for the sequence to perform its intended scans at the intended locations, the recipes and die grids are exported to the receiving system along with the sequence recipe. This export function is accomplished using the appropriate export options.

It is important to note that this procedure is recommended for like systems with the same optics. Systems with different optics might experience difficulty with the pattern recognition because the models are different sizes. In addition, sites taught on an x40 system in low magnification might not be accessible in an x20 system.

# **Sequence Transport Configuration**

The user has the option of including models and scan recipes (along with the already included basic sequence, deskew, and site by site model) when exporting a sequence to another system. If the user chooses to export the sequence recipe without including the models and scan recipes, only the basic sequence, deskew, and site by site model is exported.

## **Open the Sequence Transport Options... Dialog Box**

From the Configuration screen, click on the **Recipe Transport Options...** button to open its dialog box. (See *Figure 7.44*)

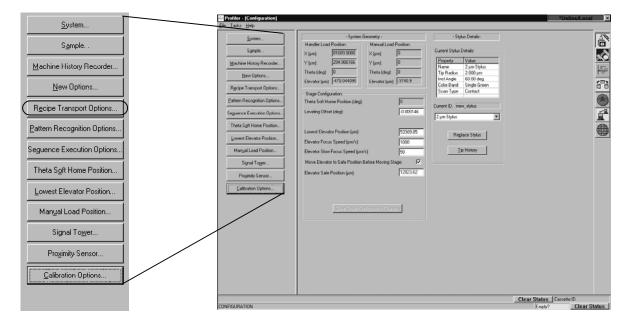


Figure 7.44 Recipe Transport Options... Configuration Screen Button

## **Export Paths**

The Recipe Transport Options dialog box, contains fields for setting the Export and Upload paths for scan and sequence recipes. The system has default paths that were established during the software installation. The default paths are displayed in *Figure 7.45*.

1. To change back to the default scan and sequence recipes, sequence recipe option defaults, and data paths (C:\EAGLE\SCANEXP and C:\EAGLE\SEQEXP), click on the **System Defaults** button.

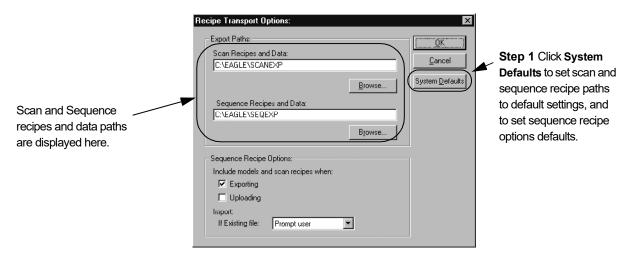


Figure 7.45 Recipe Transport Options Dialog Box

2. If setting a different path, click **Browse** and locate the desired folder in the dialog box. Click **OK** when the folder is chosen to set it active in the Recipe Transport Options dialog box. (See *Figure 7.46*.)

Figure 7.46Browse Directories Dialog Box

Browse Direc	tories		? ×	
Select Path:	Eagle	• Ē		This is the default
Cfg db diegrid dll drv dskw img	dsp     enulation     eqt     eqt_back     eq     eq     eq	hrp1 hsms klarf logs mciv	scandata scanexp scancp seqdiag seqexp seqecp	scan recipe folder.
			<u>H</u> elp	

**3.** If no other changes are to be made in the Recipe Transport Options dialog box, click **OK** to accept the changes.

## **Sequence Recipe Options**

The **Sequence Recipe Options** portion of the Recipe Transport Options dialog box is designed to give the user an opportunity to include the *models* and *scan recipes* in the sequence recipe export or upload.

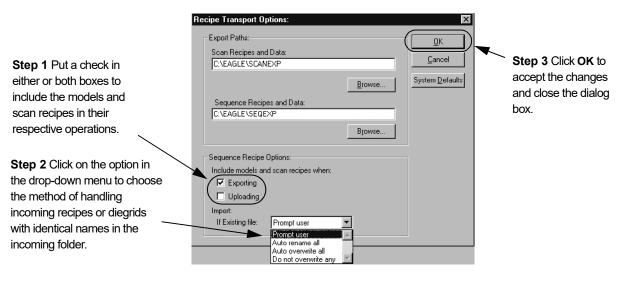
The **Export** option, when checked, adds the binary models and scan recipes to the sequence recipe when exporting it. If unchecked, the models and scan recipes are not included with basic sequence, deskew, and site by site model.

The **Upload** option, when checked, accepts the models and scan recipes when uploading the sequence recipe. If unchecked, the models and scan recipes are not included with basic sequence, deskew, and site by site model.

The **If Existing File** field contains the options necessary when recipes on the system have the same name as those being imported. (This option is only for imported recipes. If a host downloads a sequence, all existing files are automatically overwritten.) The following options are available:

- **Prompt User**: This option produces a dialog box that allows the user to rename the recipe, overwrite the current recipe having the same name, or set the option to ensure that no recipes are ever overwritten by user imported files.
- Auto rename all: This option automatically renames the scan recipes and diegrid in the sequence and placed the newly named scan recipes in the designated folder.
- Auto overwrite all: This option automatically overwrites recipes and diegrid with the same name, replacing them with the imported recipe.
- **Do not overwrite any:** This option does not allow any of the recipes, scan or sequence, to be overwritten. When an import is attempted, the user is prompted with a question asking if the existing recipe is to be overwritten with the imported one. In a sequence the prompt is given for every file, scan recipes and diegrids.

1. Put a check in the checkbox of either or both **Exporting** and **Uploading**. The checked box means the models and scan recipes, if they exist, are included in the operation.



*Figure 7.47* Recipe Transport Options with "If Existing File" Menu

- Click on the option in the drop-down menu to choose how the incoming recipes and diegrids are to be handled if there are files with the same name already resident in the selected folders. (See the explanations above regarding the operation of each option.)
- 3. Click **OK** to apply the changes and close the dialog box.

## Wafer Center Calibration

The sequence transportability depends on the system using the center of the wafer as a reference point instead of the center of the stage, as has been done in the past. This requires that the **Calibrate Wafer Center** calibration be run. The **Calibrate Wafer Center** calibrates the center of the wafer as the (0,0) reference point. After this calibration has been run, all sequence recipes and the system **Safe Area** settings use the wafer coordinates. (See "Calibrate Wafer Center" Calibration.)

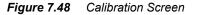
The P-15 systems do not use a handler, so this is only effective if the system has a precision locator for wafer alignment.

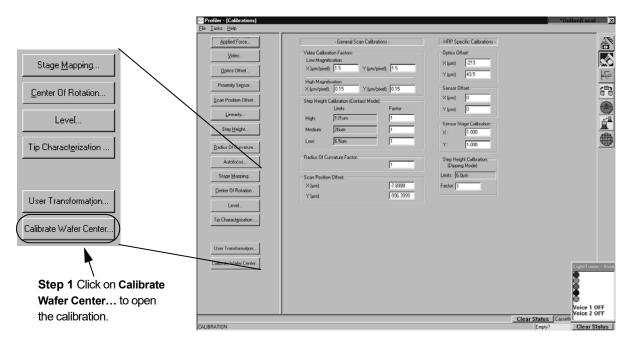
## **Calibration Procedure**

Before performing the Calibrate Wafer Center calibration, all system calibrations must be current, including the Center of Rotation and Stage Mapping calibrations. If not, perform these calibrations first along with any prerequisites. After these are acceptably completed, proceed with the following calibration. 1. From the Calibration screen, click on Calibrate Wafer Center button.

✓ N a

**NOTE:** The user must be logged in under the proper security level to access the **Calibrate Wafer Center** calibration. Without the correct level, the calibration might be missing from the menu or grayed out.





The user is prompted to load a wafer. The user selects the cassette and slot that the wafer is to be taken from as well as setting the load angle to  $45^{\circ}$ .

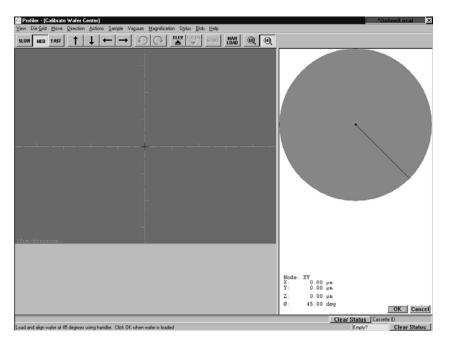


Figure 7.49 Wafer Center Calibration Screen

- 2. Load a wafer.
- 3. Click **OK** after the wafer is loaded.

The system moves the wafer to until its edge is under the optics. When the stage stops, the system focuses on a point near the wafer edge.

- 4. Align the wafer edge with the screen crosshair as prompted by the system. If the edge is not in sight, move the stage to the right using the right arrow button in the toolbar. Align the left wafer edge with the screen crosshairs.
- 5. Click **OK**.
- 6. The stage moves to a point near the right wafer edge and the system focuses on the wafer surface. The user is prompted to align the wafer edge with the screen crosshairs.
- 7. Align the right wafer edge with the screen crosshairs. Use the left-arrow button in the tool bar to move the wafer edge into alignment with the screen crosshairs. (In necessary, use the Slow speed for the arrow button movement to accurately position the edge of the wafer at the screen crosshairs.)
- 8. Click **OK** to accept the position.
- 9. Click **OK**.

The system positions the top of wafer under the optics and focuses. The user is prompted to position the top edge of the wafer at the screen crosshairs.

- 10. Align the top wafer edge with the screen crosshairs. Use the down-arrow button in the tool bar to move the wafer's top edge into alignment with the screen crosshairs. (In necessary, use the Slow speed for the arrow button movement to accurately position the top edge of the wafer at the screen crosshairs.)
- 11. Click **OK**.

The system positions the bottom of wafer under the optics and focuses. The user is prompted to position the bottom edge of the wafer at the screen crosshairs.

12. Align the bottom wafer edge with the screen crosshairs. Use the up-arrow button in the tool bar to move the wafer's bottom edge into alignment with the screen crosshairs. (In necessary, use the Slow speed for the arrow button movement to accurately position the bottom edge of the wafer at the screen crosshairs.)

## Stage to Wafer Conversion

As a result of the system converting to the use of the wafer center instead of the stage center as a reference point, all sequence recipes created before the conversion (i.e., before the "Calibrate Wafer Center" calibration) become inaccurate. They must be converted to the wafer center system in order to perform correctly. The Calibrate Wafer Center Calibration adds an offset from the stage coordinate to the wafer coordinates.

The Stage to Wafer calibration should only be performed after the Center of Wafer calibration is performed and prior to any new recipes being created. If only new recipes (recipes created after the Calibrate Wafer Center calibration) are to be used, the conversion is optional.



**NOTE:** This procedure can only be performed once.

#### **Calibration Procedure**

- From Windows Explorer, run
- User is warned to back up recipes before proceeding.
   Backup is advised. Use the Pbackup procedure.
- 3. Click Proceed. All sequence recipes are automatically converted.

# HANDLER... BUTTON OPTIONS WINDOW FOR SEQUENCING

The P-15 does not have a handler. **Manual Load/Unload** is the only active feature in this dialog box, and is available for use in the P-15 system.

This option is for an operator who is going to use the same sequence recipe to process numerous samples in a series. In this mode, at the end of each scan sequence the stage automatically moves to the manual load position and a dialog box informs the user to load a sample and click **OK** when ready. The stage positions the sample to begin the sequence scans and automatically begins the scan procedure. When the sequence is complete, process starts again. This procedure continues until the **Cancel** button is clicked to stop the sequence.

## Accessing the Handler... Button Options Window

1. In the Sequence Recipe Catalog (see *Figure 7.50*), click the View/Modify button to display the Sequence Editor. (See *Figure 7.51*.)

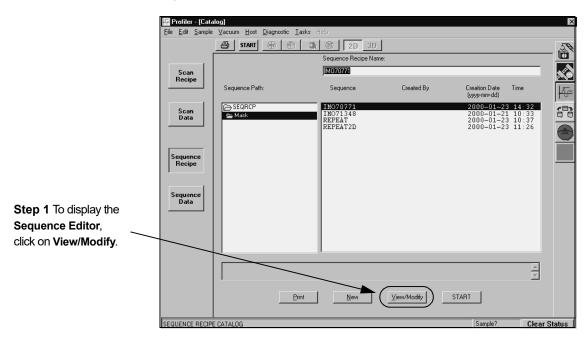


Figure 7.50 Sequence Recipe Catalog Screen

2. Click on the Handler... button (see *Figure 7.51*) to display the Handler Options dialog box. (See *Figure 7.52*.)

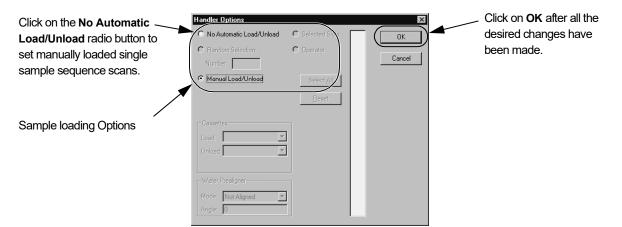
	🐺 Profiler - [Sequence E	ditor - **UNTIT	LED**]				×
	<u>S</u> equence <u>E</u> dit Sam <u>p</u> le <u>)</u>	<u>/</u> acuum Des <u>k</u> ev	v Dje Grid <u>I</u>	jiagnostics Help			
		START					
	Scan Recipe Catalog:		c:\eagle\SC4	NRCP\intel mask\1	5UM2ED		
	Type: Dipping 📀 2D	C <u>3</u> D	Loc Rec	-	X	Y Theta X-Off	Y-Off
	Browse	<u>A</u> dd >>	Video Ca Base Ang	libration le	0.39 0. NOT USED	38	
	15UM2ED	<u>C</u> hange >>					
	l i	Edit Recipe					
		Select All					
		Auto⊻erify Delete					
		Delete					
Step 2 Click on Handler	Options						
to display the Handler	🗖 Semi-Automatic Mode						
Options dialog box.	Mode: No Deskew	-					
	If Fail:	7					
	Data	andler					
	<u>S</u> ort Sort	is inactive					
			Berry	ar Scan 🔻	Teach Loc	Ieach Pat	Edit X.Y.Theta
			megu	Multi Analysis	Test	Lise Prev Site	Edit X,Y Offset
						2001107010	Converge of 1995
						Sample	Clear Status

Figure 7.51 Sequence Editor

## Using Handler Options to Set the Sample Selection Procedure

Sequence procedures can be run tow ways for the P-15 system: **No Automatic** Load/Unload and Manual Load/Unload. Each is discussed below.

Figure 7.52 Handler Options Dialog Box - Load Options



#### Manual Load/Unload (Automatic)

This options is used when the operator is going to use a sequence for processing numerous samples using the same sequence recipe. In this mode, the stage automatically moves to the manual load position and a dialog box informs the user to load a sample and click **OK** when ready. The stage positions the sample to begin the sequence scans and automatically begins the scan procedure. When the sequence is complete, the stage again moves to the manual load position and the dialog box appears. This procedure continues until the **Cancel** button is clicked to stop the sequence.

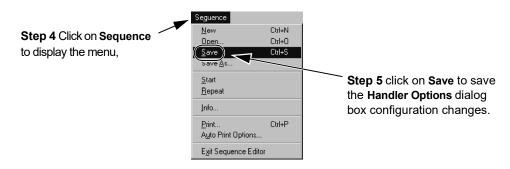
1. In the Sequence Editor click on the **Handler**... button. This displays the Handler Options dialog box. (See *Figure 7.53*.)



	Handler Options			×		
	C No Automatic Load/Unload	C Selected Slots:	25	ок	_	
Step 2 Choose the	C Random Selection:	C Operator:	25 24 23 22 21	Cancel		Step 3 Click OK
Manual Load/Unload	Number:		21 _ 20			when the selection
option for multiple	Manual Load/Unload	Select <u>A</u> ll	20 19 18 17			
samples using the		<u>H</u> eset	16 15			is complete.
manual load procedure.			14 13			
	Load:	1	12 11			
	Unload	ī	10 9 8			
			7			
	Wafer Prealigner		5			
	Mode: Not Aligned	]	3			
	Angle: 0					

- 2. Select Manual Load/Unload (place a dot in the radio button) to activate the automatic Manual Load procedure for each sample using the sequence. (See *Figure 7.53*.)
- Click OK after the Manual Load/Unload procedure has been selected. (See *Figure 7.53*.)
- 4. In the Sequence Editor, click **Sequence** in the menu bar to display its menu.
- 5. Click on Save to save the changes in the sequence. (See Figure 7.54.)

Figure 7.54 The Sequence Menu



6. When the sequence containing the Manual Load/Unload option is started, a message box appears telling the user to load a sample (substrate) then click **OK** to continue or **Cancel** to stop the sequence. (See *Figure 7.55*.)

Load a sample onto the stage then click **OK** to continue. (See *Figure 7.55*.)

Figure 7.55 Load Substrate Message

Step 6 Load a sample on the	ProfilerContainer X
stage and click <b>OK</b> to continue.	Load substrate on the stage and then press DK to proceed, Cancel to stop the sequence.
<b>Step 8</b> Click <b>Cancel</b> after the last sample is removed.	

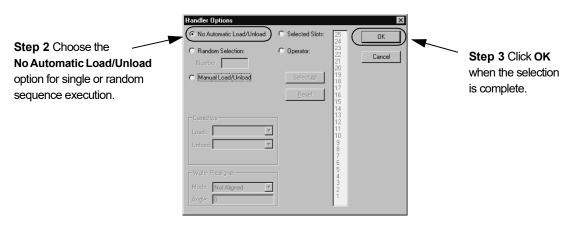
- 7. Turn on the vacuum using the switch on the top left inner door frame.
- 8. After the last sample is processed, the system moves it to stage door.
- 9. Open the door and turn off the vacuum.
- 10. Remove the sample from the stage and click **Cancel**. This terminates the sequence repetition. (See *Figure 7.55*.)

#### No Automatic Load/Unload

This options is used when the operator is going to process random samples using a sequence recipe. In this mode, all load and unload procedures are initiated directly by the operator.

1. In the Sequence Editor click on the **Handler**... button. This displays the Handler Options dialog box. (See *Figure 7.53*.)

Figure 7.56 Handler Options Dialog Box - Manual Load/Unload Option



- 2. Select **No Automatic Load/Unload** (place a dot in the radio button) to deactivate the Automatic Manual Load procedure. (See *Figure 7.56*.)
- 3. Click **OK** after the selection is complete. (See *Figure 7.56*.)
- 4. In the Sequence Editor, click **Sequence** in the menu bar to display its menu.

	<i>.</i>		e to save the changes in the sequence. (See Figure	/.
		Figure 7.57	The Sequence Menu	
<b>Step 4</b> Click on <b>Sequence</b> to display the menu,	•	Seguence New Open Save Save As Start Repeat Info Print Agto Print Options Egit Sequence Edito		

5. Click on Save to save the changes in the sequence. (See Figure 7.54.)

# ANALYZING 2D SCAN DATA

# INTRODUCTION

The 2D Analysis application displays the trace of the sample and its measurement data after scanning.

This chapter describes:

- Starting the 2D Analysis Application on page 8-1
- Leveling the Trace and Setting Up Measurements on page 8-6
- Setting the Cursor Positions Using Feature Detection on page 8-24
- *Setting the Cutoff Filters* on page 8-34
- Customizing the Graph Display on page 8-16
- Measuring the Radius on Curved Surfaces on page 8-42
- Measuring Step Height on Curved Surfaces Using Fit and Level on page 8-47
- Saving Scan Data on page 8-47
- Reevaluation of Saved 2D Scan Data on page 8-48

# STARTING THE 2D ANALYSIS APPLICATION

## Introduction

2D analysis is an operation performed on data obtained from a scan. If a 2D scan is run, immediately after the scan procedure is complete, the **Analysis** screen automatically appears. When automatically opened following a scan, the **Analysis** screen contains the analysis of the "live" data. The following apply to live data:

- It is data which has just been collected from a scan;
- It has not been saved and is therefore untitled;
- This data can be manipulated by changing the scan parameters in the Scan Recipe Editor for the recipe used to create the scan.

If the data has been saved, it is no longer "live" as described above. It has the following properties:

- Its name appears in the Scan or Sequence Data (if it was save to that location).
- It must be opened through the Analysis screen in order to view or reanalyze it.
- It can be reanalyzed by changing the scan recipe parameters.

## **Data Analysis Procedure**

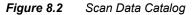
If the original scan has been saved and the Exit from the scan screen has been performed, use the following procedure to access the **Analysis** screen.

1. From the **Catalog** screen, click on the **Scan Data** button (see *Figure 8.1*) to display the **Scan Data Catalog** in the Information Display window.

Figure 8.1 Sequence Recipe Catalog

	🐺 Profiler - [Cata	log]						*Online/Loc	al X
	<u>File Edit Sample</u>	<u>V</u> acuum <u>H</u> ost <u>D</u> iag	nostic <u>T</u> asks H	elp					
		台 START 🏵	0 🕀 🐧	🕀 2D 3	D				20
	[			Scan Data Name:					
	Scan Recipe	(		2D_LONG_TRACE					
	нестре	Scan Data Path:		Scan Data	Recipe ID	Length (µm)	Number of Points	Creation Date (yyyy-mm-dd)	- 🔊 ) 🐼 (F
	Scan Data	🚈 SCAN DATA 💼 tm_Test		2d_long hl_2d_1 hl_2d_2 no_hl_2d	STI_2D_1 DIPTESTd DIPTESTd DIPTESTd	20 2 2 2	201 41 81 41	1999-06-10 1999-06-11 1999-06-11 1999-06-11	
Step 1 To display the Scan Data Catalog in the	Sequence			no_h1_2d no_h1_2d no_h1_2d	DIPTESTd DIPTESTd	4	81 401	1999-06-11 1999-06-11	
Scan screen, click on the <b>Scan Data</b> button.	Recipe								
	Sequence Data								
		Drive:	•						
Information display									)
Window			<u>T</u> humbnails	<u>R</u> eview					/
									Status
	SCAN DATA CATAL	OG					Empt	y? Clear	Status

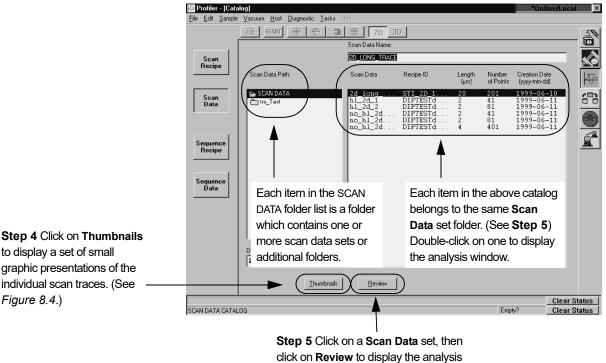
2. Click the **2D** button at the top of the screen to display the 2D Scan Data sets. (See *Figure 8.2*.)



<b>Step 2</b> Click on 2D to display 2D scan data sets in the catalog.	File       Edit       Sample       Vacuum       Host       Diagnositic       Laskis       Help       He	-
The Information Display window portion of the	Scan Recipe         20 LONG TRACE           Scan Data Path:         Scan Data         Recipe ID         Length         Number         Cireation Date           Scan Data         Recipe ID         Length         Number         Cireation Date	
<ul> <li>catalog screen contains:</li> <li>The list of folders -</li> </ul>	Scan         2± SCAN DATA         2d long STI 2D 1 20         201 1993-06-10           h1_2d_1         DIPTESTd 2         41 1999-06-11           h2_d_2         DIPTESTd 2         81 1999-06-11           h_2d_1         DIPTESTd 2         81 1999-06-11           h_2d_2         DIPTESTd 2         81 1999-06-11           no_h1_2d         DIPTESTd 2         81 1999-06-11           no_h1_2d         DIPTESTd 2         81 1999-06-11           no_h1_2d         DIPTESTd 2         81 1999-06-11	
• Displays the scan data list, the contents of the selected folder. (See <i>Figure 8.3.</i> )	Sequence Recipe Sequence Data	
Step 4 After clicking on the desired folder, click the <b>Thumbnail</b> button to display thumbnails of all data sets in		
the folder. (See Figure 8.4.)	Clear S SCAN DATA CATALOG Emply? Clear S	

- 3. Open the desired data folder by double-clicking on the folder name in the Scan Data list of folders. (See *Figure 8.3*.)
- 4. Click on the **Thumbnails** button to display small graphs (thumbnails) of all data sets in the chosen folder. (See *Figure 8.4*.)
- 5. To display the Analysis window for a particular data set, use **one** of the following procedures:
  - Double-click on the thumbnail; (See *Figure 8.4.*)
  - Click once on the thumbnail and then click on **OK**. (See *Figure 8.5*.)
  - Double-click on the scan data name in the scan data list. (See *Figure 8.3*.)
  - Click once on the name of the data set in the list (it highlights when chosen) then click on the **Review** button. (See *Figure 8.3*.)

Figure 8.3 Scan Data Catalog



screen.

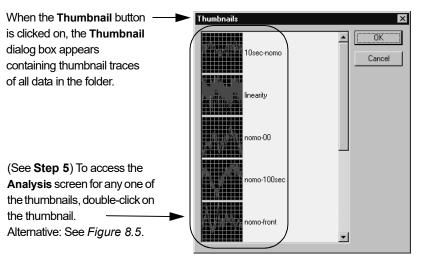
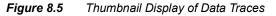
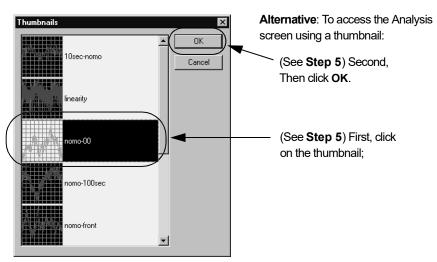


Figure 8.4 Thumbnail Display of Data Traces





# **2D Analysis Window Features**

The Analysis toolbar contains buttons that provide access to commonly used functions. (See *Table 8.1*.)

Table 8.12D Analysis toolbar

Button	Description
Q	Displays the graph view in the original view size.
Q	Activates the zoom capability. To focus on a certain part of the graph, use the cursor boundaries to define the zoom-in area.
<u>474</u>	Turns the Auto Scale Function for the zoom capability on and off.
LEVEL	First click activates the LEVEL cursors.
	Second click levels the trace according to cursor settings and activates the Measurement cursors.
STATS	Opens the Surface Parameter Summary window. If the Surface Parameter Summary window is currently minimized, it appears maximized upon clicking this button.
CALC	This initiates a recalculation of the data using newly chosen parameters from the recipe used for the scan. This can be executed on both live data (not yet saved) and saved data that was collected using the Software version 6.1 or higher.
NORM	Toggles, ON/OFF, the normal trace graph.
WAY	Toggles, ON/OFF, the waviness trace graph.
ROUGH	Toggles, ON/OFF, the roughness trace graph.
FINE	Activates Fine Cursor Movement mode of measurement and leveling cursors.
<b>3</b>	Prints the Analysis graph and the surface parameter summary.
1	Show/Hide Major Modes for the Histogram.

the margin above the

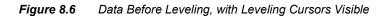
double tip arrow  $(\leftrightarrow)$ 

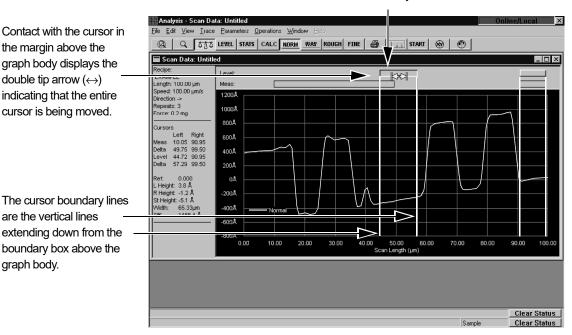
are the vertical lines

graph body.

# LEVELING THE TRACE AND SETTING UP MEASUREMENTS

To facilitate the analysis of trace data, the system uses vertical lines called cursors. Two types of cursors are used: Leveling and Measurement. Leveling cursors are used to define the baseline for the trace. Measurement cursors are used to define the region for measurement. In general, the leveling function should be performed prior to setting the Measurement cursors.





Left Cursor boundary box.

# Using Cursors

The procedure for using and moving cursors is the same for each function in which cursors are used. The cursor manipulation is the same for both the Leveling and Measurement functions.

## **Moving Cursors**

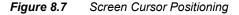
Cursors can be moved using either the track ball or the combination of keyboard space bar and arrow keys. When the scan initially appears in the Analysis screen, the left measurement cursor is highlighted.

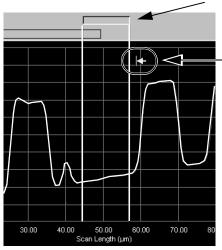
In the following discussion the screen's arrow cursor is called the *pointer*. The word *cursor* is used to describe the vertical boundary lines used to manipulate screen data.

#### Moving the Cursor with the Trackball:

1. The pointer is moved by rolling the trackball. As the pointer moves toward the right or left cursor, it interacts with the cursor's boundary line, taking on the shape of an arrow with a boundary line at its tip. (See *Figure 8.7.*) As the pointer passes the center line between the two cursors it changes direction, pointing toward the cursor boundary it is closest to. When it changes direction, it is able to interact with (reposition) the cursor boundary that it is pointing at.

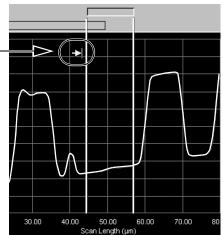
The single arrowheads demonstrate that only the nearest cursor boundary at which it is pointing, can be moved, thereby expanding or diminishing the cursor size. (See *Figure 8.7.*)





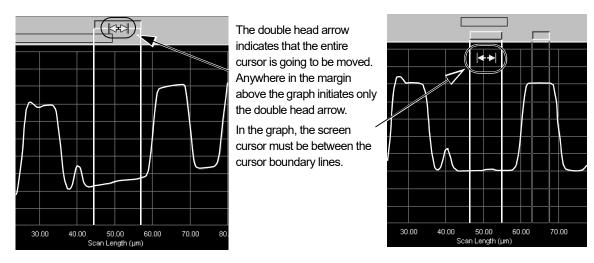
When the cursor is chosen, the boundary lines are highlighted and the boundary box appears recessed.

> The arrow direction points to the cursor boundary that is being interacted with. The pointers in these illustrations can move the boundaries they are pointing at in either direction. The trackball movement, as used in the click and drag procedure, determines the direction of cursor boundary movement.



The screen opens with the left cursor highlighted. Using the trackball, move the pointer to the cursor boundary. As the pointer passes the midpoint between the two cursors it changes direction, pointing at the closest cursor boundary. If that cursor is not highlighted, click with the left mouse button to activate the cursor. At any time after the pointer points to the boundary, as long as the cursor boundary is highlighted, the boundary can be repositioned in either direction by clicking with the left mouse button and dragging it. The pointer does not have to be directly next to the cursor boundary, only pointing at it. (In *Figure 8.7*, the pointer in the left illustration only moves the right cursor boundary.)

2. If the entire cursor is to be moved without changing its size (that is, without moving only one of its boundaries), the double arrow pointer is used. (See *Figure 8.8.*) Use the trackball to position the pointer either in the margin above the graph, or between the cursor boundaries, causing the double arrow to appear. (See *Figure 8.8.*) With the double arrow positioned to move the highlighted cursor, click and hold the left trackball button while dragging the cursor to its new location.



#### Figure 8.8 Double Cursor - Relocating the Entire Cursor

#### Moving the Cursor with the Space Bar and Arrow Keys

The combination space bar and arrow keys can be used to move the cursors to new locations on the trace. The space bar and arrow keys function independently of the trackball and the associated pointer used to change the cursor size or relocate it.

- 1. When the screen opens, the left cursor is highlighted. To select a cursor or to select another cursor, click the space bar. Each time the space bar is clicked it toggles once in the progression from left cursor to right cursor to both cursors, then back to the left cursor.
- 2. Once the desired cursor is highlighted (or both cursors are highlighted) use the left or right arrow keys to move the cursors. Notice that the cursor(s) move a small consistent distance in the direction of the arrow key each time the arrow key is clicked.

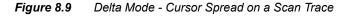
## Changing the Cursor Size Using the Space Bar and Arrow Keys

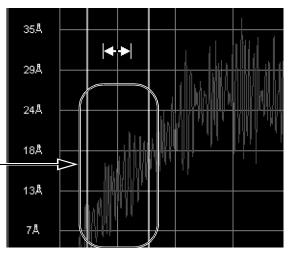
The combination space bar and arrow keys can be used to change the cursor size. They function independently of the trackball and the associated pointer used to change the cursor size or relocate it.

Once the desired cursor is highlighted (or both cursors are highlighted) use the up or down arrow keys to spread or reduce the cursor(s) size. Notice that the cursor boundaries move outward (up arrow) or inward (down arrow) a small consistent distance each time the arrow key is clicked.

## **General Cursor Use**

In the scan pictured in *Figure 8.9*, the tract is very jagged indicating a high noise level. When the scan shows evidence of this type of noise, or is very rough, the measurement cursor boundary lines set a distance over which an average is computed by the system. The resultant data is then used for the purpose of evening out the trace data. In rough or noisy scans, set the cursor boundaries further apart than would be the case in smooth scans. This technique is called the *Delta Mode*.





In this blow up of a scan in the **Analysis** screen. The spread of the cursor boundaries in this trace is wide enough to compensate for the high noise level. — Notice the spikes and valleys that depict the noise.

- 1. For rough or noisy scans, the cursor boarders should be expanded to cover a wider region. To adjust the width of the leveling or measurement cursor:
  - a. Click outside the border of the measurement cursor that is to be expanded and drag it to the new position. (See *Figure 8.7* and step *on page 8-7.*)
  - b. (Alternate resizing of cursor) With the cursor highlighted, use the up arrow key to spread the cursor and the down arrow key to shrink the cursor. Each click on the arrow key expands or shrinks the cursor a consistent amount. (See Step under *Changing the Cursor Size Using the Space Bar and Arrow Keys* on page 8-8)

The average value of the height within the region is then used for measurement or leveling.

- 2. For finer cursor control:
  - a. Click the **Operations** menu and select **Fine Movement Mode**, or click the **FINE** button.
  - b. In the **FINE** cursor mode, the movement with each arrow key click is exactly one data point.
  - c. NOTICE: The FINE cursor mode has no effect on the trackball method of movement and resizing.

# Using the Leveling Cursors

In order to obtain an accurate analysis, the trace must be given a level frame of reference. This is accomplished through the leveling procedure. For 2D scan data, two areas (defined by cursors) on the scan that are at equal heights define a reference axis for plotting the data and calculating surface parameters.

Acceptable leveling cursor positions can be determined in advance by viewing a sample in the XY View window prior to finalizing the recipe and beginning the scan. However, the proper position is not always obvious, and it is possible to accidentally set them at inappropriate locations. In an extreme case, the left leveling cursor might end up at the bottom of a large step, and the right leveling cursor on the top.

1. Click on the LEVEL button in the tool bar. (Alternative: Operations/Level Trace.) This activates the leveling cursors. They appear at the locations currently specified in the recipe, with the left cursor selected (highlighted).

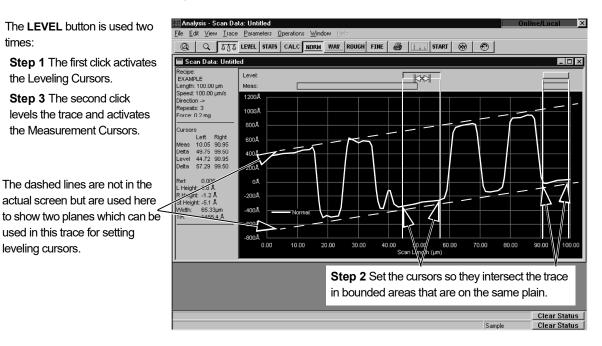


Figure 8.10 Analysis Screen with Unleveled Trace and Level Cursors

2. To set the cursors so that the trace is accurately leveled, it is important to find two areas on the trace that are on the same plain. Set the cursors to the desired positions. (For help moving cursors, see Using Cursors on page 8-6.)

times:

the Leveling Cursors.

Step 3 The second click

used in this trace for setting

leveling cursors.

3. Click the LEVEL button. (Alternative: Operations/Level Trace.) The data is leveled and replotted and the measurement cursors appear.

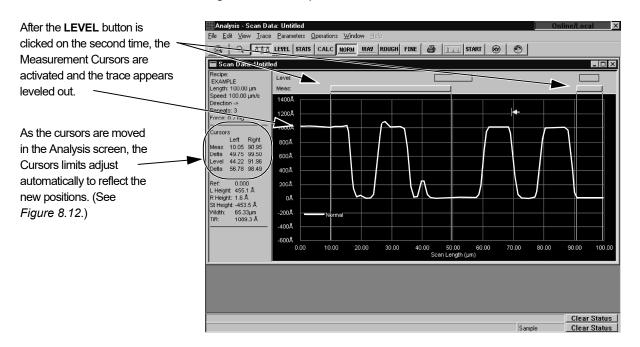


Figure 8.11 Analysis Screen with Leveled Trace and Measurement Cursors

# **Using the Measurement Cursors**

The measurement cursors are used to define the region or regions of interest for measurement.

## EXAMPLE:

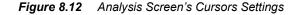
1. In order to determine the difference in height between two regions, those two regions must each be clearly identified. The measurement cursors are used to isolate both regions for measurement and subsequent calculation.

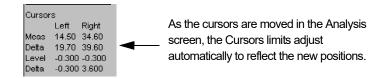
2. To determine the area in a peak or valley region, the Measurement Cursors can be moved (or adjusted if they were partially out of position) to accurately enclose those regions and the area calculated or recalculated.

The parameters affected by the measurement cursors can be added or taken out of the recipe so that the new results are displayed in the Surface Parameter Summary Window (**STATS**) of the screen after the cursors are moved and the results of the move recalculated. This procedure can be performed on "live" data or previously saved data (from scans using software version 6.1 or newer).

The **Analysis** window initially appears with the measurement cursors set at the locations specified in the scan recipe.

Like the leveling cursors, the measurement cursors can be freely moved to any location on the trace. In the **Scan Data Analysis** window the displayed cursor positions are recalculated whenever the measurement cursors are moved to new locations.





Parameters in the **Surface Parameter Summary** window are not recalculated automatically when the measurement cursors are moved. If new data is required with the adjustment of the cursors, the recipe used to create the scan can be modified to present new parameters in the Surface Parameter Summary window or remove unnecessary ones.

- 1. From the Analysis screen, click on Edit to display its menu. (See Figure 8.13.)
- 2. Then click **Recipe...** to open the scan recipe used to create the scan. (See *Figure 8.13.*)

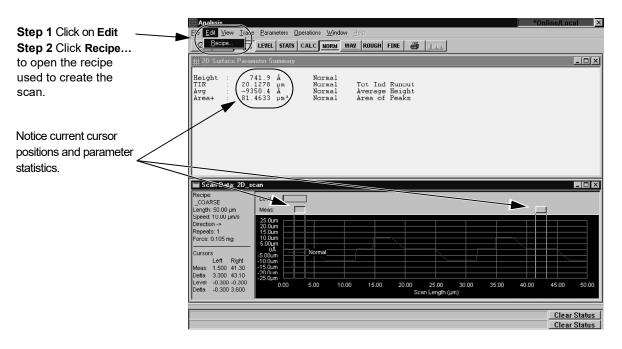


Figure 8.13 Accessing the Scan Recipe from the Analysis Screen

This displays the scan recipe screen from which parameters can be added or removed. In *Figure 8.14* the **General Parameters** window of the Recipe screen has been opened to change the parameter set to be calculated with the next cursor adjustment. (This procedure can be used with both live and saved data.)

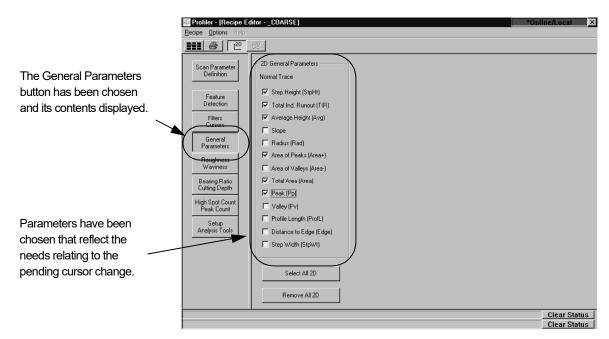


Figure 8.14 Recipe Screen - General Parameters Window

- 3. When the parameters have been chosen, click on **Recipe** to display its menu. (See *Figure 8.15.*)
- 4. Choose **Analysis** to return to the Analysis screen. The system calculated the parameter values for the chosen parameters using the current cursor settings and displays them in the **Surface Parameter Summary** window. (See *Figure 8.15*.)



Ctrl+P

Print.

Exit Recipe Editor

Figure 8.15 Exit Recipe Editor to Return to Analysis Screen

D General Parameters

ormal Trace

After repositioning the cursors, to recalculate the parameters in the **Surface Parameter Summary** window, use the following procedure:

5. Set the Measurement Cursor positions. (For help positioning the cursors, see *Using Cursors* on page 8-6.)

In the following illustration the cursors have been moved to capture the area under the two highest features in the scan. Parameters have been chosen that respond to the new position. (See *Figure 8.16*.)

to return to the Analysis

screen.

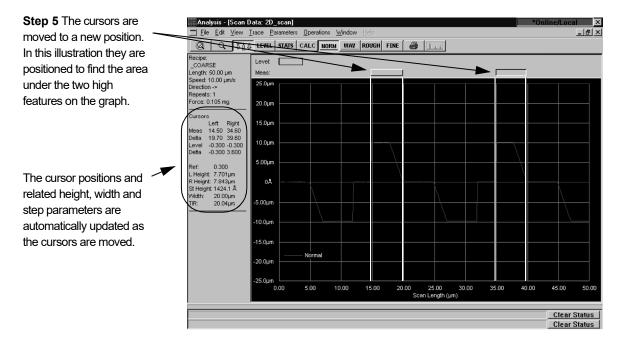


Figure 8.16 Analysis screen with Repositioned Cursors

6. After positioning the measurement cursors, the parameters in the **Surface Parameter Summary** window are ready to be updated:

Click the **CALC** button to perform the recalculation. (See *Figure 8.17*.)



Step 6 Click CALC to recalculate the parameters using the new	Analysis - [Scan D	lata: 20_scan] [race Parameters Operations Window Help [LEVEL STATE CALC NORM WAY ROUGH FINE 🖨 []
cursor positions.	Recipe: _COARSE Length: 50.00 µm Speed: 10.00 µm/s	Level:

The parameters are automatically recalculated and the **Surface Parameter Summary** window is updated. In *Figure 8.18*, the chosen parameters in the Scan Recipe display their new values in keeping with the new cursor positions. Only the chosen parameters become part of the data set that is calculated.

2D Surface Para	imeter Summary			_			
TIR 20 Avg -8 Area+ 41 Area 10	424.1 Å .0440 μm 915.8 Å .1951 μm <sup>2</sup> 0.406 μm <sup>2</sup> .0618 μm	Normal Normal Normal Normal Normal Normal	Tot Ind Ru Average He Area of Pe Total Area Peak	ight aks			
Scan Data: 2D_:			_	_	_	_	
Recipe: _COARSE	Level:	]		_	-		
Recipe: _COARSE Length: 50.00 µm Speed: 10.00 µm/s	Level: Meas:	]		-			
Recipe: _COARSE Length: 50.00 µm Speed: 10.00 µm/s Direction -> Repeats: 1	Level: Meas: 25.0um 20.0um			-			
Recipe: _COARSE Length: 50.00 µm Speed: 10.00 µm/s Direction ->	Level:						
Recipe: _COARSE Length: 50.00 µm Speed: 10.00 µm/s Direction -> Repeats: 1 Force: 0.105 mg Cursors	Level:	Normal					
Recipe: _COARSE Length: 50.00 µm Speed: 10.00 µm/s Direction -> Repeats: 1 Force: 0.105 mg Cursors 	Levet:	] Normal					
Recipe: COARSE Length: 50.00 µm Speed: 10.00 µm/s Direction -> Repeats: 1 Force: 0.105 mg Cursors Left Right	Level:	Normal 5.00 10.00	15.00	20.00 25.0	0 3000	35.00 40	00 45.00

Figure 8.18 Surface Parameter Summary Window

- 7. To retain the newly calculated values in a data file and the new cursor positions in the recipe, the data must be saved. Click **File** to open its menu. (See *Figure 8.19.*)
- 8. Choose Save Data... from the File menu to open its dialog box. (See *Figure 8.19*.)

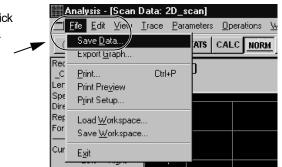


Figure 8.19 File Menu in Analysis Screen

- 9. In the Save dialog box, ensure that the proper folder is chosen, enter the name that the data is to be stored under. (See *Figure 8.20*.)
- 10. Click Save to save the data. (See Figure 8.20.)

When the recalculation procedure is performed, only the parameters chosen in the scan recipe are visible and only those are changed.

> Step 7 To save data, click File to display its menu.

Step 8 Choose Save Data... from the File menu.

	Save Scan Data	
	Save jn: 🔄 scandata 💽 🖻 📰 🏢	
Step 9 Enter the file name.	File name:     20 scar       Save     Save       Save as type:     Scan Data Files (*.dat)       Cancel	Step 10 After the name is entered click Save to save the data to the file.

Figure 8.20 Save Scan Data Dialog Box

CUSTOMIZING THE GRAPH DISPLAY

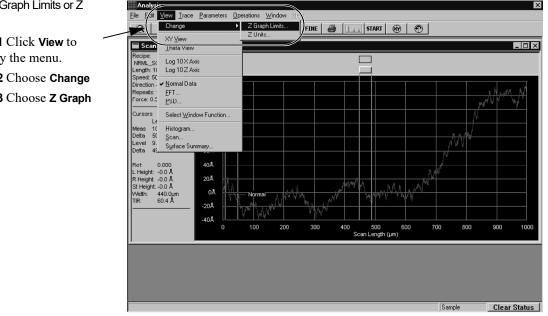
The View menu offers several options for customizing the graphical display of the data. The instrument proportions the data to the area available in the window. However, the data can be sized by setting custom graph limits.

# Changing the Z Limits Display

Changing the Z Limits Display allows the user to set the scale on the graph.

1. Click the View menu to display its menu. (See Figure 8.21.)

Figure 8.21 Analysis Screen with View Menu

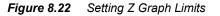


To set the Z Graph Limits or Z Units

- Step 1 Click View to display the menu.
- Step 2 Choose Change
- Step 3 Choose Z Graph Limits

- 2. Choose **Change** from the View menu. (See *Figure 8.21*.)
- 3. Select **Z** Graph Limits. (See *Figure 8.21*.)

The dialog box appears. (See Figure 8.22).





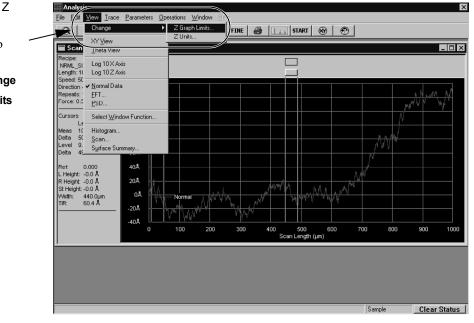
- 4. Highlight the old limit and enter the new limits in the Upper and Lower Z Limit fields: (See *Figure 8.22*.)
  - Higher to reduce the size of the trace;
  - Lower to increase the size of the trace.
- 5. Click **OK** to apply the limits to the displayed data. (See *Figure 8.22*.)

# Changing the Z Units Display

The Profiler plots the data in  $\mu$ m, nm, Å, or both  $\mu$ m and Å with a crossover value that is set by the user.

1. Click the View menu to display its menu. (See Figure 8.23.)

Figure 8.23 Analysis Screen with View Menu



2. Choose Change from the View menu. (See *Figure 8.23*.)

To set the Z Graph Limits or Z Units

- **Step 1** Click **View** to display the menu.
- Step 2 Choose Change
- Step 3 Choose Z Units

3. Select Z Units. (See Figure 8.23.)

The Set Z Units dialog box appears (see Figure 8.24).



Step 4 Choose the desired units by	Set Z Units	×	Step 5 Click on
clicking in the appropriate radio button.	Ο μm only mode	ОК	<b>OK</b> to apply the
For the bottom choice, after clicking in	O nm only mode		settings to the
the radio button, enter a distance at	O Å only mode	Cancel	displayed data.
which it changes between microns	-		
and angstroms.	<ul> <li>μm and Å mode crossover at: 10000.00 Å</li> </ul>		

4. Select the desired Z unit mode. Choose between:

- Microns only (µm only mode),
- Nanometers only (nm only mode),
- Angstroms only (**Å only mode**),
- Combination mode where the reading could be in angstroms or microns depending on the trace magnitude (µm and Å crossover at [variable] Å). In this mode, enter the trace magnitude at which the units change from microns ( $\mu$ m) to angstroms (Å) or from Å to  $\mu$ m. In Figure 8.24, the mode crosses over at 10000 Å.
- 5. Click OK to apply the settings to the displayed data.

## **Displaying Data in FFT Mode**

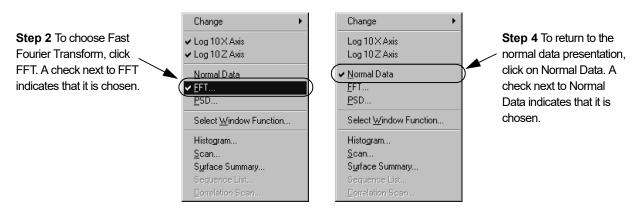
The data can be replotted using the Fast Fourier Transform (FFT) in order to expose patterns of data that indicate regularly spaced features of the same width. By default, the instrument plots the Scan View data in linear coordinates ("Normal" data).

A choice of window functions is available to apply to the endpoints of the FFT data.

Selecting FFT:

- 1. Click View to display its menu. (See Figure 8.25.)
- 2. Select FFT. (See Figure 8.25.)

Figure 8.25 View Menu with FFT Chosen



The instrument replots the data.

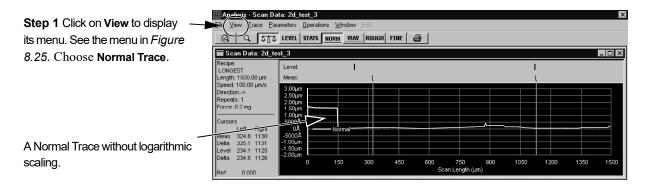
- 3. Click View to display its menu. (See Figure 8.25.)
- 4. Select **Normal Data** to return to the Normal Data mode. (See *Figure 8.25*.) The current data mode selection is one with the check next to it.

# **Displaying Data on Logarithmic Scaling**

The display can be set to plot either **Normal** or **FFT** data in logarithmic X and Z coordinates. Logarithmic scaling helps to delineate small features that are dwarfed by the larger features in a linearly proportioned scan.

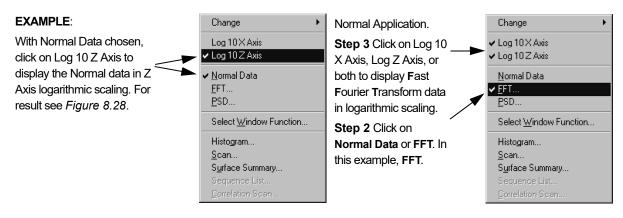
1. In the Analysis screen, click on **View** in the Menu Bar. (See *Figure 8.25* for an illustration of the menu.)

Figure 8.26 Analysis Screen with a Normal Trace



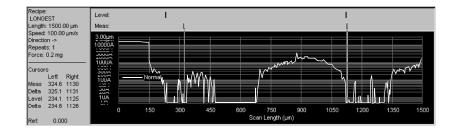
- 2. From the view menu, choose either Normal Data or FFT. (See Figure 8.28.)
- 3. Select Log 10 X or Log 10 Z or both from the menu. A check appears next to the chosen items.





A check appears beside the menu selection and the instrument replots the data for the chosen axis.

Figure 8.28 Normal Trace and Z Axis Logarithmic Scaling



4. Return to linear plotting by disabling the log 10 selection(s) (See Step 3).

# Viewing in Zoom Mode

Selected portions of the trace can be zoomed in on to help isolate features for measurement, especially when using the Fine measurement mode for small-increment cursor movement. Feature isolation can be improved with the Scale function, that allows vertical as well as horizontal scaling.

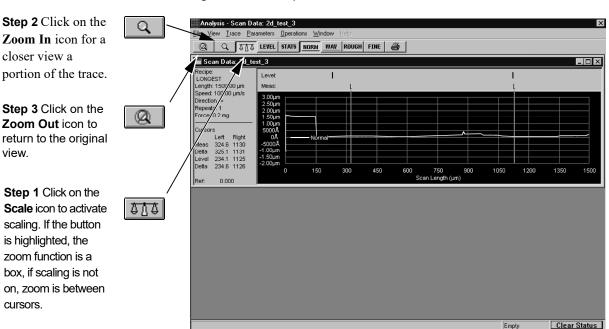
- 1. The zoom function operates using the Scale icon and the Zoom icon. (See *Figure 8.29.*) Click on the scale icon to choose the desired state of the scale function.
  - If the Scale function is on, two vertical lines appear on the scan.
  - If the Scale function is **off**, a box appears.
  - The scale icon 4 . toggles the scale function on and off.
  - 2. Click on the **Zoom-in** icon to activate the zoom function. (See *Figure 8.29*.)

This is the **Normal** trace from *Figure 8.26* with the **Z Axis** logarithmic scaling applied.

See *Figure 8.27*, **EXAMPLE**, for an illustration on setting up this display.

Zoom Procedure

3. Click on the **Zoom-out** icon to return to normal display. (See *Figure 8.29*.)

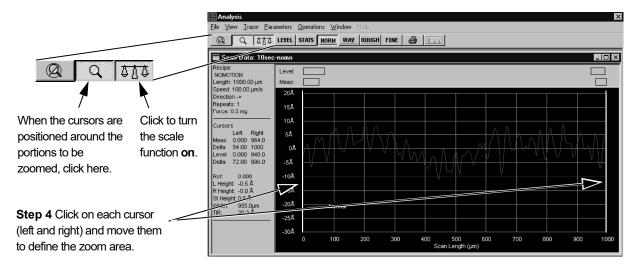


*Figure 8.29* Analysis Screen with the Zoom and Scale Function Buttons

Zoom with Scaling ON

4. Click and drag the cursors and position them, one on each side of the feature being zoomed in on. (See *Figure 8.30*.)

Figure 8.30	Analysis Screen Using Scaling Zoom
-------------	------------------------------------



#### Zoom with Scaling OFF

5. Click and drag on a border or corner of the zoom box, to enclose the portion of the scan to be zoomed in on. (See *Figure 8.31*.)

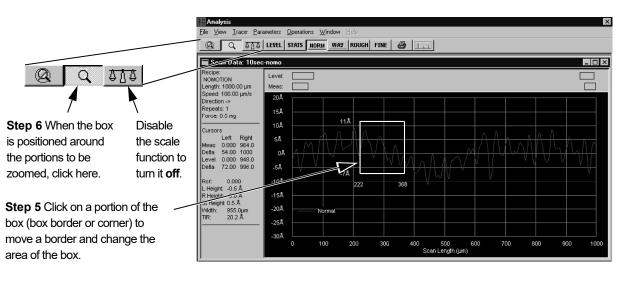


Figure 8.31 Analysis Screen Using Boxed Zoom



**NOTE:** For finer positioning, go to the **Operations** menu and select **Fine Movement Mode**, or click its button on the toolbar. Press [<] or [>] to position the vertical lines.

- 6. Click on the **Zoom In** icon to zoom into the area defined by the cursors or the zoom box. (See *Figure 8.31*.)
- 7. Perform any measurement or leveling procedure necessary to analyze the zoomed data.
- 8. Click the **Zoom In** button again to deactivate the zoom cursors and reactivate the measurement cursors. (See *Figure 8.31*.)
- 9. To save the new data and the new cursor positions, use the procedure described in *Saving Data From the Zoom Procedure* on page 8-23.

**Parameter Summary** 

Saving data and cursor position in <b>Surface</b> Parameter Summary	. To update the data in the <b>Surface Parameter Summary</b> window and to store zoomed cursor positions in the recipe, click the <b>Operations</b> menu, and select <b>Recalc with Zoomed Level Cursors.</b> (See <i>Figure 8.32</i> )
	<i>Figure 8.32</i> Recalculate and Save Zoomed Leveling Cursors
<b>Step 1</b> Click on Operations in the Menu bar.	Operations         Window         Help           Level Trace         Cancel Leveling           Eine Movement Mode         Step 2 Choose Recalc With
Step 2 Choose Recalc With Zoomed Level Cursors to recalculate data and save new cursor positions.	✓ Zoom     Undo Zoom     Hecalc With UnZoomed Level Cursors     Recalc With Zoomed Level Cursors

Unzoomed Cursors. (See *Figure 8.32*)
3. To return to the original scan view click the Undo Zoom icon , or go to

the zoomed cursor positions, go to the Operations menu and select Recalc With

the Operations menu and select Undo Zoom.

### Viewing the Trace Information

The left side of the Analysis window displays the basic data taken from the leveling and measurement cursors. These values are updated instantaneously with the positioning of the cursors (see *Table 8.2*).

Table 8.2         Trace Information Parameter
---

Parameter	Description	
Meas (µm)	Displays the X-axis value of the left vertical line of the left and right measurement cursors.	
Delta (µm)	Displays the X-axis value of the right vertical line of the left and right measurement cursors.	
Level (µm)	Displays the X-axis value of the left vertical line of the left and right leveling cursors.	
Delta (µm)	Displays the X-axis value of the right vertical line of the left and right leveling cursors.	
Ref (µm)	Displays the Feature detection reference point within the trace.	
L Height	Displays the Average height of the scan region marked by the left measurement cursor.	
R Height	Displays the Average height of the scan region marked by the right measurement cursor.	
St Height	Displays the Difference between the R Height and the L Height.	

# Saving Data From the Zoom Procedure

	Parameter	Description
	Width	Displays the Difference between the average X value of the scan region marked by the right measurement cursor, and the average X value of the scan region marked by the left measurement cursor.
	TIR	Displays the difference between the highest and the lowest points on the scan between the central points of the measurement cursors. Stands for <b>Total Indicator Runout</b> .

 Table 8.2
 Trace Information Parameter

# SETTING THE CURSOR POSITIONS USING FEATURE DETECTION

### **Feature Detection**

Feature Detection is used to enable automatic detection of some common classes of profile features (see *Figure 8.34* and *Figure 8.35*) to facilitate measurement throughput and consistency. Feature Detection makes it possible to automatically and reliably set the position of the measurement and leveling cursors relative to the rising and falling edge of a step-like feature, or the apex or an arc-like feature.

In conjunction with feature detection, both the location of the edge (or the apex of an arc) and the step width, can be calculated and displayed in the Analysis window.



**CAUTION:** It is important to ensure the accuracy of the Video Calibration and the Scan Position Offset Calibration prior to enabling Feature Detection.

1. To access the Feature Detection parameters, click on the **Feature Detection** button in the **Recipe Editor**.

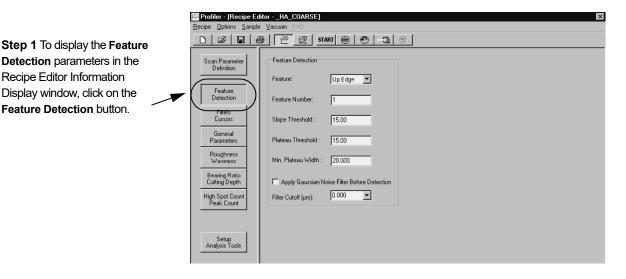


Figure 8.33 Feature Detection - Recipe Editor

2. Feature: -This parameter allows the user to choose between six different features that can be detected during a scan. (See also Quick Reference *Table 8.4 on page 8-33.*)

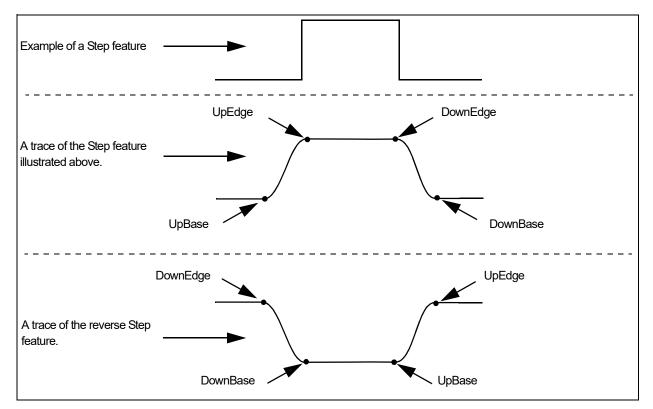
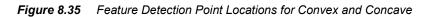


Figure 8.34 Feature Detection Point Locations on a Step



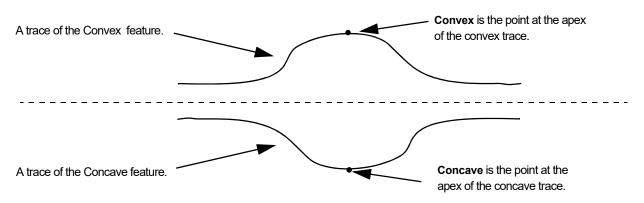


Table 8.3         Feature Detection Descriptions (See Figure 8.34 and Figure 8.35.)			
Feature	Description		
None	No feature detection is being used.		
UpEdge	At the trailing edge of a feature rise, it is the point at which the trace begins the plateau. (See <i>Figure 8.34</i> .)		
	<b>NOTE</b> : The point location can be modified using the <b>Distance to Edge</b> parameter in the <b>General Parameters</b> Window.		
UpBase	At the trailing edge of a plateau, it is the point at which the trace begins to turn upward. (See <i>Figure 8.34</i> .)		
DownEdge	At the trailing edge of a plateau, it is the point at which the trace begins to turn downward. (See <i>Figure 8.34</i> .)		
DownBase	At the trailing edge of a feature decline, it is the point at which the trace begins the plateau. (See <i>Figure 8.34</i> .)		
Convex	This is the point at the apex of a convex feature. (See <i>Figure 8.35.</i> )		
Concave	This is the point at the apex of a concave feature. (See <i>Figure 8.35.</i> )		

 Table 8.3
 Feature Detection Descriptions (See Figure 8.34 and Figure 8.35.)

Selecting a feature for detection:

- a. Click on the down-arrow next to the variable box to display its menu. (See *Figure 8.36.*)
- b. Click on the desired feature to select it. In necessary, use the scroll bar to reveal other features. (See *Figure 8.36*.)

Figure 8.36	Feature - Feature Detection - Recipe Edito
-------------	--

	- Feature Detection	
_	Feature:	Up Edge
	Feature Number:	Up Edge  Up Base Down Edge Down Base
	Slope Threshold :	10.00
	Plateau Threshold :	10.00
	Min. Plateau Width :	10.000
	🥅 Apply Gaussian No	ise Filter Before Detection
	Filter Cutoff (µm):	0.000

Feature Detection allows the user to choose from six feature option (convex and concave not shown). Click on the down-arrow to display the menu. Click on the desired feature to choose it. **3.** Feature Number: - If multiple edges are detected in the scan, Feature Number provides a way to select a specific edge for detection. (See *Figure 8.37* and also *Quick Reference Table 8.4 on page 8-33*.)

### Changing the Feature Number:

a. Double-click in its variable box to highlight the current number and type in the new number. (Use only whole numbers. 1 is Default)

#### Figure 8.37 <u>Detection Variables</u> - Feature Detection - Recipe Editor

	- Feature Detection	
	Feature:	Up Edge 💌
$\frown$	Feature Number:	1
	Slope Threshold :	10.00
)	Plateau Threshold :	10.00
	Min. Plateau Width :	10.000
	🗖 Apply Gaussian No	bise Filter Before Detection
	Filter Cutoff (µm):	0.000 💌

4. **Slope Threshold:** - This factor sets the value at which any rise or fall in a trace is considered to be a slope, not just part of the roughness or noise. This means that the **Slope Threshold** defines a point at which the system recognizes a trace line as following or preceding an *edge, convex* or *concave* point. (See also *Quick Reference Table 8.4 on page 8-33.*)

#### Changing the Slope Threshold:

- a. Double-click in its variable box to highlight the current number and type in the new number:
  - Use values between 0 and 50.000 (these numbers are proportional and have no units)
  - Default is 10.000 for a step and 1.000 for an apex point.
- b. If the artifact is much larger in comparison to the surrounding roughness of the surface:
  - Set the value higher.
- c. If the artifact is only a little larger than the surrounding roughness:
  - Set this value lower.
  - Set the Minimum Plateau Width (description follows) to avoid any ambiguity in identifying the correct edge.

- 1	*
- 1	•
- 1	1
- L	152

**NOTE:** For very noisy scans where the system is having difficulty detecting the feature, decrease the Slope Threshold. A value as low as 5.00 might work well.

Detection parameters are changed by clicking in the appropriate variable box to highlight the current number. Then type in the new number. \*

5. **Plateau Threshold:** - This factor affects the precise horizontal location calculated for an edge or arc point. This parameter allows for the positional adjustment of the point to the left or right. (See also *Quick Reference Table 8.4 on page 8-33.*)

#### Changing the Plateau Threshold:

Double-click in its variable box to highlight the current number and type in the new number:

- Use values between 0 and 50.000 (these numbers are proportional and have no units)
- Default is 10.000 for a step and 0.000 for an apex point.

**NOTE:** When comparing data from scans of identical features, find a value that works and then use it consistently. Data is changed if differing **Plateau Threshold** numbers are used.

HINTS for successfully setting the Plateau Threshold:

If setting the up edge or down edge:

- Set this value to about the same value as the **Slope Threshold** (from 0 to 50.000 these numbers are proportional and have no units).
- If the threshold is slightly greater than the **Slope Threshold**, the precise location of the edge moves slightly to the left for an **UpEdge** or to the right for a **DownEdge**.
- If the threshold slightly smaller than the **Slope Threshold**, the precise location of the edge moves slightly to the right for an **UpEdge** or to the left for a **DownEdge**.

#### If setting the UpBase and DownBase:

• Adjustments are opposite for UpBase when compared with UpEdge and for DownBase when compared with DownEdge.

#### If setting the Concave or Convex arc:

• If the default setting is not being used, set this value to a very small number (from 0 to 1.000 – these numbers are proportional and have no units).



**NOTE:** The Slope Threshold determines whether or not an edge is detected. The Plateau/Apex Threshold determines only the precise reported location of a detected edge.

6. Min. Plateau Width: - Minimum Plateau Width defines the minimum horizontal distance between rising and falling edges (or falling and rising edges). This is used in feature detection to identify true features. (See also *Quick Reference Table 8.4 on page 8-33.*)

The Minimum Plateau Width can be used to reject such peaks that may otherwise prevent the system from detecting the correct edge. For step-like features, the Minimum Plateau Width specifies a plateau as follows:

- For ascending features (such as **UpEdge**, **UpBase**), the plateau follows the detected edge.
- For descending features (such as **DownEdge**, **DownBase**), the plateau precedes the detected edge.

#### Changing the Min. Plateau Width:

Double-click in its variable box to highlight the current number and type in the new number:

- Use values between 0.005 and 1000.00 μm (0.0002 to 39.3701 mil.)
- Default is 10 µm.



**NOTE:** This is very dependent on which **Feature** is chosen for detection and which **Feature Number** is used.

HINT to successfully set the Plateau Width:

If setting the UpEdge, DownEdge, UpBase, or DownBase features:

• Set this value to be greater than the width of stray peaks, but somewhat less than the width of the step to be detected (from 0.005–1000.00 mm to 0.002–39.3701 mil.).



**NOTE:** Setting the **Plateau Width** to wide results in no edge being found.

The Minimum Plateau Width is not intended for use with Concave or Convex features. In cases of rough sample surfaces, though, it might be useful.

- For a Convex arc: The Minimum Plateau Width specifies a minimum width for the feature, and so can be used to reject narrow roughness peaks in the vicinity of the arc.
- For a Concave arc: The Minimum Plateau Width is used to specify a minimum size for a level section following a detected arc.

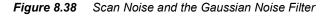


**NOTE:** The feature detection setup can be evaluated by reviewing trace data in the analysis window. The parameter "**ref**" that is listed to the left of the trace, indicates the position of the detected feature relative to the start of the scan. If this parameter reads "0" then no feature is being detected and the feature detection setup must be altered.



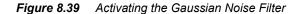
**NOTE:** It is important to set the thresholds appropriately for the type of feature being scanning so that the Feature Detection calculation is reliable. Also note that the profile scan length must include not only the entire length of the artifact but enough on both sides to set cursors for reliable data leveling.

7. Apply Gaussian Noise Filter Before Detection - This is only used to filter out unwanted noise so the feature detection can more easily detect designated features. (See *Figure 8.38.*) *It does not apply the result to scan data.* For use of the Gaussian Filter with scan data, see *Filters* on page 3-50.



A Step scan with noise, before applying the Gaussian Noise Filter. WWW-W	which have
A Step scan with noise, after applying the Gauss Noise Filter.	

Activating this feature, click in the empty check box to put a  $\checkmark$  in it. (See *Figure 8.39.*) Then set the **Filter Cutoff (mm)** size.



	- Feature Detection	
	Feature:	Up Edge 💌
	Feature Number:	1
To activate the Gaussian Noise	Slope Threshold :	10.00
Filter Before Detection feature,	Plateau Threshold :	10.00
click in its check box. A check $(\checkmark)$ indicates that it is chosen.	Min. Plateau Width :	10.000
	Apply Gaussian Noise Filter Before Detection	
	Filter Cutoff (µm):	0.45

8. Filter Cutoff (mm) - This option is only activated when there is a check in the Apply Gaussian Noise Filter Before Detection check box. (See *Figure 8.39*.) The number to be entered is in microns. This determines the noise level that is filtered out.

For an in depth discussion on filters, see *Filters* on page 3-50.

Changing the Filter Cutoff

- **a**. Ensure that a Feature has been chosen.
- b. Click on the down arrow to display its menu.
- c. Click on the desired value.

**NOTE:** A Feature must be chosen in order for the Gaussian Filter to become active. If **None** is showing in the **Feature** variable box, The Gaussian option is grayed out. To activate it, select a feature. (See *Figure 8.40.*)

 The Filter Cutoff range is from 0.25 through 800 μm. Only established variables may be chosen.

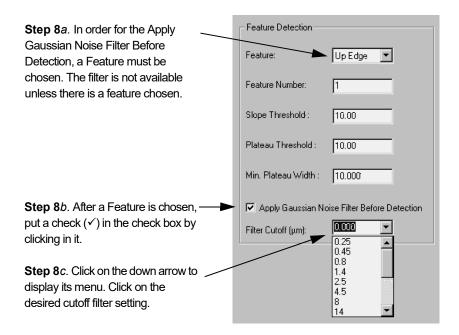


Figure 8.40 Filter Cutoff Menu

9. *Figure 8.41* through *Figure 8.43* demonstrate the usefulness of Feature Detection. Three scans were taken across the same section of the feature, beginning and ending at different points along the profile. Each time, the cursors are automatically set in the same place relative to the feature being detected, at the second UpBase.

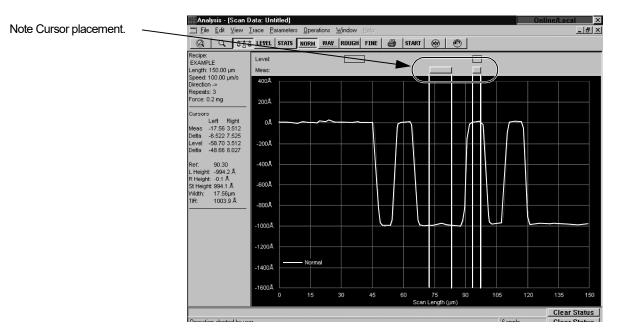
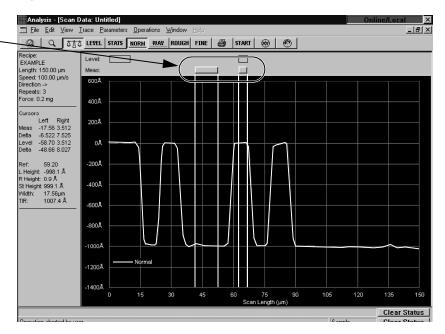
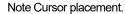


Figure 8.41 Feature Detection - Run 1 with Automatic Cursor Placement

Figure 8.42 Feature Detection - Run 2 with Automatic Cursor Placement





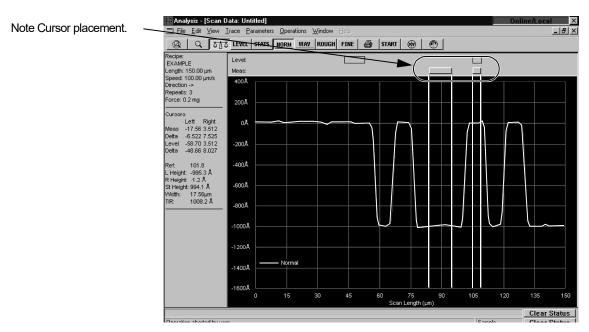


Figure 8.43 Feature Detection - Run 3 with Automatic Cursor Placement

### **Feature Detection Quick Reference Table**

Table 8.4	Feature Detection Va	ariables
-----------	----------------------	----------

Feature	Description
Feature	Identifies the type of feature to be detected, or turns Feature Detection off.
Feature Number	Provides a way to select a particular edge for detection if there are multiple edges detected in a scan.
Slope Threshold	Sets the value at which an upward slope in the trace is considered to be preceding the edge or apex; that is, when an upward slope appears that rises significantly above the general roughness of the surface.
	<b>Slope Threshold</b> is very similar to a signal-to-noise ratio. The best values for a given sample will depend on the relative scales of the artifact being examined and the surrounding surface roughness, as well as parameters such as scan speed, sampling rate, and so on. For step heights, <b>10</b> is a good typical value.
Plateau Threshold	Affects the precise horizontal location calculated for the edge or arc. Since the edge of a step is rarely a perfectly defined location, this factor allows for the adjustment of the value to the left or right, depending on whether the edge is to be the bottom of the step, the top of the step, or somewhere in between. Generally, the best way to specify the <b>Plateau Threshold</b> is to set the same value as the <b>Slope Threshold</b> .
Min. Plateau Width (µm)	This value specifies the minimum horizontal length between a rising and falling edge, which is used in the feature detection calculation to determine the correct edge.
	This is useful in preventing erroneous feature detection of spikes due to noise, particles, rough surfaces, etc.

# SETTING THE CUTOFF FILTERS

Setting Cutoff Filters can be accomplished using "live" data or previously saved data. "Live" data has not yet been saved, and the **Analysis** window is still open, displaying the scan data from the current scan (i.e., the **Analysis** window has not been closed on the current scan data).

The scan data does not come directly from the sensor, but instead is filtered through three stages:

- an analog hardware filter
- a digital decimation filter
- digital software filtering
- 1. The sensor output is filtered by the analog hardware filter so that it can be digitized with minimal distortion. The filter also reduces noise by attenuating higher frequencies. It has a fixed cutoff frequency of 2 kHz.
- 2. The signal then passes through an analog-to-digital (A/D) converter. The A/D converter has a nominal sampling frequency of 31.25 kHz.
- **3**. Next, the signal passes into the digital decimation filter. This step reduces the signal sampling rate from the original31.25 kHz down to the sampling rate selected in the recipe by the user.

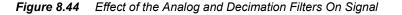
The cutoff wavelength depends on the scan speed as described by the following equation:

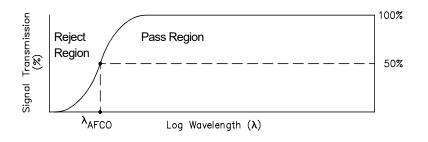
 $Cutoff Wavelength = \frac{Scan Speed}{Cutoff frequency of combined filters}$ 

For example, with a scan speed of 100  $\mu$ m/s, and a sampling rate of 200 Hz or 100 Hz, the cutoff wavelength is 5.6  $\mu$ m. With this same scan speed, however, at a sampling rate of 50 Hz, the cutoff wavelength is 7.1  $\mu$ m.

The action of a cutoff filter can be illustrated by plotting the percentage of signal transmission as a function of wavelength (usually plotted as the logarithm of wavelength). Note that there is always some slope in the transmission curve of a cutoff filter; that is, the transmission percentage is not exactly zero for all values on one side of the cutoff value and exactly 100 for all values on the other side of the cutoff value. The cutoff wavelength of a filter is defined by that wavelength at which 50% of the signal is passed.

*Figure 8.44* shows the transmission curve of the combined analog and decimation filters. For every factor of 10 in scan speed, the curve moves to the right by a factor of 10 in wavelength.





### Setting the Short-Wave Filter Cutoff Values

See also the discussion on Short-Wavelength Cutoff Filters

Data can be filtered to provide the following specific results:

- Reduce the effect of small surface irregularities or environmental noise;
- Remove large-scale waviness and form error so that roughness can be evaluated unambiguously;
- Isolate specific frequency bands, allowing determination of intermediate components of roughness or waviness.

Long-wave, short-wave, or both filters can be used. Combining the short and long wave filters forms a band pass filter that cuts off all short wavelengths below the short-wave cutoff value and all long wavelengths above the long-wave cutoff value.



**NOTE:** The software does not allow setting a short-wave cutoff that is larger than the long-wave cutoff, which would result in a zero-width band of wavelengths, attenuating all of the data (see *Figure 8.45*).

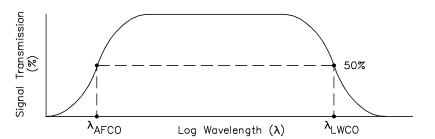


Figure 8.45 Defining a Band Pass With The Short-wave & Long-wave Cutoff Filters

0104396-000 AA 3/05

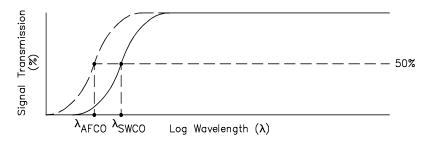
# Transmission

The short wavelength cutoff or noise filter attenuates data with wavelengths below the specified cutoff valve. This has the effect of removing noise from the data. This filter is always active, set either to a specified or a default value.

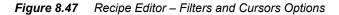
#### Select the short-wave cutoff (or long-wave pass) filter.

This cuts off the short-wavelengths in the data; those short-wavelengths below the filter's cutoff value. (See *Figure 8.46*).

Figure 8.46 Effect of the Short-wave Cutoff Filter



- 1. Go to the Recipe Editor, click **Filters/Cursors** to open its window. (See *Figure 8.47.*)
- 2. At the **Noise Filter** (shortwave cutoff) variable field, click the drop-down arrow to select a value from the range of cutoff filters provided. In this menu, the filter can also be turned off by clicking the **Off** option in the menu. The chosen filter appears in the variable field. (See *Figure 8.47*.)



Step 1 Click on the         Filter/Cursors button to display         the Filter and Cursor options.         Feature         Feature         Filter         Peature         Filter         Step 2 To display the Noise         Filter menu, click on the         down-arrow next to the         variable field. Click to         choose the filter or click on         Off at the top of the menu to         turm the filter Off.		Profiler - [Recipe Edi Recipe Options Help	itor - 13X13]	×
Step 2 to display the Noise     Cuting Depth       Filter menu, click on the     High Spat Count       down-arrow next to the     30 Cursors       variable field. Click to     Setup       choose the filter or click on     Setup       Off at the top of the menu to     Setup       turm the filter Off.     Filter off.	Filter/Cursors button to display	Can Parameter Definition Feature Detection Filters Cursors General Parameters Roughness	Filters Filter Option: Characteristic Classian Filter Gaussian Filter Characteristic Classian Characte	
Substr. Clear Status	Filter menu, click on the down-arrow next tot he variable field. Click to choose the filter or click on <b>Off</b> at the top of the menu to	Cutting Depth High Spot Count Peak Count 3D Cursors Setup	Left Level:         0.024         0.024           Right Level:         0.024         0.024           Relative to Feature Detected         0.024	

Up to 22 standard settings (including the default) are available depending on the scan speed. Entering a short-wave cutoff that is longer than the currently selected long-wave cutoff, or shorter than the value of the analog cutoff is prevented by the system. For scan speeds greater than 5  $\mu$ m/s, the shortest short-wave cutoff selection turns off the short-wave cutoff filter.

If subsequent changes to the scan speed or scan length cause the short-wave cutoff setting to become invalid, the cutoff is automatically changed to the nearest available valid value (possibly the default).

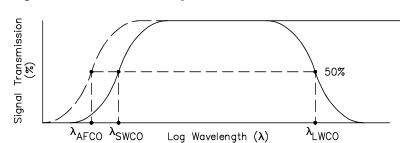
The default cutoff depends on the scan speed and sampling rate.

- 3. From the Filter Option variable menu, select from the following filters:
  - Gaussian For Windows-based systems; and
  - **RC** For comparison to scan data obtained with DOS-based systems, such as the KLA-Tencor P-2 Long Scan Profiler.

### Setting the Long-Wavelength Filter Cutoff Values

#### Select the long-wave cutoff (or short-wave pass) filter.

This cuts off the higher wavelengths in the data (those above the filter's cutoff value, see *Figure 8.48*).



#### Figure 8.48 Effect of the Long-wave Cutoff Filter

1. Go to the recipe window, click **Filters/Cursors** to open its window. (See *Figure* 8.49.)

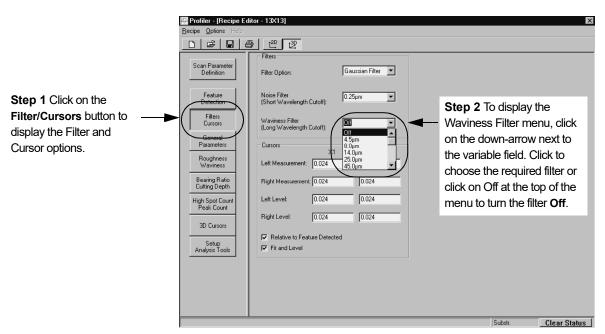


Figure 8.49 Waviness Filter (Long Wavelength Cutoff Filter)

2. In the **Waviness Filter** variable field, click the drop-down arrow to select a value from the range of cutoff filters provided. From this menu, the filter can also be turned off by clicking **Off** in the menu. (See *Figure 8.49*.)

Up to 17 standard filter choices are available depending on the scan speed. A long-wave cutoff that is shorter than the currently selected short-wave cutoff or the value of the analog cutoff, is prevented from being entered.

If subsequent changes to the scan speed or scan length cause the long-wave cutoff setting to become invalid, the cutoff is automatically changed to the nearest available valid value.

*Figure 8.50* shows the effect of different cutoff filter settings on the same set of scan data.

Figure 8.50	Signal Transmission Curves And Their Effects On Scan Data
-------------	---

Signal Transmission Curve	Scan Data Effect	Description
$\lambda_1$ $\lambda_2$ $\lambda_3$ Log Wavelength	×3	<b>Normal Data</b> Only the analog filter acts on the data. Three wavelengths, labeled $\lambda_1$ , $\lambda_2$ , and $\lambda_3$ , are identified.

Signal Transmission Curve	Scan Data Effect	Description
(23)		Roughness 1 The long-wavelength cutoff filter is applied with a cutoff value just higher than $\lambda_1$ .
$\lambda_1$ $\lambda_2$ $\lambda_3$ Log Wovelength	råntestenterionalisentenesperingerestentententesteretenten	The resulting data trace shows only features of the scale of $\lambda_1$ ; higher wavelengths, including $\lambda_2$ and $\lambda_3$ , are suppressed.
Trun shruseion		<b>Roughness 2</b> A different long-wavelength cutoff value is applied, it value is just higher than $\lambda_2$ .
μ λ1 λ2 λ3 Log Wavelength	, and all is a special for the special sector of the special sector of the special sector of the special sector special sector of the special sector of th	The resulting data trace shows features of the scale of $\lambda_1$ to $\lambda_2$ ; higher wavelengths, including $\lambda_3$ , are suppressed.
Signal from smission	~~~~~	Roughness 3 A short-wavelength cutoff filter with a value just higher than $\lambda_1$ is applied, in addition to the long-wavelength cutoff, to the Roughness 2 curve.
λ1 λ2 λ3 Log Wavelength		The resulting data trace shows only features of the scale of $\lambda_2$ ; higher wavelengths, including $\lambda_3$ , and lower wavelengths, including $\lambda_1$ , are suppressed.
(%)		Waviness 1 The short-wavelength cutoff filter is applied with a cutoff value just lower than $\lambda_3$ .
μ δ λ1 λ2 λ3 Log Wavelength		The resulting data trace shows only features of the scale of $\lambda_3$ ; lower wavelengths, including $\lambda_1$ and $\lambda_2$ , are suppressed.
(A)		<b>Waviness 2</b> The short-wavelength cutoff filter is applied with a cutoff value just lower than $\lambda_2$ .
log Wovelength	$\sim$	The resulting data trace shows features of the scale of $\lambda_2$ and $\lambda_3$ ; lower wavelengths, including $\lambda_1$ , are suppressed.

Figure 8.50 Signal Transmission Curves And Their Effects On Scan Data

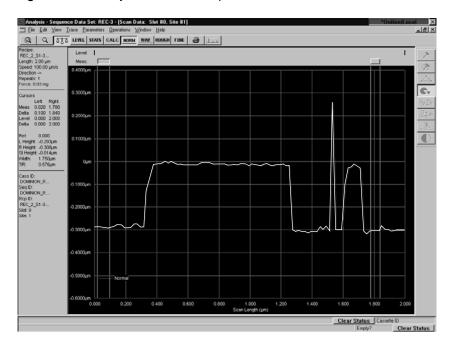
# **2D GLITCH REMOVAL**

### Introduction

The 2D glitch removal is designed to remove erroneous data caused by environmental noise or particulate contamination. The 2D glitch removal process is designed to work in conjunction with the repurposed measurement cursors. The glitch removal operates using a median point filter that can be set by user to either  $1 \times 3$ ,  $1 \times 5$ , or  $1 \times 7$  data points. (For more information on median filters, see *Median Filter for 2D and 3D Data* on page 3-61.) The filter is reset with each new data set.

This procedure can be used with new unsaved data, saved data, and a 2D slice of a 3D image.

### Procedure

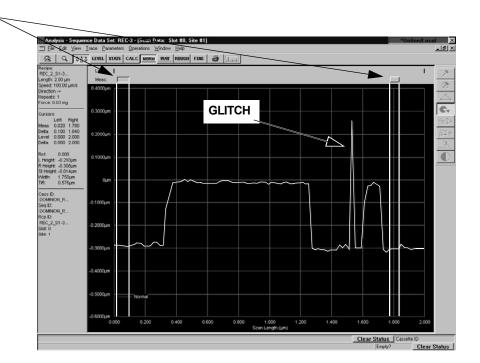


*Figure 8.51* Analysis Screen with Operations Menu

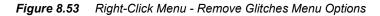
1. Move the left cursor to the next position to the left of the glitch that models the trace where the glitch occurs. Place the cursor's left and right borders to include the data set that is to be used to remove the glitch. (See *Figure 8.52*.)

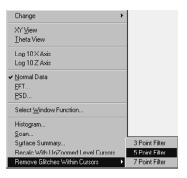
2. Move the right cursor to the next position to the right of the glitch that models the trace where the glitch occurs. Place the cursor's left and right borders to include the data set that is to be used to remove the glitch. (See *Figure 8.52*.)

Figure 8.52 Analysis Screen with Operations Menu



3. Right-click to display the Right-Click menu. (See Figure 8.53.)





4. Move the cursor over **Remove Glitches Within Cursors** to display its menu. (See *Figure 8.53*.)

Set the cursors on data that is a model for the glitch removal. In this case, the bottom of the trace. 5. Click on the required filter.(See Figure 8.53.)

The glitch is removed using the chosen filter. (See Figure 8.54.))

Figure 8.54 Analysis Trace Window with Glitch Removed

# **MEASURING THE RADIUS ON CURVED SURFACES**

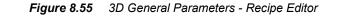
The average radius of a circular segment defined by the measurement cursors is calculated from a data set using the least squares fit method. This method is capable of high precision, covering a range from  $0.5 \ \mu m (20 \ \mu in.)$  to 200 mm (7.9 in.), provided that the sample fits on the stage.

The radius of the measurement stylus is added to the sample radius in the measurement. The following sample might be:

- Acceptable Where the radius of a 2-μm stylus added to a 20-mm radius sample might be considered negligible (0.01%),
- Unacceptable Where a 5-µm stylus added to a 1-mm radius is a 0.5% error, which is generally unacceptable.

This can be avoided if the instrument is calibrated with a high precision cylindrical standard whose radius is within a factor of 5 of the sample to be measured. This is the Radius of Curvature calibration. For the highest accuracy, KLA-Tencor recommends that this calibration is performed by a trained technician.

1. Go to the Scan Recipe Editor and click on General Parameters. Step 1 (See *Figure 8.55.*)



	🐖 Profiler - [Recipe Editor - 13X13]			
	<u>Recipe Options</u> Help			
Step 1 In the Recipe Editor,		S 2 2		
click on the <b>General</b> <b>Parameters</b> button to display the 2D General Parameters	Scan Parameter Definition Feature	2D General Parameters Normal Trace Step Height (StpHt)	3D General Parameters Full Scale For Total Ind. Runout (TIR3D)	
in the Information Display	Detection	Total Ind. Runout (TIR)	SlopeX	
Window.	Filters	🗖 Average Height (Avg)	🗖 🗖 Slope'Y	
window.	Lursors	Slope		
	General Parameters	Radius (Rad)		
	Roughness	Area of Peaks (Area+)		
Step 2 Click in the empty check box next to Radius so the radius information is displayed in the Analysis screen, in the Surface Parameter Summary	Wavings Busing Ratio Cutting Depth High Spot Count Peak Count 3D Cursors Setup Analysis Tools	Area of Valleys (Area-) Total Area (Area) Profile Length (ProfL) Distance to Edge (Edge) Step Width (StpWt) Select All 2D	Select All 3D	
window.		Remove All 2D	Remove All 3D	
				Substr Clear Status

- 2. Click in the check box next to **Radius** to enable the radius measurement and display the results in the Analysis screen. (See *Figure 8.55*.)
- If measuring other types of samples with no required radius measurement, disable the radius measurement by clicking on the check mark (✓) in the check box so that the check box is left empty.

### **Measuring for Maximum Precision**

1. The height of the measured arc should be no more than 77% of the vertical range of the measurement head.

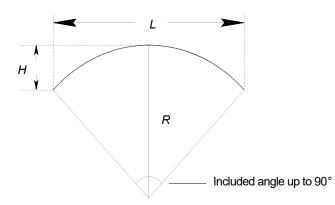
Measurements <u>can</u> be made up to 90% of the vertical range of the measurement head in arc height but precision of the scan cannot be certain. (See *Figure 8.56*).

2. The size of the included angle should be no more than  $90^{\circ}$ .

Measurements can be made up to  $110^{\circ}$  in included angle with a small loss of precision. (See *Figure 8.56*).

These limits depend on the type of measurement head being used.

*Figure 8.56* Arc Segment Dimensions



**3**. To measure another portion of the radius, physically rotate the sample about the radial axis.

Precise measurement is also restricted to arc segments that are symmetric to the radial axis of the measured artifact.

4. To measure using a given radius *R*, optimum arc height *H* (*Figure 8.56*), and the optimum scan length *L*, use the following formula:

$$L = 2\sqrt{2RH - H^2}$$

Scan length and scan speed are dependent on the radius of the sample, the arc height allowed by the measurement head, and its vertical range.



**NOTE:** Scans taken at the lowest possible horizontal resolution for the optimal scan length generally yield the most repeatable and precise radius measurements.

### Measuring for the Lowest Horizontal Resolution

Various combinations of scan speed and sampling rate can be experimented with.

- 1. Set the sampling rate to 200 Hz.
- 2. Set the scan speed to get a scan time that is as close as possible to 25 seconds without exceeding it.
- 3. If the longest scan time possible under these restrictions is 12 seconds or less:
  - a. Set the sampling rate to 100 Hz.
  - b. Set the scan speed so that the scan time is as close as possible to 50 seconds without exceeding it.

- 4. If the arc height *H* is less than 40% to 45% of the range available for the measurement head, the recommended profile type is the center bias profile type ¬¬ ¬.
- 5. Set the stylus force high enough for the stylus to reach the lowest points of the scan.

The stylus force needed depends on the arc height H and on the profile type (peak, valley, or center bias).

a. If, during radius measurement, the trace flattens out and no **data out of** range message appears, try a higher stylus force setting.

# Measuring with a 1- $\sigma$ Repeatability (precision) of 0.002% of the Radius

- 1. Do not set both leveling cursors to zero.
- 2. Preset the position of the measurement cursors.

Ensure that the following parameters are properly set. (See Table 8.5).

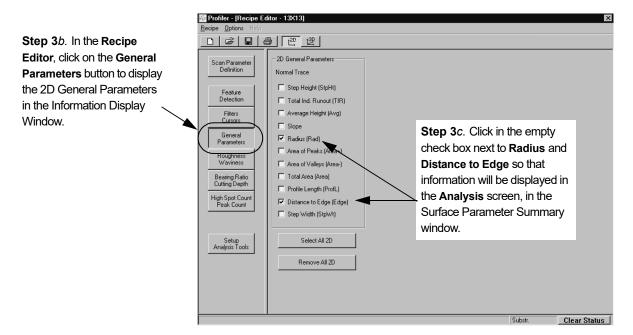
Table 8.5Scan Recipe Parameters

Recipe Field	Setting
Scan Length	See changing <b>X Scan Size</b> .
Scan Speed	See changing Scan Speed
Sample Rate	200 Hz is optimum. See Sampling Rate.
Surface Parameters	Use the General Parameters window in the Recipe Editor to enable Radius and Distance to Edge.
Stylus Force	See Applied Force.
Profile Type	See Profile Type.
Vertical Range	See Range/Resolution.

- 3. To measure a convex radii:
  - a. Go to the Scan Recipe Editor.
  - b. Click on the General Parameters button

c. Ensure that there is a check (✓) in both the Distance to Edge and Radius check boxes. (See *Figure 8.57*.)





d. From the Recipe Editor click on the **Feature Detection** button to display the Feature Detection options in the Information Display Window. The display is shown in *Figure 8.58*.



	Feature Detection		Step 3e. Click on the down-arrow next to the
Step 3f. Scroll down to the	Feature:	Convex 🔽 🗲	Feature variable box.
bottom of the menu. Click on Convex from the drop-down	Feature Number:	Down Base	
menu.	Slope Threshold :	10.00	
	Plateau Threshold :	10.00	
	Min. Plateau Width :	10.000	
	🗖 Apply Gaussian N	oise Filter Before Detection	
	Filter Cutoff (µm):	0.000	

e. Click on the down-arrow next to the **Feature** variable box. The menu is displayed.

- f. Scroll down to the bottom of the menu. Click on **Convex**. The cursors automatically adjust.
- 4. To measure with 0.002% repeatability, adjust the measurement cursors in the Analysis window until the height values for the cursors are equal within 0.5  $\mu$ m (20  $\mu$ in.) for radii larger than 2.5 mm (0.1 in.).

# **MEASURING STEP HEIGHT ON CURVED SURFACES USING FIT AND LEVEL**

Step height can be measured on curved surfaces such as lenses or glass optical fibers, or in a bow in a profile that has been leveled in the normal manner. This capability is enabled or disabled in the Scan recipe.



**NOTE:** The Profiler application can remove a simple convex or concave curve from the data, but not more complex curves like waves.

1. From the **Recipe Editor** click on the **Filters/Cursors** button. This displays the Filters and Cursors options in the Information Display Window.

Figure 8.59 Cursor Options - Filters/Cursors - Recipe Editor

– Cursors –––––	×1	X2
Left Measurement:	10.000	50.000
Right Measurement:	450.000	490.000
Left Level:	10.000	50.000
Right Level:	450.000	490.000
☐ Relative to Feature Fit and Level	ure Detected	

- 2. In the **Cursors** portion of the display, check the **Fit and Level** check box. (See *Figure 8.59*.)
- **3**. Save the changes.

# SAVING SCAN DATA

Step 2 Click on the empty check box next to Fit and Level to enable it.

Scan data can be saved for reviewing at a later time. This is especially important because the data that is saved can be reanalyzed at a later date using different scan parameters.

1. Click on File in the Menu Bar to display the File menu.

### 2. Select Save Data.

The Save Scan Data dialog box appears. (See Figure 8.60).

Figure 8.60 Save Scan Data Dialog Box

Step 4 From the drop-down	Save Scan Data	? ×
menu, click on the desired drive and directory.	Save in: Scandata	Step 3 Click on the menu arrow to reveal the
<b>Step 5</b> Double-click on the folder → in which the data is to be saved.	Capture	available drives and directories.
Step 6 Enter the name being	File name:     good data       Save as type:     Scan Data Files (*.dat)	Save Step 7 Click Cancel Help

- **3**. Click on the menu arrow next to **Save In** to reveal the available drives and directories. (See *Figure 8.60*)
- 4. Select the drive and directory from the drop-down menu. (See *Figure 8.60*)
- 5. Double-click on the folder that the data is to be stored in. A list of all current data files appear. (See *Figure 8.60*)
- 6. Enter a name for the data set in the File name variable box. (See *Figure 8.60*)
- 7. Click **Save** to save the data in the new file. (See *Figure 8.60*)

Once a data set has been saved, it is added to the Scan Data catalog. The Scan Data catalog window allows selection of individual data sets for reviewing. Unwanted data sets can be deleted.

# **REEVALUATION OF SAVED 2D SCAN DATA**

The version 6.2 software provides a the user with an opportunity to review scan data that was saved and to change parameters in the scan recipe for recalculation of the data. This is possible because the system saves the raw scan data from the scans.

The recipe determines which parameters are calculated in the Analysis screen's Statistics window after the scan. Once the data is saved, it can be revisited in the Catalog screen. The general procedure is as follows.

- 1. Access the Catalog screen.
- 2. Choose either the Scan Data or Sequence Data windows.
- 3. From the Scan Data window, navigate to the data set that is to be recalculated.
- 4. From the Sequence Data window, choose a sequence.
- 5. Double-click the scan data set. This opens the Analysis screen for the data set.
- 6. In the analysis screen, click on Edit to display its menu.
- 7. Choose Recipe. This opens the Recipe that was used to create the original scan.

8. Change the parameters that require addition or removal. This is accomplished by opening each parameter window and choosing the new parameter to be included in the analysis statistics or removing parameters no longer required.

The following parameters can be edited:

- Feature Detection Filters and Cursors General Parameters Roughness and Waviness Bearing Ratio/Cutting Depth Automatic Histogram Leveling
- The Scan Parameter Definition cannot be edited.
- **9**. After all changes have been made, click on the Analysis icon in the tool bar to return to the Analysis screen.

Figure 8.61 Scan Recipe Tool Bar for Analysis Editing

**Step 9** Click on the Analysis icon in the tool bar to return to the Analysis screen.



10. The Analysis screen returns with the statistics in place in the 2D Surface Parameter Summary window. There is no need to recalculate this information because the system automatically does that when it regenerates the Analysis screen.

If there are any manipulations to the image that are being done, click in the 2D Data portion (the window with the 2D image) of the Analysis screen to make it active.

- 11. Adjustments that effect the parameters are cursor placement or leveling. Change these if required.
- 12. In the Analysis screen click the CALC button CALC to perform a recalculation of the statistics for the new cursor or leveling.
- 13. To save the data, click on File to display its menu.
- 14. Choose Save Data... to open its dialog box.
- 15. Navigate to the correct folder in which the data is to be stored.
- 16. Name the file.
- 17. Click on Save to save the data in the folder.

# **ANALYZING 3D SCAN DATA**

# INTRODUCTION

The 3D scan data analysis displays the 3D scan image and trace information after a scan is completed. A 3D scan is an image built by taking a series of 2D scans, arranged in a raster pattern, to form a picture of the sample surface at the scan location. With 3D analysis, complete surface analysis can be performed.

This chapter describes:

- Starting the 3D Analysis Application on page 9-2
- 3D Analysis Screen Features on page 9-3
- Line-by-Line Leveling on page 9-33
- Customizing the Scan Image on page 9-40
- Changing the View Angle on page 9-41
- *Customizing the View* on page 9-42
- Using Image Arithmetic to Compare Data on page 9-43
- Saving Scan Data on page 9-45
- on page 9-50

# STARTING THE 3D ANALYSIS APPLICATION

1. Click the **Scan Data** or **Sequence Data** command button to display the data information in the Catalog window. (See *Figure 9.1*.)

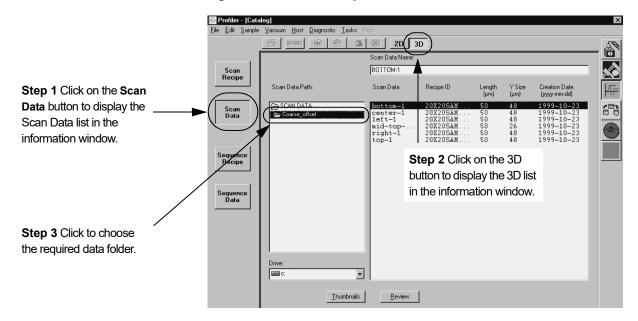
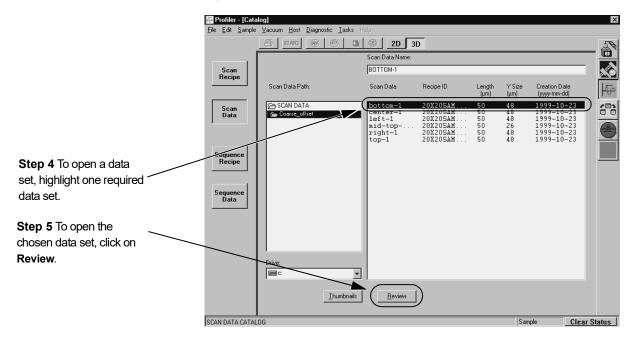


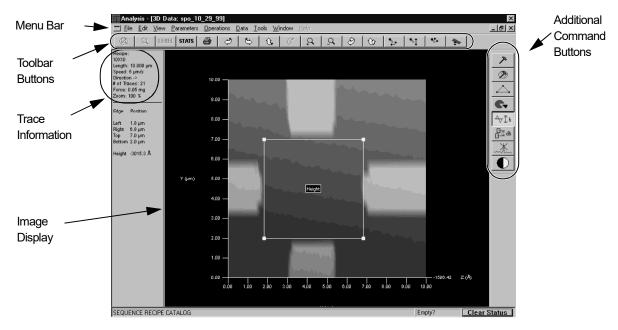
Figure 9.1 Scan Catalog Screen with Scan Data Active.

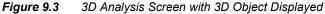
2. Click the **3D** button. (See *Figure 9.1*.)

Figure 9.2 Scan Catalog Screen with Scan Data Active.



- 3. In the Scan Data Path column, click the folder name. (See *Figure 9.1*.)
- 4. In the Scan Data list, click on a data set to be analyzed. (See *Figure 9.2*.)
- 5. With the data set highlighted, click the **Review** button. The Analysis window appears. (See *Figure 9.3*.)



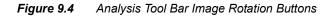


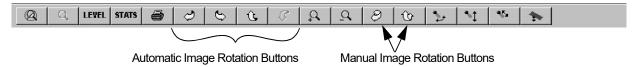
# **3D ANALYSIS SCREEN FEATURES**

### Analysis Screen – Image Orientation

The image in the Analysis Image Display area can be rotated to orient it for analysis and viewing. Four options exist for rotation of the object. All four are presented, with the Recommended procedure coming first.

Recommended Image Rotation Procedure Option 1 – Automatic Image Rotation. Use the Image Rotation buttons in the tool bar. (See *Figure 9.4*) These are Automatic Image Rotation buttons, described in *Table 9.1*.





Button	Description of Action
\$	Rotates the image to the left on its horizontal plane. Each click moves the image a small distance. (Identical to the <b>left</b> arrow key.)
Ð	Rotates the image to the right on its horizontal plane. Each click moves the image a small distance. (Identical to the <b>right</b> arrow key.)
Û	Rotates the image in a backward roll. Each click moves the image a small distance. (Identical to the <b>up</b> arrow key.)
G	Rotates the image in a forward roll. Each click moves the image a small distance. (Identical to the <b>down</b> arrow key.)

#### Table 9.1 Automatic Image Rotation Buttons

**Option 2 – Manual Handle Drag.** There are also Manual Image Rotation buttons, described in *Table 9.2*.

 Table 9.2
 Manual Image Rotation Buttons

Button	Description of Action	
Ð	Rotates the image on its horizontal plane using four handles that are manipulated by click-and-drag method. (See <i>Figure 9.5</i> .)	
Ċ	Rotates the image on its horizontal plane using a single handle that is manipulated by the click-and-drag method. (See <i>Figure 9.5</i> .)	

 Click on the button representing the plane in which the required rotation is to take place. The image appears to have handles attached to it. (See *Figure 9.5*) Click on the button

plane of rotation.

image in the chosen

rotation.

2. Click on one of the handles (see Figure 9.5) and, while holding down the mouse button, drag the image to rotate it to a different orientation in the chosen plane. Release the mouse button to set the image in its new orientation.

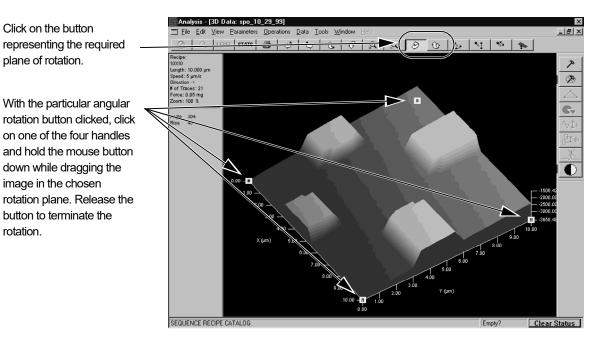
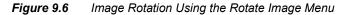


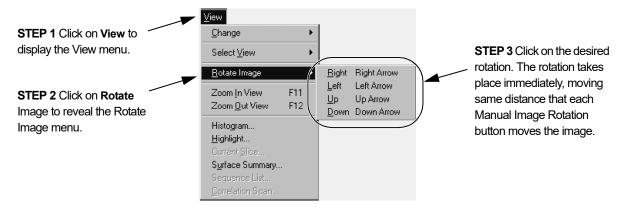
Figure 9.5 Manual Image Rotation Handles

Option 3 – Arrow Keys. Use the arrow keys on the keyboard. The movement provided by each key is described in Table 9.3.

Table 9.3	Table 9.3         Image Rotation Using the Arrow Keys	
Button	Description of Action	
-	Rotates the image to the left on its horizontal plane. Each click moves the image a small distance. (Identical to the <b>left</b> rotation button.)	
-	Rotates the image to the right on its horizontal plane. Each click moves the image a small distance. (Identical to the <b>right</b> rotation button.)	
<b>A</b>	Rotates the image in a backward roll. Each click moves the image a small distance. (Identical to the <b>up</b> rotation button.)	
*	Rotates the image in a forward roll. Each click moves the image a small distance. (Identical to the <b>down</b> rotation button.)	

**Option 4 – Rotate Image Menu.** Use the **Rotate Image** menu rotation options. The rotation provided by each menu item is identical to that provided by the representative arrow key (cited next to each option) as described in *Table 9.3*, and the related Image Rotation button described in *Table 9.1*.





Menu Item	Description of Action
Left Left Arrow	Rotates the image to the left on its horizontal plane. This action only move the image one increment each time. The menu must be opened again for each move.
<u>R</u> ight Right Arrow	Rotates the image to the right on its horizontal plane. This action only move the image one increment each time. The menu must be opened again for each move.
Up Up Arrow	Rotates the image in a backward roll. This action only move the image one increment each time. The menu must be opened again for each move.
Down Down Arrow	Rotates the image in a forward roll. This action only move the image one increment each time. The menu must be opened again for each move.

 Table 9.4
 Rotate Image Menu Options (From View Menu)

Use the Mouse Tool in the Right-Click menu.

- 1. Right-click to display the **Right-Click** menu. (See *Figure 9.7.*)
- 2. Click on Mouse Tools to display its menu. (See Figure 9.7.)
- 3. Choose Rotate Image from the Mouse Tools menu. (See Figure 9.7.)
- 4. Choose the required rotation from the menu. This menu is the same as the Rotate Image menu from in the View drop-down menu in the Menu Bar. (See *Figure 9.6* and *Table 9.4*.)

Each click moves one increment only. The entire menu process must be completed for each single movement.

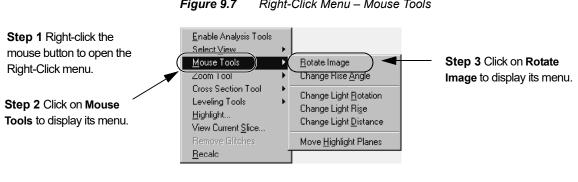


Figure 9.7 Right-Click Menu – Mouse Tools

### **Graphics Buttons and Their Function**)

Figure 9.8	Analysis	Tool Bar	Graphics	Buttons
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#### **Automatic and Manual Image Rotation Buttons**

The Automatic and Manual Image Rotation buttons are displayed in Figure 9.4. They are discussed beginning in Analysis Screen - Image Orientation on page 9-3 and explained in Table 9.1 through Table 9.4.

In general, the automatic rotation buttons move the image in the depicted direction by one increment of movement each time they are clicked on. The manual rotation buttons place handles on the image to allow it to be moved in the indicated direction.

#### **Zoom Features**

The Zoom features are designed to facilitate zooming in on a portion of the 3D graphic for closer inspection. The zoom can be accomplished through the use of several zoom tools.

- The View menu contains zoom features.
- ٠ The tool bar contains zoom features shaped like magnifying glasses.
- The Right-Click menu contains zoom tools. ٠

The following explanation demonstrates the use of the zoom tools in the most efficient manner. Other combinations of zoom tool usage exist, but this combination should be the simplest.

1. In the Analysis screen, click on the **Tool Activation** icon at the top of the tool bar on the right side of the screen. This activates (enables) the side tool bar tools. (See Figure 9.9.) When the side tool bar is activated, the graphic image is changed to top view.

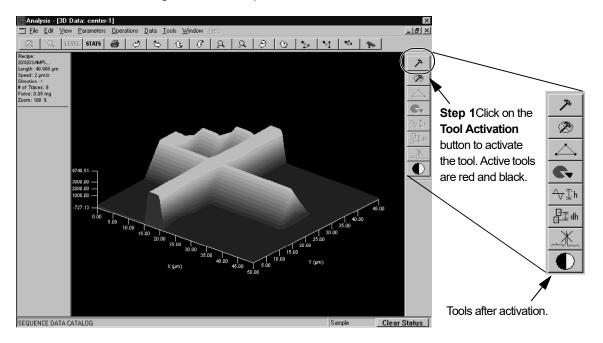


Figure 9.9 Analysis Screen - Tool Activation

2. Place the cursor over the graphic display and right-click to display the tool menu. (See *Figure 9.10*.)

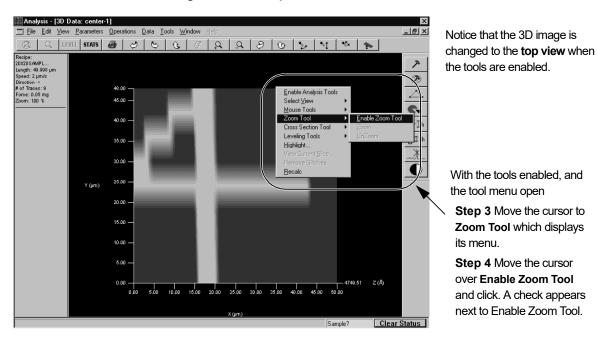
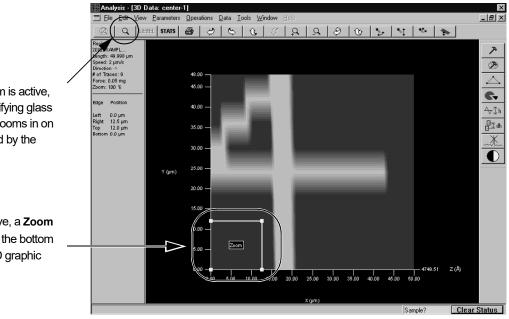


Figure 9.10 Analysis Screen - Enable Zoom Tool

- 3. In the tool menu, move the cursor over **Zoom Tool** to display its menu. (See *Figure 9.10.*)
- 4. Click on Enable Zoom Tool to activate the zoom process. (See Figure 9.10.)

Figure 9.11 Analysis Screen - Zoom Active



5. When the zoom process is activated, the **Zoom In** magnification glass is activated and the **Zoom** box is deployed at the bottom left of the 3D graphic display. (See *Figure 9.11*.)

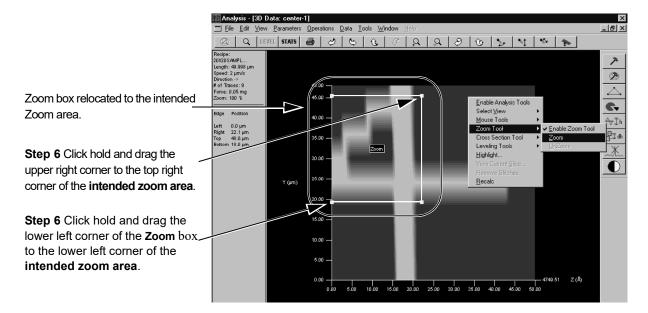
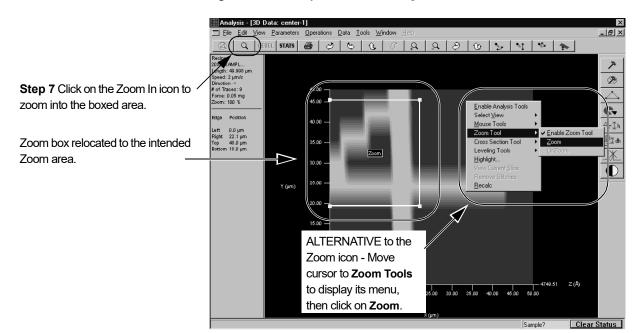


Figure 9.12 Analysis Screen with Zoom Box

**Step 5** When zoom is active, the **Zoom In** magnifying glass icon is enabled. It zooms in on whatever is outlined by the **Zoom** box.

When zoom is active, a **Zoom** box is displayed at the bottom left corner of the 3D graphic display.

6. A good way to position the **Zoom** box is, click and hold on the top right handle (boxed corner) of the **Zoom** box and position it where the top right corner of the intended zoom area. Repeat the process with the bottom left corner, placing it at the bottom left corner of the intended zoom area. (See the intended zoom area in *Figure 9.12.*)





7. When the **Zoom** box is positioned as the boundary of the intended zoom area,

click on the **Zoom In** icon  $\bigcirc$  in the tool bar. (See *Figure 9.13*.)

The 3D graphic image changes, displaying only the bounded area within the **Zoom** box. (See *Figure 9.14*.)

**ALTERNATIVE** procedure for activating the zoom to display the area within the **Zoom** box:

- a. Right-click to display the Right-Click menu. (See Figure 9.13.)
- b. Click on Zoom Tools. (See Figure 9.13.)
- c. Choose Zoom. (See Figure 9.13.)

While in the view containing the zoomed image, all the procedures contained in the right side tool bar can be executed on the image. The Level, Slice, Height, Step Height, and Glitch Removal, all function the same way with a zoomed image that they do with a standard top view image.

While in the view containing the zoomed image, it is not possible to zoom in further. To zoom in closer, return to the original image and repeat the zoom procedure using a smaller area within the Zoom Box for the zoom image.

When the Zoom In procedure is complete, the Zoom Out icon is activated to allow the User to return to the pre-zoom image. (See *Figure 9.14*.)

Working with a Zoomed Image

Step 8 When the Zoom In

procedure is complete, the

**Zoom Out** icon is activated to allow the user to return to the

pre-zoom image. The Zoom In icon is deactivated.

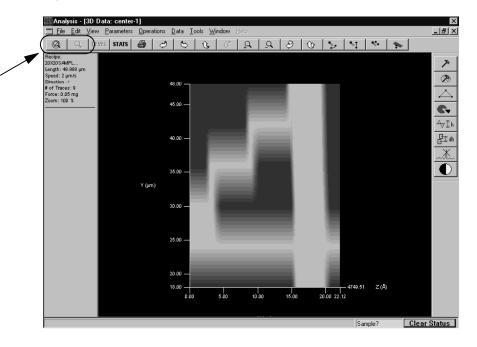
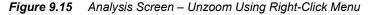


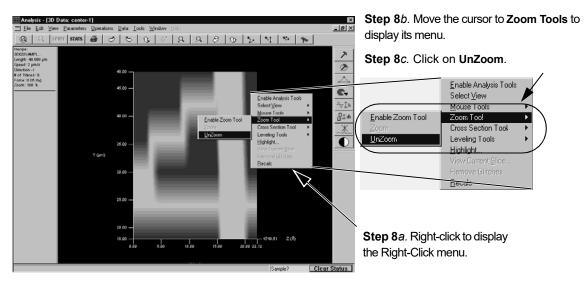
Figure 9.14 Analysis Screen – Zoomed In Area

8. To return to the pre-zoom image, click on the **Zoom Out** icon. The image returns to the prior display. (See *Figure 9.14*.)

ALTERNATIVE: (See Figure 9.15.)

- a. Right-click on the graphic display area to display its menu.
- b. Move the cursor to Zoom Tools, to display its menu.
- c. Choose Unzoom and click. The image returns to the prior display.





### Analysis Screen Toolbar Button Functions

### Table 9.5 Analysis Toolbar Buttons

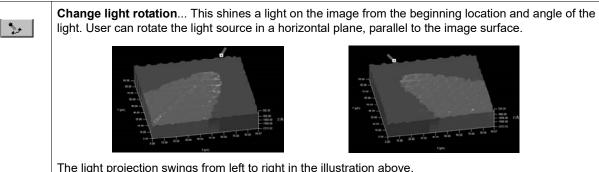
Button	Description of Action					
Q	<b>Zoom In</b> on the area bounded using a zoom box to form the boundary. This is for use with the Zoom Box. This icon is used as a trigger to execute zoom of the data according to the parameters set using the Zoom Box.					
	<ul> <li>Procedure: (See procedure as described beginning with STEP 1. on page 9-7.) The following is an abbreviated version of the procedure.</li> <li>1. Click on the Hammer in the Analysis Tool box to enable the Analysis Tools.</li> <li>2. Right-click to display its menu.</li> </ul>					
	3. Move the cursor to the <b>Zoom Tools</b> .					
	4. Click on <b>Zoom</b> in the Zoom Tools menu.					
	5. Adjust the size and position of the zoom box so it forms the boundary of the area to be zoo					
	6. Click on the <b>Zoom In</b> icon <b>Q</b> to zoom to the area bounded by the zoom box (or click on					
	Zoom in the Tools menu - as illustrated below).					
	1. Click on Tools to display its menu.       Iools         2. Click on Zoom       Zoom					
	Tools     3. Click on Enable     4. Click on Zoom					
	Zoom Tool to enable the Zoom In icon.					
Q	<b>Zoom Out</b> tool. This returns the image to its pre zoom magnification. This tool works with the Zoom In tool described above. It is for use after zooming in on a bounded area. (See <i>STEP 8. on page 9-11.</i> )					
LEVEL	<b>LEVEL</b> icon. This is for use with the three point leveling tool. It is used as a trigger to execute leveling of the data according to the three vertex positions set using the Leveling Tool.					
	Procedure:					
	1. Click on the <b>Hammer</b> <i>i</i> in the Analysis Tool box (on the right side of the image), The					
	Analysis Tools are enabled.					
	2. Click on the Leveling Tool . The LEVEL icon LEVEL is enabled.					
	<b>3</b> . Use the click-and-drag procedure (click on the center of each vertex) to position them. (For more information on the procedure, see <i>Activate Leveling Tool on page 9-15</i> .)					
	4. Click on the <b>LEVEL</b> icon <b>LEVEL</b> to complete the leveling procedure.					

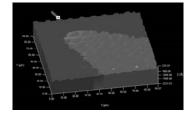
Button	Description of Action
STATS	<b>Statistics</b> information box. This displays the statistics information box on the screen, usually beneath the analysis image. The positioning can be manipulated.
5	<b>Print</b> . This causes the system to print the analysis information.
Ą	<b>Positive Magnification</b> . This causes the entire image to be magnified by one increment each time it is clicked on. The image continues to grow in size, having its outside edges cropped as its size increases past the image area of the screen.
<u>_</u>	<b>Negative Magnification</b> . This causes the entire image to be reduced in magnification by one increment each time it is clicked on.

#### Table 0 5 Analysis Toolbar Buttons (Continued)

The following three buttons activate the Ray Trace Mode and allow the user to illuminate the surface with a light source from different angles. The Spotlight effect has been used in the following graphics to illustrate the lights distance and direction. The spotlight was activated for the illustration and, if on, can be turned off for complete lighting of the surface, while maintaining directional integrity of the lighting process.

> **NOTE:** For the three following buttons it is important to remember that the light can be moved over and over, through a series of different locations and angles. Each time a different light button is chosen, the light moves differently depending on its beginning position and angle. The following descriptions are designed to give general guidelines for moving the lights. Light angles, beginning, and ending positions vary depending on the position and angle that the light is in when the next button is clicked.





The light projection swings from left to right in the illustration above.

Button	Description of Action				
*1	<b>Change light rise</b> From the starting location and angle, the light moves in an arc over the image surface (like a sunrise/sunset).				
	The light swings from centered above toward a lower left side angle.				
<b>N</b> 5	<b>Change light distance</b> From the starting position and angle of the light, the light moves close further from the image at the current angle.				
	The light moves from high left to a lower position near image center.				
-	<b>Move highlight planes</b> This moves each highlighted plane for visibility. Up to 10 planes can be identified for viewing.				

### Table 9.5 Analysis Toolbar Buttons (Continued)

### **Analysis Screen Side Toolbar Buttons**

These buttons, located at the right of the image, are active in the **Top View** only (looking directly down on the image surface). (See *Table 9.6*).

### **Analysis Screen Side Toolbar Button Functions**

Table 9.6	Analysis Side Toolbar Buttons
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Button	Description of Action
*	<b>Enable Analysis Tools (Top View)</b> . This button enables the remaining tools in this tool bar. It moves the image to the <b>Top View</b> because all the tools require this view.
Ø	<b>Disable analysis Tools</b> . This button disables active tools. This includes the tools in this tool bar as well as those in the top tool bar.

Button	Description of Action
$\bigtriangleup$	<ul> <li>Activate Leveling Tool. This button activates the leveling tool that places three interactive boxes on the image surface for leveling the image. Each box represents a corner of the leveling triangle.</li> <li>Procedure: <ol> <li>Click-and-drag the center of the boxes (labeled vertexes in the data column at the left) to locations on the image surface that are to be used as leveling points. The information in the</li> </ol> </li> </ul>
	square is averaged to form a height for leveling that point in the triangle.
	2. If desired, use the handles at the corners of the squares to resize the squares so the surface bounded by each vertex creates the average desired height for that point.
	<b>NOTE:</b> It is very important that the area covered by each box is on the same plane. In addition, the contents of all three boxes must also be on the same plane, or the image is not properly leveled and the image itself could become distorted. Boxes 1 and 2 in the illustration below are too large to properly level the image.
	3. Click the <b>LEVEL</b> button <b>LEVEL</b> on the top tool bar to level the image.
	Analysis - 100 Date petidid
	Huge 40:14 Werk 40:1 Werk 40:1
	Each box has its location statistics displayed in the data column, to the left of the image.
Art In	Activate Height Tool. This button activates the tool that places a box on the image surface. The box borders an area containing data that is averaged to give a single average height of the contents of the box. Using the center of the box, it can be moved using the click-and-drag procedure. The handles at the corners of the box can be used to change the area of the box. The data is automatically calculated as the box is moved, or as its area is changed by moving its borders.

 Table 9.6
 Analysis Side Toolbar Buttons (Continued)

D. #					
Button	Description of Action				
6.	Activate Slicing Tool. This button activates the tool that allows the user to slice the image down from the top surface to the foundation of the image and display a 2D image of the cross section at the slice. This tool provides three options (see also <i>Table 9.14</i> ) for the slice: horizontal, vertical, and diagonal. (Diagonal can be adjusted to any angle.) All three options can be adjusted to any length. (See <i>Table 9.9</i> , in the <b>Current Slice</b> section.)				
	Procedure:				
	a. When this tool is clicked, a slice line is displayed on the 3D image in the chosen orientation.				
	b. Click and hold while dragging the slice line to the desired location on the image.				
	c. Adjust the length of the slice by using the click-and-drag procedure with one of the handles at the end of the slice line.				
	d. Right-click to display the Right-click menu. (See below.)				
	In the View menu, click on View Current Slice to display the 2D image at the slice indicated in the 3D image.				
	e. Click on View Current Slice (shown above) to view the current slice trace. To display both the 2D image along with the 3D image (as illustrated below), click on Window, then choose Cascade. (See Creating and Saving 2D Slice Data from a 3D Scan on page 9-46 for information on creating a slice and saving current slice data.)				
	If Y Way       Table Detained is generations Window 1960         Image: State Detained is generation 1960         Image: State D				
	Bit Date         P III X           Insertion - 3         40.00           Insertion - 3         50.00           Insertion - 300 µm         6.00           Insertion - 30.00         5.00           Insertion - 30.00         5.00				
₽₽dh	Activate Step Height Tool. This button activates the tool that places two boxes on the image surface. Using using the click-and-drag procedure with the center of each box, it can be moved to a new location on the image surface. It can then be resized using the corner handles. The software determines the difference between the average height in one box and the average height in the other box. This difference is automatically calculated as the boxes are moved or resized.				

### Table 9.6 Analysis Side Toolbar Buttons (Continued)

Table 9.6	Analysis Side Toolbar Buttons (Continued)				
Button	Description of Action				
	<ul> <li>Activate 3D Glitch Removal Tool.</li> <li>This button activates the 3D glitch removal option. The tool is used in the following manner: <ol> <li>Activate the glitch removal button by clicking on it. A box is displayed at the bottom right of th top view of the 3D image.</li> <li>Drag the box over an area that presents the identical but correct formation of the area that contains the glitch. Resize the box to capture only those attributes and only the size that is to be corrected in removing the glitch. (See left side illustration below. Note that it is important to gather enough data points for the system to make the analysis and remove the glitch.)</li> <li>Right-click to display the right-click menu.</li> </ol> </li> </ul>				
	4. Move cursor to Remove Glitches Within Cursors and choose the median filter to be used; 3 x 3, 5 x 5, or 7 x 7. (See right side illustration above.) (For more information on median filters, see also <i>Median Filter for 2D and 3D Data</i> on page 3-61.)				
	<ul> <li>5. Move the box over the glitch area, placing it in the same relative position that the initial box was placed. (See left side illustration below.)</li> <li>Image: A state of the glitch area.</li> <li>Image: A state of the glitch are</li></ul>				
	7. Move the cursor to <b>Remove Glitches</b> and click.(See right side illustration above.) The glitch is removed using the chosen filter and the data gathered in the first box.				

#### Table 9.6 Analysis Side Toolbar Buttons (Continued)

### Analysis Menu Bar

Most of the functions available in the two Analysis Tool Bars and the Right-click menu, are also available using the Menu Bar at the top of the screen. In addition, there are numerous other menu items that facilitate functions necessary for the processing of 3D scan data.

Figure 9.16 A	alysis Screen Menu Bar
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$\underline{F}ile  \underline{E}dit  \underline{V}iew  \underline{P}arameters$	<u>Operations</u>	<u>D</u> ata	<u>T</u> ools	<u>₩</u> indow	
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### File Menu

Table 9.7File Menu Operations

Menu Item	Description of Action
Save <u>D</u> ata	Saves the current data to a file. This option displays the Save Dialog box with its associated options.
Export <u>G</u> raph	Exports the current data. This option displays the Export dialog box with its associated options.
<u>P</u> rint Ctrl+P	Prints the current data. This option displays the Print dialog box with its associated options.
Print Pre <u>v</u> iew	This option displays a thumbnail presentation of the material that is to be printed so it can be reviewed.
P <u>r</u> int Setup	This option displays the Print Setup dialog box with its printer/print setup options.

Menu Item	Description of Action
Load Workspace	This option allows the user to choose a specifically designed work space from a drop-down menu in the Select Work Space dialog box.
	Select Work Space       Work Space Name       DEFAULT       OK         Cancel
Save Workspace	This option presents a dialog box that allows the user to establish a named work space.
	Save Work Space       Enter Workspace Name       OK         Cancel
E <u>x</u> it	This option Exits from the Analysis screen.

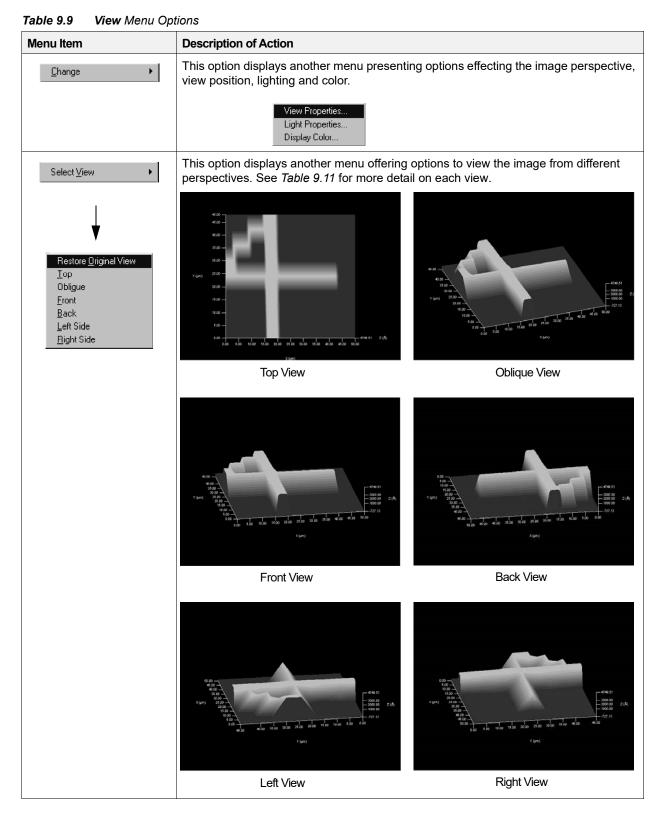
 Table 9.7
 File Menu Operations (Continued)

#### Edit Menu

### Table 9.8Edit Menu Option

Menu Item	Description of Action
Copy Ctrl+C	This option places the image and data information on the clipboard.

### View Menu



Menu Item	Description of Action
<u>R</u> otate Image →	This option displays another menu presenting options, each of which rotate the image by one increment each time they are chosen. (See <i>Table 9.4</i> for a complete explanation of the movement of each option.)
	<b>NOTE:</b> This is the most inefficient way of image rotation since each time an option is used, the menu disappears and must be accessed again for another single movement rotation. The rotation buttons in the tool bar or the arrow keys on the keyboard are much more efficient.
	<u>R</u> ight Right Arrow Left Left Arrow Up Up Arrow <u>D</u> own Down Arrow
Zoom In View F11	This option causes the magnification of the entire image by one increment of magnification each time it is clicked on.
Zoom <u>O</u> ut View F12	This option causes the reduction in size of the entire image by one increment of magnification each time it is clicked on.
Histogram	This option opens the Analysis screen where it presents a graphical representation of the histogram of the data in the chosen data file.

 Table 9.9
 View Menu Options (Continued)

lenu Item	Description of Action
<u>H</u> ighlight	This option displays the Highlight dialog box with its highlight options for chosen planes in the analysis image.
	Plane Height:       0.00       Å         Set Highlight Plane Color
Current <u>S</u> lice	This options presents the trace of the <b>Current Slice</b> as an Analysis Screen graph.
	2D image of the slice. 3D image with a horizontal slice displayed.
Surface Summary	This option displays the Surface Summary box in the Analysis Screen.
	So Suface Parameter Summary      Xoffset : -12.60 µm RavLeveled Feat. Find Xoffset     Yoffset : 0.50 µm RavLeveled Feat. Find Xoffset     (-Information-) Some calculated how presenters lose their significance if the box
Sequence List	Ignore this button

Table 9.9View Menu Options (Continued)

Menu Item	Description of Action
Correlation Scan	Ignore this button

 Table 9.9
 View Menu Options (Continued)

## Change Menu From the View Menu

Table 9.10	Change Menu Option From the View Menu
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Menu Item	Description of Action
View Properties	This option displays the <b>Set Viewing Parameters</b> dialog box with its options and settings.
	Set Viewing Parameters       Image: 30 deg         View       Rise Angle: 30 deg         Rotation Angle: 20 deg       Data Height Mag: 0.20         Data Height Mag: 0.20       Far         Close       Image: Far         Image: Ray trace mode       Image: Height gradient mode         Image: View Using Perspective       Image: Use smooth shading
Light Properties	This option displays the Light Properties dialog box with its options and settings.
	Set Lighting Parameters     Light Source     Light 1     Image: 0     OK     Cancel     Distance from Center:   42   Image: 0   Close   Select Light Color   Range: 0   deg     OK     Cancel     Cancel     OK     Cancel     OK     Cancel     OK     Cancel     Select Light Color     Range: 0     deg     OK     Cancel     OK     Cancel     OK     Cancel         Cancel         OK

Menu Item	Description of Action
Color	This option displays the <b>Light Properties</b> dialog box with its options and settings. The color is applied to the primary image on the Analysis screen.
	Color ? ×   Basic colors:

 Table 9.10
 Change Menu Option From the View Menu (Continued)

### Select View Menu From the View Menu

 Table 9.11
 Change Menu Option From the View Menu

Menu Item	Description of Action
Restore <u>O</u> riginal View	Restore Original View returns the image view to the first view that it is presented in when the Analysis screen opens.
<u>I</u> op	Top turns the image surface flat, giving the user a top down view of the image. This is the same view that is presented when the side tool bar is activated. $\int_{0}^{1} \int_{0}^{1} \int_{0}^{$

Menu Item	Description of Action
Obligue	Oblique turns the image so that it is rotated to the left and down from the Original View, giving more view of the top surface. $ \\ \\ \hline \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\$
<u>F</u> ront	Front is rotated a short distance in the counter-clockwise direction from the Original View. $ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\ \\$
<u>B</u> ack	Back rotates the image so that the surface is in the same basic orientation as the Original View, only with the front to the rear and rear of image to the front.

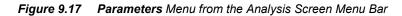
 Table 9.11
 Change Menu Option From the View Menu (Continued)

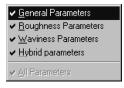
Menu Item	Description of Action
<u>L</u> eft Side	Left Side rotates the image so that the surface is in the same basic orientation as the Original View, only with the front to the right, the rear of image to the left and the left side to the front of the display.
<u>B</u> ight Side	Right Side rotates the image so that the surface is in the same basic orientation as the Original View, only with the front to the left, the rear of image to the right and the right side to the front of the display.

 Table 9.11
 Change Menu Option From the View Menu (Continued)

#### **Parameters Menu**

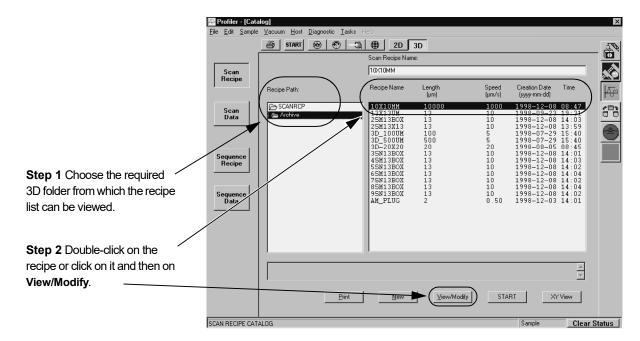
The Parameters Menu is designed to display the checked parameters in the analysis data. This information is included and saved in the Surface Summary record. To include the menu parameter in the Surface Summary, click next to it so that a check appears. (See *Figure 9.17*.)





The General, Roughness, Waviness and Hybrid parameters are sets of parameters found in the Recipe Editor for the recipe being used to create the 3D scan that is being analyzed. For details on each parameter set, see *Chapter 3*. To cause these parameters to be displayed in the **Surface Summary** information, use the following procedure:

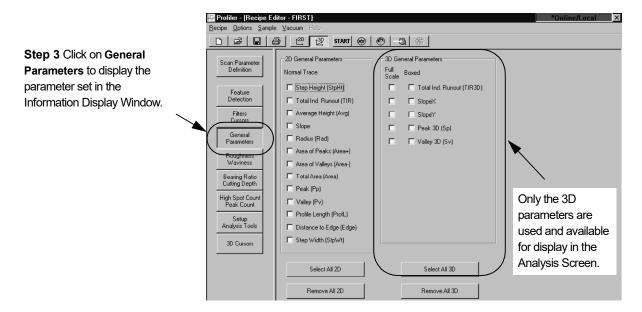
- 1. From the 3D **Recipe Path**, choose a folder containing the 3D recipe, or from the Scan Sequence Recipe list choose a sequence. (See *Figure 9.18*.)
- 2. Double-click on the recipe to open the **Recipe Editor** for that recipe, or click on **View/Modify** at the bottom of the screen.





- **General Parameters**
- **3**. Click on the **General Parameters** button (see *Figure 9.17*.) to display the **General Parameters** information in the Information Display Window.

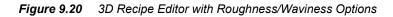
Figure 9.19 3D Recipe Editor

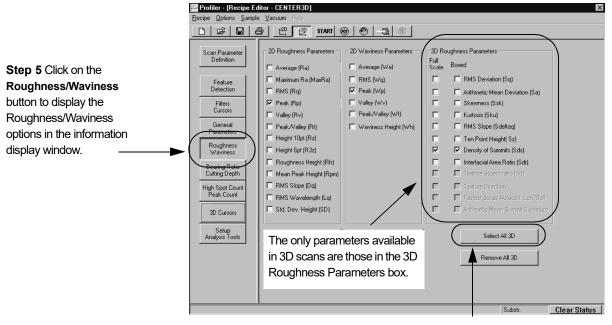


4. Ensure that the required parameters for the scan are chosen. (*Figure 9.19*.)

#### Roughness/Waviness Parameters

5. Click on **Roughness/Waviness** button to display the **Roughness/Waviness** options in the information display window. (See *Figure 9.20*.)





**Step 6** Click on Select All 3D to choose all the available parameters for inclusion in the Analysis data.

6. Click in each empty check box next to the parameters that are to be displayed in the **Surface Summary** box after the scan. This activates the procedure so that the information is available for data analysis. (See *Figure 9.20*.)

To choose all of the available parameters, click on the **Select All 3D** button at the bottom of the column.

7. This is the set of parameters contained in **Bearing Ratio**, **Cutting Depth**, **High Spot Count**, and **Peak Count**. Click on the **Bearing Ratio/Cutting Depth** button. (See *Figure 9.21*.)

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### Hybrid Parameters

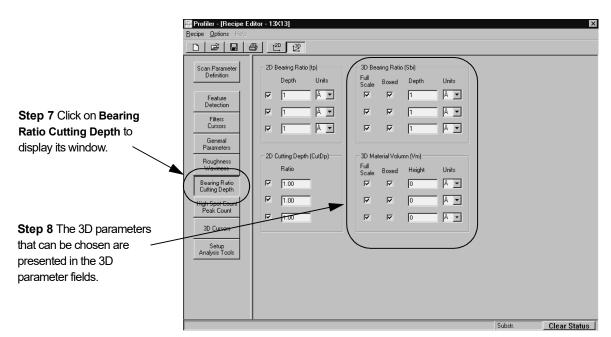


Figure 9.21 Bearing Ratio/Cutting Depth in Recipe Editor

8. Make the required adjustments to the 3D parameter settings. (See Figure 9.21.)



**NOTE:** The **High Spot Count/Peak Count** parameters are only for 2D analysis and do not show up in 3D analysis.

- 9. In the 3D Analysis screen, click on View in the menu bar to display its menu.
- 10. From the View menu, click on Parameters Menu.
- 11. Click next to each parameter that is to be displayed in the **Surface Summary** box. The checkmark ensures that the information prescribed in the Recipe Editor and collected during the scan, is displayed in the **Surface Summary** box. (See *Figure 9.17.*)

#### **Operations Menu in the Analysis Screen Menu Bar**

Table 9.12 Op	erations Menu	Options	(From Menu Bai	)
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Menu Item	Description of Action
Level	This option activates the Leveling procedure by activating the tool bar to the right of the image, orientating the image to the <b>Top View</b> , and placing the leveling cursors on the image surface. (See <i>Table 9.5</i> , <b>Level tool</b> .)

-	nu Options (From Menu Bar) (Continued)		
Menu Item	Description of Action		
<u>C</u> ancel Leveling	This button is activated when the Leveling procedure is activated. If the Leveling procedure is begun and the user wishes to cancel it prior to completion, this button can be clicked to abort the procedure.		
Line Le <u>v</u> el	This option displays the Line Leveling dialog box for use in leveling the image. There are two sets of lines that work just like setting cursors. There is a left and right side of the "line" that will be used for leveling. It is very important that the bounded area in both "lines" is all in the same plane. For this reason, the example shown below would not be a good candidate for this type of leveling since no vertical line could be drawn on a single plane.		
	Line Leveling		
Image Arithmetic	This displays the Image Arithmetic dialog box which allows the user to compare the current image with other images using various mathematical operators.		
<u>R</u> ecalc	This option allow the user to <b>recalculate</b> the current data using <b>new</b> parameters.		

 Table 9.12
 Operations
 Menu
 Options (From Menu Bar) (Continued)

Menu Item	Description of Action
<u>S</u> ummary Display Options	

 Table 9.12
 Operations Menu Options (From Menu Bar) (Continued)

### Data Menu from the Analysis Screen Menu Bar

 Table 9.13
 Data Menu Options (From Menu Bar)

Menu Item	Description of Action		
Data Inverted	This option inverts the data and changes the screen image to reflect the inverted data.		
<u>G</u> ranularity	This option allows the user to choose how many of the collected data points will be used. It opens a dialog box that with the necessary settings.		
	This feature sets the gain of the image.		
	The computer records more data points than are possible to plot on-screen, so it uses a subset of the points taken to build the image. In general, the smaller the subset, the coarser the image and the faster it can be displayed and rotated.		
	To control the image granularity from coarse to fine, set the parameters for the data subset, using the Data Granularity dialog box.		
	Data Granularity       X         Rotation Data Set Screen Display Limit       OK         Maximum Number of X data points:       50         Maximum number of Y data points:       50         Low Resolution Data Set Screen Display Limit       Cancel         Maximum Number of X data points:       100         Maximum Number of Y data points:       100         High Resolution Data Set Screen Display Limit       Maximum Number of Y data points:         High Resolution Data Set Screen Display Limit       Maximum Number of Y data points:         Maximum Number of Y data points:       200		
High Resolution	This option is for display purposes only. If checked (like Low Resolution in the following field), the image will be presented in a higher resolution. This slows generation time when the image is rotated or magnified but offers greater detail.		
✓ Low Resolution	This option is for display purposes only. If checked, as in the illustration, the image will be presented in a lower resolution. This enhances generation time when the image is rotated or magnified.		

### Tools Menu from the Analysis Screen Menu Bar

 Table 9.14
 Tools Menu Options (From Menu Bar)

Menu Item	Description of Action		
Enable Tools (Top View)	This options enables the Side Tool Bar Buttons. (See <i>Table 9.6</i> .)		
<u>D</u> isable Tools	This options disables the Side Tool Bar Buttons.		
Analysis <u>T</u> ools →	This option displays the Analysis Tools menu. Leveling Slice Height		
✓ <u>E</u> nable Zoom Tool	This option changes the image to Top View, places the zoom box at the bottom left corner of the image, and activates the Zoom In (magnification) icon 2 in the top tool bar. (See <i>Table 9.5</i> , Zoom In.)		
Zoom	Once the Zoom In boundary box is set on the area to be zoomed in on, this option completes the zoom procedure to magnify the surface bounded by the box.		
UnZoom	This button restores the pre zoom image.		
Mouse Tools →	This option displays the <b>Mouse Tools</b> menu. These tools are all duplications of tools on the top tool bar. For <b>Rotate Image</b> and <b>Change Rise Angle</b> , see <i>Table 9.2</i> . For three <b>Change Light</b> options, see <i>Table 9.5</i> , look for the same titles. For the <b>Move</b> <b>Highlight Planes</b> , see <i>Table 9.5</i> , look for the same title.		
	Change Light <u>Distance</u> Move <u>Highlight</u> Planes		
Lock to <u>H</u> orizontal Cross-Sections	This option is used with the Slicing Tool. (See <i>Table 9.6</i> , in the Activate Slicing Tool section.) When this option is chosen, the slicing tool will automatically go to the horizontal position and only operate in that position for the slicing procedure.		

Menu Item	Description of Action
✓ Lock to <u>V</u> ertical Cross-Sections	This option is used with the Slicing Tool. (See <i>Table 9.6</i> , in the Activate Slicing Tool section.) When this option is chosen, the slicing tool will automatically go to the vertical position and only operate in that position for the slicing procedure.
Unlock Cross-Sections	This option is used with the Slicing Tool. (See <i>Table 9.6</i> , in the Activate Slicing Tool section.) When this option is chosen, the slicing tool automatically set the slicing line at a diagonal across the image. This line can be changed to any angle or length.

 Table 9.14
 Tools Menu Options (From Menu Bar) (Continued)

# LINE-BY-LINE LEVELING

### Introduction

Line-by-Line Leveling is designed to provide a tool for leveling 3D images where planes at the same "Z" level can be detected running from top to bottom (along the Y-axis) of the 3D image. This process is used to remove errors caused by scan drift. This is accomplished by the system which averages the points between the cursor borders to come up with a single value. The 3D image is leveled using the trace line along the x-axis and the averaged value for the leveling cursor.

Each cursor is color coded with a right and left side and progressively higher headers that help the user to set them in their proper order. All four lines can be used for leveling. The left line (shorter cursor border) of each color set is the left cursor border. This keeps the lines identifiable so they are not placed out of order. It is important that the lines be kept in order.

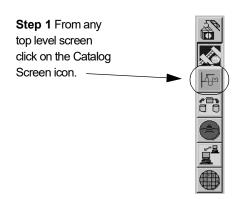
# **Activating Line Leveling**

### **Opening the 3D Cursor Parameters Window**

Line-by-Line Leveling is activated in the Recipe Editor. It is used only in 3D images and is only accessible through a 3D recipe.

1. From any top level screen, open the Catalog Screen by clicking on its icon. (See *Figure 9.22*.)

Figure 9.22 Program Level Icons

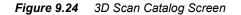


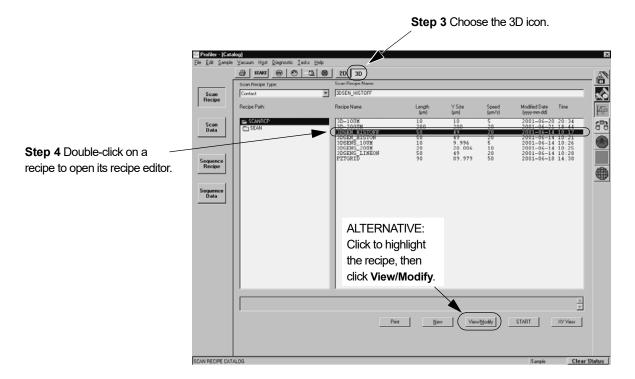
2. From the Catalog Screen choose the **Scan Recipe** button to display the scan recipe names in the list field portion of the screen.

Figure 9.23	Catalog Screen with Scan Recipe Chosen
-------------	--

File Edit Sample	leg) ⊻acuum Host Diagnostic Iasks He	sip					
	START 🛞 🕙 坑	🖶 2D 3D					
	Scan Recipe Type:	Scan Recipe Name:					
Scan Recipe	Contact	3DSEN_HISTOFF					
	Recipe Path:	Recipe Name	Length (ym)	Y Size (µm)	Speed (µm/s)	Modified Date (yyyy-mm-dd)	Time
Scan Data Sequence Recipe	SEANIGP SEANI	DD-100M 3D-2000M HGSNN HESODE DDSEN_HISTON JDSENS_100M JDSENS_200M JDSENS_LINEON FZTGRID	10 200 50 50 20 20 50 90	10 200 49 9.996 20.006 49 89.979	5 20 20 5 10 20 50	2001-06-20 2001-06-21 2001-06-14 2001-06-14 2001-06-14 2001-06-14 2001-06-14 2001-06-18	18:44 10:17 10:21 10:26 10:25 10:28
Sequence Data							

**Step 2** Click on the Scan Recipe button to display the scan recipes in the list field. **3**. Ensure that the 3D icon is active so the 3D Scan Recipes are displayed in the lit field. (See *Figure 9.24*.)





4. Select the 3D recipe to be edited by double-clicking on the recipe name. This opens the recipe editor. (See *Figure 9.24*.)

(ALTERNATIVE: Click to highlight the recipe, then click on **View/Modify** at the bottom of the screen. See *Figure 9.24*.)

- 5. In the Recipe Editor, click on **3D Cursors** to display the 3D Cursor parameters. This displays the four sets of 3D cursor parameters that are available for defining in the recipe:
  - 3D Leveling Cursor
  - 3D Line by Line Leveling Cursor
  - 3D Measuring Cursor
  - 3D Step Height Cursor

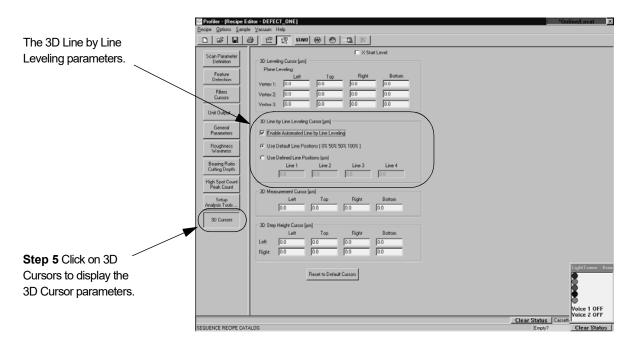
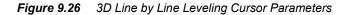


Figure 9.25 Recipe Editor - 3D Cursors Window

### **Enabling 3D Line-by-Line Parameters**

The 3D Line-by-Line Leveling option is enabled by putting a check in the **Enable Automated Line by Line Leveling** checkbox. After the option is enabled, the user can choose between two leveling options, or manually set the cursors in the Analysis screen after the scan. Enable the 3D Line-by-Line Leveling by clicking in the empty **Enable Automated Line** by Line Leveling checkbox to put a check in it. (See *Figure 9.26*.)



Step 5 Click in the	- 3D Line by Line Leveling Cursor [μm]
empty checkbox to	Enable Automated Line by Line Leveling
enable 3D Line-by-Line	Use Default Line Positions [ 0% 50% 50% 100% ]
Leveling.	🕐 Use Defined Line Positions (μm)
	Line 1 Line 2 Line 3 Line 4

After the Line-by-Line Leveling is enabled, the two leveling options are also active so one or the other can be enabled. Clicking in the empty radio button toggles between the options.

#### Use Default Line Position [0% 50% 50% 100%]

This option can be used best when scanning a sample with uniform texture typical of film roughness scans. This function operates best when there are known flat regions throughout the Y axis direction. This preset option automatically levels the scan by placing the left cursor's left border at the origin of the scan, the left cursor's right border at the mid point of the scan, the right cursor's left border also at the midpoint of the scan, and the right cursor's right border at the end point of the scan.

#### **Use Defined Line Positions**

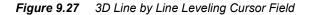
The Defined Line Positions can be set in two ways:

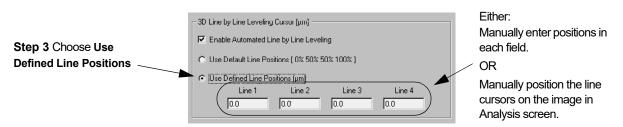
- The operator chooses **Use Defined Line Positions** as the leveling tool. The operator manually enters (sets) the positions of the cursors in microns. These settings are between 0 µm and the number of microns in the scan length, as defined in the recipe.
- The operator can enable line-by-line leveling and choose **Use Defined Line Positions** as the leveling tool. The operator then either runs the scan to obtain the data, or opens saved data that used the same recipe. The Line-by-Line procedure is used to level the data and the data is saved. Once saved, the positions of the newly placed cursor lines is displayed in the recipe.

#### Manual Entry of Line Position in Line Field

- 1. Follow the instruction in *Opening the 3D Cursor Parameters Window* on page 9-33.
- 2. In the 3D Cursor Parameters window, ensure that **Enable Automated Line by Line** Leveling is enabled. (See *Figure 9.27*.)

**3**. Click on the empty radio button next to **Use Defined Line Positions** to enable it. (See *Figure 9.27*.)





Once Use Defined Line Positions is enabled, the four Line fields become active.

- 4. If the positions for the line spacing is known, enter the respective positions in each of the fields. Remember the following when entering the position:
  - The units are microns (μm).
  - The range is [0 μm to (Length of scan) μm] (length as defined in the scan recipe being used).
  - 0 ≤ Line 1 position < Line 2 position < Line 3 position < Line 4 position ≤ Scan Length
  - If the cursor line entries fall outside the scan limits, the system automatically adjusts the cursors according to the sequential priority in the above bullet.

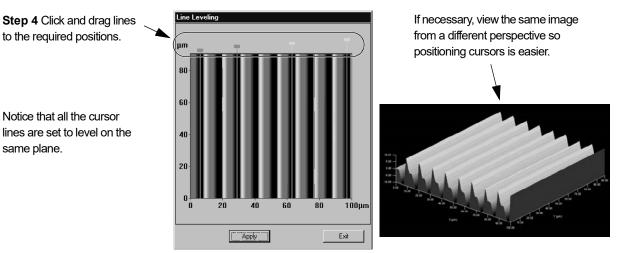
#### Manually Position Line Cursors on Image to Enter Line Position

- 1. Run the scan using the recipe that is modified as illustrated in Figure 9.27.
- 2. From the Analysis screen choose Operations in the Menu Bar.
- 3. Select Line Leveling from the Operations menu.

The graphic display of the data appear midscreen in the top view with the four line cursors in place at opposite borders of the image.

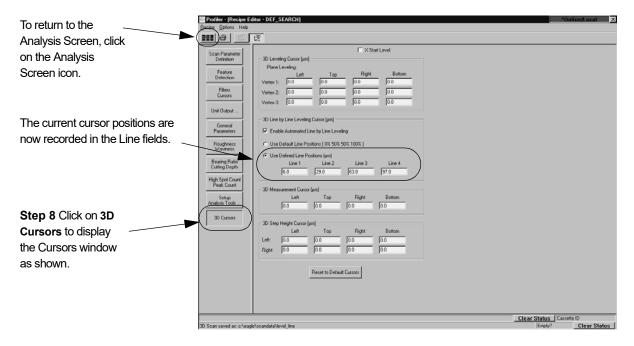
4. Click and drag each line to its required position. All four line cursors must be on the same plane for the data to be properly leveled. (See *Figure 9.28*.)

Figure 9.28 Line Leveling Top View Analysis Screen



- 5. It is not necessary to save the data for the new cursor position to be recorded in the recipe.
- 6. To observe the recipe, click Edit in the Menu Bar to display its menu.
- 7. Select **Recipe** from the Edit menu to return to the Recipe Editor.
- 8. In the Recipe Editor, click on the **3D Cursors** button at the bottom of the parameter window icon column. (See *Figure 9.29*.)

Figure 9.29Recipe Editor with 3D Cursors Window Displayed



**9**. To preserve the current 3D Line by Line Leveling Cursors positions, save the recipe.

# CUSTOMIZING THE SCAN IMAGE

### **Setting the Image Proportions**

1. Go to the View menu, and select Change.

The View Properties dialog box appears.

2. Type a number that gives an appropriate value for the image height in Data Height Mag. (See *Table 9.10 on page 9-23*, View Properties.)

Since the number depends on the relative heights of the features in the image, select a higher value to obtain a taller image, a smaller value to reduce it. Click **OK**.

# Setting the Shading Mode

- 1. In the View menu, click on Change...
- 2. In the Change... menu, click on View Properties. The Set Viewing Parameters dialog box appears.

Figure 9.30	Set Viewing Parameters Dialog Box
-------------	-----------------------------------

	Set Viewing Parameters	×
Shading mode options. Chose the one that best fits the requirements by clicking in its empty radio button.	View Rise Angle: 20 deg Rotation Angle: 10 deg Data Height Mag: 0.20 Close S Far Ray trace mode Height gradient mode View Using Perspective View Use smooth shading	Cancel

- **3**. Select one of the following shading modes to customize the 3D data images to better represent the sample type:
  - By Height to emphasize high features, click on the radio button next to Height gradient mode. (See *Figure 9.30*.)
  - By Light to enhance smooth surfaces, click on the radio button next to Ray trace mode. (See *Figure 9.30*.)

The results will appear in the Analysis screen, showing the three-dimensional, color representation of the data points collected in one of three selectable formats. (See *Table 9.15*.)

Table 9.15 3D Analysis graphs

Graph	Description
215474 -	By Height Good for viewing rough features.
Z (Å) 10000- 240- 200-	The higher the feature, the lighter the color.
% (m) 7 (m)	
X (µm)	
245474 200000 240 240 200 200 7 (m) 100 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	By Light Good for viewing smooth features since contours are more obvious. Features appear as if illuminated by a light source.
X (µm)	

### **Changing the View Angle**

- 1. The image can be viewed from various angles by doing one of the following:
  - Press the arrow keys on the keyboard. (See *Analysis Screen Image Orientation* on page 9-3.)
  - Go to the View menu, click on Change...

Click on one of the seven views listed: (See Table 9.11 on page 9-24.)

Restore Original View	Тор
Oblique	Front
Back	Left Side
Right Side	

• Click the **Rotation** buttons at the bottom of the 3D view window to quickly examine the image from any angle. (See *Table 9.1 on page 9-4* and *Table 9.2 on page 9-4*.)

# **CUSTOMIZING THE VIEW**

## Changing the Image Colors

- 1. Go to the View menu, and select Change...
- 2. Click on Display Color.
- Select a color from the palette or create a custom color.
   Saving the scan file also saves custom colors. (See *Table 9.10 on page 9-23.*)
- 4. Click **OK** to close the dialog box and apply the choice.

# **Changing the Scan Height Colors**

Images can be color-coded and displayed in the Height Gradient Mode format to better delineate height features. The Highlight feature allows the user to define a highlight plane to bring out certain features of the image.

1. Go to the View menu, and select Highlight.

A dialog box appears with the minimum and maximum heights obtained in the scan.

- 2. Go to the Plane Height entry field, and type the desired height.
- 3. Click Set Headlight Plane Color.
- 4. Select a color from the palette or create a custom color.
- 5. Click OK.
- 6. If desired, repeat to define additional planes.

# **Removing Banding with Line Leveling**

Line leveling can be used to remove banding caused by environmental signal drift with each successive trace in a 3D scan baseline. Line leveling calculates corrections by comparing line segments line-by-line rather than by averaging areas. Line leveling should generally be used when calculating 3D roughness, area, volume, and other parameters.

- 1. Click on **Operations** in the Analysis screen menu bar.
- 2. Click on Line Level...

**3**. Go to the **Operations** menu, and select **Line Level**. The dialog box appears (see *Figure 9.31*).

Step 4 The cursors in	Line Leveling
this illustration must be	
placed close together to	
ensure that they are	
covering the same plane.	80 / 1 //
sevening the same plane.	
	40
Step 5 After the cursors	
are set, click Apply to	20
preview the results.	20
F	
	8 0 20 40 60 80µm
	0 20 40 60 80µm
	Exit

Figure 9.31 Line Leveling Dialog Box After Cursors Positioned

4. Click and drag the lines of each pair of boundary cursors to define segments of the scan lines on the same plane.

Do not include features, only flat areas (see *Figure 9.31* for placement of cursors). Notice that in the image, the lines must be vary close together in order to keep from including unwanted features.

The instrument compares the bounded segments and calculates an average baseline for the scan.

- 5. Click the Apply button to preview the results. The Undo button become active.
- 6. Click the **Exit** button to return to the scan data window and view the results on the scan image.
- 7. If the new leveling is to be retained, it must be saved. If the screen is closed without saving, the changes are lost.

# **USING IMAGE ARITHMETIC TO COMPARE DATA**

Two 3D scans can be compared with similar surfaces or the same site to evaluate noise and roughness. Both scans must use the same recipe:

- Recipe
- X-size and Y-size
- 1. Open the data file that is to be use in the calculations. This is **Image 1**.

2. Go to the **Operations** menu, and select **Image Arithmetic**. The dialog box appears (see *Figure 9.32*)

Figure 9.32	Image Arithmetic Dialog Box

	Image Antometic	~
	μm 80	<u>D</u> isplay Apply
	60 ·	<u>U</u> ndo <u>C</u> lose
	40	
Step 3 Enter the name of the second image or click the Browse button to search for the image.	20- 0- 0 20 40 60 80μm	
	Select the second image (Image2):	
	Browse	
	Processing Formula: (Image1 - Image2 ) / 1  Operator 1 Operator 2 Scale Factor:	
	Subtraction     Operator 2     Scale Pactor	
	C Addition	

- Type in the name of the second image or Browse for the second image. The second image must have used the same recipe as the first image, and it must be the same size.
- 4. Press ENTER, or click the Display button.

The second image appears in the display area in the dialog box.

- 5. Go to the **Operator** panels, and click one of the buttons for:
  - Subtraction or addition
  - Division or multiplication

The Processing Formula above the panels displays the selection.

- Scale Factor sets the value for Operator 2.
- If division or subtraction are not being performed on the data, go to the **Scale Factor** field, and enter **1**.
- 6. Click the Apply button to perform the operations.
- 7. To revise the operations and recalculate, click the Undo button.
- 8. When the results are satisfactory, click the **Close** button.

A Save message dialog box appears.

9. Click **OK** to save the resulting image.

# SAVING SCAN DATA

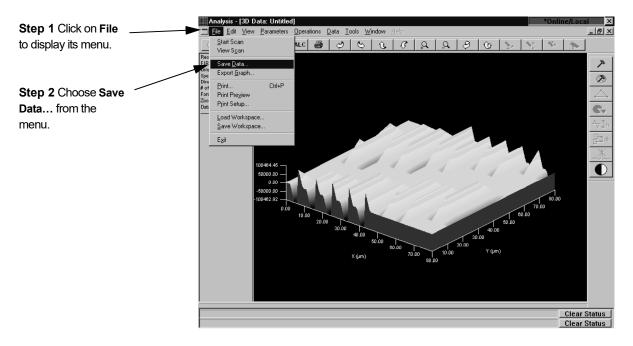
Scan data can be saved for reviewing at a later time. This is especially important because the data that is saved, using software version 6.1 or newer, can be reanalyzed at a later date using different scan parameters.

In addition to saving the 3D data, current slice data can be save. This procedure is covered at the end of this section.

# Saving 3D Scan Data

1. Click on **File** in the Menu Bar to display the File menu.

Figure 9.33 3D analysis Screen with File Menu



#### 2. Select Save Data...

The Save Scan Data dialog box appears. (See Figure 9.34).

Figure 9.34 Save Scan Data Dialog Box

Step 4 From the drop-down menu, click on the desired drive and directory.	Save Scan Data ?	X Step 3 Click on
Step 5 If folders are present, double-click on the folder in which the data is to be saved.	lanit_scn.3dd ■ scan_3.3dd ■ scan_4.3dd	the down-arrow to reveal the available drives and directories if needed.
Step 6 Enter the name being given to the new data set.	File name:     scan_5       Save as type:     Scan Data Files (*.3dd)       Cancel       Help	Step 7 Click Save to save the data to the file.

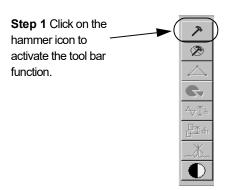
- 3. Click on the menu arrow next to **Save In** to reveal the available drives and directories. (See *Figure 9.34*)
- 4. Select the drive and directory from the drop-down menu. (See Figure 9.34)
- 5. Double-click on the folder that the data is to be stored in. A list of all current data files appear. (See *Figure 9.34*)
- 6. Enter a name for the data set in the File name variable box. (See *Figure 9.34*)
- 7. Click **Save** to save the data in the new file. (See *Figure 9.34*)

Once a data set has been saved, it is added to the Scan Data catalog. The Scan Data catalog window allows selection of individual data sets for reviewing. Unwanted data sets can be deleted.

## Creating and Saving 2D Slice Data from a 3D Scan

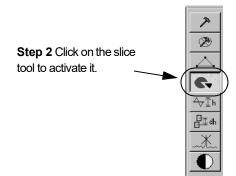
1. From the Analysis Screen, click on the hammer tool to activate the tool bar.

Figure 9.35 Analysis Screen - Analysis Tool Bar

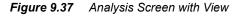


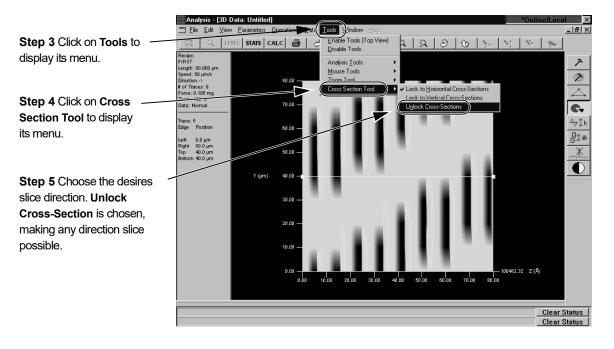
2. In the activated tool bar, click on the slice tool to activate the slice tool.

Figure 9.36 3D Analysis Tool Bar with Slice Tool Activated



**3**. Choose the desired slice direction. Click on Tools to display its menu. (See *Figure 9.37.*)





- 4. Click on Cross Section Tool from the Tools menu to display its menu. (See *Figure 9.37*.)
- 5. Choose the desired cross section tool for the slice direction. (See Figure 9.37.)
- 6. For the **Horizontal** and **Vertical** tools, click and drag the slice line to the desired location on the 3D image to display the 2D trace of the scan at that location. For the **Unlock Cross-Section** tool, click and drag the slice line end points to the desired location on the border of the image as seen in *Figure 9.38*.

Step 6 Top create the slice,

the unlocked slice tool or the

line segment of the vertical or

horizontal slice tools.

click and drag the endpoints of

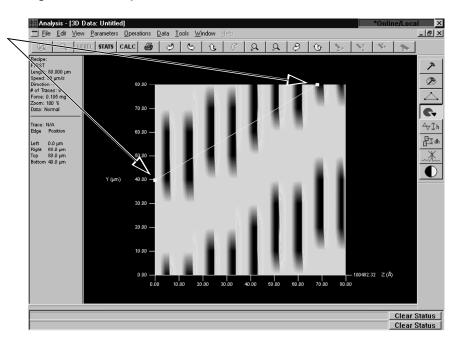
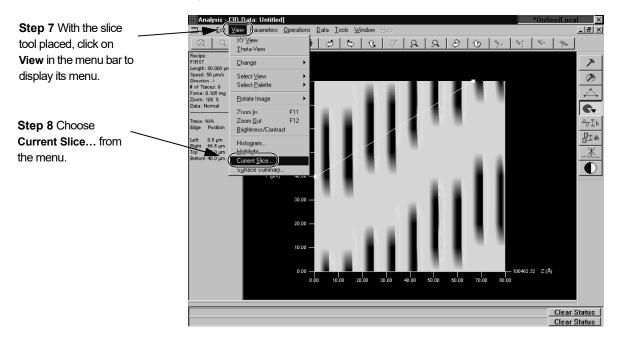


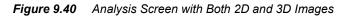
Figure 9.38 Analysis Screen with Slice Tool Active

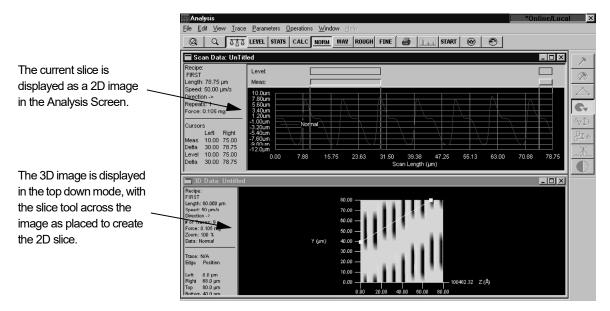
- 7. When the slice line has been placed, click **View** in the menu bar to display its menu. (See *Figure 9.39*.)
- 8. Choose Current Slice... to display the 2D slice trace. (See Figure 9.39.)

Figure 9.39 Analysis Screen with Both 2D and 3D Images



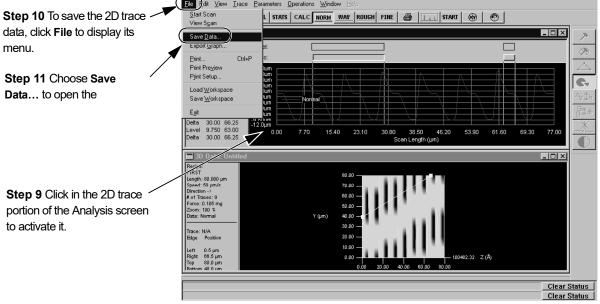
If the Window option is set to Tile Horizontal then the image is displayed as illustrated in *Figure 9.40*. The 2D slice trace is displayed above the 3D image. The 3D image is shown with the slice tool placed across the image at the place where the 2D image is generated.



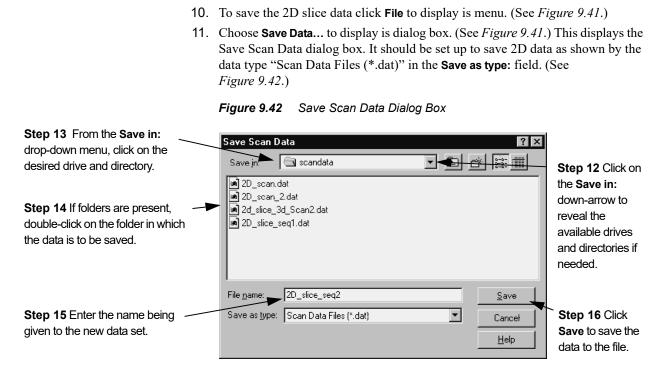


9. To save the 2D trace data from the 3D scan, click in the 2D trace portion of the Analysis screen to activate it.





×



- 12. Click on the down-arrow next to **Save In** to reveal the available drives and directories. (See *Figure 9.42*)
- 13. Select the drive and directory from the drop-down menu. (See *Figure 9.42*)
- 14. Double-click on the folder that the data is to be stored in. A list of all current data files appear. (See *Figure 9.42*)
- 15. Enter a name for the data set in the File name variable box. (See *Figure 9.42*)
- 16. Click **Save** to save the data in the new file. (See *Figure 9.42*)

Once a data set has been saved, it is added to the Scan Data catalog. The Scan Data catalog window allows selection of individual data sets for reviewing. 2D slice data saved from a 3D scan can be reevaluated in the Analysis screen by changing the recipe parameters and performing a recalculation of the information. Unwanted data sets can be deleted.

# SYSTEM SECURITY

# INTRODUCTION

The Profiler system security is designed to provide users with membership in various groups for access to the Profiler functions for which they are responsible. Each group access is provided by an interface between the Windows software and the Profiler Software. Each group is defined and named in the Windows software. Windows defines three user groups: Administrator, Power Users, and Users. The Profiler software defines 16 additional groups. The additional groups are as follows:

P_Configuration	P_Calibration	P_AdvCalibration
P_EditScanRecipe	P_TranScanRecipe	{+EditScanData
P_TranScanData	P_EditSeqRecipe	P_TranSeqRecipe
P_EditSeqData	P_TranSeqData	P_Stress
P_Diagnostics	P_VirtualArtifacts	P_StageMapping
P_GemSecs		

Each of these groups provide access to system functions that are necessary for the job actions associated with the security level. There can be as many people assigned to each level as is necessary.

This chapter includes discussions on:

- Windows Defined Groups on page 10-2
- *Profiler Defined Groups* on page 10-2
- Opening the User Manager on page 10-4
- User Manager on page 10-6
- Creating a New User on page 10-6
- Results of Limited Access on page 10-11
- Adding a User to a Users Group on page 10-9

# Windows Defined Groups

The Windows defined groups have functions as follows:

- Administrator and Power Users: A user who is a member of either of these predefined groups has all of the Profiler privileges. That is, he is allowed to use any and all Profiler software features and can create, delete, or modify any Profiler system or data files.
- User: A user who is a member of predefined Users group has the basic set of Profiler privileges:

View a scan or sequence recipe

Run a scan or sequence recipe

Save the data in a new data file, including thumbnail files

View data, including thumbnail files

Perform the Applied Force calibration procedure because it is a daily operation that requires relatively few Profiler skills

# **Profiler Defined Groups**

The Profiler defined groups have privileges as follows:

- **P\_Configuration**: This group allows a user to select the **Configuration** button in the program level screens and to perform any configuration procedures. The only exception is that in System Configuration, only Administrators and Power Users are allowed access to Registry Maintenance.
- P\_Calibration: This group allows a user to perform any of the calibration procedures except Center of Rotation (Administrators and Power Users only), Linearity, Pulse ratio, Tilt/Level, Virtual Artifacts, and Stage Mapping. These other calibrations are included in other groups.
- **P\_AdvCalibration**: This group allows a user to access these calibration procedures: Linearity, Pulse Ratio, and Tilt/Level.
- **P\_EditScanRecipe**: This group allows a user to modify an existing scan recipe and save it. The edit can be done explicitly in the recipe editor or implicitly by using a function that automatically changes the recipe, such as the CALC function in the Analysis window in a live scan or in review mode.
- P\_TranScanRecipe: This group allows a user to import a new scan recipe but not to overwrite an existing one, unless the user is also a member of P\_EditScanRecipe. The user can also export a scan recipe to an external file. The Profiler imposes no restrictions on the user privileges of the external file.
- **P\_EditScanData**: This group allows a user to modify existing scan data and save it. The user can also overwrite existing scan data with different data or delete scan data.



**NOTE:** If the user is not also a member of P\_EditScanRecipe, then the user cannot implicitly modify a scan recipe in the Analysis window in either a live scan or review mode. Examples of this are the CALC and RECALC button which are disabled.

- P\_TranScanData: This group allows a user to import new scan data but not to overwrite existing data, unless the user is also a member of P\_EditScanData. The user can also export scan data to an external file. The Profiler imposes no restrictions on the user privileges of the external file.
- **P\_EditSeqRecipe**: This group allows a user to modify an existing sequence recipe and save it. The edit can be done either directly in the recipe editor or implicitly by using a function that automatically changes the recipe. The user can also overwrite an existing sequence recipe with a different recipe or delete a sequence recipe.
- P\_TranSeqRecipe: This group allows a user to import a new sequence recipe but not to overwrite an existing one, unless the user is also a member of P\_EditSeqRecipe. The user can also export a sequence recipe to an external file. The Profiler imposes no restrictions on the user privileges of the external file.
- **P\_EditSeqData**: This group allows a user to modify existing sequence data and save it. The user can also overwrite existing sequence data with different data or delete sequence data.

*
*
/

**NOTE:** If the user is not also a member of P\_EditSeqRecipe, then the user can not implicitly modify a sequence recipe in the Analysis window. Examples of this are the CALC and RECALC button functions which are disabled.

- **P\_TranSeqData**: This group allows a user to import new sequence data but not to overwrite existing data, unless the user is also a member of P\_EditSeqData. The user can also export sequence data to an external file. The Profiler imposes no restrictions on the user privileges of the external file.
- **P\_Stress**: The group allows a user to access the Stress application. The user can create, delete, or modify stress recipes. The user can also create, delete, or modify stress scan data. This group can be restricted to users who have stress characterization responsibilities.
- **P\_Diagnostics**: This group allows a user to access the Diagnostics application. This group can be restricted to users who have machine troubleshooting responsibilities.
- **P\_VirtualArtifacts**: This group allows a user to generate virtual artifacts. This group can be restricted to user who have this responsibility.
- **P\_StageMapping**: This group allows a user to perform the Stage Mapping calibration. Only users with special training should be members of this group.
- **P\_GemSecs**: This group allows a user to change the host/equipment GEM/SECS settings. Only users with special training should be members of the group.

# MANAGING THE SYSTEM SECURITY

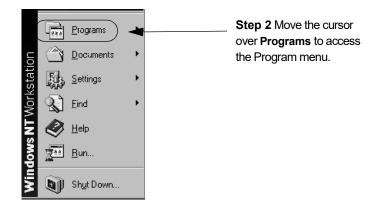
## **Opening the User Manager**

During the logon procedure the user must enter a combination of logon ID and password. This logon is necessary for the Windows software to complete the system initiation. The logon ID establishes which group(s) the user has access to. The password completes the access to group functions. When opening the **User Manager** screen, where the security system resides, the logon will have already determined what groups the user has access to. Only those with Administrator or Power User access can perform any of the functions in the User Manager screen.

- 1. Click on the **START** button at the bottom left of the screen. This displays the Windows menu. (See *Figure 10.4*.)
- 2. Click on the Programs option to display its menu. (See Figure 10.1.)

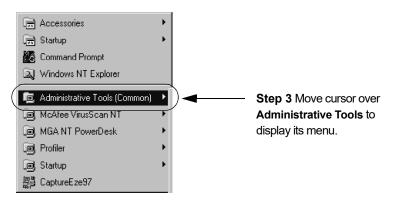
Figure 10.1 Windows Screen START Menu

**Step 1** Click on **START** at the bottom left corner of the screen to open this menu.



**3**. Move the cursor over **Administrative Tools (Common)** to display its menu. (See *Figure 10.2* and *Figure 10.4*)

Figure 10.2 Programs Menu



4. Move the cursor over User Manager (see *Figure 10.3* and *Figure 10.4*) to display the User Manager screen. (See *Figure 10.5*.)

Figure 10.3 Administrative Tools Menu

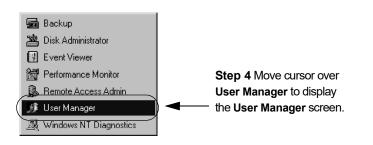
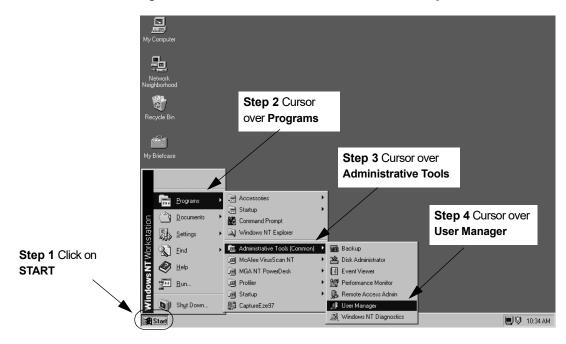


Figure 10.4 Windows Screen with Path to User Manager Screen



## **User Manager**

The **User Manager** is the security system interface for Windows. The P-15 Profiler uses the Windows security system. All assignment of users to user groups and creation of user passwords is set in this screen.

**User Manager** User <u>P</u>olicies <u>O</u>ptions <u>H</u>elp - 8 × Usemame Full Name Description 🗜 Administrator Built-in account for administering the c List of user names. Dummy Guest mantest Process Eng 2 User 2 Peggy Fleming Built-in account for guest access to the computer/domain Manufacturing Test first shift operator Bob Shaw The process engineer 2nd shift operator Mike Smith Sam Davis Groups Description P-EditScanData
 P-EditScanData
 P-EditScanData
 P-EditScapData
 P-EditScapData
 P-StageMapping
 P-StageMapping
 P-TranScanData
 P-TranScanData
 P-TranScapData
 P-TranSc List of User Groups Power Users Members can share directories and printers Replicator Supports file replication in a domain rdinary users sers

#### Figure 10.5 User Manager

# Creating a New User

For the P-15 system users, a User Group is a secured access group with specific system privileges.

To create a new user, use the following procedure:

1. Click on User to display its menu. (See Figure 10.6.)

۷.			dialog box. (See Figure 10.0.)
	Figure 10.6	ser Manager	
	🖘 User Manager		Online/Local ×
Step 1 To create a	<u>User</u> <u>Policies</u> <u>Options</u> <u>H</u> elp		
-	New <u>U</u> ser	Full Name Description	
new user, click on	New Local Group	Built-in acco	unt for administering the computer/domain
User.	<u>C</u> opy F8 <u>D</u> elete Del <u>B</u> ename	Built-in acco	unt for guest access to the computer/domain
	Properties Enter		
Step 2 Click on	E <u>x</u> it Alt+F4		
New User			
	_	<b>1</b>	
	Groups R Administrators	Description Members can fully administer the comp	uter/demoin
	Backup Operators	Members can bypass file security to be	
	Backup Operators     Guests     P_AdvCalibration	Users granted guest access to the com	
	峰 P_AdvCalibration 峰 P_Calibration		
	P_Configuration P_Diagnostics		
	🚅 P_Diagnostics 🚅 P_EditScanData		
	P_EditScanRecipe		
	P_EditSeqData		-
	P_EditSeqRecipe     GemSecs	P GemSecs	
	P_GemSecs P_StageMapping		
	P_Stress		a. a 1
			Empty? Clear Status

2. Click on New User to open the New User dialog box. (See Figure 10.6.)

#### **BEGIN: Setting a** Password

- 3. Enter the User Name in the first field. This is the name that the user enters into the User ID field during the logon process. (See Figure 10.7.)
- 4. Enter the Full Name in the second field. This is the actual identity of the user. (See *Figure 10.7.*)
- 5. Enter the **Description** in the third field. This describes the duties of the user. (See *Figure 10.7.*)
- 6. Enter the **Password** in the fourth field. This is the password that the user enters in the Password field at logon. (See Figure 10.7.)
- 7. Enter the Confirm Password in the fifth field. This is the Password that was entered in the fourth field, now entered a second time to verify that the first entry was correct (verification is difficult since the password is not displayed). If the two entries are different correction can be made. (See Figure 10.7.)



CAUTION: It is extremely important that the Administrator password be protected. If the passwords are changed and lost or forgotten, it is a very expensive and time consuming process to establish new access to the system. To avoid potential system downtime, the original Administrator password should be kept in a secure place by the administrator and not changed.

END: Setting a Password

Step 3 Enter the user name. This is the logon name.	New User
Step 4 Enter the user name This is the identity of the person.	Username:         ProcessEng 2         OK           Full Name:         MortamerSnerd         Cancel           Description:         The2ndProcessEng         Help
Step 5 Enter the user name. This is what the person does in the system.	Bassword:     Instant       Confirm     Instant       Password:     Instant       User Must Change Password at Next Logon
Step 6 Enter the Password. A confirmation is requested so there is less chance of misspelling since it is not visible.	✓       Uger Cannot Change Password         ✓       Password Never Expires         ✓       Account Disabled

Figure 10.7 New User Dialog Box - Variables

- 8. There are four logon variables that can be selected from. To enable one of the variables, click in the empty checkbox so that a check ( $\checkmark$ ) appears in it. The variables are as follows: (See Figure 10.8.)
  - User Must Change Password at next logon. If checked, the user will be ٠ required to enter a new Password the next time the user logs on.
  - User Cannot Change Password. This makes it impossible for the user to change the password. This is helpful if several people use the same logon.
  - Password Never Expires. If checked, the password always stays the same. If this is not checked, the user will be required to periodically choose another password. This is a way of forcing a periodic change of password.
  - Account Disabled. If checked, the user will not be able to logon until it is unchecked. This way a users logon can be stopped without wiping out the connections that the user has in the system. The connections cannot be reestablished if the user is deleted.

Figure 10.8 New User Dialog Box - Variables

1	New User		×
	<u>U</u> sername:	ProcessEng 2	OK
	Full <u>N</u> ame:	MortamerSnerd	Cancel
	Description:	The2ndProcessEng	Help
Click on the empty checkbox of the desired password logon variables.		resense t Change Password at Next Logon not Change Password	
To change or add access to a group for a user, click on <b>Group</b> to display its dialog box.	Password	I Never Expires Disabled Profile Djalin	

## Changing or Adding Access to a User Group

- 1. Click on the **Groups** button at the bottom left of the **New User** dialog box to display the **Group Membership** dialog box.
- 2. Remove the current user group. This is done by double-clicking one or more of the current user groups in the Member of field, like one of the P\_XxxXxxXxx groups in *Figure 10.9*. (OR by highlighting the current user group in the **Member** of variable box and clicking on **Remove**. See *Figure 10.9*.)

Figure 10.9	Group	Membership	Dialog Box
-------------	-------	------------	------------

	Group Memberships	×	
<b>Step 2</b> Double-click one or more of the current user group. In this case, one of the P_XxxXxxXxx groups.	User: Process Eng 2 (Mortamer Snerd) Member of: Users P_EditScanData P_EditScanRecipe P_EditSeqData P_EditSeqRecipe	OK Cancel Help Not member of: P_TranSeqData P_TranSeqData P_VritualArtifacts Power Users Repticator	OR Highlight the current user group, and click on <b>Remove</b> to delete the highlighted user group.

# Adding a User to a Users Group

It is possible to add user to a profiler specific users group. This is primarily for those who are in the Windows defined **Users** group, because they have limited access to the profiler groups.

Use the following procedure to add a person already having the Users group access to a user specific users group.

1. From the **User Manager**, double-click on the name of the user in the users name list. (See *Figure 10.10*.)

Figure 10.10 User Manager

Username	Full Name	Description
😰 Administrator		Built-in account for administering the computer/domain
🕵 Dummy	Peggy Fleming	
🕵 Guest		Built-in account for guest access to the computer/domain
🕵 mantest	Manufacturing Test	
🕵 operator	Bob Shaw	first shift operator
👲 Process Eng 2	Mike Smith	The process engineer
횿 User 2	Sam Davis	2nd shift operator
Groups	Description	
Administrators	Members can fully adn	ninister the computer/domain
🕼 Backup Operators 🕼 Guests	Members can bypass	file security to back up files
🗳 Ruests	Users granted guest a	ccess to the computer/domain
🕼 P_AdvCalibration	Users granted guest a	ccess to the computer/domain
R P_AdvCalibration	Users granted guest a	ccess to the computer/domain
R P_AdvCalibration	Users granted guest a	ccess to the computer/domain
R P_AdvCalibration P_Calibration P_Configuration R P_Diagnostics	Users granted guest a	ccess to the computer/domain
P_AdvCalibration P_Calibration P_Configuration P_Diagnostics P_EditScanData	Users granted guest a	ccess to the computer/domain
P_AdvCalibration P_Calibration P_Configuration P_Diagnostics P_EditScanData P_EditScanRecipe	Users granted guest a	ccess to the computer/domain
P_AdvCalibration P_Calibration P_Configuration P_Diagnostics P_EditScanData P_EditScanRecipe P_EditScanRecipe	Users granted guest a	ccess to the computer/domain
AdvCalibration     P_Calibration     P_Calibration     P_Diagnostics     P_Diagnostics     P_EditScanData     P_EditScanRecipe     P_EditScanRecipe     P_EditScanRecipe     P_EditScanRecipe	Users granted guest a	ccess to the computer/domain
P_AdvCalibration P_Calibration P_Configuration P_Diagnostics P_EditScanData P_EditScanRecipe P_EditScanRecipe	Users granted guest a	ccess to the computer/domain

Step 1 Double-click on the name of the user that is to be added to the profiler specific group. (In this case, User2.) This opens the User Properties dialog box.

.

2. Click on the **Groups** button at the bottom left of the **User Properties** dialog box to display the **Group Membership** dialog box. (See *Figure 10.11*.)

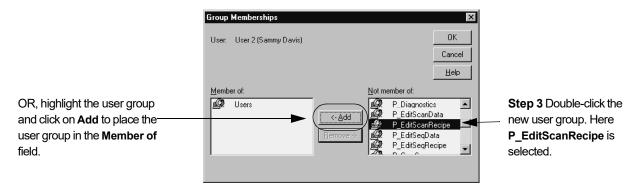
Figure 10.11 User Properties Dialog Box

	User Propert	ies			X
	Username:	User 2			OK
	Full <u>N</u> ame:	SamDavis			Cancel
	Description:	2ndShift0perat	or		Help
	Password:	****			
	<u>C</u> onfirm Password:	*****			
	🔲 User <u>M</u> usl	t Change Passw	ord at Next	Logon	
Step 2 Click on the Groups	🔽 U <u>s</u> er Canr	not Change Pas:	sword		
button to open the Group	✓ Password	Never Expires			
Membership dialog box.	🗖 Account 🛙	Disa <u>b</u> led			
	🗖 Account L	Loc <u>k</u> ed Out			
(	<u>G</u> roups	) 😨 Profile	-B Djalin		

**3**. Scroll to find the desired user group in the **Not member of** variable box. (See the user groups defined in *Profiler Defined Groups* on page 10-2.) Double-click on the group to move it into the **Member of** field.

OR, highlight the desired group in the **Not Member of** field and click on the **<-Add** button. The selected group moves to the **Member of** field. (See *Figure 10.12.*)





4. After adding all the necessary groups, click on **OK** to finalize the choices. (See *Figure 10.13*.)

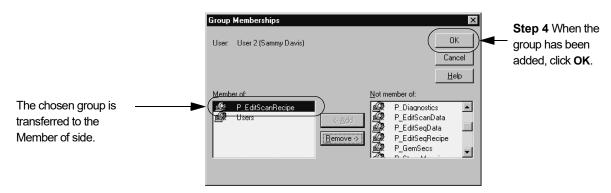


Figure 10.13 Group Memberships Dialog Box

5. The User Properties dialog box appears. Click **OK** to close and save the changes.

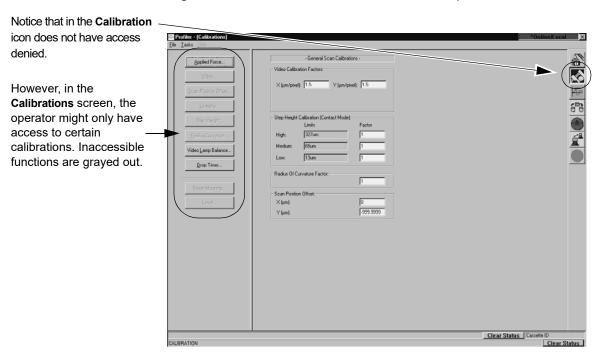
Figure 10.14 User Properties

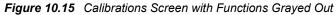
User Properties	×
Username: User 2	ОК
Full <u>N</u> ame: SamDavis	Cancel
Description: 2ndShift0perator	
Bassword:     Interest contracts at the contract of	Step 5 When all the desired changes and additions have been completed, click on OK to complete and save them.
Image: Constraint of the second sec	

## **Results of Limited Access**

When a user group is added to a user, the user access is limited to only those P-15 processes indicated by the user group membership. With limited access, certain screens and contents are not accessible for change or use. In other cases, the screens or specific functions in a screen are blocked from user access.

When a screen has limited access to its functionality, the inaccessible functions are grayed out. In the illustration in *Figure 10.15*, the **Applied Force**, **Video Lamp Balance**, **and Drop Timer** calibrations are active but all other calibration functions are grayed out to indicate that they are inaccessible to the operator under the current security limitations.





# CONFIGURATION

# INTRODUCTION

## This chapter describes:

- Operating Environment on page 11-1
- *Facility Specifications* on page 11-2
- Introduction to System Configuration on page 11-2
- Setting the Date and Time on page 11-3
- *Configuration Window* on page 11-4
- Theta Soft Home Position on page 11-6
- Teach Lowest Elevator Position on page 11-10
- System Configuration on page 11-14
- Safe Area Configuration on page 11-21
- Machine History Recorder Configuration on page 11-23
- Enable New Options (Proprietary) on page 11-26
- Export Path Defaults on page 11-27
- Pattern Recognition Options and Deskew on page 11-29
- Sequence Execution Options on page 11-35
- Teach Manual Load Position on page 11-38
- Proximity Sensor Configuration on page 11-40
- Loss of Power on page 11-44
- *Turning Off or Resetting the Instrument* on page 11-44
- Installing a Precision Locator on page 11-47
- Optional Precision Locators on page 11-58

# **OPERATING ENVIRONMENT**

The KLA-Tencor systems use an internal, passive vibration isolator system to allow operation in a normal production-line environment. For highly sensitive measurements (i.e., for artifacts below 500 Å or when the system is located in excessively noisy areas), KLA-Tencor recommends a solid floor.

For service access, approximately 50 cm (20 in.) of air space on both sides and to the rear of the instrument is required.



**CAUTION:** The installation site must be free from sudden temperature changes or extreme drafts. Do not place the instrument directly in the airstream or an air-conditioning vent or heating outlet.

# **FACILITY SPECIFICATIONS**

FACILITY	SPECIFICATION					
Vacuum	<b>Required to hold down the samples</b> : 6 mm (0.25 in.) nominal line providing a minimum of 500 mm (20 in.) mercury of vacuum at a flow of 27 liters/min. (1 cfm).					
Dimensions	Instrument (without monitor): 57 cm (23 in.) wide, 78 cm (31 in.) deep, 46 cm (17.5 in.) high. Monitor (15-in.) SVGA:					
Electrical	90-110 V, 50/60 Hz 110-130 V, 50/60 Hz 208-260 V, 50/60 Hz UL, CSA, European-qualified.					
	<b>NOTE:</b> If the power source is susceptible to radio-frequency interference, an isolation transformer is required for providing additional filtering. Sensitive computer components require a power source that is free from spikes, dips, and surges.					
	<b>NOTE:</b> If power failure is a common occurrence, use ar Uninterruptable Power Supply (UPS) device. A UPS device supplies post interruption power for 30 minutes so an orderly system shutdown can be accomplished during a power failure. See <i>Loss of Power</i> on page 11-44 for details.					
Ambient	Specified operating range: 16°–26°C.					
Temperature	Maximum rate of temperature change: $\leq 1^{\circ}$ C/hr.					
Vibration	Floor vibration must be less than 250 $\mu in./sec.~(6.4~\mu m/s)$ RMS, 1-100 Hz					
Audio Noise	≤ 80 dB (C weighting scale)					
Air Pressure	90-125 psi, flow (6.4 kg/cm <sup>2</sup> - 8.9 kg/cm <sup>2</sup> )					
Laminar Air Flow	≤ 100 ft/min (30 m/min), down-blowing					

#### Table 11.1 Facility Specifications

# INTRODUCTION TO SYSTEM CONFIGURATION

The KLA-Tencor system application software must have the correct information in its internal configuration files to properly run the instrument. The following sections cover checking and editing these configurations.

# SETTING THE DATE AND TIME

#### To Set the Date and Time

- 1. Before starting the Profiler system, click **Start** to display its menu.
- 2. Move the scroll cursor to **Settings** to display its menu.
- 3. Click on Control Panel to display the Control Panel window. (See Figure 11.1.)

Figure 11.1 Start Menu with Setting Menu Displayed

							×	
	Eile Edit Sample	<u>⊻acuum Host D</u> iagnostic <u>I</u> asks						
		🖨 STANT 🛞 😷 🕄	1 🕀 🛛 2D	3D				9
Step 1 Press CTRL+ESC		Scan Recipe Type:	Scan Recipe Nam	ie:				1
to display the Start menu.	Scan Becipe	Disping	_HA_COARSE					ò
to display the Start menu.	1	Recipe Path:	Recipe Name	Length (µm)	Max Depth (µm)	Creation Date (ysysymmidd)		
	Scan Data	SCANRCP Steel 1 st	HA_COAR HA_FINE STI_2D	. 1000 85 5	0.50 0.50 0.50	1999-05-14 1999-05-14 1999-06-08	18001 17:57 13:19	20
Step 2 Move the cursor to								2
Settings in the menu.	Sequence Recipe						*	•
	Sequence Data							
	Elogra							
	KStatt	a Control Panel	I					
Stop 2 Olight on Operating	T Cred	' 🖻 Isekba					(A) (Y)	
Step 3 Click on Control	Bun	Erint	New	⊻iew/Modify	STAF	IT XY	View	
	Š 🗊 shat	kown	/			Substr.	Clear Status	1

4. In the Control Panel window, click on **Date/Time** (it is either in a list or displayed under its icon). (See *Figure 11.2*.)

Figure 11.2 Control Panel

🔯 Control Pa	anel					_ 🗆 🗡	
<u>F</u> ile <u>E</u> dit <u>V</u> ie	ew <u>H</u> elp			$\frown$			
Accessibility Options	Add/Remove Programs	Console	CSNW	Date/Time	<b>Vives</b>	Display	
Ð	Ø	62	ļŶ	Ð		- P	Step 4
Modems	Mouse	Multimedia	Network	ODBC	PC Card (PCMCIA)	Ports	Double-click Date/Time to
5	*	<b>S</b>			<b>\$</b>	50	open the
Server	Services	Sounds	System	Tape Devices	Telephony	UPS	Date/Time window.
4						F	
27 object(s)							

- 5. Choose the new value from the drop-down menu or highlight the part of the date or time (e.g., month, hour) that requires updating.
- 6. Enter the new value. (See *Figure 11.3*.)

Figure 11.3 Date/Time Properties Window

Dat	e/Tir	ne P	rope	ertie	\$				? ×
D	ate &	Time	Ti	me Z	one				
Пг	<u>D</u> ate								_ <u></u>
	Apri	1	-	1 6	1999	-	-	4	and the second second
	,				_	_	_		
	S	М	T	W	T	F	S		
					1	2	3		
	4	5	6	7	8	9	10		
	11	12	13	14	15	16	17		
	18	19	20	21	22	23	24		
	25	26	27	28	29	30			
									11:54:21 AM ÷
									,
C	urrent	time	zone	e: Pa	acific	Dayl	ight '	Time	e
		_	_	_	_	_	_		
								ОK	Cancel Apply

- 7. Repeat for each new value that requires updating.
- 8. Click **OK** to reset the system with the new date or time and to exit from the dialog box.
- 9. Close the Control Panel

# **CONFIGURATION WINDOW**

The Configuration screen is password protected. If the icon or the function buttons in the Configuration screen are not active, the user should logon with the appropriate log-on ID and password for access.

To access the **Configuration** screen, click on the **Configuration** icon in any system level screen. (See *Figure 11.4*.)

KLA-Tencor Confidential

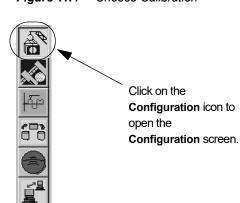
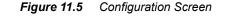
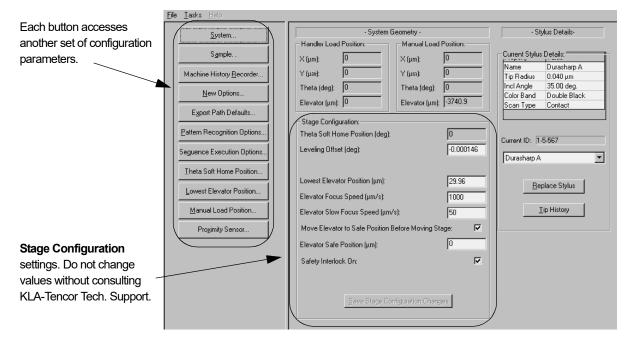


Figure 11.4 Choose Calibration

The Configuration window is displayed. (See Figure 11.5)

The left side of the screen contains a series of access buttons that open configuration parameter dialog boxes in which configuration values can be set. The right side of the window shows some of the current configuration values. Most of these values are set by manufacturing technicians prior to shipment of the system. Although these values are editable, they should not be changed without advice from KLA-Tencor Technical Support personnel.





# **STAGE CONFIGURATION**

The items in the Stage Configuration area are all editable using Configuration screen options. All of the variable fields except the Theta Soft Home Position, the ones with the active variable fields (white background), can be edited directly in the field itself. The Theta Soft Home Position must be changed using the configuration procedure presented by clicking its configuration button. (See *Teaching the Soft Home Position* on page 11-6.)

0
-0.000146
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ng Stage: 🔽
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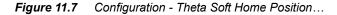
Figure 11.6 Stage Configuration Parameters

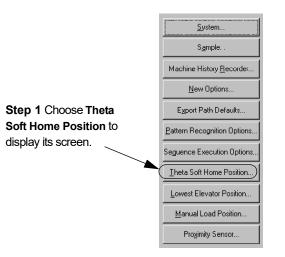
## **Theta Soft Home Position**

The Soft Home position is related to the X- Y-stage Theta Home Switch and the puck cutout. It is set at manufacturing and should not require further adjustment unless the entire Y-drive is replaced. Prior to performing this adjustment, the Y-orthogonality should be adjusted. The Soft Home position might be changed by teaching a new position.

This procedure should only be attempted by a KLA-Tencor trained technician. An error in this position could create further alignment difficulties.

#### **Teaching the Soft Home Position**





1. Choose **Theta Soft Home Position**... from the buttons on the left side of the **Configuration** screen. (See *Figure 11.7.*) The **Teach Soft Home Position** screen appears. (See *Figure 11.8.*)

The stage rotates to the current Soft Home, theta, position.

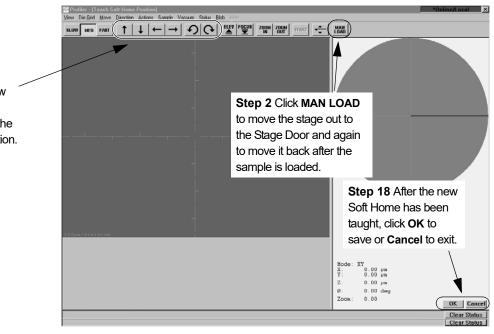
- 2. Click MAN LOAD to move the stage to the stage door. (See *Figure 11.8.*)
- **3**. Open the stage door.



**CAUTION:** A system safety shutdown occurs if an attempt is made to activate any stage or elevator motion when the stage door is open (unless the interlock switch has been disabled).

- 4. Load the **orthogonality fixture** onto the stage. (If the fixture is not available, use a patterned wafer, seated in a precision locator.)
- 5. Close the door.
- 6. Click MAN LOAD to move the stage back under the stylus.

Figure 11.8 Teach Soft Home Position Screen



- 7. Click on **FOCUS** to focus on the sample surface.
- 8. Find a line or row of attributes using the arrow buttons in the tool bar, move the sample to the desired new position. If necessary, use the rotation buttons to rotate the stage to a new theta position. (See *Figure 11.8*) For a more precise setting, use the Align Sample procedure detailed in Step 9. through Step 9.
- 9. Click on View in the tool bar to display its menu. In the menu, click on Align Sample. (See *Figure 11.9.*) This sets up the Align Sample procedure used to align the XY axis of the screen with the tool's pattern.

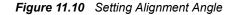
#### **Step 8** Use the arrow buttons to move and rotate the stage into the new Soft Home position.

Begin: ALIGN SAMPLE

<b>Step 9</b> To align the Stylus Alignment Tool with the XY	Profiler - [Teach Soft Home View Die Grid Move Direction Eccus			MAN	*Online/Local X
axis of the screen, click on Align Sample.	Save Image To File Bint Image Align Sample Zoom (n Zoom (n	)			
	200m got Beset Zoom Save ≩oom Position				

Figure 11.9 Align Sample Procedure - Scan Offset Calibration

10. The alignment Angle dialog box appears requesting input of the intended alignment angle. The default is "0" and should appear in the variable box. Click on **OK** in the dialog box to accept the "0" value. (See Figure 11.10.)



Step 10 Click on OK to accept	Alignment Angle		x
the " <b>0</b> " angle alignment.	Alignment Angle:		)egrees
	ОК	Cancel	Help

11. The message prompt at the bottom of the screen appears as follows:

Figure 11.11 Message Prompt After Alignment Angle is Set

Click the left mouse button to teach the first point

Using the **right** arrow button  $(\rightarrow)$ , scroll across the a horizontal pattern.

- 12. Place the crosshairs cursor on the horizontal line or die border and click. The system performs adjustments that align the screen grid dashes to the crosshairs.
- 13. The message prompt displays the following:

Figure 11.12 Message Prompt to Accept of First Alignment Location

Press OK to accept the first alignment location

Click **OK**, at the bottom right of the screen, to accept the first alignment location.

14. The following message appears in the message prompt:

Figure 11.13 Message Prompt for Selecting Second Alignment Location

Click the left mouse button to teach the second point

Using the **left** arrow button ( $\leftarrow$ ), scroll across the wafer or sample. Stay close to the chosen horizontal feature. Travel at least one centimeter. Place the crosshairs cursor on the horizontal feature (in the same relative position as the first position) and click with the left mouse button. The system performs final adjustments, aligning the screen grid to the horizontal feature (the sample pattern is now aligned with the XY axis.)

15. The message prompt appears as follows:

Figure 11.14 Message Prompt to Accept Second Alignment Location

Press OK to accept the second alignment location

Click **OK**, at the bottom right of the screen, to accept the second alignment location.

16. The message prompt appears as follows:

Figure 11.15 Message Prompt to Accept the Alignment

#### Press OK to accept new alignment

After the adjustments have been completed by the system, the message prompt at the bottom of the screen requests the user to click **OK** to accept the new alignment adjustment. (See *Figure 11.15*.) Click **OK** (bottom right of screen) to accept, or click **Cancel** to run a new alignment calculation.

End: ALIGN SAMPLE

- This completes the Align Sample procedure.
- 17. Click at the X- Y-junction on the video image to record the new position's coordinates.
- 18. Click **OK** to save the new position, or click **Cancel** to keep the original value and return to the Configuration screen. (See *Figure 11.8*)

## Leveling Offset

The Leveling Offset is set at manufacturing. It should not be necessary to adjust it unless other mechanical procedures have been performed on the stage or drive systems. The leveling calibration procedure is automated and, when completed, provides a value for this field. (See *Level Calibration* on page 12-41)

KLA-Tencor recommends that this number not be changed except by a KLA-Tencor trained technician.

# **Teach Lowest Elevator Position**

#### Introduction

The Lowest Elevator Position sets the vertical motion range of the stage. Using this feature, a limit (**Z coordinate**) can be set for the elevator so that the measurement head cannot descend past the level of the sample surface.

Correctly teaching the Lowest Elevator Position protects the measurement head when the Proximity Sensor (which is used to switch from **Elevator Focus Speed** to **Elevator Slow Focus Speed**) is not being used.



**CAUTION:** It is very important to reset the correct **Lowest Elevator Position** after a precision locator is installed. The stylus can be damaged if the stage remains configured to the original setting.

## **Procedure to Teach Lowest Elevator Position**

This positioning procedure requires that the stylus make contact with the stage surface, precision locator surface, or a ample (if samples of consistent thickness are used) in order to assign a lowest elevator position that allows the system to locate and use the sample support surface or embedded standards. It is best to use a sample if the samples tested are of a consistent thickness. **Make sure that the stylus stops on the top surface and not in a hole or grove.** Once the stylus is aligned with the proper surface position, the remainder of the procedure is automatic.

1. From the **Configuration** screen, choose **Lowest Elevator Position...** from the menu buttons at the left side of the screen. (See *Figure 11.16*.)

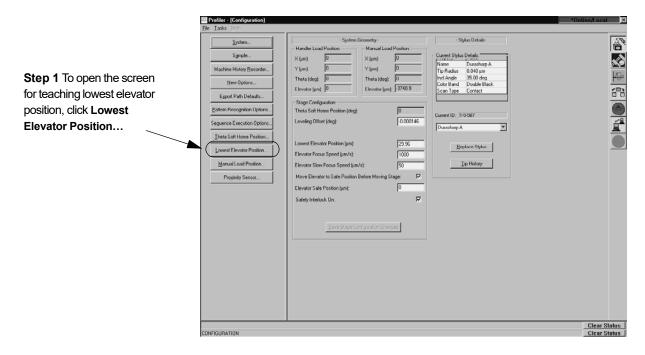
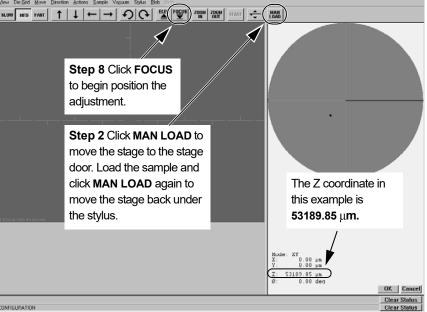


Figure 11.16 Configuration Screen - Lowest Elevator Position

2. The window shown in *Figure 11.17* appears. Assuming that the samples of consistent thickness are being used, load one of the samples onto the stage.

To manually load a wafer or other sample, click **MAN LOAD** to move the stage to the stage door. (See *Figure 11.17*.)





3. Open the stage door.



**CAUTION:** A system safety shutdown occurs if an attempt is made to activate any stage or elevator motion when the stage door is open (unless the interlock switch has been disabled).

- 4. Load the sample from the stage.
- 5. Switch on the vacuum using the switch on the upper left inside door frame.
- 6. Close the door.
- 7. Click MAN LOAD to move the stage under the stylus. (See *Figure 11.17.*)
- 8. Click **FOCUS** in the tool bar to move the head down to focus on the sample. (See *Figure 11.17.*) The system is set to protect the stylus so this final null could take a relatively long time.
- **9**. When the null is complete, click **OK** to accept the Lowest Elevator Position (Z coordinate) position or **Cancel** to reject the new position (Z coordinate) and retain the previous one. The screen should close and return to the Configuration screen.

The system takes the null position Z coordinate and adds 500  $\mu$ m to it. The new accepted position is automatically entered into the Lowest Elevator variable field in the Configuration screen. (See *Figure 11.18*.)

The new value for Lowest Elevator Position. In this case it is: <b>53389.85</b> .	Profiles - [Configuration]     En Tasks Hete:     System     System     System     Machine History Becoder     Hew Options     Egood Path Defaults     Editem Recognition Options     Segures Execution Options     Interaction Position     Lowest Elevator Position     Morual Load Position	System Growely -           Handler Load Position:         Marxial Load Position:           Y (µm)         0         Y (µm)         0           Theta (deg):         0         Y (µm)         0           Theta (deg):         0         Theta (deg):         0           Stage Coefig action:         Theta (deg):         0         0           Levelog Office (deg):         0         0         0           Levelog Office (deg):         0         0         0           Levelor Position (µm)         53300.05         5         1000           Elevator Focus Speed (µm/s):         1000         50         5	- Stylue Detale Durared Stylue Detale Name Durarburg A Tip Radiu 0.040 µm Irel Angle 35.00 deg Colate Bard Double Black. Scan Type Contact Cuerent ID: 1:45:687 Durarburg A Beplace Stylue Lip History	
Step 10 When an acceptable change to the Lowest Elevator Position has been entered, click on Save Stage Configuration Changes.	Proginity Sensor	Move Elevator to Safe Position Balore Moving Stage: Elevator Safe Position (jum): Safety Interlock Dr. Serve Stage Configuration Changes		Clear Status
	CONFIGURATION			Ctear Status

Figure 11.18 Configuration Screen - Lowest Elevator Position

10. In the Configuration screen, if the Lowest Elevator Position (**Z coordinate**) is acceptable, click **Save Stage Configuration Changes** to accept the new value; or, to retain the previous position, close the screen without saving the changes.

# **Elevator Focus Speed**

This is the speed at which the elevator lowers the head toward the sample surface until it reaches the Proximity Sensor Trip Position. When it reaches the trip position, it proceeds with the Elevator Slow Focus Speed until Soft Null or Null is reached, depending on whether the proximity sensor is being used. (See *Figure 11.6 on page 11-6* also *Figure 11.18.*)

#### **Settings Determining Trip Position**

- If the proximity sensor is *not on*, the Elevator Focus Speed is active until the elevator reaches 1mm above the Lowest Elevator Position, at which point the Elevator Slow Focus Speed is activated.
- If the proximity sensor is *on*, the Elevator Focus Speed is active until the proximity sensor trip position is reached, at which time the Elevator Slow Focus Speed is activated.

#### **Elevator Speed**

The elevator speed in this setting cannot exceed 1000  $\mu$ m/second if the proximity sensor is off. Otherwise, if it is on, the speed is 2000  $\mu$ m/second

## **Elevator Slow Focus Speed**

The Elevator Slow focus Speed is the speed at which the elevator lowers the head from the Elevator Focus Speed trip position until null is accomplished. (See *Figure 11.6 on page 11-6* also *Figure 11.18*.)

## Move Elevator to Safe Position Before Moving Stage

This checkbox works in conjunction with the Elevator Safe Position variable. If this box is checked, the elevator moves the head up to the recorded height in the Elevator Safe Position variable field. This prevents the stylus from contacting the surface of an ununiform or tilted sample as the sample moves from one location to another. (See the checkbox in *Figure 11.6 on page 11-6* also *Figure 11.18.*)

## **Elevator Safe Position**

This feature works in conjunction with the Move Elevator to Safe Position Before Moving Stage checkbox. If there is a check in the box, this variable is used. If there is no check in this box, the head is not lift up this distance. This is the absolute elevator height that the system moves the head to every time the stage is moved under the prescribed circumstance. (See *Figure 11.6 on page 11-6* also *Figure 11.18.*)



**NOTE:** The smaller the number, the longer it takes for the head to rise before the move and lower after the move. Set this number carefully if processing time is a concern, especially in sequence scans.

# Safety Interlock On

The door to the P-15 has an interlock that should be used to protect the user from injury and the instrument from damage. When the safety interlock is ON, the interlock system is active. This protective status prevents the system motors from engaging if the measurement chamber (stage) door is open. If any of the system stage or elevator motors are active when the stage door is opened, they are immediately turned off. They remain inoperative until the door is closed.

A check in the check box shows that the interlock system is ON. Like many of the Configuration features, this feature requires a security log on to enter and change. It is View Only to those without the clearance.



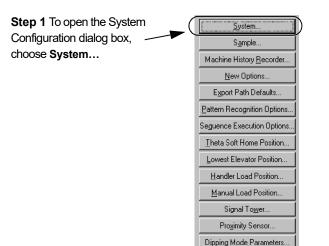
**CAUTION:** the Safety Interlock should not be defeated except for service requiring the service engineer to operate the motors with the door open. There are no operator defined functions requiring the door to be opened during system operation. **Only KLA-Tencor trained service personnel should ever defeat the Safety Interlock System**.

# SYSTEM CONFIGURATION

The System Configuration options can only be observed in the System Configuration dialog box, not edited. The System Configuration screen contains tabbed windows that allow the user to observe the process and hardware settings for the instrument. Changes must be performed by KLA-Tencor trained technicians.

# **Editing the System Configuration**

1. Click on the **System...** button at the left side of the Configuration screen. (See *Figure 11.19*).





The System Configuration dialog box appears. (See Figure 11.20)

Figure 11.20 System Configuration Dialog Box

System Configura	ation		Configuration
Serial Number:	457645756	<u>0</u> K	Dialog Box
Customer:	34534645	<u>C</u> ancel	
Model:	P-15	Configuration	
Machine Type:	Instrument	Instrument	
Handler Type:	None	<u>H</u> andler	K l
		S <u>u</u> mmary	Instrument
Enable Wafer I	Presence Check 🛛 🗖		Dialog Box
Enable Stage I	vlapping 🗖		
		<u>H</u> elp	
Registry <u>M</u> a	intenance		

# **Instrument Setup Configuration Dialog Box**

Figure 11.21 Instrument Setup Dialog Box

Step 1 Change the Software Options by clicking on them. The chosen options will have an X next to them. Deactivated options have no X.

Instrument Setup		x
Software Options:	Hardware Options:	<u>0</u> K
X 3-D Analysis X Combine Statistics	Video Hardware: Corona	Cancel
X GEM/SECS X Pattern Recognition X Sequence	Head Type: MH2 SR	
X Stress X HPPC/HPPM	- Vacuum Options:	
	Vacuum Control:	
	Time Delay From 2nd Deskew to 1st Measurement in Sequence (s):	
	Vacuum Feedback	<u>H</u> elp

The **Instrument Setup** dialog box provides access to the **Software Options** activation box and the **Vacuum Options** box. The **Hardware Options** box is a display box that reports the current Video Hardware and MicroHead type. The following steps detail the operation and function of each activity box and check box. (See *Figure 11.21*.)

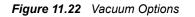
#### **Software Options**

- All of the purchased software options should appear in this box. (See the circled area in *Figure 11.21.*) An X before the option name indicates that it has been enabled. Click on the option to toggle between enabled and disabled. Choose the options that are to be enabled in the upcoming scanning session. When the configuration changes are complete, a system warning tells the user that the system must be restarted to initiate the new options and other changes.
- 2. The vacuum system is manually operated so no changes are required in the Vacuum Options field. Click OK to confirm the Software Options selection.
- **3**. The **System Configuration** window appears again. If no further changes are required, click **OK** to confirm the current changes. A window appears advising the operator that the system must be restarted to activate the newly enabled software configuration (selected options). The system MUST BE RESTARTED TO ACTIVATE THE NEW SOFTWARE OPTION CONFIGURATION.

#### Vacuum Options

Vacuum Control Option

1. Vacuum Control contains three options that are presented in the Vacuum Control drop-down menu: None/Manual; Automatic; and Load/Unload Only. (See *Figure 11.22*. It might be necessary to scroll down to see all options.) The P-15 system operates using a manual set of vacuum controls. The only valid option in the Vacuum Control menu is None/Manual. The vacuum control for the P-15 is a manual switch on the upper left inner portion of the system door frame.



	Instrument Setup	×
<b>Step 1 Vacuum Control</b> : Choose how the vacuum operation is to be controlled.	Software Options:       Hardware Options:         X 3-D Analysis       Video Hardware:         Combine Statistics       Video Hardware:         X GEM/SECS       Pattern Recognition         X Sequence       Head Type:         X Stress       Vacuum Options:         X Wafer Sorting       Vacuum Control:         Load/Unload Only       Measurement in Sequence of Vacuum Feedback	<u>□</u> K <u>C</u> ancel

Click on the **Vacuum Control** menu arrow to display the **Vacuum Control** options. Select the desired option. (See *Figure 11.22*.)

Vacuum Feedback Option

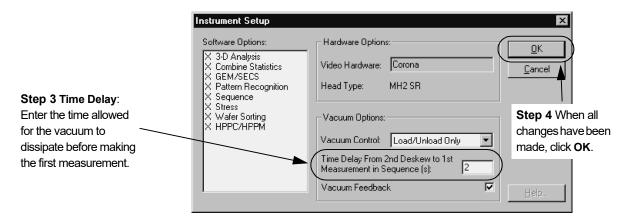
2. Vacuum Feedback: Vacuum Feedback is not available in the P-15 system.

Figure 11.23 Vacuum Feedback

	Instrument Setup		×
Step 2 Vacuum Feedback: Not for use with the P-15 system.	Software Options: X 3-D Analysis X Combine Statistics X GEM/SECS X Pattern Recognition X Sequence X Stress X Wafer Sorting X HPPC/HPPM	Hardware Options: Video Hardware: Corona Head Type: MH2 SR Vacuum Options: Vacuum Control: Load/Unload Only Time Delay From 2nd Deskew to 1st Measurement in Sequence (s): 2 Vacuum Feedback	<u>©</u> к <u>C</u> ancel

Time Delay Option
 3. Time Delay Between 2nd Deskew and 1st Measurement in Sequence (in sec): is designed to provide enough time, after the last stage movement and before the beginning of a scan sequence, to dissipate the vacuum holding a sample. This option is only available for entering a value when the Load/Unload Only option in the Vacuum Control menu is enabled. (See Load/Unload Only in Step 1 on page -15 of the Vacuum Options section.)

Figure 11.24 Vacuum Options



To enable the **Delay**, highlight the number in the box next to **Time Delay From 2nd Deskew to 1st Measurement in Sequence (s)**: (See Vacuum Options on page 15.) Enter the number of seconds that the system must pause for the dissipation of the vacuum holding the sample. (See *Figure 11.24*.)

If there is a number in this box, and the field behind it is white, the Delay is already enabled. If the number is **0**, it has no delay effect on the scan. If the **0**, or other number in the box, has a gray background, enable the **Load/Unload Only** option in the **Vacuum Control** menu to activate the field so it can receive a value (enabled and accessible for change).

- 4. If no other changes are to be made in the Instrument Setup window, click **OK** to confirm the changes.
- 5. The **System Configuration** window appears again. If no further changes are to be made, click **OK** to confirm the current changes. A window appears advising the operator that the system must be restarted to enable the new software configuration (selected options). If there were changes to the Software Options, the system MUST BE RESTARTED TO ENABLE THE NEW SOFTWARE OPTION CONFIGURATION.

# **Summary Configuration**

The Summary Configuration is a display of information regarding the current system configuration. None of the items are configurable in this screen; it is read only. The items covered in this screen inform the user of the following system configuration parameters:

• The Software version and the build number for that version is indicated in the first field at the to top left of the window, Version 6.20.(Build XX). In this example, the software version is 6.30.00, and Build number is XX. (See *Figure 11.25*.)

System Configuration	×
Summary	
KLA-Tenco	r Corporation
Version 6.20.(Build 🔀)	Serial Number: 457645756
Built: 02-Jan-2001; time: 01:36:46	Customer: 34534645
	Model: P-15

CIB DSP n.a. MH2 DSP: 156.71.237 Stage mapping disabled

Figure 11.25 System Configuration Summary Window

• The Build date for the specific build of the current Software version is presented in the second field down in the left panel, Built 02Jan-2001; time: 01:36:46. The date and time of the software compilation are recorded for identification of the exact software build being used on the system.

ОK

- The version of software operating the CIB is presented in the third field down in the left panel, CIB DSP n.a. In this example, *no CIB is present* so no software version is operating the CIB.
- The system scanning head being used, and the software version operating the head are presented in the fourth field down in the left panel, MH2 DSP: 156.71.237. In this example, the MH2 head is being used and the 115.71.237 version software is driving it.

- Stage mapping can be enabled or disabled. The current status is displayed in the fifth field down in the left panel, Stage mapping disabled. In this case, Stage Mapping is disabled. (See also *Figure 11.27*.) This feature is only available with the pattern recognition option.
- The Mechanical assembly serial number of the system is recorded in the first field of the right panel, Serial Number. 457645756.
- The customer number, assigned for use in conjunction with the serial number to enable easy access for the user to Customer Services, Customer. 34534645.
- The system Model type is displayed in the third field down in the right panel, Model: P-15. In this case, it is a P-15 profiler.

### **Registry Maintenance**

The Registry Maintenance dialog box is provided so that the registry can be either updated with the new information or reset to the previous registry information. The registry should only be accessed by KLA-Tencor Field Service Engineers. Certain calibration information is stored here and must be used by a trained technician who understands the registry requirements.

Figure 11.26 Registry Maintenance Dialog Box

Registry Maintenance	X
Save Registry	
Restore Registry	
	[]

# **Completing the Configuration**

1. Check the configurable information in the System Configuration box itself.

• Machine Type: This presents a choice between **Desktop** and **Instrument**. **Desktop** means that the software is actually being run as a simulation on a desktop computer (this is primarily for data assessment), not on the instrument itself. **Instrument** indicates that the software is being used to run the instrument. (See *Figure 11.27*.)



**CAUTION:** Do not Change the Machine Type information. This information has been set at installation and changing it renders the tool useless. It is not possible to restore the system exactly to it previous state because vital information is lost at conversion.

• Handler Type: The P-15 does not have a handler. The only option available is None. (See *Figure 11.27*.)

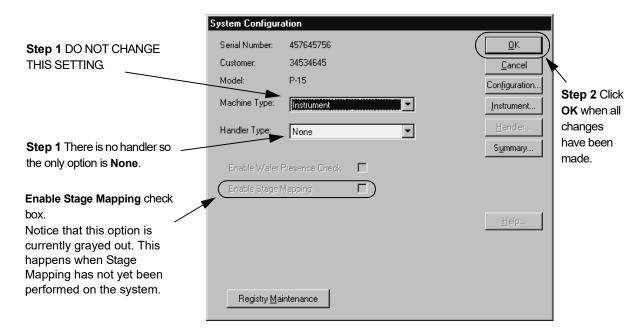


Figure 11.27 System Configuration Dialog Box

- 2. After all necessary changes are made, from the **System Configuration** dialog box, and click **OK** to accept the changes, or **Cancel** to close this dialog box and return to the **Configuration** window with the original settings unchanged. A message box appears warning the operator to reboot the system if any changes have been made.
- **3**. To reboot the system, follow the instructions in *Turning Off or Resetting the Instrument* on page 11-44.

# SAFE AREA CONFIGURATION

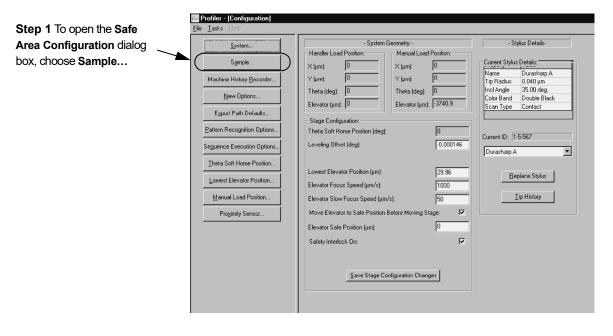
The Stage Limit setting is designed to limit the movement of the stage to the current setting parameters. The setting defines the mechanical movement limit called the **SAFE AREA**. There is also a hardware limit switch that automatically stops the stage movement if the setting in the Radius box is too large.



**NOTE:** If the Safe Area is set too large, as would be the situation after original installation, the die grid application cannot be loaded and the Die Grid button in the Sequence Recipe Editor is grayed out. To correct this, set the Safe Area to coincide with the sample being used.

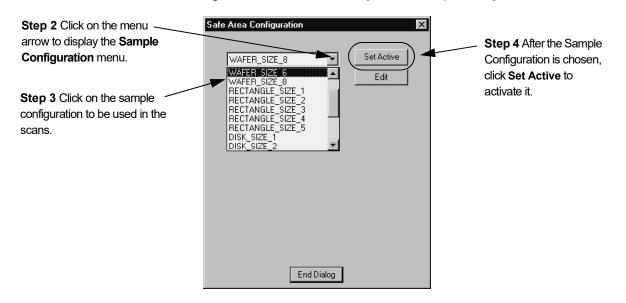
1. Click on Sample... to open the Safe Area Configuration dialog box. (See *Figure 11.28.*)

Figure 11.28 Configuration Screen



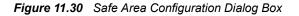
The Safe Area Configuration dialog box opens with only the wafer configuration drop-down menu active.

2. Click on the menu arrow to access the Sample Configuration menu. (See *Figure 11.29.*)



*Figure 11.29* Safe Area Configuration - Sample Configuration Menu

- **3**. Choose the required sample configuration. (See *Figure 11.29*.) This changes the information in the Safe Area configuration display (circled in *Figure 11.31*).
- 4. Click on **Set Active** to activate the new Safe Area configuration. (See *Figure 11.29.*)
- 5. To edit the safe area configuration parameters, click Edit. (See Figure 11.30.)



When the Safe Area Configuration dialog box opens, only the sample configuration drop-down menu is active.	Safe Area Configuration	<b>Step 5</b> To open up and edit the safe area parameters, click on <b>Edit</b> .
	End Dialog	

The Safe Area Configuration dialog box safe area can now be edited. (See *Figure 11.31*.)

Begin: Changing Safe 6 Area Values

6. Change the safe area parameters by highlighting the appropriate box and entering the new parameter. (See *Figure 11.31*.)



**CAUTION:** DO NOT CHANGE these parameters without consulting a KLA-Tencor system specialist. Incorrectly set parameters could seriously damage the system.

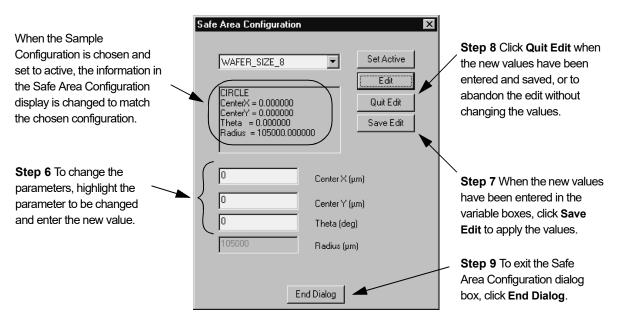


Figure 11.31 Safe Area Configuration - Edit Safe Area Values

- 7. After the parameters have been entered, click **Save Edit** to accept the new safe area. (See *Figure 11.31*.)
- 8. If the edit is to be abandoned without accepting the new parameters, click Quit Edit. (See *Figure 11.31*.)
- 9. To exit the Safe Area Configuration dialog box, click **End Dialog**. (See *Figure 11.31*.)

# MACHINE HISTORY RECORDER CONFIGURATION

The Machine History Recorder is designed to provide a log of certain system activities as a process record and for review. The log information is limited to messages generated by the system. Each of the five message types can be entered in the log. The log itself can be maintained as a continuous log or can be set to generate a separate log for each processing session.

1. From the **Configuration** screen, choose **Machine History Recorder...** (See *Figure 11.32.*)

Figure 11.32 Configuration Screen

Step 1 To open the Machine	File Tasks Help		
History Recorder Configuration dialog box, click on Machine History Recorder	Ele Tasks Edep System Sample . Machine History Becorder New Options Egrout Path Defaults Eattern Recognition Options Seguence Execution Options Inteta Soft Home Position Lowest Elevator Position Manual Load Position Progimity Sensor	- System Geometry -         Handler Load Position:         X (µm):       0         Y (µm):       0         Theta (deg):       0         Elevator (µm):       0         Stage Configuration:       0         Theta (deg):       0         Leveling Offset (deg):       0         Leveling Offset (deg):       0         Leveling Offset (deg):       0         Elevator Position (µm):       23 96         Elevator Speed (µm/s):       50         Move Elevator Speed (µm/s):       50         Move Elevator Safe Position Before Moving Stage:       If         Elevator Safe Position (µm):       0         Safety Interlock On:       If	Stylus Details:     Current Stylus Details:     Name Durasharp A     Tip Radus     Outed ym     Incl Angle     Stold deg     Color Band     Double Black     Scan Type Contact      Current ID: 11-5:567      Durasharp A     Eeplace Stylus      Ip History

- Create: Recorder File Name 2. The **Recorder File Name** variable box allows the user to set another file name for the log that is to be generated. The default is MHRLog.log. To change the current log name, highlight the current name and enter the new one. (See *Figure 11.33*.)
  - **3**. The **Recorder Actively Recording** check box allows the user to enable or disable the active log entry process. If this feature is enabled, the recorder makes real time entry of system messages into the designated log. (See *Figure 11.33*.)



Step 2 To change the file name for the log, highlight the current name and enter the	Machine History Recorder Co Recorder File Name: MHRLoc		ОК
new one.	Recorder Actively Recording Maximum number of items per rec	) order file: 10.000	Cancel
Step 3 A check in the check box activates the recorder to make message entries in the designated log file.	Items To Be Recorded	Output Format  Space Delimited  C Comma Separated Values  Tab Separated Values	
<b>Step 4</b> A check in the check box includes that message type in the designated log file when the recorder is active.	Fatal Error Messages     Debugging Messages	Output Mode C Append to existing log file C Start new log file each session	

Enable: Recorder Actively

Recording

Select: Items To Be Recorded

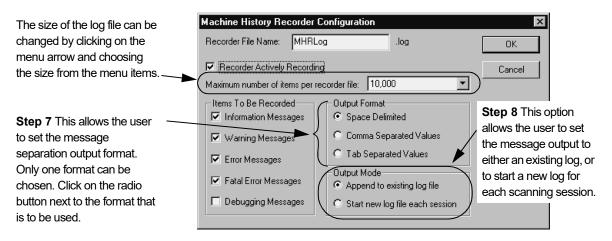
- Set: Maximum number of items per recorder file
- 4. In the **Items To Be Recorded** menu box, ensure that there is a check ( $\checkmark$ ) in each check box of the messages that are to be recorded in the log. (See *Figure 11.33*.)
- 5. To set the log file size, click on the menu arrow next to the **Maximum number of** items per recorder file variable field. This displays its menu. (See *Figure 11.35*.)

Figure 11.34 Machine History Recorder Configuration with Drop-Down Menu

Machine History Recorder C	Configuration	×
Recorder File Name: MHRLo	g .log	OK
Recorder Actively Recording		Cancel
Maximum number of items per re	corder file 10,000 💌 🔪	\
Items To Be Recorded Information Messages Warning Messages Fror Messages Fatal Error Messages Debugging Messages	Output Fc 1,000 © Speci 100,000 Unlimited C Comma Separated Values © Tab Separated Values Output Mode © Append to existing log file © Start new log file each session	)

6. Choose the number of items from the drop-down menu by clicking on the number, either **1,000**, **10,000**, **100,000** or **Unlimited**. The new number is displayed in its field. (See *Figure 11.35*.)

Figure 11.35 Machine History Recorder Configuration Dialog Box



7. The **Output Format** allows the user to determine what type of spacing is used in the log to separate the messages. The separator is either a space, a comma or a tab.

A selected option has a dot in its radio button. To choose an unselected option, click in the empty radio button next to it.

#### Step 5 Click on the menu arrow to display its menu, then click on the Maximum Number \_ of Items Per Recorder File.

Choose: Output Format

Choose: Output Mode8. The Output Mode allows the user to choose to add new messages to the existing<br/>log file, or put the messages in a new log file for each session.A selected option has a dot in its radio button. To choose an unselected option,<br/>click in the radio button next to it.

# **ENABLE NEW OPTIONS (PROPRIETARY)**

In most cases, options can be added to an installed instrument without additional software or hardware installation. The system software contains all the options. The options that are enabled and available for use are activated by entering the configuration code programmed into the Configuration Key during manufacturing. Using this dialog box and a code provided by the KLA-Tencor Sales representative, desired options can be enabled for the instrument.

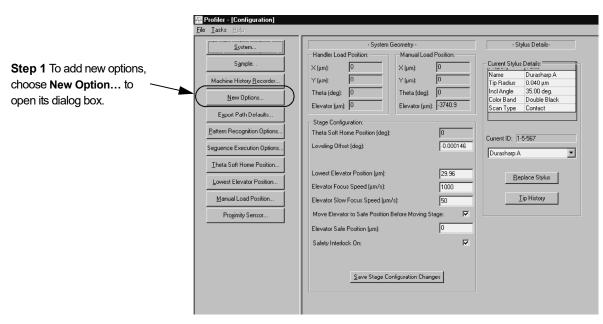


Figure 11.36 Configuration Screen

1. To add an option that is purchased after the system is installed, choose **New Options...** to open the New Options dialog box. (See *Figure 11.36*.)

Figure 11.37 Enable New Options Dialog Box

Step 4 Current Model	Enable New Options	X
Identification No. (MIN). Record the new number on the form after	Model Identification No.: Current Options:	
the new option is enabled.	56140-5889-60159-60159-60159	]
<b>Step 2</b> Enter the number provided on the Configuration Key Update Form in these boxes.	Customer No.: 523223 GEM/SECS Pattern Recognition Serial No.: 6111111 Sequence Stress Model No.: Hardware Wafer Sorting	
Step 3 After the number is entered, click <b>Program</b> to enable the option.	New Option No.:        Image: Cancel     Help	D

2. The option to be added is identified in the software by a series of numbers similar to that displayed under the **Model Identification No:** in *Figure 11.37*. When the option is purchased from KLA-Tencor, the series of numbers is provided on the **Configuration Key Update Form**.

Enter each set of numbers into the provided series of boxes using the dash between number segments as the indicator to move to the next box. (See *Figure 11.37*.)

- **3**. When the number has been entered, click **Program** to initiate enabling of the option program. (See *Figure 11.37*.)
- 4. Once enabled, the Model Identification No. (MIN) changes. Record the new MIN on the **Configuration Key Update Form** for future reference. This is the number that KLA-Tencor uses for identification of the customer and current options when ordering software upgrades or new options for the system. (See *Figure 11.37.*)
- 5. After the program is enabled, a system message box might request that the system be restarted to initialize the new option. Follow the instructions; they differ depending on the option purchased.

# **EXPORT PATH DEFAULTS**

**Export Path Defaults** set the default path for exporting scan and sequence recipes and data.

### **Data Export Paths Configuration**

1. Choose Export Paths in the Configuration screen. (See *Figure 11.38*). The Export Path Defaults dialog box opens. (See *Figure 11.39*)

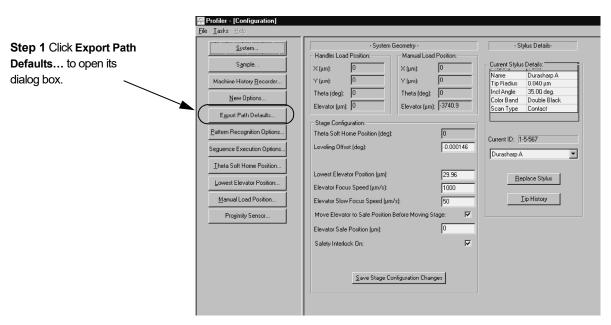
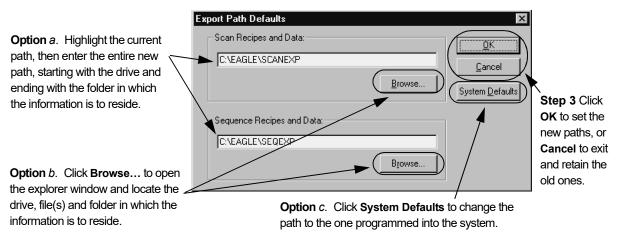


Figure 11.38 Configuration Screen

- 2. To set the default path for either the Scan or Sequence recipe and data, use one of the following:
  - a. Enter the desired path, starting with the drive and continuing through the entire sequence, ending with the folder in which the information is to reside. (See *Figure 11.39*.)
  - b. Click **Browse**... to find the drive and folder in which the information is to reside. (See *Figure 11.39*.)
  - c. Click **System Defaults**. This sets the path to the one programmed into the system as displayed in *Figure 11.39*.



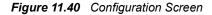


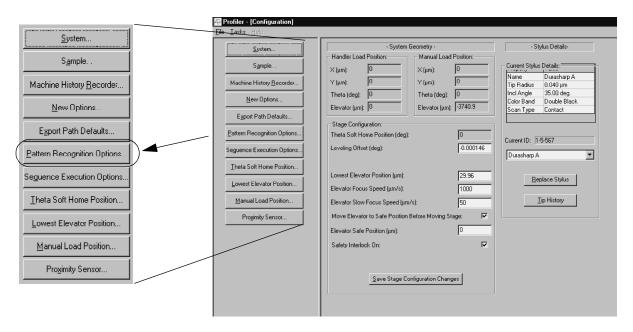
 Click OK to save the new values and return to the Configuration window, or click Cancel to return to the Configuration screen without changing the previous values. (See *Figure 11.39*.)

# PATTERN RECOGNITION OPTIONS AND DESKEW

#### Introduction

Configuration of the Pattern Recognition and Deskew options is performed in the **Pattern Recognition and Deskew Options** dialog box, and the Deskew Options dialog box. Access to the Pattern Recognition and Deskew Options dialog box is through the Configuration screen's **Pattern Recognition Options**... button. (See *Figure 11.40.*) Access to the Deskew Options dialog box is through the **Deskew** menu in the Sequence Recipe screen. (See *Using Groping with Pattern Recognition* on page 7-44.) Notice that, the parameter, "Minimum Match Score" in the Pattern Recognition dialog box. *The values set in the Deskew Options dialog box for each sequence recipe override those set in the Pattern Recognition Options dialog box.* 





# **Deskew Twice To Align Theta**

With a single deskew operation, there is no stage rotation to compensate for the small rotational error in sample placement. A second deskew can be performed to compensate for this error by enabling this option in the **Pattern Recognition and Deskew Options** dialog box. This allows accurate sample rotations within a sequence.

A second deskew operation is, therefore, sometimes necessary to improve the accuracy of pattern recognition deskew, in the Pattern Recognition Option. (See *Figure 11.41.*)

	Figure 11.41 Pattern	Recognition and Deskew Op	tions Dialog Box
The variables all deal with groping functions that are defined in the these parameters.	Pattern Recognition and Do Pattern Recognition Option Number of Groping Retry L Minimum Match Score (%): Minimum Score to Stop Gro Edge based Pattern Reco	s: .ayers: <b>1 (8 Sites)</b> 44 oping (%): 64	D <u>Lancel</u>
A check in the check box signals that the second deskew is enabled. Click in the empty box to enable the second deskew.	Save/Apply Video Setting Deskew Option: Perform Deskew Twice to		<b>ਪ</b>

## **Using Groping with Pattern Recognition**

Pattern Recognition options can be set so that the system performs a pattern search if the pattern is not found within the field of view when the sample is positioned at the deskew site. This search is called groping.

The three groping parameters are described. (See Figure 11.41).

- 1. From the Configuration screen, choose Pattern Recognition Options. The Pattern Recognition and Deskew Options dialog box appears. (See Figure 11.41)
- 2. Edit the fields by using the parameters described in *Table 11.2*.

Table 11.2 Groping Parameters

Parameter	Description
Save/Apply Video Settings	The lamp brightness setting is important in pattern recognition. If the lamp brightness is different from when the original sequence was established, the pattern recognition images could be difficult for the system to detect. A check in the <b>Save/Apply Video Settings</b> checkbox ensures that the lamp brightness is saved with each deskew site pattern so future scans have the same image view with the same light for pattern recognition.
Perform Deskew Twice to Align Theta	With a single deskew operation, there is no stage rotation to compensate for the small rotational error in sample placement. By enabling this option in the <b>Pattern Recognition and Deskew Options</b> dialog box, a second deskew is performed to compensate for this error. This allows accurate sample rotations within a sequence.

Parameter	Description
Edge Based Pattern Recognition	The <b>Edge Based Pattern Recognition</b> option is used for low contrast image recognition on a sample surface or where there is a large surface light variation. If this option is chosen (with a check in the check box), the normal image contrast grayscale processing takes place first, then a series of filters are applied that further contrast and sharpen edges for a better pattern recognition. The image data is stored before these filters are applied so the data is not effected by this option. It is strictly a tool used for pattern recognition where contrast is low or where light varies significantly. If the option is not chosen, only the image contrast grayscale processing is performed.
	<b>NOTE:</b> When this option is enabled, the pattern recognition process takes longer than if it is not chosen. The filtering and sharpening procedures require significant extra time.

**Table 11.2**Groping Parameters (Continued)

Parameter	Description	
Number of Groping Retry Layers	This parameter controls how much of the area around the deskew site is searched looking for the pattern. Each layer consists of a square area constructed by evenly surrounding the deskew site with squares the size of the camera field of view. (See <i>Figure 11.42</i> .)	
	Figure 11.42       Groping Retry Layers         Groping disabled searches only camera field of view       1st Retry Layer searches for 8 more square areas       2nd Retry Layer searches for 24 more square areas         Image: Comparison of the searches only camera field of view       Image: Comparison of the searches for 8 more square areas       Image: Comparison of the searches for 8 more square areas         Image: Comparison of the searches for 8 more square areas       Image: Comparison of the searches for 8 more square areas       Image: Comparison of the searches for 8 more square areas         Image: Comparison of the searches for 8 more square areas       Image: Comparison of the searches for 8 more square areas       Image: Comparison of the searches for 9 more square areas         Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas         Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas         Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas         Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas       Image: Comparison of the searches for 9 more square areas         Image: Comparison of the searches for 9 more squa	
	3rd Retry Layer searches for 48 more squares; 4th Retry Layer searches for 80 more squares. It stops after the 4th try.	
	<ul> <li>Options in the drop-down menu are: (See Figure 11.43.)</li> <li>None (the default)</li> <li>1 (8 Sites)</li> <li>2 (24 Sites)</li> <li>3 (48 Sites)</li> <li>4 (80 Sites)</li> </ul>	
	NOTE: It takes 10 seconds to move the stage, null the stylus, and search one such area; 8 search sites (1 layer of retry) takes as long as 90 seconds; and 24 sites (2 layers) takes as long as 250 seconds, and so on.	
	First, the deskew site field of view is searched. If the pattern is not found, the stage moves to one corner of the next layer and searches the field of view there. This continues until the pattern is found or until all search sites have been examined. If the pattern is still not found, the stage moves to one corner of the next layer and continues.	

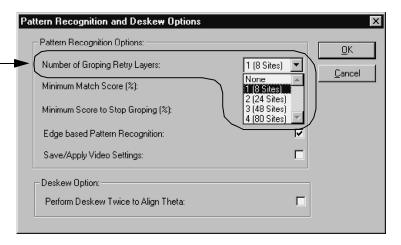
 Table 11.2
 Groping Parameters (Continued)

Parameter	Description
Minimum Match Score	This parameter allows adjustment of the threshold at which the pattern recognition system concludes that it has found a candidate for the desired deskew site.
(Renamed in Deskew Options dialog box to: <b>Lowest Match Score</b> )	Lowest Match Score is used to compare all the groping positions in the given groping levels. Once the groping stops (assuming that the Minimum Score to Stop Groping is not found) the highest score achieved, among those scores that qualified for Lowest Match Score acceptance, is chosen as the search pattern (model). This score must be smaller than the Minimum Score to Stop Groping. Allowed values range between 20 to 100%; the default is 65%.
	If the pattern does not show up in the original field of view, the search begins, and if any images score greater than the Lowest Match Score, the pattern recognition system concludes that the best of these is the correct deskew site (unless it finds a match equal to or greater than the Maximum Score and stops groping). Allowed values range from 20 to 100%; the default is 65%.
	For Desktop versions, use the minimum value, 20.
Minimum Score To Stop Groping	If the pattern recognition system is groping to find the desired pattern, sometimes the matching pattern is found with little ambiguity. If a score equal to or better than the Minimum Score to Stop Groping occurs, the searching process stops and the deskew site is placed. Allowed values range from 20 to 100%; the default is 70%.
	For Desktop versions, use the minimum value, 20.
	If no matches are found that are as good as this setting, the search continues until the retry layer areas are all searched. If this occurs, the best score above the <b>Minimum Match Score</b> setting determines the placement of the deskew site.

 Table 11.2
 Groping Parameters (Continued)

Figure 11.43 Pattern Recognition and Deskew Options Dialog box

Step 3 The drop-down menu for Number of Groping Retry Layers displays the number of tries and the number of sites associated with the groping level.



Setting: Number of Groping Retry Layers	3.	Click on the menu arrow to display the <b>Number of Groping Retry Layers</b> drop-down menu. (See <i>Figure 11.43</i> and <i>Table 11.2.</i> )
	4.	From the drop-down menu, choose the number of groping layers (sites) to be searched in pattern recognition attempts. (See <i>Figure 11.43</i> and <i>Table 11.2.</i> )
Setting: Minimum Match Score (%)	5.	Highlight the current value in the variable box associated with <b>Minimum Match</b> <b>Score (%)</b> and enter the new percentage value. Values can be from 20-100%. Default is 65%. (See <i>Figure 11.44</i> .)
		Figure 11.44 Pattern Recognition and Deskew Options Dialog Box
<ul> <li>Step 5 Highlight the current percentage and enter the new one. Values must be between 20 and 100%.</li> <li>Step 7 For low contrast images or large surface light variations, enable the Edge Based Pattern Recognition option.</li> </ul>		Pattern Recognition and Deskew Options         Pattern Recognition Options:         Number of Groping Retry Layers:         Minimum Match Score (%):         Minimum Score to Stop Groping (%):         Edge based Pattern Recognition:         Save/Apply Video Settings:    Step 9 When all changes are complete, click
<b>Step 8</b> To save lamp brightness settings for pattern recognition consistency, choose this option.		Deskew Option: Perform Deskew Twice to Align Theta:
Setting: Minimum Score to	6.	Highlight the current value in the variable box associated with Minimum Score to

- to Stop Groping (%) and enter the new percentage value. Values can be from 20-100%. Default is 70%. (See Figure 11.44 and Table 11.2.)
- 7. The Edge Based Pattern Recognition option is used for low contrast image recognition on a sample surface or where there is a large surface light variation. If the option is not chosen, only the image contrast grayscale processing is performed.

To select this option, ensure that there is a check in the check box. Click in the empty check box to place a check ( $\checkmark$ ) in it. (See *Figure 11.44*.)



NOTE: When this option is enabled, the pattern recognition process takes longer than if it is not chosen. The filtering and sharpening procedures require significant extra time.

8. The Save/Apply Video Settings option saves the lamp brightness settings so image processing for pattern recognition is the same when the same recipe is used for the scan or sequence.

To select this option, ensure that there is a check in the check box. Click in the empty check box to place a check ( $\checkmark$ ) in it.

9. Click **OK** to set the options and close the dialog box. (See *Figure 11.44*.)

Set Stop Groping (%)

> Selecting: Edge Based Pattern Recognition

Selecting: Save/Apply Video Settings

# SEQUENCE EXECUTION OPTIONS

This option is only for those systems that have the Sequence Option as part of the system package. It automatically saves sequence data under a lot ID and/or operator ID. To enable and define this option, the **Sequence Execution Option** must be set to display an ID information prompt before each sequence.

# **Open Sequence Execution Options Dialog Box**

Choose Sequence Execution Option from the option buttons in the Configuration screen. (See *Figure 11.45*).

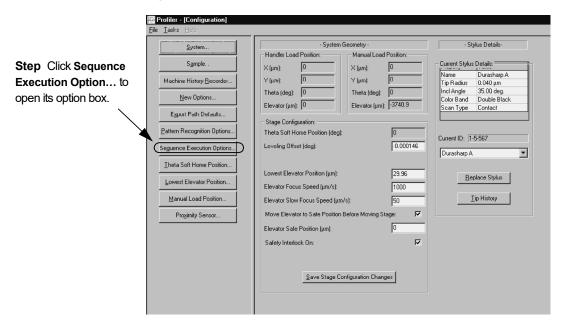


Figure 11.45 Configuration Screen

The Sequence Execution Options dialog box appears. (See Figure 11.49.)

Figure 11.46 Sequence Execution Options Dialog Box

equence Execution Options		
Prompt for Lot ID Before Sequence Execution:		<u>0</u> K
Prompt for Operator ID Before Sequence Execution	: 🗖	<u>C</u> ancel
Show Measurement Sites		
Low Mag. Camera 💿 High Mag. Camera	0	
Automation		
Confirm Start:		
Prompt for Cassette ID(EMID) if reader fails		
Operator input required (slot map).		

### **Enable Sequence ID Prompts**

The first combo box in the Sequence Execution Options dialog box contains options for operator identification. (See *Figure 11.47*.)

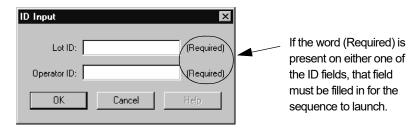
Figure 11.47 Sequence Prompts Combo Box

Prompt for Lot ID Before Sequence Execution:	
Prompt for Operator ID Before Sequence Execution:	

The first item, **Prompt for Lot ID Before Sequence Execution**, requires the operator to enter a **Lot ID** code in the Lot ID field before the sequence can proceed. If there is a check in the checkbox, the word (**Required**) appears next to the ID field. (See *Figure 11.48*.) If (**Required**) is *not* present, then the sequence can be started without entering the ID.

The second item, **Prompt for Operator ID before Sequence Execution**, requires the operator to enter an operator ID code before the sequence can proceed. If there is a check in the checkbox, the word **(Required)** appears next to the ID field. (See *Figure 11.48.*) If **(Required)** is *not* present, then the sequence can be started without entering the ID.

Figure 11.48 ID Input Dialog Box



 To choose one or both of the listed options, put a check (✓) in its check box. (See *Figure 11.49*.)

Before the sequence begins, each option is displayed in a dialog box. If the option was chosen in the options dialog box, that option must be responded to by the operator before sequence processing starts. (See *Figure 11.48*.)

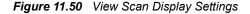
<b>Step 1</b> Click on the empty — check box to put a check in the box and enable the option.	Sequence Execution Options Prompt for Lot ID Before Sequence Execution: Prompt for Operator ID Before Sequence Execution:		Step 2 Click OK to accept the changes or Cancel to retain previous settings.
	Show Measurement Sites Low Mag. Camera O High Mag. Camera	0	providuo solarigo.
	Confirm Start: Prompt for Cassette ID(EMID) if reader fails Operator input required (slot map).		

Figure 11.49 Sequence Execution Options

2. Click **OK** to save the new settings and return to the **Configuration** screen, or click Cancel to return to the Configuration screen retaining the previous settings.

### View Scan Display Settings

The View Scan Display Settings are designed to give the operator the opportunity to choose which view is presented in the View Scan screen during a sequence scan. If the Show Measurement Sites option is chosen, then the operator has the option to view either the scan site on the sample surface or the site map showing the individual scan sites for the current sequence. (See Figure 11.50.) See Show Measurement Site During Sequence Run on page 6-21 for explanation and examples of the settings.





1. Click in the empty **Show Measurement Sites** checkbox to ensure that the operator can view both the measurement site map and the scan site by toggling between them in the View Scan screen during a sequence. (See *Figure 11.50*.)

The Low Mag. Camera is automatically chosen for the scan site view.

2. Click **OK** to accept the changes and close the dialog box. (See *Figure 11.49*.)

#### Automation Settings

Automation settings found in this dialog box are not functional in the P-15 system. These settings are used with systems having a handler and cassettes that have slot map criteria available for the system. The checkboxes might appear to be enabled but there is no affect on the system. (See *Figure 11.51*.)

Figure 11.51 Automation Combo Box in Sequence Execution Options

Automation Confirm Start:	
Prompt for Cassette ID(EMID) if reader fails	
Operator input required (slot map).	

# **TEACH MANUAL LOAD POSITION**

This procedure sets the manual load position of the stage and elevator. The Manual Load position can be changed by teaching the new position.

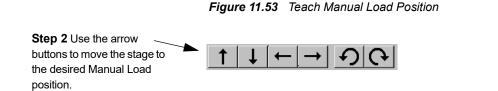
### **Teach Procedure**

 To open the Teach Manual Load Position screen, click on the Manual Load Position... button on the left side of the Configuration screen. (See *Figure 11.52.*)

	Profiler - [Configuration] File Iasks Help System	- System Geometry -	- Stylus Details-
Step 1 To open the Teach Manual Load Position screen, click Manual Load Position	System Sgmple . Machine History Becorder New Options Egrout Path Defaults Battern Recognition Options Iheta Soft Home Position Lowest Elevator Position Progimity Sensor	- System Geometry - - System	- Stylus Details: Varient Stylus Details: Tip Radius 0.040 µm Lincl Angle 55.00 deg. Color Band Double Black. Scan Type Contact Current ID: 1-5-567 Durasharp A

Figure 11.52 Configuration Screen - Manual Load Position

2. The **Teach Manual Load Position** screen appears. (See *Figure 11.53*.) The stage moves to the current Manual Load position. Using the arrow and rotation buttons on the tool bar, move the sample to the desired position. It is also possible to click the destination point in the wafer map on the XY View screen.



3. If desired, adjust the Z coordinate by raising the head with the **ELEV** button. Or, lower it using the **FOCUS** to start the head lowering and the **ESC** key on the key board to stop it at the desired height. (See *Figure 11.54*.)

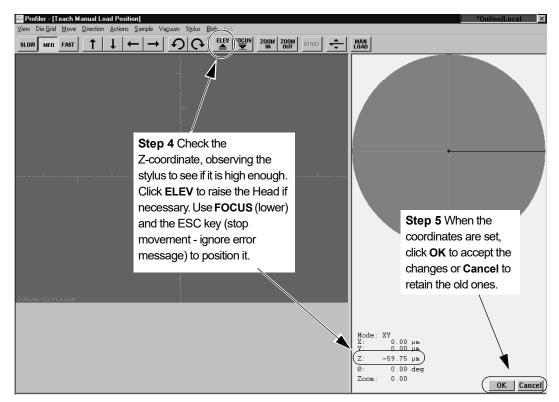


Figure 11.54 Teach Manual Load Position Screen

- 4. If desired, adjust the Z coordinate by raising the head with the **ELEV** button. Or, lower it using the **FOCUS** to start the head lowering and the **ESC** key on the key board to stop it at the desired height. (See *Figure 11.54*.)
- 5. Click **OK** to save the new position, or click **Cancel** to keep the original values and return to the Configuration screen. (See *Figure 11.54*.)

# **PROXIMITY SENSOR CONFIGURATION**

The proximity sensor is responsible for signalling when the stylus is in near proximity to the sample surface. The proximity sensor activity has configurable parameters that can be accessed in the **Proximity Sensor Configuration** dialog box.

# **Configuration Procedure**

1. To open the **Proximity Sensor Configuration** dialog box, click **Proximity Sensor...** at the bottom of the Configuration screen menu buttons. (See *Figure 11.55*.)

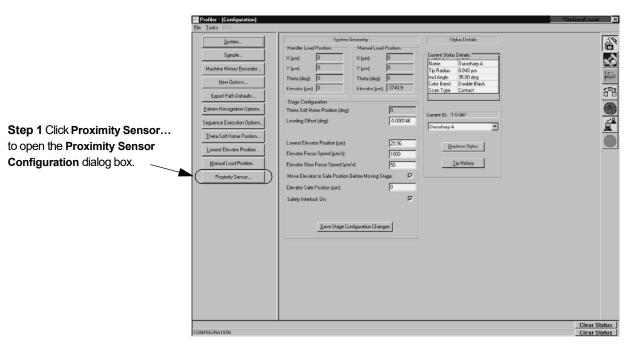


Figure 11.55 Configuration Screen - Proximity Sensor

The Proximity Sensor dialog box (see *Figure 11.56*) is divided into four sections:

- Options
- Proximity Sensor to Camera Offsets

The options and the variables within each one are discussed in the following sections.

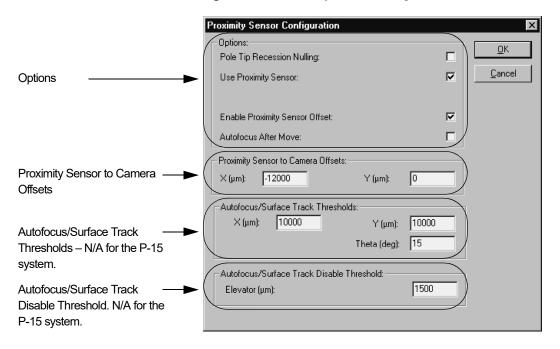


Figure 11.56 Proximity Sensor Configuration

### Options

A check in the checkbox next to each option indicates that it is enabled.

- *Pole Tip Recession Nulling:* The MicroHead II optics are perpendicular to, and focus directly on, the sample surface. When the instrument is to *scan a very small sample*, the sample stage moves the sample from under the optics focal point to a position under the stylus. When this options is enabled, the proximity sensor is not used in the focusing operation. The stylus is lowered and nulls directly on the small sample.
- Use Proximity Sensor: This option is active and can be changed to meet processing requirements. Before enabling this option, the **Pole Tip Recession Nulling** must be disabled. With this option enabled (a check in the check box), the Proximity Sensor signal causes the system to slow the head descent at a preset distance from the sample surface, then stops the head before the stylus touches the surface.
- *Enable Proximity Sensor Offset:* This option is used to prevent the stylus from hitting the sample too hard in situations where the proximity sensor is out of position to detect the sample surface; e.g., beyond the edge of the sample. This option should be used for Scan Position Offset and Step Height Calibrations. When this option is enabled, the following sequence of events occurs during the nulling procedure:
  - a. The sample stage moves the sample under the proximity sensor.
  - b. The head is lowered until the proximity sensor detects the sample surface, causing the head to stop.

- c. The sample stage moves the sample under the stylus.
- d. The head is lowered until the stylus nulls on the sample surface.
- In the **Options** section of the Proximity Sensor Configuration dialog box, put a check (✓) in the check box of every option that is to be used. (See *Figure 11.56.*)
- 2. If no other changes are to be made in the Proximity Sensor Configuration dialog box, click **OK** to accept the configuration. (See *Figure 11.56*.)

## Proximity Sensor to Hi Mag Camera Offsets



**CAUTION:** Do not change this number unless told to by an authorized KLA-Tencor representative.

This is a hardware parameter. At manufacturing, it is precisely set according to the distance from the Proximity Sensor to the Hi Mag Camera. This number is used by the software to perform certain centering functions. Currently this number is set at **0** in the **Y**-axis and -12000 in the **X**-axis. (See *Figure 11.56*.)

# **PASSWORD – MID-SESSION CALIBRATION OR CONFIGURATION ACCESS**

### Introduction

If a system is currently being used by an operator who *is not* logged in as a member of the Administrators, P\_Configuration, P\_Calibration, or P\_AdvCalibration security group, most of the Calibration and Configuration screen functions are not available to the operator. This feature provides an operator, who has a valid password, the ability to enter the Calibration or Configuration screen procedures in the current session without the necessity of exiting and restarting the Profiler software under the required security level.

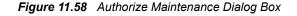
### Accessing the Maintenance Functions

To access the Calibration or Configuration functions, the user must enter the Authorize Maintenance dialog box from either the Configuration or Calibration screen, depending on which screen's functions are to be accessed. If a calibration is to be performed, enter through the Calibration screen. If configuration changes are to be made, enter through the Configuration screen. Access is granted only as long as the user stays in the Configuration or Calibration screen. Access is terminated when the user clicks on one of the other Program icons. 1. In the Calibration or Configuration screen, click on File to display its menu. (See *Figure 11.57.*)

Figure 11.57 File Menu for Choosing Authorize Maintenance



2. From the File menu choose Authorize Maintenance... This opens a Authorize Maintenance dialog box. (See *Figure 11.57*.)



Authorize <u>M</u> aintenance	X
Enter maintenance <u>p</u> assword:	
ОК	Cancel

- 3. Enter the password required for access to the Calibration or Configuration screen. (See *Figure 11.58*.)
- 4. Click **OK** when the password has been entered. (See *Figure 11.58*.)

If the valid password was correctly entered, access is granted to the Calibration or Configuration functions until the user exits the accessed screen.

### **Changing the Maintenance Password**

#### Introduction

A member of the **Administrators** security group can change the Maintenance Password. Once changed, the same password is used for entrance to either the Configuration or Calibration screen functions.

#### **Choosing a Password**

Choose a password with the following parameters in mind:

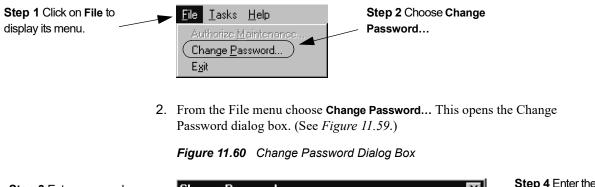
- It can only have alphabetic and/or numeric characters.
- It is case sensitive.
- It must have between 6 and 14 characters.

#### **Password Change Procedure**

Use the following procedure to change the password.

1. From either the Configuration or Calibration screen click on **File** to display its menu. (See *Figure 11.59*.)

Figure 11.59 File Menu for Change Password... Dialog Box Access



Step 3 Enter password	Change Password 🛛 🗙	
here first.		password here
	New maintenance password:	again.
	( <u>C</u> onfirm new password:	
Step 5 Click OK only after		
both password entries have been completed.	OK Cancel	

- 3. Enter the new password first in the New maintenance password field. *Do not* click OK.
- 4. Enter the identical password into the **Confirm new password** field. (See *Figure 11.60.*)
- 5. Click **OK**. If both passwords were the same, the system receives it and it becomes the new password for both screens.

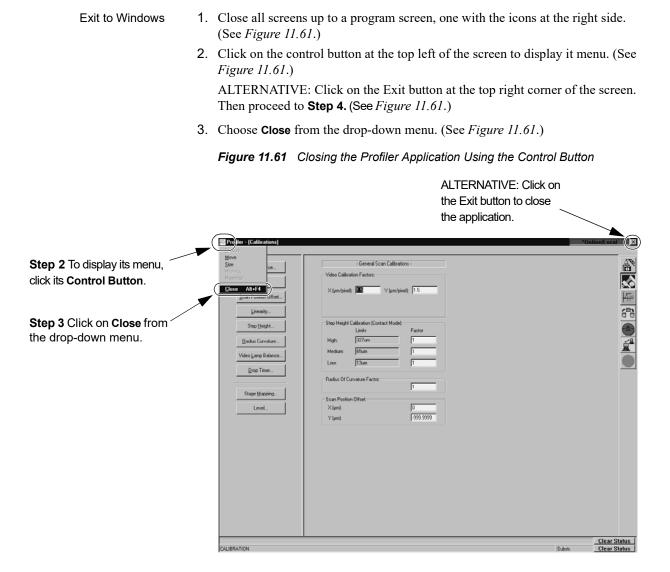
## LOSS OF POWER

The KLA-Tencor profiler should be protected from power loss.

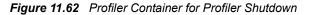
- The head of the hard disk drive auto-parks at power loss so that the hard disk drive does not suffer damage. However, if power returns and cycles quickly on and off two or three times within 100 to 200 ms, there is a remote possibility of a head crash and permanent damage.
- If power failure is a common occurrence, use an Uninterruptable Power Supply (UPS) device that supplies power for 30 minutes to provide time for an orderly shutdown.

# **TURNING OFF OR RESETTING THE INSTRUMENT**

When powering down the instrument, use the following procedure to ensure against loss of data and recipes.



4. A Message box is displayed asking, "Are you sure you want to exit the Profiler?" Click on **Yes** to exit. (See *Figure 11.62*.)

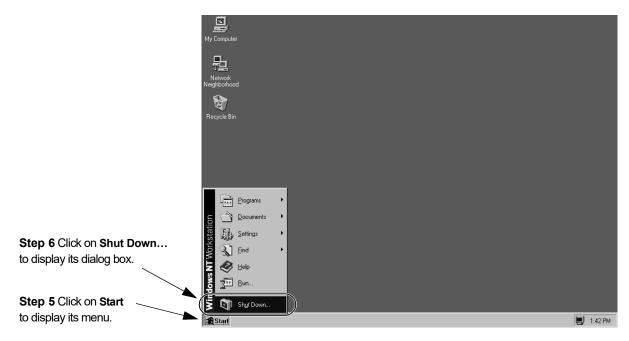




Step 4 Click on Yes to exit the Profiler application.

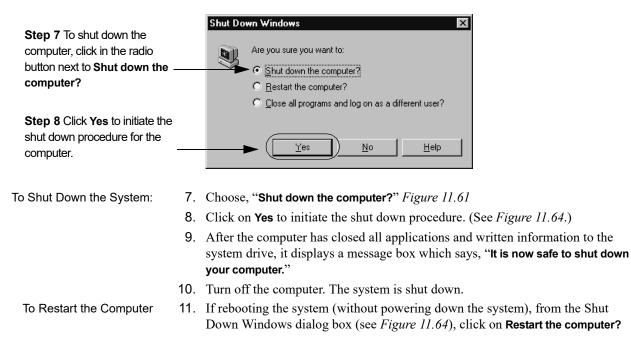
- To log off to shut down the system
- 5. If exiting from the program so that another user can log on, click on the **Start** button at the bottom left of the screen to display its menu. (See *Figure 11.63*.)

Figure 11.63 Start Menu



Choose Shut Down... from the menu. (See *Figure 11.63*.)
 This displays a dialog box that presents three options. (See *Figure 11.64*.)

Figure 11.64 Shut Down Windows Dialog Box



12. Click Yes at the bottom of the dialog box to initiate the reboot.

# INSTALLING A PRECISION LOCATOR

Various precision locators are available to provide for exact positioning of a sample relative to a fixed reference point. See *Standard Precision Locators* on page 11-54 and *Optional Precision Locators* on page 11-54 for graphic representations of the available precision locators.

The stage table is removable so the *precision locators* can be bolted directly to the stage. *Disc locators* bolt directly to the stage table.

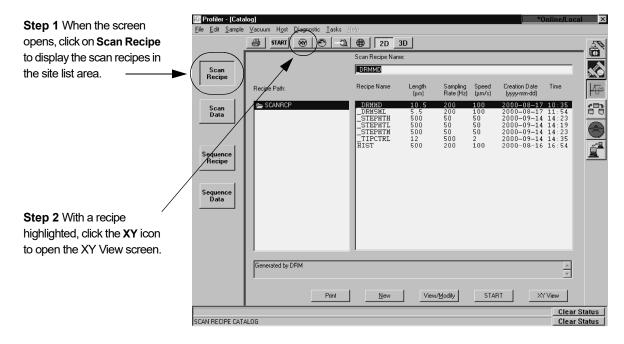
# **Standard Precision Locators**



**CAUTION:** Nominally, the top surface of a standard precision locator should be at the same level relative to the measurement head as the top surface of the stage tabletop. Still, it is a good idea to confirm the accuracy of the setting for Lowest Elevator Position when a precision locator is installed. The stylus can be damaged if the existing settings are incorrect. Refer to the procedures in *Teach Lowest Elevator Position* on page 11-10 for details.

#### **Installing the Precision Locator:**

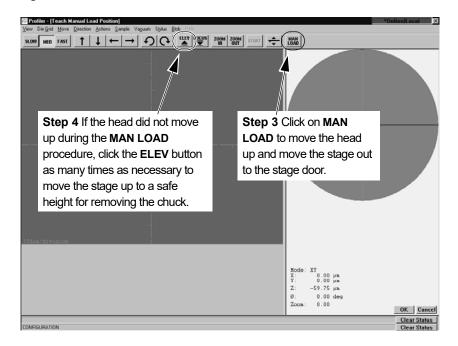
1. In the **Catalog** screen, choose **Scan Recipe** to display the scan recipes in the site list area. (See *Figure 11.65*.)



#### Figure 11.65 Catalog - Scan Recipe Screen

2. With a recipe highlighted, click on the **XY** icon in the tool bar to open the XY View screen. (See *Figure 11.65.*) The XY View screen opens. (See *Figure 11.66.*)

Figure 11.66 XY View Screen



- 3. Click on **MAN LOAD** to move the head up and bring the stage out to the stage door. (See *Figure 11.66*.)
- 4. If the head does not move up during the **MAN LOAD** procedure, click the **ELEV** button (see the Tool Bar in *Figure 11.66*) as many times as necessary to move the head to a high enough position so that contact with the stylus can be avoided when removing the stage table.
- 5. Open the door.



**CAUTION: If Interlock is ON, do not open the door before** moving the stage into position or the system might shut down due to the safety interlock activation on the stage door.

6. Remove the three screws (see *Figure 11.67*) that hold the stage table to the stage. Remove the table. It might be necessary to rotate the stage using the rotational arrow buttons (in the tool bar) for easier access to the screws.

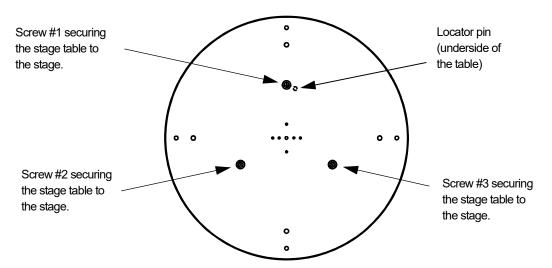
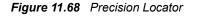
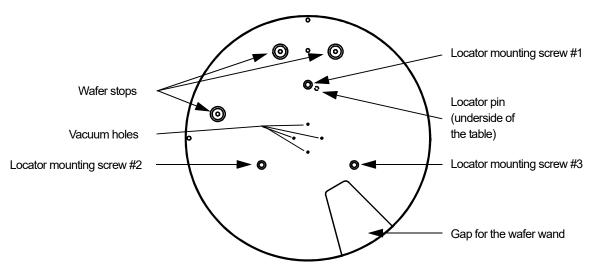


Figure 11.67 Lightweight Stage Table Top

7. Place the precision locator on the stage so that the three holes line up with the mounting holes. A pin on the bottom of the locator fits into the groove on the stage just to the right of the 12 o'clock position as seen from above. (See *Figure 11.68.*)





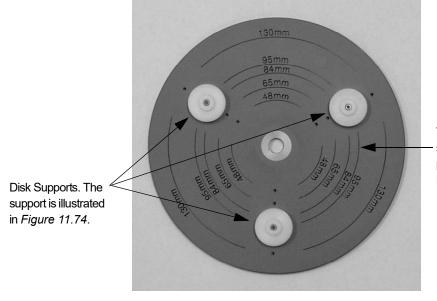
Press down on the precision locator to slide the pin into the groove. When positioned as shown in *Figure 11.68*, the precision locator is in the "0" theta position (that is, theta equals 0 degrees).

8. Screw in the mounting screws to secure the locator to the stage. (See *Figure 11.68.*)

#### **Three Point Disk Locator**

The KLA-Tencor three point disk locator for profilers (Part No. 304247) is shown in *Figure 11.69*.

Figure 11.69 Three Point Disk Locator

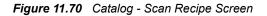


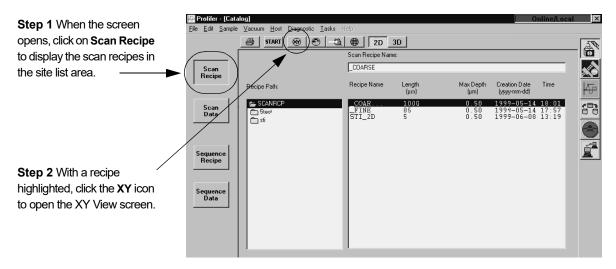
The current locators are situated at the 95 mm position on the Three Point Disk Locator.

The three point Disk Locator has three disk supports that can be situated to support five sizes of disk: 48 mm, 65 mm, 84 mm, 95 mm, and 130 mm disks.

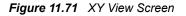
#### Installing the 3-point Disk Locator on the Stage:

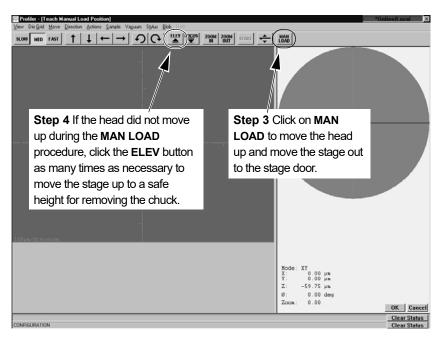
1. In the **Catalog** screen, choose **Scan Recipe** to display the scan recipes in the site list area. (See *Figure 11.70.*)





2. With a recipe highlighted, click on the **XY** icon in the tool bar to open the XY View screen. (See *Figure 11.71.*) The XY View screen opens. (See *Figure 11.71.*)





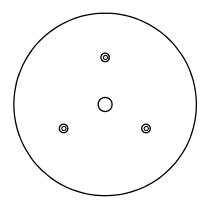
- 3. Click on MAN LOAD to move the head up and bring the stage out to the stage door. (See *Figure 11.71*.)
- 4. If the head does not move up during the **MAN LOAD** procedure, click the **ELEV** button (see the Tool Bar in *Figure 11.71*) as many times as necessary to move the head to a high enough position so that contact with the stylus can be avoided when removing the stage table.
- 5. Open the door.



**CAUTION: If Interlock is ON, do not open the door before** moving the stage into position or the system might shut down due to the safety interlock activation on the stage door.

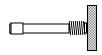
- 6. Remove the three screws (8-32×3/8 in.) that hold the stage table to the stage. Remove the table.
- 7. The Three Point Disk Locator has a base plate (see *Figure 11.72*) that has three holes for mounting it in place of the stage table. Place the disk locator base plate on the stage so that the three mounting holes line up.
- 8. Insert the three mounting screws and tighten. (See Figure 11.72.)

Figure 11.72 Three Point Disk Locator Base Plate



9. Place the Three Point Disk Locator on its base plate and screw in the center hub screw. (See *Figure 11.73*.) Be sure that the washer is between the screw and the Three Point Disk Locator.

Figure 11.73 Center Hub Screw



10. Close the door



**PINCH POINT:** Keep fingers, hands, and other body parts clear of the closing door to prevent a pinch injury.



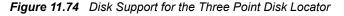
**CAUTION:** If Interlock is ON, do not open the door before moving the stage into position or the system might shut down due to the safety interlock activation on the stage door.

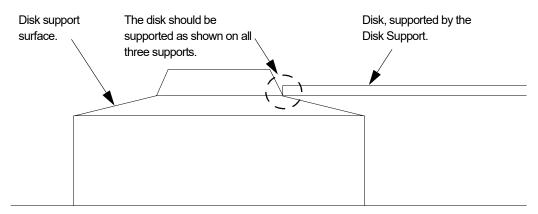
11. Click MAN LOAD to move the stage back under the measurement head

The Lowest Elevator Position is set at the factory to allow the stylus to be nulled on the stage surface for both the standard stage and a precision locator. When a wafer locator is installed, a new lowest elevator position must be redefined, and that position entered into the stage configuration file. See *Teach Lowest Elevator Position* on page 11-10 for details.

#### Adjusting the Disk Size:

- 1. Remove the screws  $(2-56 \times 1/2 \text{ in.})$  securing each of the three disk supports.
- 2. Position each disk support to the required disk size. The five disk sizes are identified by concentric circles on the locator surface, with the representative disk size printed over each circle. The are three disk support mounting holes associated with each disk size. (See *Figure 11.69*.)
- **3**. Insert the screws and loosely tighten, leaving some play in the position of each disk support. Place a representative disk on the supports and adjust them so that the disk is supported snugly between the three supports. The final positioning of the disk should resemble that illustrated in *Figure 11.74*.





4. When the three disk supports are adjusted, tighten the three disk support screws and recheck the disk position. Leave enough clearance to take into account manufacturing tolerances so that all disks of this size fit. Try to get the disk centered around the central hub of the locator.

## **Precision Locators - Description**

Precision locators are fixtures that provide for exactly positioning of a sample relative to a fixed reference point. KLA-Tencor provides the following types of precision locators:

#### **Standard Precision Locators**

These locators provide positioning for square samples, wafers with flats, and notched wafers. Instruments are shipped with a choice of the standard stage table or one of the locators in this list. (See *Figure 11.75* through *Figure 11.80*.)

Standard precision locators include:

- 4-in. for Wafer with Flat/Square Substrate
- 4-in. for Wafer with Notch
- 5-in. for Wafer with Flat/Square Substrate
- 5-in. for Wafer with Notch
- 6-in. for Wafer with Flat/Square Substrate
- 6-in. for Wafer with Notch

## **Optional Precision Locators**

These locators allow positioning of less common sizes of square substrates and wafers. They bolt on top of the standard stage table.



NOTE: These locators must be purchased separately.

Optional precision locators include (See Figure 11.81 through Figure 11.88)

- 2-in. for Wafer with Flat/Square Substrate
- 3-in. for Wafer with Flat/Square Substrate
- 82-mm for Wafer with Notch
- 4-in. for Wafer with Flat/Square Substrate
- 5-in. for Wafer with Flat/Square Substrate
- 5-in. for Wafer with Notch

#### **Optional Disk Precision Locators**

These locators are used for holding hard disk samples to the stage. They bolt on top of the standard stage table. Note: These locators have to be purchased separately.

Instructions for installing precision locators can be found in *Installing the Precision Locator:* on page 11-47,

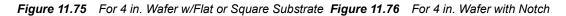
Optional disk precision locators include (See Figure 11.89)

- 48-mm for Disk
- 65-mm for Disk
- 95-mm for Disk
- Adjustable Three Point Disk Locator (48 mm, 65 mm, and 95 mm)

#### **Optional Stress Precision Locators**

These locators are used for holding wafers in place, suspended at three points, for measurement of stress related to a deposition on the wafer surface. The Manual Load Stress Locator is attached to the stage table. The Adjustable Stress Locator is mounted to its own base place that is secured to the stage.

Optional, Stress Locator - Manual Load for 200 mm Wafers (see Figure 11.90).



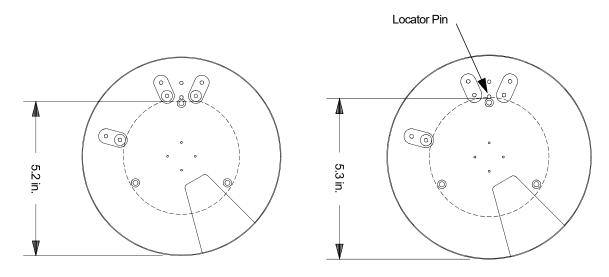
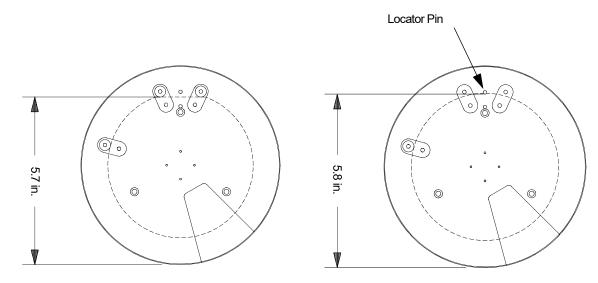


Figure 11.77 For 5 in. Wafer w/flat or Square Substrate Figure 11.78 For 5 in. Wafer with Notch



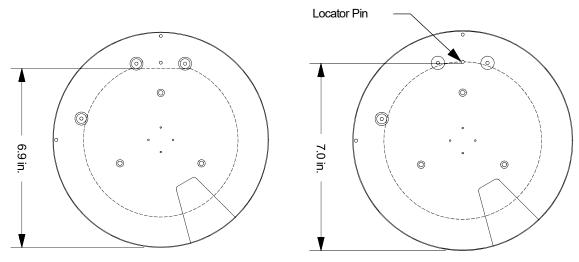


Figure 11.79 For 6 in. Wafer w/flat or Square Substrate Figure 11.80 For 6 in. Wafer with Notch

# **OPTIONAL PRECISION LOCATORS**

Figure 11.81 For 2 in. Wafer w/Flat or Square Substrate Figure 11.82 For 3 in. Wafer w/Flat or Square Substrate

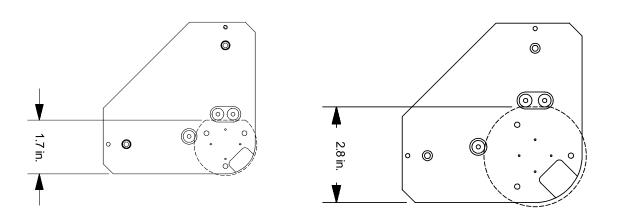
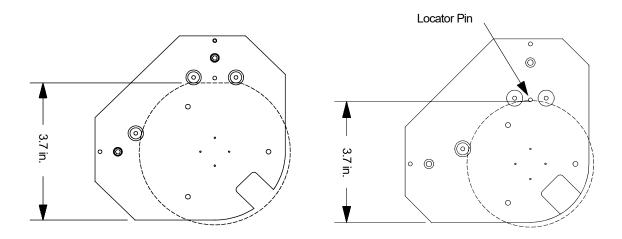
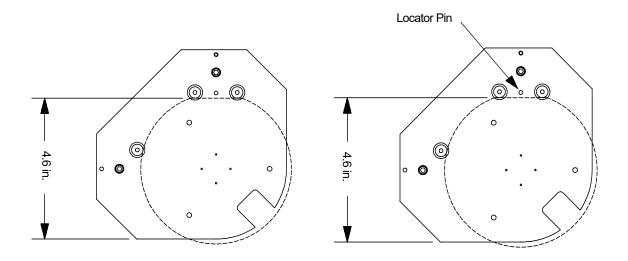


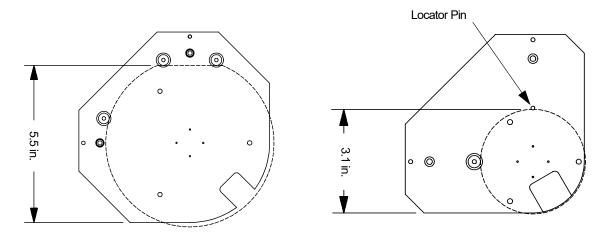
Figure 11.83 For 4 in. Wafer w/Flat or Square Substrate Figure 11.84 For 4 in. Wafer with Notch





#### Figure 11.85 For 5 in. Wafer w/Flat or Square Substrate Figure 11.86 For 5 in. Wafer with Notch

Figure 11.87 For 6-in. Wafer w/Flat or Square Substrate Figure 11.88 For 82-mm Wafer with Notch



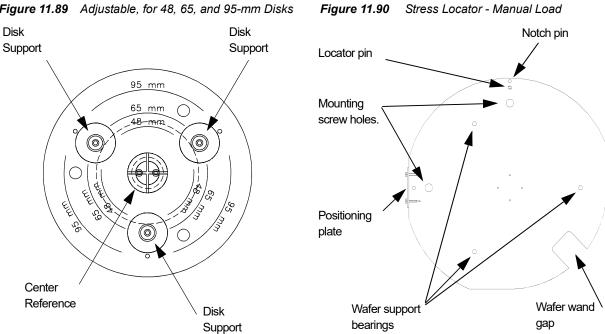


Figure 11.89 Adjustable, for 48, 65, and 95-mm Disks

# CALIBRATIONS

# INTRODUCTION

## This chapter describes:

- Password Mid-Session Calibration or Configuration Access on page 12-1
- Applied Force Calibration on page 12-3
- Video Calibration on page 12-5
- Scan Position Offset Calibration on page 12-10
- Scan Position Offset Calibration on page 12-10
- *Step Height Calibration* on page 12-28
- Level Calibration on page 12-41
- Level Calibration on page 12-41
- Standard Calibration Matrix on page 12-51

# PASSWORD – MID-SESSION CALIBRATION OR CONFIGURATION ACCESS

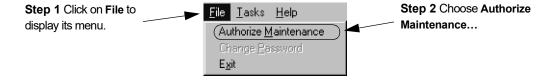
## Introduction

If a system is currently being used by an operator who *is not* logged in as a member of the Administrators, P\_Configuration, P\_Calibration, or P\_AdvCalibration security group, most of the Calibration and Configuration screen functions are not available to the operator. This feature provides an operator, who has a valid password, the ability to enter the Calibration or Configuration screen procedures in the current session without the necessity of exiting and restarting the Profiler software under the required security level.

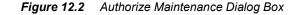
## Accessing the Maintenance Functions

To access the Calibration or Configuration functions, the user must enter the Authorize Maintenance dialog box from either the Configuration or Calibration screen, depending on which screen's functions are to be accessed. If a calibration is to be performed, enter through the Calibration screen. If configuration changes are to be made, enter through the Configuration screen. Access is granted only as long as the user stays in the Configuration or Calibration screen. Access is terminated when the user clicks on one of the other Program icons. 1. In the Calibration or Configuration screen, click on **File** to display its menu. (See *Figure 12.1.*)

Figure 12.1 File Menu for Choosing Authorize Maintenance



2. From the File menu choose Authorize Maintenance... This opens a Authorize Maintenance dialog box. (See *Figure 12.1*.)



Authorize <u>M</u> aintenance	X
Enter maintenance <u>p</u> assword:	
ОК	Cancel

- **3**. Enter the password required for access to the Calibration or Configuration screen. (See *Figure 12.2*.)
- 4. Click **OK** when the password has been entered. (See *Figure 12.2*.)

If the valid password was correctly entered, access is granted to the Calibration or Configuration functions until the user exits the accessed screen.

## **Changing the Maintenance Password**

#### Introduction

A member of the **Administrators** security group can change the Maintenance Password. Once changed, the same password is used for entrance to either the Configuration or Calibration screen functions.

#### **Choosing a Password**

Choose a password with the following parameters in mind:

- It can only have alphabetic and/or numeric characters.
- It is case sensitive.
- It must have between 6 and 14 characters.

#### **Password Change Procedure**

Use the following procedure to change the password.

	1.	From either the Configuration or Calibration screen click on <b>File</b> to display its menu. (See <i>Figure 12.3</i> .)
		Figure 12.3 File Menu for Change Password Dialog Box Access
Step 1 Click on File to display its menu.		Eile       Lasks       Help       Step 2 Choose Change         Authorize       Maintenance       Password         Change       Password         Exit       Kathorize
	2.	From the File menu choose <b>Change Password</b> This opens the Change Password dialog box. (See <i>Figure 12.3</i> .) <i>Figure 12.4</i> Change Password Dialog Box
Step 3 Enter password here first.		Change Password Step 4 Enter the password here again.
		Confirm new password:
<b>Step 5</b> Click <b>OK</b> only after both password entries have been completed.		
	3.	Enter the new password first in the <b>New maintenance password</b> field. <i>Do not</i> click <b>OK</b> .

- 4. Enter the identical password into the **Confirm new password** field. (See *Figure 12.4.*)
- 5. Click **OK**. If both passwords were the same, the system receives it and it becomes the new password for both screens.

# **APPLIED FORCE CALIBRATION**

Check the Calibration Matrix on *page 12-51* for possible interaction with other calibrations.

## Windows - Applied Force Calibration Procedure

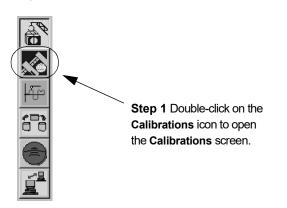
#### Introduction

Applied force is the force between the stylus tip and the sample when the stylus is in contact with the sample. Mechanical changes in the stylus arm can affect calibration settings.

## **Applied Force Calibration Procedure**

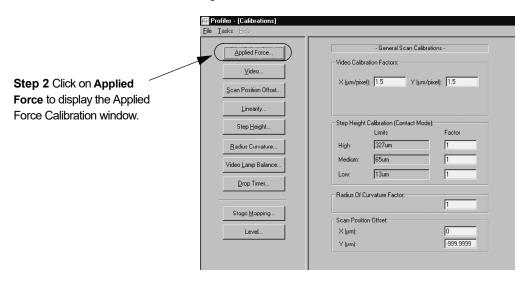
1. Double-click on the Calibration icon. (See Figure 12.5.)

Figure 12.5 Catalog Screen - Choose Calibration



2. Click on the **Applied Force** button in the **Calibration** screen. (See *Figure 12.6.*) The Applied Force Calibration dialog box is displayed. (See *Figure 12.7.*)

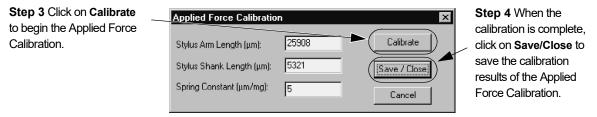
Figure 12.6 Calibrations Screen



3. Click on **Calibrate** to begin the calibration procedure.

The system performs the calibration and displays the results in the three fields of the Applied Force Calibration dialog box. (See *Figure 12.7.*)

Figure 12.7 Applied Force Calibration Window



4. Click on **Save/Close** button to save the calibration results. (See *Figure 12.7.*) OR, click on **Cancel** to retain the old calibration results.



CAUTION: Do Not Manually Change any of the numbers in the fields.

# VIDEO CALIBRATION

Check the Calibration Matrix on page 12-51 for possible interaction with other calibrations.

## Introduction

Video calibration ensures that the stage position is correlated to the video image on the screen. The calibration calculates the <sup>video pixels</sup>/<sub>micron</sub>. This means that when a position on the video screen is clicked, that position moves to the screen crosshair. This calibration works two different ways depending on whether or not the P-15 system has the Pattern Recognition option. Both calibration procedures are presented.

In this procedure, the Stylus Alignment Tool, Stage Mapping Wafer, or another sample with distinctive features can be used. The Stylus alignment Tool is recommended. The directions in this procedure include loading a sample, like the Stylus Alignment Tool (KLA-Tencor part number 219517).

## **Video Calibration Procedure**

1. Click on the **Calibration** icon. (See *Figure 12.8.*) The **Calibrations** screen is displayed. (See *Figure 12.9.*)

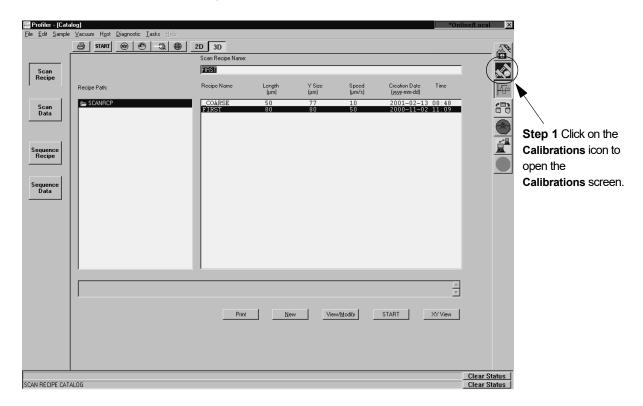


Figure 12.8 Catalog Screen - Choose Calibration

2. Choose Video. (See *Figure 12.9*.) The XY View Video Calibration screen appears. (See *Figure 12.10*.)

Figure 12.9 Calibrations Screen- Accessing the Video Calibration

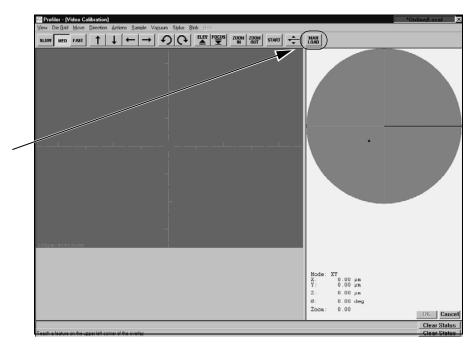
	🐺 Profiler - [Calibrations]		
	<u>File Tasks H</u> elp		
Step 2 Click on the Video button to display the Video Calibration window.	Line Laks       Edu         Applied Force       Video         Scan Position Diffset       Linearity         Step Height       Badius Curvature         Video Lamp Balance       Video Lamp Balance         Drop Timer       Stage Mopping         Level       Level	- General Scan Calibrations - Video Calibration Factors: X (µm/pixel): 1.5 Y (µm/pixel): 1.5 Step Height Calibration (Contact Mode): Limits Factor High: 327um 1 Medium: E50m 1 Low. 13um 1 Radius Of Curvature Factor: Radius Of Curvature Factor: Scan Position Offset: X (µm): 0 Y (µm): -399.3933	
		Y (µm): -999.9999	

#### Loading the Stylus Alignment Tool

**3**. From the **Video Calibration** screen choose **MAN LOAD** to move the stage out to the stage door. (See *Figure 12.10*.)

The Stylus Alignment Tool should be used to perform this calibration. A patterned sample that provides very distinct features could also be used if the Stylus Alignment Tool is not available.

Figure 12.10 Manual Load from the Video Calibration Screen



Step Click MAN LOAD to bring the stage to the door so the sample can be loaded.

Step 8 After the sample is loaded on the stage, click MAN LOAD to return stage under stylus. 4. Open the stage door.



**CAUTION:** A system safety shutdown occurs if an attempt is made to activate any stage or elevator motion when the stage door is open, unless the interlock defeat switch has been disabled.

- 5. Place the Stylus Alignment Tool (or other sample) on the stage. Position it in the center of the stage as squarely as possible with respect to the XY axis.
- 6. Turn of the vacuum using the switch just inside the left side of the door.

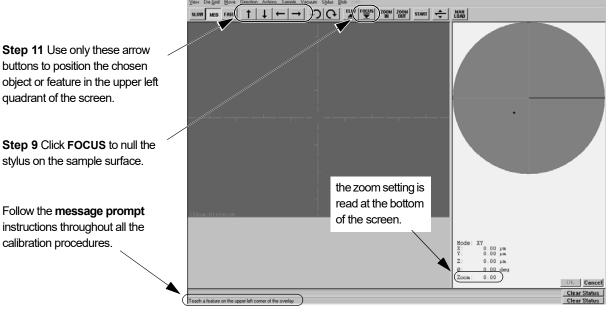


**NOTE:** The vacuum menu in the screen's menu bar is disabled. It does not effect the stage vacuum.

- 7. Close the door.
- 8. Click MAN LOAD to move the stage back into position under the stylus and the optics. (See *Figure 12.10*.)
- 9. Click **FOCUS** in the tool bar. (See *Figure 12.11*.) The system nulls on the sample (nulls = brings the head down and focuses the optics according to the currently set magnification with the stylus very near contact with the sample surface).
- 10. Ensure that the current zoom setting is correct for the measurements that this calibration is preparing for. The zoom setting is read at the bottom right of the screen. A setting of 0.00 is zoomed all the way out. (See *Figure 12.11*.)
- 11. The prompt in the lower left corner of the screen reads, "**Teach a feature on the upper left corner of the overlay**." Use the linear arrow keys to position a feature in the upper left quadrant of the screen for use in teaching the calibration. *Avoid features that are identical or similar to other features nearby*. (See *Figure 12.11*.)
- Teaching for Systems with Pattern Recognition
- 12. To TEACH the feature, drag a pattern recognition box around the chosen feature. (Pattern recognition box: Move the cursor above and to the left of the feature. Click and hold the mouse button, drag the box down below and to the right of the feature, and release the button.)

The system moves the feature and pattern recognition locates it again. If the system locates the feature go to Step on page -10. Otherwise continue on to the next step.





- 13. If the pattern recognition program does not find the pattern, perform the calibration again. If the system locates the feature, go to the results that are explained in Step 15. If the system still does not locate the feature, use the procedure for systems without pattern recognition as described in Step 14 and Step 15.
- 14. Choose a feature in the upper left quadrant of the screen. To choose the feature, move the cursor crosshair over the feature and click on it at a precise point that can be exactly identified again. The system moves the feature to another location nearby.

calibration procedures.

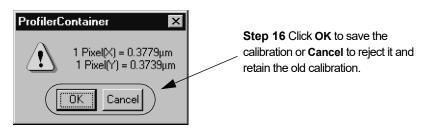
Teaching for Systems without Pattern Recognition 15. Click on the same feature again in exactly the same place on the feature as the first click.

The Profiler Container message box is displayed (this is true also if the pattern recognition finds the chosen pattern after Step 12 on page -8).

The calibration results are presented as calculated ratios of:

vertical and horizontal screen units called pixels to X and Y stage coordinates in microns (a ratio of Pixels to microns, see *Figure 12.12*.)

Figure 12.12 XY Video Display Message Box



16. Click **OK** to save the calibration or **Cancel** to reject it and retain the old calibration. The **Calibration** screen is then displayed. (See *Figure 12.12*.)

## SCAN POSITION OFFSET CALIBRATION

## Introduction

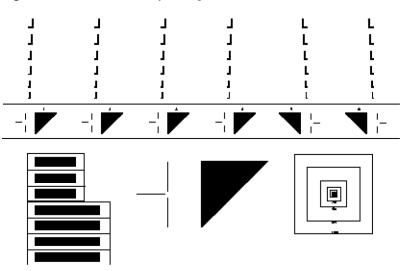
The Scan Position Offset Calibration procedure scans for data that it then uses to calculate the X-, Y-axis offsets from the optics and stylus, for positioning the sample stage.

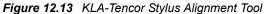
During the Stylus Change procedure, the system automatically sets up the Scan Position Offset Calibration to be performed as part of the procedure.

For the standard styli this procedure is performed in the following order:

- 1. 150 µm (standard) calibration
- 2. If the 150  $\mu$ m scan fails to locate the triangle, then the 500  $\mu$ m (backup) calibration is performed.
- 3. If the 500  $\mu$ m was performed successfully, the 150  $\mu$ m calibration must be performed again.

Use the Stylus Alignment Tool (KLA-Tencor Part Number 219517 – see *Figure 12.13*) to perform the Scan Position Offset Calibration and determine the distance that the stylus tip is offset from the crosshair overlay in the XY View window.





## 150 $\mu$ m (Standard) Scan Position Offset Calibration

- 1. From the Scan Offset Calibration screen click MAN LOAD to move the stage out to the stage door. (See *Figure 12.14*.)
- 2. After the system has completely stopped moving, open the stage door.



**CAUTION:** Wait until the stage motion has completely stopped before opening the door. If the stage is still in motion when the door is opened, the system stops. (Unless the interlock is disabled)

**CAUTION:** Do not activate the stage motion system with the door open or the system stops. (Unless the interlock is disabled)

Step 1 To move the stage to

the open door, click on the **MAN LOAD** icon. It highlights and the stage moves

**Step 6** After loading the Stylus Alignment Tool, click on **MAN LOAD** again to send the stage back under the

forward.

stylus.

Figure 12.14 Manual Load from the Scan Offset Calibration Window

- **3**. Place the **Stylus Alignment Tool** precisely in the center of the stage, squarely positioned with respect to the XY axis.
- 4. Turn the vacuum on using the switch on the left inside edge of the door.

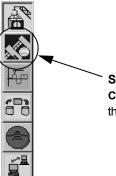
**NOTE:** The Vacuum menu in the screen's menu bar is disabled. It does not effect the stage vacuum.

5. Close the stage door.

×

- 6. From the **Scan Offset Calibration** screen, click **MAN LOAD** in the tool bar to move the stage back beneath the stylus. (See *Figure 12.14*.)
- 7. From the **Catalog** screen click on the **Calibration** icon to display the **Calibration** screen. (See *Figure 12.15.*)

Figure 12.15 Catalog Screen - Click on the Calibration Icon



Step 7 Click on the Calibration icon to display the Calibration screen.

8. Ensure that the Video Calibration is correct at the zoom setting being used for the Scan Position Offset calibration. (If, when clicking on an object to center it in the XY View screen, the object does not move to the crosshair junction, perform the Video Calibration. This should correct the symptom. See *Video Calibration* on page 12-5.) *Zoomed out all the way out is recommended*.



**CAUTION:** Use the zoom-lock or zoom all the way out when performing the Scan Position Offset calibration.

Each zoom setting has a slightly different Scan Position Offset. It is important that the system be calibrated at the zoom setting which is being used for the scans. It is very important that the zoom setting be consistent when using pattern recognition and that the pattern recognition image be captured at the zoom setting being used to locate the pattern. Scans zoomed all the way out are consistent as is any zoom position that has been locked.



**NOTE:** Ensuring that the Video Calibration is correct helps to avoid introducing error into the Scan Position Offset calibration.

- **9**. Ensure that the proximity sensor is ON (see *Proximity Sensor Configuration* on page 11-40) or reteach the Lowest Elevator Position using the alignment tool as the sample surface. (See *Teach Lowest Elevator Position* on page 11-10.)
- 10. In the XY View screen, click and hold the **ZOOM-IN** button until the optics are fully zoomed out.
- 11. From the Calibration screen, click on the **Scan Position Offset**... button. (See *Figure 12.16*.)

	File Tasks Help	
Step 11 Click on the Scan Position Offset calibration button to display the SCAN OFFSET CALIBRATION OPTION dialog box.	Applied Force         Video         Scan Position Offset         Linearity         Step Height         Radius Curvature         Video Lamp Balance         Drop Timer         Stage Mapping         Level	- General Scan Calibrations - Video Calibration Factors: X (μm/pixel): 1.5 Y (μm/pixel): 1.5 Step Height Calibration (Contact Mode): Limits Factor High: 327um 1 Medium: 65um 1 Low: 13um 1 Radius Of Curvature Factor: Radius Of Curvature Factor: X (μm): 0 Y (μm): 339,3939

Figure 12.16 Scan Calibrations Screen

The **Scan Offset Calibration Option** dialog box is displayed (see *Figure 12.17*) on top of the Calibration screen.

Two columns present the two options used to set up the Scan Offset Calibration. The first column is the **Size** column. It is used to determine the width of the triangle that is to be scanned and therefore, which triangle the scan is to be performed on. If the width is 150  $\mu$ m then the 300  $\mu$ m triangle is being used. If the width is 500  $\mu$ m then the 1000  $\mu$ m (1 mm) triangle is being used.

12. Choose 150  $\mu$ m (standard) to continue with the calibration. (See *Figure 12.17*)

Step 13 Choose Recipe	Scan Offset Calif	bration Option	×
type: Custom or Default	Size:	Recipe:	Continue
Step 12 Click on 150 $\mu$ m.	► © 150 µm	Default	Cancel
	Ο 500 μm	Default	Default
			Custom

*Figure 12.17* Scan Position Offset Calibration Options dialog box

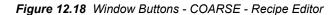
13. Choose a recipe type, Default or Custom.

**RECIPE TYPES.** Two calibration options exist in the **Scan Offset Calibration Option** dialog box. Each option provides the user with the opportunity to choose between using a default recipe or to create/use a custom recipe. Default and Custom recipes are explained below:

- **Default**: This recipe is designed to operate with a scan speed and stylus force setting that is safe for any contact stylus. The default settings are the KLA-Tencor recommended recipe settings for all the calibrations.
- **Custom:** (CUSTOM RECIPE CREATION IS AN OPTION BUT IS NOT NOT RECOMMENDED BY KLA-TENCOR.) This recipe type offers the user the option to customize recipe parameters to meet specific scan requirements. In the Recipe Editor there are seven windows, each with configurable parameters. (See *Figure 12.18*.) For the **Scan Position Offset**

**Calibration**, the only **Recipe Editor** window necessary is the **Scan Parameter Definition** that appears when the editor is first opened (see *Figure 12.21*). When chosen, the **Scan Parameter Definition** button (in the top left corner of the screen, circled in *Figure 12.18*) appears to be indented.

	🐺 Profiler - [Recipe Editor0FF150]		
/	<u>Recipe Options</u> He	lp.	
Scan Parameter			
Definition: displays the 2D		2D Scan	
Scan window shown in the	(Scan Parameter)	X Scan Size (µm): 500.000	
illustration			
	Feature Detection		
	Filters	Scan Speed (µm/s): 10 💌	
	Gutsors		
		Sampling Rate (Hz): 50	
-	Unit Output	Multi-Scan Average : 1 Show Position: - Start: •	
	General	Start:  Center:  C	
Each button in this column	Parameters	Scan Direction:each End: C	
displays a user configurable	Roughness Waviness		
· , ·		Scan Time:	
window in which recipe	Bearing Ratio Cutting Depth	Individual Trace (s): 50.0 Total Data Points: 2501	
parameters can be defined for	High Spot Count	Approx. Total (h::min:s): 0 : 1 : 6.7 Point Interval (μm): 0.200000	
use in various types of scans.	Peak Count	Stylus:	
NOTE: SOME OF THESE	Setup	Applied Force (mg): 1.00 💌 Recommended Maximum (mg): 0.20	
BUTTONS ARE PASSWORD	Analysis Tools	Stylus Radius (μm): 0.04	
PROTECTED WITH		Vertical Ranging:	
		Range/Resolution: 327um/0.1953A 💌	
RESTRICTED ACCESS.		Profile Type : -Ur -	





**CAUTION:** The DuraSharp stylus should only be used with the low force head. If using the DuraSharp stylus, DO NOT set the Scan Speed higher than the default, **10**  $\mu$ **m/second**, and do not set the Applied Force higher than the default, **0.2 mg**. In general, these settings should be established through the Stylus Change procedure only, and not changed manually in their fields.

#### 14. The recipes are set as follows:



**CAUTION:** KLA-Tencor recommends using the Default recipes unless there is a very good reason for creating a custom recipe.

To use the currently selected recipe:	a.	To use the calibration recipe indicated to the right of the <b>Size</b> selection (see <i>Figure 12.19</i> ), click <b>Continue</b> to proceed.
The current recipe type is		Figure 12.19 Scan Position Offset Calibration Options dialog box           Scan Offset Calibration Option         Image: Calibration Option
displayed here.		Size: Recipe: Continue Step 14a. Click I 150 µm Default Cancel 500 µm Default Default Custom
To change the recipe from Custom to Default	b.	To apply the <b>Default</b> recipe when <b>Custom</b> is indicated, click on <b>Default</b> . The message box, " <b>Copy default to custom recipe?</b> " appears. Click <b>Yes</b> in the message box to replace the parameters in the custom recipe with default values. (See <i>Figure 12.20</i> .) <i>Figure 12.20</i> Set Default Dialog Box
<b>Step 14</b> <i>b.</i> To change from Custom to Default, click on <b>Yes</b> to set default values in the custom recipe.	_	Set Default     Image: Copy default to custom recipe?       Image: Yes     Mo       Cancel
To change the recipe from Default to Custom	C.	To apply a <b>Custom</b> recipe when <b>Default</b> is indicated, or to modify the custom recipe that is indicated, click <b>Custom</b> . The <b>Recipe Editor</b> opens, displaying the custom recipe. Change the parameters as required. (See <i>Figure 12.21</i> .)
15.		se the <b>Recipe Editor</b> by clicking on the control button in the upper left corner choosing <b>Close</b> from the drop-down menu. (See <i>Figure 12.21</i> .)
16.	user Cho	the new parameter values were not already saved, a dialog box requires the to choose between the save options before exiting the Recipe Editor. Soose <b>Save Changes</b> to set the changes to the Custom recipe so they are used the scan.

Step 15 Click to display the Control Button menu. Choose Close from the menu. This window (Scan Parameter Definition) is the only one required if there are to be recipe changes related	Yotiker - [Recipe Editor - OFF150]         ipe Dptons Hep         Cast Parameter         Definition         Performer         Scan Parameter         Detection         Feature         Detection         Filters         Cursors         Unit Output         General         Parameters         Roughness         Wavness         Beating Ratio         Lutting Depth         Approx. Total (hr:mn:s):         Difference         Setup         Analysis Tools         Vertical Ranging:         Range/Resolution:         327un/0.1953A         Profile Type :
--	---

Figure 12.21 Scan Parameter Definition - \_OFF150 - Recipe Editor

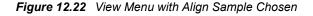
17. (BEFORE CONTINUING see CAUTION below.) Click FOCUS in the tool bar. The Stylus Alignment Tool's surface image comes into focus.

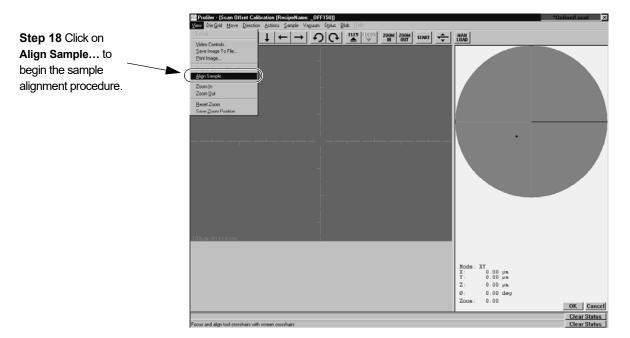


**CAUTION:** As the stylus lowers toward the Stylus Alignment tool, watch carefully to ensure that both the proximity sensor and the stylus come down on the tools measurement surface. With the Proximity Sensor Offset option chosen in the Proximity Sensor Configuration box, the proximity sensor is coming down directly on the position where the stylus makes its measurement. If the stylus and the sensor are not descending directly onto the stylus alignment tool's measurement area, press the ESC key, on the computer keyboard, to stop the stylus descent. Manually relocate the tool under the stylus. Click on **FOCUS** again to resume the procedure.

BEGIN Align Sample Procedure
18. The Stylus Alignment Tool must be aligned with respect to the X-, Y-axis in order for the calibration to be as accurate as possible. Click on View in the menu bar to display its menu. (See *Figure 12.22*.)

This displays the Alignment Angle Dialog Box.





19. In the Alignment Angle dialog box, leave the setting at the default, "0" and click **OK** to accept the alignment angel of  $0^{\circ}$ .

Figure 12.23	Alignment Angle	Dialog Box
--------------	-----------------	------------

Alignment Angle		×
Alignment Angle:		Degrees
ОК	Cancel	Help

The prompt at the bottom of the screen now says,.

#### Click the left mouse button to teach the first point

- 20. Use the arrow buttons to locate the border line between the 300  $\mu$ m triangles and the 1000  $\mu$ m triangle. Still using the arrow buttons, follow the line to the left side of the tool. (See *Figure 12.24*.)
- 21. Move the cursor to the line and click precisely on the line.
  - The prompt at the bottom of the screen now says,

Press OK to accept the first alignment location

- 22. Click **OK** at the bottom right corner of the screen.
  - The prompt at the bottom of the screen now says,

Click the left mouse button to teach the second point

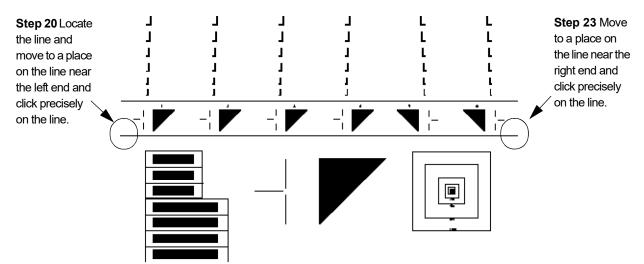


Figure 12.24 KLA-Tencor Stylus Alignment Tool

- **23**. Use the left arrow button follow the dividing line to the right until it reaches the end of the line. (See *Figure 12.24*.)
- 24. Move the cursor directly over the line and click precisely on the line.

The system adjusts the theta alignment so the Stylus alignment tool is lined up with the X- and Y-axis. The prompt at the bottom of the screen now says,

#### Press OK to accept the second alignment location

25. Click **OK** at the bottom right of the screen to accept the stage alignment of the Stylus Alignment Tool.

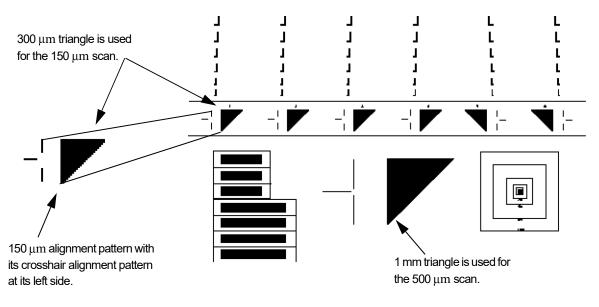
The prompt at the bottom of the screen now says,

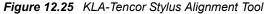
#### Focus and align tool crosshairs with screen crosshairs

There are two different alignment patterns that can be used in the Scan Position Offset Calibration. Each scan is conducted at the midpoint of the triangle where the step distance is one half the length of both right angle triangle sides. The first and primary alignment pattern is the 300  $\mu$ m triangle which is called the 150  $\mu$ m alignment pattern. It has this name because the scan traverses the triangle at it midpoint where the distance is 150  $\mu$ m. The second is the 1000  $\mu$ m (1 mm) triangle which is called the 500  $\mu$ m alignment pattern because its midpoint scan distance is 500  $\mu$ m. It is used when the 150  $\mu$ m scan fails to locate the 300  $\mu$ m triangle.

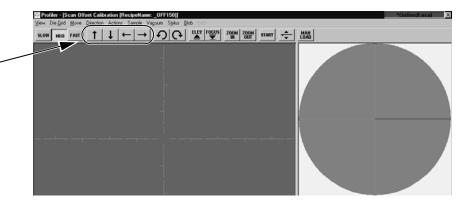
END Align Sample Procedure When making this calibration, first use the 300  $\mu$ m triangle to complete the 150  $\mu$ m scan. If the stylus offset is too great, the scan misses the triangle. If this happens, try the 1000  $\mu$ m (1 mm) triangle to complete the 500  $\mu$ m scan. If that is successful, retry the 300  $\mu$ m triangle.

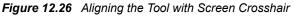
If the 500  $\mu$ m scan missed the 1000  $\mu$ m triangle, the stylus needs to be physically realigned by an authorized KLA-Tencor service representative.





26. Use the linear movement arrow buttons (see *Figure 12.26*.) to locate one of the 150 μm alignment patterns with its crosshair alignment pattern at its left side, or, if they are in view on the video screen, click on one to move it to the screen crosshair. (See *Figure 12.25*.)





27. Click at the center of the Crosshair Pattern to align it with the screen crosshair. (See *Figure 12.27*.) The crosshair pattern should align precisely with the screen crosshair.

**Step 26** Use the arrow buttons to locate one of the 300 μm triangles with its crosshair pattern next to it.

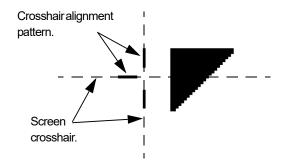
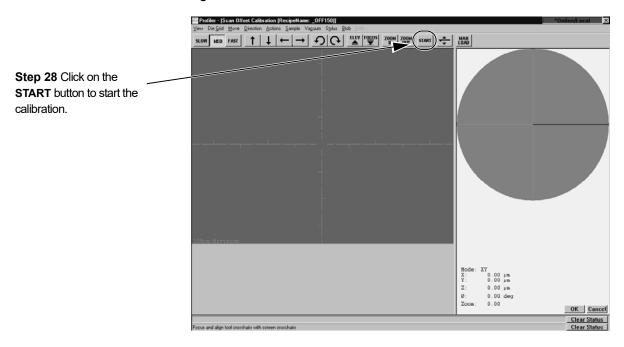


Figure 12.27 Align Screen Crosshair with 150 µm Crosshair Pattern

28. Click the START button located in the screen tool bar. (See Figure 12.28.)

Figure 12.28 Manual Load from the Scan Offset Calibration Window



The video image changes to side view as the stage moves to position the start of the scan on the beginning of the start pattern near the calibration triangle.

When the stylus has reached the beginning of the 150  $\mu$ m scan trace, the screen changes to the **Scan: \_OFF150** window. The scan automatically begins.

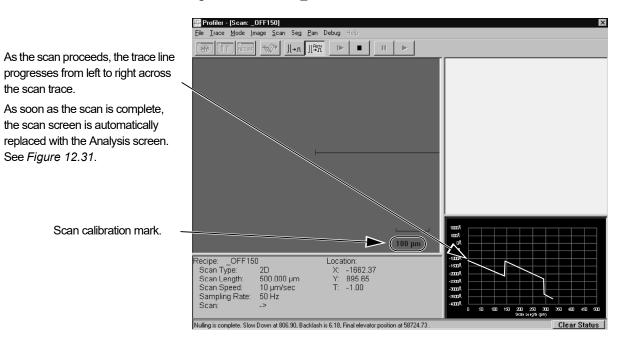
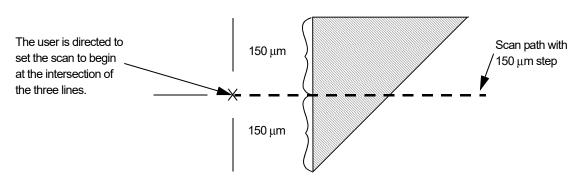


Figure 12.29 Scan: \_OFF150 Window

The scan can be viewed at the bottom right of the **Scan: \_OFF150** screen as it progresses from left to right across the scan trace window, forming a linear image of the scanned surface. The Start pattern next to triangle is set up to direct the scan through the middle of the triangle using the **\_OFF150** recipe. In a perfectly calibrated system, the scan trace goes directly through the center of the 300  $\mu$ m triangle creating a 150  $\mu$ m trace step. However, this is not a common occurrence for a system that has not yet been calibrated after a stylus change.

The system uses the step and the distance across the triangle to determine where the trace was performed and then automatically calculates the offsets.

Figure 12.30 Trace Path Through the Triangle



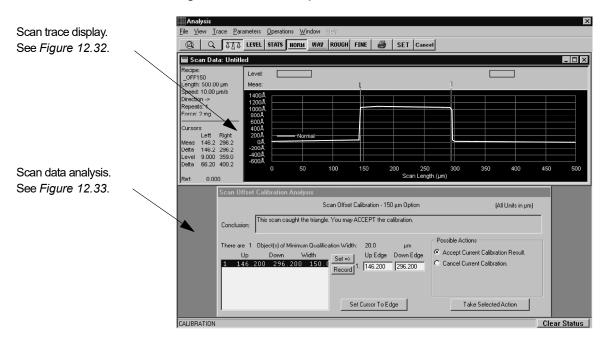


Figure 12.31 Data Analysis Window.

When the scan is complete, the **Data Analysis** window automatically replaces the **Scan: \_OFF150** screen. The window contains a scan data trace as shown in *Figure 12.32*. If the scan was successful, the system detected the triangle and set cursors at the edges of the triangle for visual inspection. It is possible to observe the scan and determine, visually, where the trace is running through the triangle.

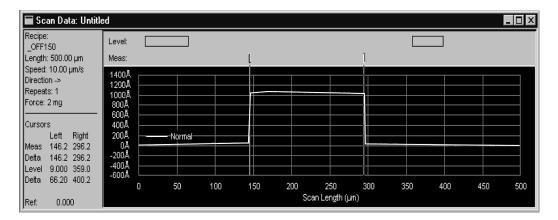


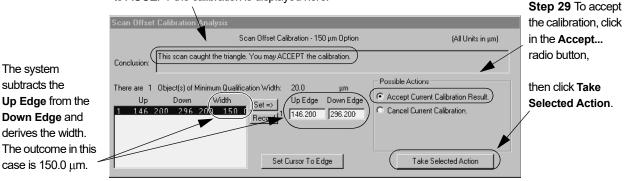
Figure 12.32 Scan Data Portion of the Analysis Window

In the bottom half of the window, the **Scan Offset Calibration Analysis** appears. In *Figure 12.33* the system has subtracted the Up Edge from the Down Edge and calculated the result to be  $150.0 \,\mu\text{m}$ . Using this analysis of the scan, the system makes a recommendation based upon its recognition of the **Stylus Alignment Tool** triangle pattern.

**29**. To accept the recommendation, ensure that **Accept Current Calibration Result** is chosen, then click on **Take Selected Action**. (See *Figure 12.33*.)

*Figure 12.33* 150 µm Scan Data Analysis Window

If the scan was recognized by the system, a recommendation to ACCEPT the calibration is displayed here.



If the trace misses the triangle or is unable to identify it, one of several messages can be displayed. The message could say that scan might have caught the triangle and ask the user to choose either to accept it, change the location, or reject it. The message might read, "Unknown situation..." in which case the user should perform the 500  $\mu$ m scan. If the message is uncertain, perform the entire scan procedure again, this time using the 1000  $\mu$ m (1 mm) triangle and the 500  $\mu$ m scan recipe, \_OFF500.

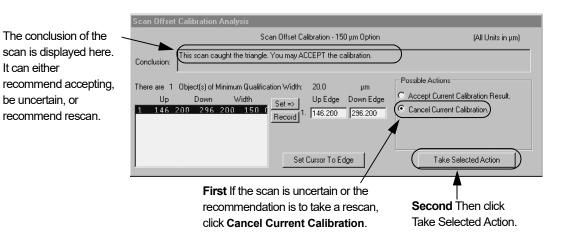


Figure 12.34 "Unknown Situation" Corrective Action

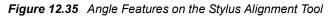
After the scan calibration has been accepted, the **Calibrations** screen returns with the **Scan Offset Calibration Option** dialog box open on top.

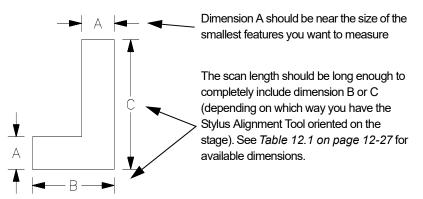
## Scan Position Offset Calibration Validation

#### Introduction

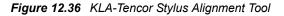
This procedure is used to verity the accuracy of the Y dimension in the offset. If the calibration result was 150  $\mu$ m, the offset error should be **0**. The offset error is determined by subtracting the scan result from the intended width, 150  $\mu$ m.

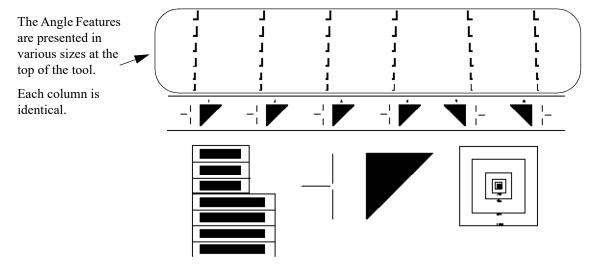
To verify the calibration for a specific sample size the Scan Position Offset Verification procedure is used. The Stylus Alignment Tool provides a set of various sized right angle test features that can be used to ensure that the calibration is effective for the sample size being scanned. Use the right angle test feature that has features closest in size to features that are to be measured.





The right angle features are at the top of the Stylus Alignment Tool (KLA-Tencor Part Number 219517 – see *Figure 12.36*). They are used to validate the effectiveness of the Scan Position Calibration. Each of the six columns contain the same sized angle features, duplicated above each triangle that is available for use in the calibration procedure.





Each angle feature has its own "Dimension A" displayed just above it on the tool. The top angle feature in *Figure 12.37* is 14  $\mu$ m in the "A" direction as demonstrated in *Figure 12.35*. The bottom feature is 10  $\mu$ m. The displayed size is also a key in determining the length of the angle feature arms, features "B" and "C" in *Figure 12.35*. Each size ("A" dimension) is recorded in the first column of *Table 12.1*, Angle Feature Dimensions. Find the size and the corresponding lengths are displayed in that row.

Figure 12.37 Angle Features



-		
Dimension A (µm)	Dimension B (μm)	Dimension C (µm)
4	16	50
6	24	60
8	32	80
10	40	100
14	56	100
18	72	100

Table 12.1Angle Feature Dimensions

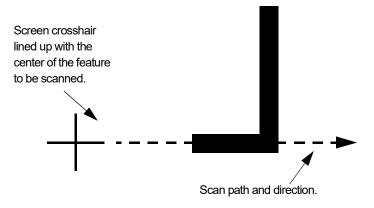
#### **Verification Procedure**

The verification procedure can be performed using the recipe that the scan is being used to verify.

- 1. With the Scan Recipe screen open, select the recipe to be used.
- 2. Click on the **XY** icon to open the XY View screen.
- **3**. Ensure that the zoom setting is exactly the same as was used in the calibration procedure. It is best to perform the calibration zoomed all the way out.
- 4. Click on FOCUS. The system focuses on the Stylus Alignment Tool.
- 5. Find an angle feature that has the dimension size needed to verify that the system can find and scan a feature of that size.

If the need arises to use a feature that is vertically positioned on the screen, use the rotation buttons to reorient the stage so the feature is horizontally positioned. Or, right-click on the navigation window to display the **Move To** dialog box and enter  $90^{\circ}$  in the Theta field.

- 6. Use the arrow buttons to approximately position the feature for the scan.
- 7. Position the cursor crosshair and click such that the screen crosshairs are exactly lined up horizontally with the left side of the feature, far enough from the feature to allow the stylus room to scan the approach to the feature before actually scanning the feature itself.



8. Click **START** to begin the scan. The scan progresses like other scans, with the real-time trace displayed at the bottom right of the screen.

Observe the stylus image on the screen to ensure that it contacts the feature at the intended location.

When the scan is complete, the Analysis screen is displayed. On the left side of the Analysis screen are some of the statistics of the scan itself.

9. In the Analysis screen, set the measurement cursors to the edges of the step.

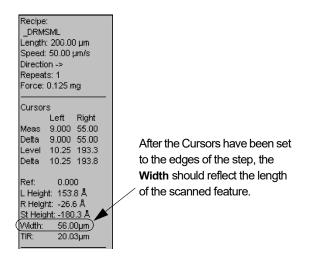


Figure 12.38 Scan Information Display in Analysis Screen

10. In the Analysis screen, look in the Analysis display (see *Figure 12.38*) and locate the Width.

The Width should show that the correct feature was scanned. In *Figure 12.38* the scan Width of 56 µm would show that the "B" dimension of the right angel feature labeled "14" (see *Figure 12.37 on page 12-26* and *Table 12.1 on page 12-27*) was scanned.

If the stylus passed over the intended object and the Width verifies that the object scanned was the correct one, the verification is complete and the system is ready to be used for scans.

If the scan missed its intended object, repeat the Scan Position Offset Calibration. After the calibration is complete, repeat the verification procedure.

# **STEP HEIGHT CALIBRATION**

Check the Calibration Matrix on *page 12-51* for possible interaction with other calibrations. The vertical sensing transducers in the system are not absolute devices and, therefore, require calibration. The calibration factors for the available vertical ranges are set to approximately 1.00 at the factory. (See *Figure 12.39*.)

**CAUTION:** All vertical ranges must be calibrated. Each calibration must be performed independently. Use the 2  $\mu m$  stylus fo this calibration

The best calibration results come from precision techniques carefully repeated. To promote uniformity in results, the procedure for Step Height Calibration is automated for each range. The recipes are written for use with VLSI Standards Inc. step height calibration standards. The *step height calibration should be performed periodically*, depending on the amount of system use, *for each of the three ranges*.



	🜆 Profiler - [Calibrations]		×
	<u>File I</u> asks <u>H</u> elp		
	Applied Force	- General Scan Calibrations -	
	<u>V</u> ideo	Video Calibration Factors:	
	Scan Position Offset	Х (µm/pixel): 1.4706 У (µm/pixel): 1.4706	⊸과
	Step Height		60
	<u>R</u> adius Curvature	Step Height Calibration (Contact Mode): Limits Factor	
	Video Lamp Balance	High: 327um 0.994319	
	Drop Timer	Medium: 65um 0.993563	
	Stage Mapping	Low: 13um 0.996031	
	Level	Radius Of Curvature Factor:	
Step Height Calibration			
Factors are presented in		Scan Position Offset: × (μm):	
the Calibrations screen.		Y (µm): 198.9	
	CALIBRATION		Clear Status
	CADDIATION		

# **Calibration Procedure:**

All three ranges must be calibrated.

- 1. From any top level screen choose the Scan Catalog icon to open the Catalog screen.
- 2. From the Scan Catalog screen, click on the **XY** icon in the tool bar to open the XY View screen.
- 3. Click **MAN LOAD** in the tool bar, to move the sample stage to the door.

Check the Calibration Matrix on page 12-51 for possible interaction with other calibrations. 4. Open the stage door.



**CAUTION:** A system safety shutdown occurs if an attempt is made to activate any stage or elevator motion when the stage door is open (unless the interlock defeat switch has been disabled).

5. Place the **Step Height Standard** so it is centered on the stage, positioned squarely with respect to the X-Y axis.

If the step height standard does not cover the vacuum holes so they can be effective, it might be necessary to rotate the standard  $90^{\circ}$  so it does cover the vacuum holes.

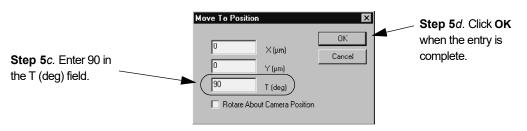
If the standard was rotated  $90^{\circ}$ , it is necessary to rotate the stage  $90^{\circ}$  in the same direction so the step and other scan features are properly oriented for a scan. To accomplish this

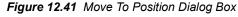
- a. Right-click in the navigation window to display the menu dialog box.
- b. Click on Move To... to open its dialog box. (See Figure 12.40.)

Figure 12.40 Navigation Window Right-Click Menu



c. In the Move To Position dialog box, enter 90 or -90 in the T (deg) field, depending on which way the step standard was rotated on the stage. (See *Figure 12.41.*)





- d. Click **OK** to rotate the stage and close the dialog box. (See *Figure 12.41*.)
- 6. Turn ON the Vacuum using the switch on the upper left inside jam of the door.
- 7. Close the door.
- 8. Click MAN LOAD in the tool bar, to move the sample stage back under the stylus.
- 9. Close the XY View screen. This returns to the Scan Catalog screen.
- 10. Click on the Calibration icon to open the Calibration screen.

From the Calibrations screen, choose Step Height... (See *Figure 12.42*.) The Step Height Calibration Options dialog box appears in the center of the window. (See *Figure 12.43*.)





12. Range: Choose the range to be calibrated. Select the appropriate step height standard for use in calibrating the selected range. (See the circled area in Figure 12.43.) If using the Low range, the step limit should be 3.5 µm or less, if using the Medium range, the step limit should be 13 µm or less, and if using the High range, the step limit should be 65 µm or less.

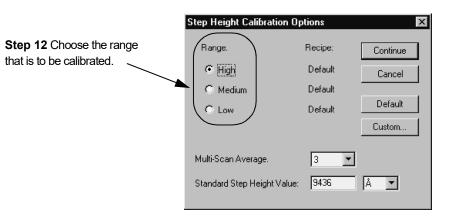
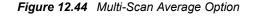


Figure 12.43 Step Height Calibration Options Dialog Box

Step 11 From the Calibration screen, choose Step Height... to open the Step Height calibration screen. 13. Multi-Scan Average: This determines the number of times the profiler scans the same feature during each scan procedure. Data from all scans are automatically averaged and their average is presented as the scan result. Click on the down-arrow next to the Multi-Scan Average value box to display the menu. Select the number of scans per calibration from the drop-down menu. (See *Figure 12.44* below.) The value should be at least 3, with 5 being optimum.



	Step Height Calibr	ation Options	×
	Range.	Recipe:	Continue
	💿 High	Default	Cancel
Step 13 Click on the down	C Medium	Default	
arrow to display the menu. Choose the number of scans per	O Low	Default	Default
calibration.			Custom
	Multi-Scan Average.	3	)
	Standard Step Heigl	ht Value: 9436	🔻

14. *Standard Step Height Value*: Enter the nominal step height value, for the standard being used, into the Standard Step Height Value field. Select the correct units from those available in the drop-down list to the right. See the circled area in *Figure 12.45*.



**NOTE:** Units in Å correspond to recipes for VLSI Thin Film standards; units in  $\mu$ m correspond to the longer scan VLSI Thick Film standards.

Step 14 The step height standard	Step Height Calibrat	ion Options	×	
being used should have an absolute	Bauaa	<b>D</b> anian		Encure that the unite diaple and
height value on it. Double-click on the	Range.	Recipe:	Continue	Ensure that the units displayed are identical to the step height
numerical box next to Standard Step	🖲 High	Default	Cancel	units. To change the units,
Height Value: and type in the height	C Medium	Default		click on the menu-arrow and
displayed on the standard.	O Low	Default	Default	click on the correct units.
	Multi-Scan Average. Standard Step Height	3 🔽 Value: 9436	Custom	

Figure 12.45 Setting Standard Step Height Value

## 15. *Recipe:*



**CAUTION:** KLA-Tencor recommends using the Default recipe for all calibrations. Default recipes should always be used unless there is a very good reason for creating a custom recipe. Creating a custom recipe for a calibration procedure could result in inaccurate calibration results. The system is designed to operate using Default recipes only.

The system provides both default and customizable calibration recipes for each of the three ranges. When a range is chosen, either the Default or a Custom recipe can be used to perform the calibration. The currently applied calibration recipe is displayed to the right of the chosen range. If nothing is changed, the currently displayed recipe is used for the calibration procedure.

Choose **Default** for the calibration unless there is a very good reason to change the recipe.



**CAUTION:** In Low Force Head systems, the Default recipe for the short scan (6.5 µm) should be used for systems operating with the DuraSharp stylus. This stylus requires a slow scan speed to protect its tip. If using a DuraSharp tip, do not modify a custom recipe scan speed to operate at faster than the recommended 10 µm/second (5 µm/sec is best), to protect this delicate stylus.

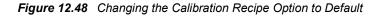
16. To proceed with the calibration using the recipe indicated to the right of the range (Default or Custom), click **Continue**. (See *Figure 12.46*.)

	Figure 12.46	Confirming the Displayed Calib	ration Recipe
--	--------------	--------------------------------	---------------

	Step Height Calibration Op	otions 🛛 🗙
Step 16 Click on Continue to apply the	Range.	Recipe:
Recipe type indicated next	• High	Default Cancel
to the <b>Range</b> choice.	C Medium	Default
	C Low	Default
		Custom
	Multi-Scan Average. Standard Step Height Value:	3 <b>•</b> 9436 A •

**Default Recipe Option** 17. To apply the Default recipe when "Custom" is indicated, click on Default. (See the circled areas in Figure 12.48.) The message, "Copy Default to Custom recipe?" appears. (See Figure 12.47.) Clicking on Yes replaces the parameters in the Custom recipe with Default values. Clicking No retains the current Custom value. Figure 12.47 "Copy default to custom recipe?" Message Set Default х Step 17 Click NO to retain Step 17 Click Yes to Copy default to custom recipe? the custom recipe values. replace custom recipe Yes <u>N</u>o TCancel values with default values. 18. To apply a Custom recipe when "Default" is indicated or to modify the Custom **Custom Recipe Option** recipe that is indicated, click on Custom... (See the circled areas in Figure 12.49.) The **Recipe Editor** opens, displaying the parameters for the custom recipe. A custom recipe for each Range is already in the Scan Recipe Catalog File with a name representing the recipe; STEPHTL for Low step; \_STEPHTM for Medium step; and \_STEPHTH for High step. (The procedure continues

on page 12-36.)



	Step Height Calibration O	ptions	×	
The type of recipe being used in a given range is listed next to it in the Recipe column. In this case, a Custom recipe is being applied to the Low Range scan.	Range: O High O Medium O Low	Recipe: Contin Default Cance Default Defau Custom Custom		Step 17 To change from Custom to Default recipe, click on <b>Default</b> .
	Multi-Scan Average: Standard Step Height Value:	3 V 9461 Å V	I	

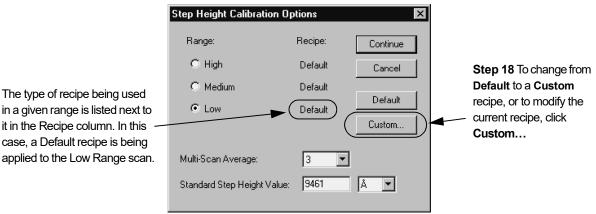


Figure 12.49 Changing the Calibration Recipe Option to Custom

it in the Recipe column. In this case, a Default recipe is being applied to the Low Range scan.

> 19. The parameters that can be modified are included in the Recipe Editor screen. (See Figure 12.50.) Each recipe, including the Default, has a specific name that is included in the Scan Recipes screen under the 2D recipe catalog. Custom recipes can be modified to meet special scan requirements including custom calibration scans. If the Default recipe is not going to be used, great care should be taken to modify only those parameters absolutely necessary to provide the best step height calibration



CAUTION: Step Height Calibration is a critical procedure, vital to future process scan integrity. Do not modify the calibration recipe parameters without understanding the consequences of such modification. Only parameters included in the Step Height Calibration Options dialog box are used for the calibration.

	Profiler - [Recipe EditorSTEPHTH] Recipe Options Sample Vacuum Help	
Step 20 From the Recipe drop-down menu, click on Save.	New         Chi+N         22         122         Start         100<	*
Step 21 Choose Save.	X_View Iheta View Qenter Übject Treach Die Grid Start Scan Analysis ampling Rate (Hz): 50 ▼	
	Diagnostic     Info     UtiliScan Average : 3 •       Info     Ctrl+I       Erint     Ctrl+P       Egit Recipe Editor     Image: State S	Show Position: Start: © Center: © End: ©
	Cutting Depth High Spot Count Peak Count Stylus:	ata Points: 501 kerval (µm): 1.000000 ended Maximum (mg): 0.20
	Vertical Ranging. Range/Resolution: 327um/0.1953A	

*Figure 12.50 Recipe Editor for*\_STEPHTL

The parameters that can be modified for the scan calibration are: Scan Length; Scan Speed; Sampling Rate; Multi-Scan Average; Stylus Force; Contact Speed; Range/Resolution; and Profile Type.

- **Range/Resolution** and **Multi-Scan Averaging** should have already been set in the **Step Height Calibration Options**. There should be no need to change these in this screen. Range/Resolution is not available for change at this point in the procedure.
- Profile Type only contains options for the High (131 μm/0.357Å) Range. Both of the other ranges have only one profile type available.
- Scan Speed can be changed. If the speed is increased, the accuracy could suffer. The Step Height Calibration is critical to scan data accuracy. If the speed is set at a higher rate than the Default value, the number in the **Multi-Scan Average** should also be set to at least 5.
- When using the DuraSharp tip (not recommended for P-15), the Scan Speed defaults to 5 μm/s and the associated drop-down menu contains only 2, 5, and 10 μm/s options.
- Scan Length should reflect about 200 µm on each side of the step.
- **Stylus Force** should never be set higher than the recommended value (indicated next to the box containing the current value.) If it is set too high, a message box might appear that prompts the user to consider changing back to within the safe force limits. (See *Figure 12.51*.)

This should not be a problem if the recommended 2 µm stylus is used.

Figure 12.51 Stylus Force Change Message

Warning	: RE505
$\underline{\mathbb{A}}$	Stylus force exceeds the recommended safe limit. Would you like to change the stylus force?

- 20. When the required modifications to the recipe have been completed, click **Recipe** in the menu bar to display the menu.
- 21. Choose Save from the drop-down menu. (See Figure 12.50.)
- 22. To close the Recipe Editor, first click on the control button at the top left corner of the screen to display its menu.
- 23. If the recipe was not saved, and **Exit** is chosen from the control button drop-down menu, a dialog box opens requesting a decision on the changes made to the recipe. Choose **Save Changes** to save the changes so they can be used in the Step Height Calibration. (See *Figure 12.52*.)

#### Figure 12.52 Recipe Editor - Saving Recipe Changes

	RecipeEditor X
<b>Step 23</b> Click on the radio button next to <b>Save Changes</b>	Recipe _STEPHTL has been modified. Before continuing, do you want to:
then on <b>OK</b> so the new parameters are in effect for the Step Height Calibration.	<ul> <li>Save Changes</li> <li>Save Changes as a New Recipe</li> <li>Discard Changes</li> </ul>
	OK Cancel Help

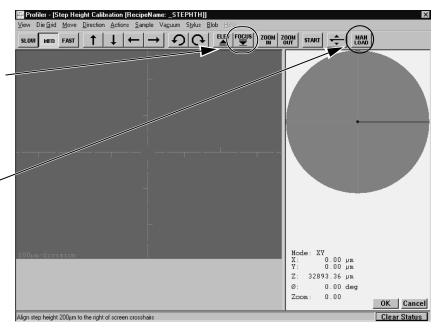
24. After the modifications to the recipe are saved, the **Step Height Calibration Options** dialog box appears again. Click on **Continue**. (See *Figure 12.53*.) This displays the **Step Height Calibration** screen.

Figure 12.53 Completing the Options Selection

Step Height Calibration O	ptions	×	
Range.	Recipe:	Continue	
<ul> <li>High</li> </ul>	Default	Cancel	
O Medium	Default		$\backslash$
C Low	Default	Default	Step 24 After all modifications
		Custom	have been saved, click Continue to proceed to the
Multi-Scan Average.	3	2	Calibration screen for the Step Height Calibration scan.
Standard Step Height Value:	9436	À 🔻	

25. Click on **FOCUS** to null the stylus near the VLSI Step Height Standard surface and bring the standard into focus. (See *Figure 12.54*.)





**Step 25** After the Step Height Calibration Standard has been placed on the stage and the stage centered under the stylus, Click **FOCUS** to null the stylus.

**Step 3** Click on **MAN LOAD** to move the stage to the open door.

Step 8 After the Step Height Calibration Standard is centered on the stage, click MAN LOAD to send the stage back under the stylus. 26. Use the arrow buttons to locate the calibration step on the standard.

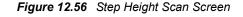
If the Video Calibration has been performed in the current zoom position, the hash marks on the crosshair are 100 µm apart. (See Figure 12.55.)

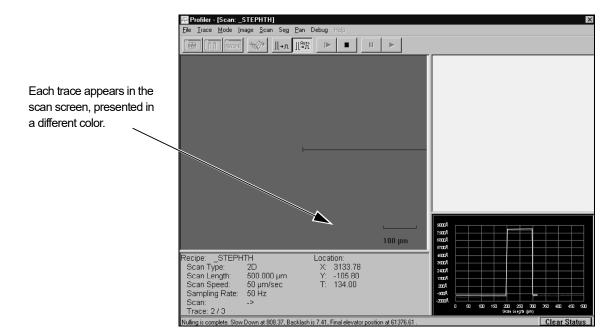
Figure 12.55 Step Height Calibration Window

	🖙 Profiler - [Step Height Calibration [RecipeName: _STEPHTH]]		×
	View Die Grid Move Direction Actions Sample Vacuum Stylus Blob Help		
		DOM START - MAN LOAD	
Step 26 Use the arrow			
buttons to locate the			
	-		
calibration step on the Step			
Height Standard.			
0	_		
		•	
	'		
If Video is calibrated for the	n n		
current zoom, the distance			
between the hash marks on			
the centerline is displayed in	$\checkmark$		
this screen position.			
	100µm/division	Mode: XY X: 0.00 µm	
		Υ: 0.00 μm	
		Z: 32893.36 μm	
		Ø: 0.00 deg	
		Zoom: 0.00	OK Cancel
	Alian step height 200µm to the right of screen crosshairs		Clear Status

- 27. Position the crosshair about 200 µm from the left side of the step and click OK (at the bottom right of the screen), or click Start in the tool bar. The instrument performs the same scan through the exact same location as many times as prescribed in the recipe (the Multi-Scan Average on page 12-32, set in the Step Height Calibration Options dialog box, *Figure 12.44*).
- 28. During the Step Height Calibration Scan procedure, the progression of each scan can be observed in the lower right corner of the screen, on the scan graph. Each scan is displayed in a different color. (See Figure 12.56.)

between the the centerline this screen p 29. The individual scans (Multi-Scan Average) are averaged to arrive at a single step height. The system then compares the average of the scans with the known VLSI standard step height that was entered into the Step Height Calibration Option dialog box. (See Step 14 on page -32.)





When complete, the calibration factor is automatically calculated and displayed at the end of the information area of the Analysis window. (See the circled area at the bottom left in *Figure 12.57*.)

The calibration factor is displayed with the last calibration factor. Both should be close. See the circled area at the bottom left of *Figure 12.57*.

To compare the step height standard value with the averaged measured height, click on STATS in the tool bar to open the Surface Parameter Summary statistics window. The step height result is displayed in the Statistics window. See the white area just above the Analysis trace window in *Figure 12.57*.

30. Click on the **SET** button in the tool bar to save the calibration factor, or the **Cancel** button to keep the original value and return to the Calibrations screen. (See the circled area at the top right in *Figure 12.57*.)

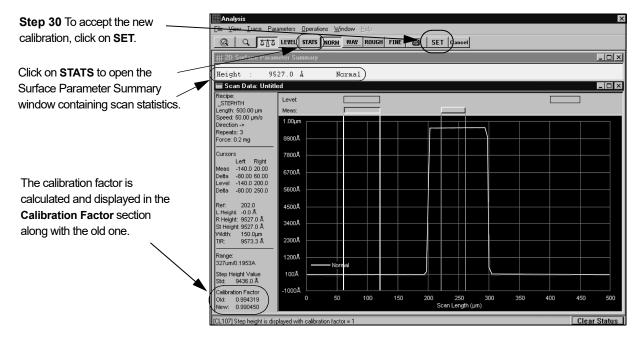


Figure 12.57 Saving the New Calibration

**31.** Use the above procedure to repeat the step height calibration for the remaining ranges. Each range is significant and important for the integrity of future scans.

# LEVEL CALIBRATION

Check the Calibration Matrix on page 12-51 for possible interaction with other calibrations. Accurate scans depend on the X- and Y-axis planes of the Sample Stage being parallel to the stage motion in the respective planes. Two independent calibrations, Tilt and Level, are required to ensure that these planes are parallel to the stage motion in their respective directions.

The Tilt Calibration (adjustment) sets the Y-axis plane of the Sample Stage surface parallel to the stage motion, which is defined by the surface of the reference flat. The Tilt calibration requires the manual adjustment of a screw that is difficult to locate. This calibration should be performed by a KLA-Tencor trained technician. The Tilt calibration is described in the Service Manual.

The Level Calibration sets the X-axis plane of the Sample Stage surface parallel to the stage motion, which is defined by the surface of the reference flat. The Level calibration is totally automated for the P-15.

**Check the Calibration** Matrix on page 12-51 for possible interaction with

other calibrations.

The Level calibration should be performed whenever one of the listed conditions arise:

- Removing and replacing the carriage
- Changing the reference flat
- Replace motorized stage
- Replacing the leveling motor
- System does not complete the initialization procedure.

When performing this calibration, use a Contact Mode stylus, preferably a 2 µm tip, that has been properly installed using the Stylus Replacement procedure. For information on changing the stylus, see Chapter 4 Stylus Change Procedure on page 4-1.



CAUTION: Be sure that the system is using a sturdy stylus.

# Level Calibration Procedure

1. From from any top level screen, click on the **Calibrations** icon



2. Click Level... to open the Level Calibration screen.

#### Figure 12.58 Calibration Screen

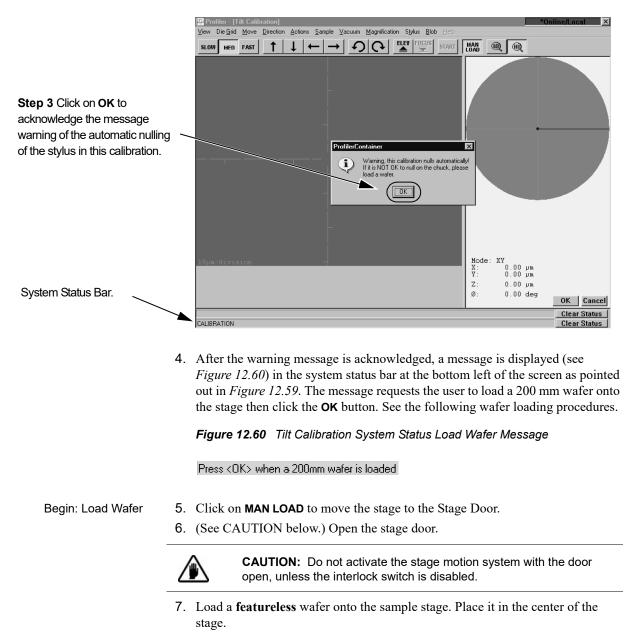
	🔤 Profiler - [Calibrations]		×
	<u>File I</u> asks <u>H</u> elp		
	Applied Force	- General Scan Calibrations -	P
		Video Calibration Factors:	
	Scan Position Offset	× (µm/pixel): 1.4706 Y (µm/pixel): 1.4706	
	Linearity Step Height		
	Step Height		00
	<u>R</u> adius Curvature	Step Height Calibration (Contact Mode): Limits Factor	6
	Video Lamp Balance	High: 327um 0.994319	
	Drop Timer	Medium: 65um 0.993563	
Step 2 Click Level to		Low: 13um 0.996031	
-	Stage <u>M</u> apping		
open the calibration screen.	Level	Radius Of Curvature Factor:	
		Scan Position Offset	
		Х (µm):	
		Υ (μm): 198.9	

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**3**. A warning appears in the **Profiler Container** message box. It states that the system automatically nulls in this calibration and advises that a sample be placed on the stage to prevent stylus damage. (See *Figure 12.59*.)

Read the message and click **OK** to close the message box. (See *Figure 12.59*.)

Figure 12.59 Level Calibration Warning

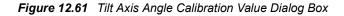


- 8. Turn the vacuum ON using the switch on the upper left door jam.
- 9. Close the stage door.
- End: Load Wafer Manually 10. Click MAN LOAD to move the stage back under the optics.

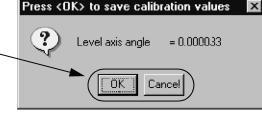
11. Click **OK** to begin the calibration.

The stylus nulls twice, once each near the left and right extremes of the wafer. With each nulling, the Z value is registered. The system then calculates and corrects the stage level status such that, when the calibration is performed again, the entire surface of the stage has nearly the same Z value (assuming the wafer has a minimal bow and that the Tilt calibration is correct).

12. When the Level calibration is complete, the system presents a dialog box with the results and an option to accept or reject the calculation. Click **OK** to accept the calculated value or **Cancel** to reject it. (See *Figure 12.61*.)



**Step 12** Click **OK** to accept the Level calibration value, or **Cancel** to reject it.

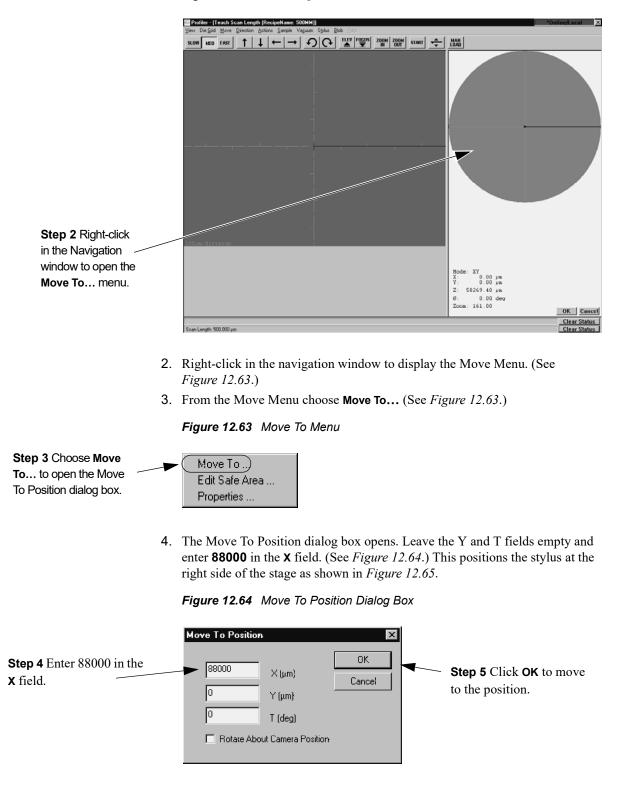


# Level Calibration Confirmation

After the Level calibration is complete, a confirmation test must be made of the calibration results. The test consists of nulling near the left edge of the wafer and recording its Z height at null, and then nulling near the right edge of the wafer and recording its Z height at null. This can be done using the Lowest Elevator Position procedure accessed through the Configuration screen. The difference between the left and right Z value should be 20  $\mu$ m or less for the calibration to be acceptable. If the Z value is greater than 20  $\mu$ m, perform the Level calibration again.

1. Open the XY View screen. (See Figure 12.62.)

Figure 12.62 Activating Focus in the XY VIEW Screen



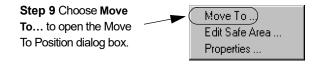
5. After the entry is complete, click **OK** to close the dialog box and position the stylus at the new coordinates. (See *Figure 12.64*.)

E Profiler - [Teach Lowest Elevator Position] *Online/Local ×	Step 6 After the stylus is in
View Die Grid Move Direction Actions Sample Vacuum Stylus Blob Help	position, click FOCUS to null the
	stylus on the sample surface.
	After the OK button is clicked the stylus is positioned near the right or left of the wafer as shown by the blue tracking dot.
	The navigation window is used to position the scan and view the null position.
	Notice that <b>X</b> coordinate is the 88000 that was set before the move.
10 μ×Givision         Hode: XV           Y:         0.00 μm           Y:         0.00 μm           Y:         0.00 deg           Ø:         0.00 deg           Clear Status           Clear Status	<b>Step 7</b> The <b>Z</b> value is the relative height of the stylus. Record this number after the null is complete.

## Figure 12.65 Teach Lowest Elevator Position Screen

- 6. After the stylus is in position, click on **FOCUS** to null the stylus near the back of wafer. (See *Figure 12.65*.)
- 7. When the focus procedure is complete, record the **Z** value as indicated in the lower right corner of the screen. (See *Figure 12.65*.)
- 8. Right-click in the navigation window to display the Move Menu.
- 9. From the Move Menu choose **Move To...** (See *Figure 12.66*.)

#### Figure 12.66 Move To Menu



12-46

10. The Move To Position dialog box opens. Leave the Y and T fields empty and enter **-88000** in the **X** field. (See *Figure 12.67.*)

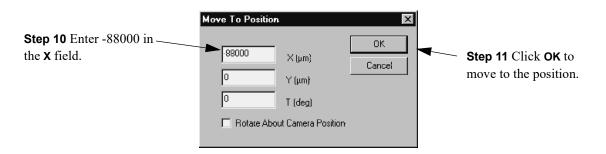


Figure 12.67 Move To Position Dialog Box

- 11. After the entry is complete, click **OK** to close the dialog box and position the stylus at the new coordinates. (See *Figure 12.67*.) The blue tracking dot appears at the left edge of the wafer.
- 12. After the stylus is in position, click on **FOCUS** to null the stylus near the front of wafer.
- 13. When the focus procedure is complete, record the **Z** value as indicated in the lower right corner of the screen. (See *Figure 12.65*.)
- 14. The numerical difference between the Z value near the right edge of the wafer and the Z value near the left edge of the wafer represents the level calibration results. If this number is less than 20  $\mu$ m, the calibration is within specifications. If it is not within the specifications, perform the Level calibration again and check the results.

# WAFER CENTER CALIBRATION

The sequence transportability depends on the system using the center of the wafer as a reference point instead of the center of the stage, as has been done in the past. This requires that the **Calibrate Wafer Center** calibration be run. The **Calibrate Wafer Center** calibrates the center of the wafer as the (0,0) reference point. After this calibration has been run, all sequence recipes and the system **Safe Area** settings use the wafer coordinates. (See "Calibrate Wafer Center" Calibration.)

The P-15 does not use a handler, so this is only effective if the system has a precision locator for wafer alignment.

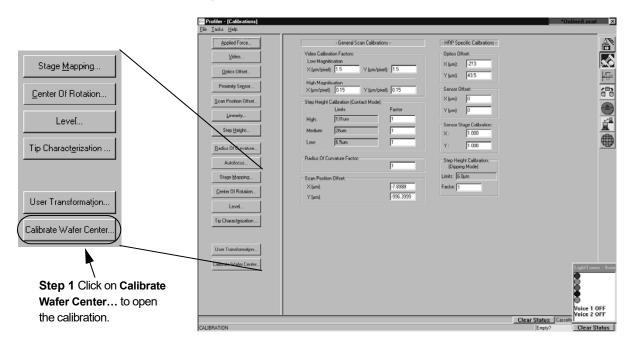
# **Calibration Procedure**

Before performing the Calibrate Wafer Center calibration, all system calibrations must be current, including the Center of Rotation and Stage Mapping calibrations. If not, perform these calibrations first along with any prerequisites. After these are acceptably completed, proceed with the following calibration. 1. From the Calibration screen, click on Calibrate Wafer Center button.

×

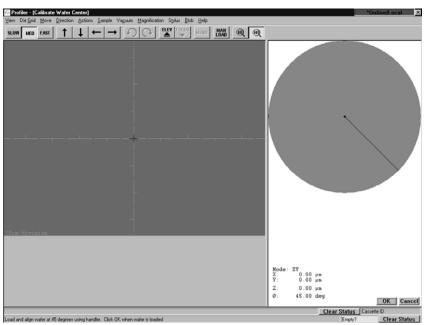
**NOTE:** The user must be logged in under the proper security level to access the **Calibrate Wafer Center** calibration. Without the correct level, the calibration might be missing from the menu or grayed out.





The user is prompted to load a wafer. The user selects the cassette and slot that the wafer is to be taken from as well as setting the load angle to  $45^{\circ}$ .

Figure 12.69 Wafer Center Calibration Screen



- 2. Load a wafer on the precision locator.
- 3. Click **OK** after the wafer is loaded.

The system moves the wafer to until its edge is under the optics. When the stage stops, the system focuses on a point near the wafer edge.

- 4. Align the wafer edge with the screen crosshair as prompted by the system. If the edge is not in sight, move the stage to the right using the right arrow button in the toolbar. Align the left wafer edge with the screen crosshairs.
- 5. Click **OK**.
- 6. The stage moves to a point near the right wafer edge and the system focuses on the wafer surface. The user is prompted to align the wafer edge with the screen crosshairs.
- 7. Align the right wafer edge with the screen crosshairs. Use the left-arrow button in the tool bar to move the wafer edge into alignment with the screen crosshairs. (In necessary, use the Slow speed for the arrow button movement to accurately position the edge of the wafer at the screen crosshairs.)
- 8. Click **OK** to accept the position.
- 9. Click **OK**.

The system positions the top of wafer under the optics and focuses. The user is prompted to position the top edge of the wafer at the screen crosshairs.

- 10. For all tools: Align the top wafer edge with the screen crosshairs. Use the down-arrow button in the tool bar to move the wafer's top edge into alignment with the screen crosshairs. (In necessary, use the Slow speed for the arrow button movement to accurately position the top edge of the wafer at the screen crosshairs.)
- 11. Click OK.

The system positions the bottom of wafer under the optics and focuses. The user is prompted to position the bottom edge of the wafer at the screen crosshairs.

12. Align the bottom wafer edge with the screen crosshairs. Use the up-arrow button in the tool bar to move the wafer's bottom edge into alignment with the screen crosshairs. (In necessary, use the Slow speed for the arrow button movement to accurately position the bottom edge of the wafer at the screen crosshairs.)

# Stage to Wafer Conversion

As a result of the system converting to using the wafer center instead of the stage center as a reference point, all sequence recipes created before the conversion (i.e., before the "Calibrate Wafer Center" calibration) become inaccurate. They must be converted to the wafer center system in order to perform correctly. The Calibrate Wafer Center Calibration adds an offset from the stage coordinate to the wafer coordinates.

The Stage to Wafer calibration should only be performed after the Center of Wafer calibration is performed and prior to any new recipes being created. If only new recipes (recipes created after the Calibrate Wafer Center calibration) are to be used, the conversion is optional.



NOTE: This procedure can only be performed once.

## **Calibration Procedure**

- From Windows Explorer, run
- User is warned to back up recipes before proceeding. Backup is advised. Use the Pbackup procedure.
- 3. Click Proceed. All sequence recipes are automatically converted.

# STANDARD CALIBRATION MATRIX

The system is facilitated by a series of interconnected calibrations. The interdependency of the calibrations makes it important that those who calibrate the systems understand the which calibrations affect other calibrations. When performing any of the calibrations for the system, ensure that all prerequisite calibrations are performed prior to performing the target calibration. When the target calibration is completed, ensure that any necessary subsequent calibrations are performed or the possibility exists for inaccurate scans.

Calibration to be Performed	Calibration Prerequisites	Post Calibration Requirements	System Performance Results
Applied Force	none	none	Protects stylus and sample during nulling procedure.
Video Calibration	Applied Force	none	Objects chosen (clicked on) in the screen are accurately positioned in the center of the screen. Improves accuracy of pattern recognition deskew and site-by-site pattern recognition.
Scan Position Offset Calibration	Applied Force, Video	Fine Scan Position Offset Calibration	When performing a scan with the sample stage, the general location taught for the scan is accurate. The scan occurs very near the taught position.
Linearity	Applied Force	Step Height	Linearity ensures that a sensor that has been calibrated using only one step height standard can accurately measure other values. For example, a sensor calibrated with a 24 $\mu$ m standard should accurately measure a 100 $\mu$ m step.
Step Height	Applied Force, Linearity, Scan Position Offset	none	Feature steps on the sample surface are more accurately measured.
Radius of Curvature	Applied Force, Step Height	none	Radii of curved surfaces are more accurately measured.
Pulse Ratio	Applied Force, Video, Center of	none	Calibrates the stage movement distance to match the move distance requested by the user.
	Rotation		All previously taught sites in a sequences become invalidated (are slightly off from their original position.)
Stage Mapping	Applied Force, Video, Center of	none	Enhances accuracy of movement between identical positions in a die grid.
	Rotation, Pulse ratio		All previously taught sites in a sequences become invalidated (are slightly off from their original position.)
Level	Applied Force	none	Scans in excess of 1000 $\mu$ m are more level. Ensures that the stylus does not exceed its vertical range due to the excessive tilt or level orientation of the stage.
Lamp Balance	Applied Force, Drop Timer	none	
Drop Timer	Applied force	none	

 Table 12.2
 Standard Calibration Matrix

# **GEM/SECS OPTION**

# INTRODUCTION

The GEM/SECS option is designed for environments in which the system is controlled by, or requires communication with a remote Host computer. GEM/SECS also provides a communication link with the Host for receiving and sending process programs (recipes).

This chapter includes:

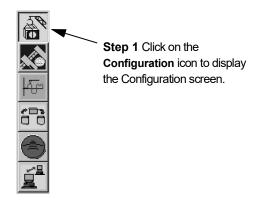
- Establishing GEM/SECS Communication
- Using the GEM/SECS Application
- GEM/SECS Configuration Options
- GEM Status Window

# **ESTABLISHING GEM/SECS COMMUNICATION**

Communication between the system and the Host computer is established through the GEM/SECS program. Use the following procedure to open the GEM/SECS link between the system and the Host:

1. From any top level screen, click the **Configuration** icon. (See *Figure 13.1*.)

Figure 13.1 Database File Manager Icon Choice



2. This brings up the **Configuration** window. To display the **Machine Configuration** dialog box:, click **System...** (circled in *Figure 13.2*).

Figure 13.2 Configuration Screen

	Profiler - [Configuration]			*Online/Local ×
Step 2 Click on the System	Ele Iaska Help			
button to select System	System	System Geometry -	- Stylus Details-	20
-	Sample.	Handler Load Position Manual Load Position	Current Stylus Details	
Configuration.		×(µm); 0 ×(µm); 0	Name Durasharp A	<u></u>
e en ingen etterni	Machine History Recorder	Y (µm): 0 Y (µm): 0	Tip Redius 0.040 µm	
	New Options	Theta (deg): 0 Theta (deg): 0	Incl Angle 35.00 deg. Color Band Double Black	Por
		Elevator (µm): 0 Elevator (µm): -3740.9	Scan Type Contact	<u>북</u> 83
	Egport Path Defaults	Stage Configuration		00
	Pattern Recognition Options	Theta Soft Home Position (deg): 0		
	Seguence Execution Options	Leveling Offset (deg): 0.000146	Current ID: 1234 Durasherp A	
	Iheta Soft Home Position			
	Lowest Elevator Position	Lowest Elevator Position (µm): 29.96	Replace Stylus	
	Lowest Elevator Posison	Elevator Focus Speed (µm/s): 1000		
	Manual Load Position	Elevator Slow Focus Speed (µm/s): 50	Lip History	
	Progimity Sensor	Move Elevator to Sale Position Before Moving Stage:		
		Elevator Safe Position (µm): 10		
		Safety Interlock On:		
		Save Stage Configuration Changes		

**3**. This brings up the **System Configuration** dialog box. (See *Figure 13.3*.) From the **System Configuration** dialog box, choose **Instrument...** (circled in *Figure 13.3*). This brings up the **Instrument Setup** dialog box. (See *Figure 13.3*.)

Figure 13.3 Machine Configuration Dialog box

System Configura	tion		
Serial Number:	1111		<u>0</u> K
Customer:	1111		<u>C</u> ancel
Model:	P-15		Configuration
Machine Type:	Instrument		Instrument
Handler Type:	None		<u>H</u> andler
E 11 1 1 4 5		/	
	Presence Check	Step 3 Click on Instrume	
Enable Stage N	lapping	display the Instrument Se dialog box.	tup
FFU Alarm M	onitoring		
© <u>D</u> isable	d		<u>H</u> elp
C Notify			
C Notify a	nd <u>A</u> bort		
Registry <u>M</u> ai	ntenance		

4. To activate automatic GEM/SECS connection when the system is booted up: from the **Instrument Setup** dialog box, double-click on the check box next to GEM/SECS (circled in *Figure 13.4*). The Instrument Setup dialog box contains a list of all purchased system options. An X next to the option name indicates that it has been chosen to be active. Click in the empty column next to GEM/SECS to put an X next to it. The system is now set up to initiate the GEM/SECS connection every time the system is booted up. (See *Figure 13.4*.)

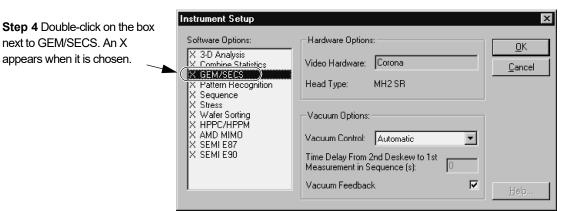
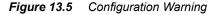


Figure 13.4 Instrument Setup Dialog Box

- 5. Click on **OK** to set the change and close the dialog box.
- 6. A message box appears instructing the user to restart the system. GEM/SECS is not activated unless the system is restarted. (See *Figure 13.5.*)







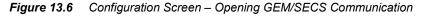
**NOTE:** A Message Box appears instructing the user to reboot the system. This must be done to ensure proper GEM/SECS connection.

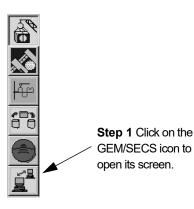
7. Use the same procedure described above (except that the check box should be **empty**), to **deactivate** the automatic connection of GEM/SECS each time the system is booted up.

# Enabling GEM/SECS from the GEM User Interface Screen

1. If the GEM+SECS option in the **Instrument Setup** dialog box is enabled, then it is possible to activate GEM/SECS using the **GEM User Interface** screen.

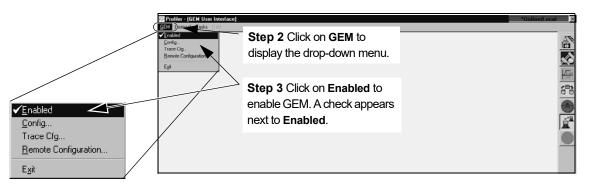
From any top level screen, click on the GEM+SECS icon. (See Figure 13.6.)





- 2. Open the **GEM User Interface** screen. From the **GEM User Interface** dialog box, click on **GEM**, located at the top left of the screen (indicated in *Figure 13.7*).
- **3**. In the drop-down menu, click on **Enabled** to enable GEM/SECS. A check appears next to **Enabled** when GEM is running (illustrated in *Figure 13.7*).



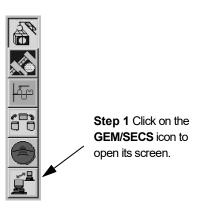


4. **Disabling** GEM/SECS is accomplished by clicking on **Enabled** when the check mark appears next to it. The check mark is absent when GEM/SECS is disabled.

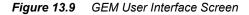
# USING THE GEM/SECS APPLICATION

The GEM/SECS application has functions that are accessed in different ways. Establishing the GEM/SECS communication link can be set up through both the **GEM User Interface** and **Configuration** screens. GEM/SECS configuration is accessed through the **GEM** drop-down menu in the **GEM User Interface** screen. Message TTY communication with the Host, using GEM/SECS, is accomplished through the **GEM Status** window. 1. To access the **GEM User Interface** screen from any top level screen, click on the **GEM+SECS** icon. (See *Figure 13.6.*)

Figure 13.8 Configuration Screen – Opening GEM/SECS Communication



2. From the GEM User Interface screen, click on GEM at the top left of the screen, to access the drop-down menu (indicated in *Figure 13.9*).



	Field Profiler - [GEM User Interface]	*Online/Local ×
	GEM Protocol Istka Help	
Step 2 Click on GEM	✓ Embled [Conto Tione Clg	8
to display the	Benote Configuration	*
drop-down menu.	Ept	ন্দ্র্
•		678
Step 3 Drop-down		
menu containing GEM		1 State
related dialogue boxes.		
Choose the required		
option.		

3. Choose the required option.

Four options are available in the drop-down menu. The first is the Enable/Disable option, and has already been discussed in *Enabling GEM/SECS* from the GEM User Interface Screen on page 13-4. The other three are discussed in the following sections.

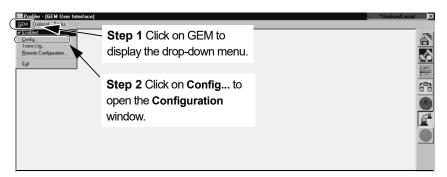
# **GEM/SECS** CONFIGURATION OPTIONS

These options should only be exercised by those totally familiar with the GEM+SECS operation. The function definition for each of the configurable states is set by **Semi Standard E30**. Refer to that document for any questions regarding GEM+SECS communication. Use the following procedure to configure the GEM/SECS options:

1. From the **GEM User Interface** screen, click on **GEM** to display its menu.

2. From the GEM menu click on Config... to display the Configuration window.

Figure 13.10 GEM User Interface Screen



The Configuration screen is displayed as shown in Figure 13.11.

Figure 13.11 Configuration Screen

GEM Configuration	×
Communication       Init. Comm. State:       Poll Delay       20       Estab. Comm. Delay:	Control States Init. Control State: Online Online Failed State: Equipment Offline
Spooling Spooling Enabled Overwrite Spool Max. Spool Transmit: Max Spool File Size.	Event Reports Annotated Reports (S6F13) W-Bit for S6 Alarms W-Bit for S5
Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE	Terminal ✓ W-Bit for S10 □ Buffer TTY Msgs Summary Format □ Send Blanks
OK	Cancel Help

The GEM Configuration window has seven category boxes containing GEM related options and control information. This section provides user interface information on four of the categories:

- Communication
- Spooling
- Control States
- Equipment Identification.

# **Communication Configuration Options**

The Communication box deals with establishing and continuing the communication link between the system and the Host computer. The communication link establishes the ability of the system and Host to send and receive messages.

## **Initial Communication State**

In the **Communication** box, **Init. Comm. State:**, determines the initial communication link status between the system and the Host when the system is booted up. (See *Figure 13.12.*)

Figure 13.12 Communication Option - Initial Communication States

Communication Box	GEM Configuration	X
Initial Communication State: Choose Enabled or Disabled.	Communication Init. Comm. State: Poll Delay Estab. Comm. Delay: Spooling Spooling Enabled	Control States Init. Control State: Online  Control State: Equipment Offline Control State: Equipment Offline Control State: Event Reports Control States Annotated Reports (S6F13)
	Max Spool Transmit: 0 Max Spool Transmit: 0 Max Spool File Size: 10000	W-Bit for S6
	Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE	Terminal ✓ W-Bit for S10 Buffer TTY Msgs Summary Format ✓ Send Blanks
	ОК	Cancel Help

From the drop-down menu, choose the desired option. The selected option appears in the field. (See *Figure 13.12*.)

- **Enabled:** This means that when the system is booted up, it attempts to initiate a link between itself and the Host computer.
- **Disabled:** This means that when the system is booted up, it does not attempt to initiate a link between itself and the Host computer.

- E	
1	
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. L	

**NOTE:** After boot up, once the system initialization is complete, the initial communication state can be overridden using the GEM drop-down menu in the GEM User Interface screen. (See *Enabling GEM/SECS from the GEM User Interface Screen* on page 13-4.)

## **Poll Delay**

The system continually checks to determine if the Host computer is still communicating with it. The number of seconds between these "**polls**" of the Host computer is indicated in this box. (See *Figure 13.13*.) This number should only be

changed under the supervision of those responsible for GEM/SECS communication between the system and the Host.

Figure 13.13 Communication Option - Poll Delay

	GEM Configuration	×
Communication Box	Communication       Init. Comm. State:       Poll Delay       20       Estab. Comm. Delay:	Control States Init. Control State: Online
<b>Poll Delay</b> : To change the number, highlight the box, delete its contents and enter the new number.	Spooling Spooling Enabled Overwrite Spool Max. Spool Transmit: Max Spool File Size: 10000 Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P.15 PROFILE OK	Event Reports Annotated Reports (S6F13) W-Bit for S6 Alarms W-Bit for S5 Terminal W-Bit for S10 Buffer TTY Msgs Summary Format Send Blanks Cancel

To change the number of seconds between "polling incidents," highlight and delete the current contents of the box. Type in the new "polling interval" in seconds.

## **Establish Communication Delay**

Figure 13.14 Communication Option - Poll Delay

Communication Box	GEM Configuration	x
Estab. Comm. Delay: To	Communication Init. Comm. State: Enablec Poll Delay 20 Estab. Comm. Delay: 20 Spooling Spooling Enabled Overwrite Spool	Control States Init. Control State: Online ▼ Online Failed State: Equipment Offline ▼ Event Reports Annotated Reports (S6F13) ▼ W-Bit for S6
change number, highlight the box, delete contents and enter new time.	Max. Spool Transmit. 0 Max Spool File Size: 10000 Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE OK. C	Alarms W-Bit for S5 Terminal W-Bit for S10 Buffer TTY Msgs Summary Format Send Blanks Cancel Help

During the system initialization, if the **Init. Comm. State:** is set to **Enable**, the system attempts to establish a communication link between itself and the Host computer. If the link is not established immediately, it continues to attempt the link at intervals set in the **Estab. Comm. Delay**. This number should only be changed under the supervision of those responsible for GEM/SECS communication between the system and the Host.

To change the number of seconds between communication link attempts, highlight and delete the current contents of the box. Type in the new "link attempt interval" in seconds.

# **Control States**

After a communication link is established between the system and the Host, the Online status can take the form of either ONLINE/REMOTE or ONLINE/LOCAL. Control of the system processing can be transferred from the system to the Host or remain with the system.



	GEM Configuration	×
Control States Box	Communication       Init. Comm. State:     Enabled       Poll Delay     20       Estab. Comm Delay.     20	Control States Init. Control State: Online Failed State: Equipment Offline Host Offline Unline
Init. Control State: Click — on the menu-arrow to display its menu.	Spooling ✓ Spooling Enabled ✓ Overwrite Spool Max. Spool Transmit. Max Spool File Size: 10080	Event Reports Annotated Reports (S6F13) W-Bit for S6 Alarms W-Bit for S5
	Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE OK	Terminal       Image: W-Bit for S10       Image: Buffer TTY Mags       Summary Format       Image: Send Blanks       Cancel       Hielp

#### **Initial Control State**

If the Initial Communication State is set to Enabled (see *Initial Communication State* on page 13-7), then the system and the Host are set to be in communication with each other. This does not mean that the Host is controlling the system. For the Host to assume control of the processing at boot up time, **Init. Comm. States** must be set to **Enabled** and the **Control** must be set to **Online**.

• Online: In this state, when the system is fully initilized, its activity is controlled by either the Host (ONLINE/REMOTE) or the system (ONLINE/LOCAL) according to preprogrammed parameters. To set this option, click the menu arrow next to the Init. Control State: interaction box. Click Online. (See *Figure 13.15.*)

- Equipment Offline: In this state, the system is being operated by the operator and not the Host. For allowable communication between Host and system while in this state, see Semi Standard E30. While in this state, the operator must initiate Online status. (See *Figure 13.15.*)
- Host Offline: In this state, the system is ready to accept Host interaction whenever the Host is responding. This state allows the system to continue operation while waiting for Host interaction. (See *Figure 13.15.*)

### **Online Failed State:**

This setting establishes a default state in the event that Initial Communication was set to Online, and the Online status fails. If Online fails, the system automatically resets to the state chosen in the **Online Failed State** selection. (See *Figure 13.16*.)

GEM Configuration	×	
Communication Init. Comm. State: Enablec Poll Delay 20 Estab. Comm. Delay: 20 Spooling Spooling Enabled Overwrite Spool Max. Spool Transmit: 0 Max Spool File Size. 10000	Control States Init: Control State: Online  Online Failed State: Equipment Offline  Equipment Offline Host Offline Host Offline Kevent Reports V-Bit for S6 Alarms V-Bit for S5	Online Failed State: Click on the menu arrow to display drop-down menu. Click on the desired state.
Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE OK	Terminal  W-Bit for S10 Buffer TTY Msgs Summary Format Send Blanks Cancel Help	

Figure 13.16 GEM Configuration - Online Failed State:

- **Equipment Offline**: With this setting, if the Online status fails, the system resets to Equipment Offline. In this state, the operator must initiate generation of the Online status.
- Host Offline: With this setting, if the Online status fails, the system resets to Host Offline. In this state, the system is open to initiation of the Online status from the Host.

## Spooling

When enabled, spooling is activated during communication failure between the Host and the system. In the event of communication failure between the host and the system, the system no longer sends events to the host. When spooling is enabled, the events are written to a file. When the system is in this spooling mode, an asterisk (\*) appears in the status bar. When communication is restored, the host must send an S6F23 (RSD) message to the system requesting that queued messages be purged or requesting that they be transmitted. After the host message is received, the asterisk is removed from the status bar. When activated, this allows the system to queue messages intended for the host so they can be delivered when the communication is restored. (See *Figure 13.17*.)

Figure 13.17 GEM Configuration - Spooling

	GEM Configuration	×
Spooling category box.	Communication     Control States       Init. Comm. State:     Init. Control State:       Poll Delay     20       Estab. Comm. Delay:     20	
	Spooling Enabled         Image: Spooling Enabled         Image: Spool Transmit:         Image: Max Spool Transmit:         Image: Max Spool Transmit:         Image: Max Spool Transmit:         Image: Spool	
	Equipment Identification       Terminal         Model (MDLN):       P15         Rev.       6.3         Device Name:       P-15 PROFILE         Summary Format       Image: Summary Format         Image: Summary Format       Image: Summary Format	
	OK Cancel Help	

#### • Spooling Enabled:

This option enables the spooling activity during periods of communication laps between the system and the Host. Click on the empty checkbox next to **Spooling Enabled** to enable this option. The **X** in the box enables the option. (See *Figure 13.17.*)

## Overwrite Spool:

This option requires that **Spooling Enabled** is active (**X** in the checkbox). When activated, this option allows a full spool file to have its oldest messages overwritten with new messages. Click on the empty checkbox next to **Overwrite Spool** to enable this option. The **X** in the box indicates that the option is active. (See *Figure 13.17.*)

#### Max. Spool Transmit:

This is the maximum number of messages that can be sent in response to a S6F23 message from the Host. (See *Figure 13.17*.)

Max. Spool File Size:

This specifies the maximum size, in bytes, of the disk file that is used for the spool area. (See *Figure 13.17*.)

## **Equipment Identification**

This information identifies the system, and the software being used to operate it. These fields are generated by the system when the software is loaded.

Figure 13.18 GEM Configuration - Equipment Identification

	Communication       Communication       Init. Comm. State:       Poil Delay       20       Estab. Comm. Delay:       20
Equipment Identification category box.	Spooling       Event Reports         Image: Spooling Enabled       Annotated Reports (S6F13)         Image: Spool Transmit:       Image: Spool Transmit:         Max. Spool Transmit:       Image: Spool Transmit:         Image: Spool Transmit:       Image: Spoo
	OK Cancel Help

- Model (MDLN):
  - This field contains the model number (e.g., P-15). (See Figure 13.18.)
- Rev.:

This field contains the version number of the software operating the system. (See *Figure 13.18.*)

Device Name:

A default name is applied to the system by the system software when it is installed. The name can be changed by the host, at host discretion. (See *Figure 13.18.*)

#### **Event Reports**

Figure 13.19	GEM Configuration	- Event Reports
--------------	-------------------	-----------------

GEM Configuration	×	
Communication Init. Comm. State: Enclarer Poll Delay 20 Estab. Comm. Delay: 20	Control States Init. Control State: Online	Event Reports options.
Spooling Spooling Enabled Overwrite Spool Max. Spool Transmit: 0 Max Spool File Size. 10000	Event Reports  Annotated Reports (S6F13)  W-Bit for S6  Alarms W.Bit for S5	
Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE OK	Terminal W-Bit for S10 Buffer TTY Msgs Summary Format Send Blanks Cancel Help	

### • Annotated Reports (S6F13):

This option provides annotation with the S6F13 event reports sent to the Host. (See *Figure 13.19*.)

• W-Bit for S6:

This option specifies whether S6 messages are to be sent to the Host with the **Wait Bit** set to **0** or **1**. If the check box contains an **X**, the Wait Bit is set to **1**. (See *Figure 13.19*.)

#### Alarms

This option sets the S5 Alarm message **Wait Bit** to either **0** or **1** for transmission to the Host. If the check box contains an **X**, the Wait Bit is set to **1**.

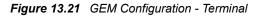
Figure 13.20 GEM Configuration - Alarms

GEM Configuration	×	
Communication Init. Comm. State: Poll Delay 20 Estab. Comm. Delay: 20 Spooling	Control States Init: Control State: Online Online Failed State: Equipment Offline Event Reports	
Spooling Enabled       Overwrite Spool       Max. Spool Transmit:       Max Spool File Size.	Annotated Reports (S6F13) W-Bit for S6 Alarms W-Bit for S5	Alarms options.
Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE OK	Terminal  W-Bit for S10  Buffer TTY Msgs  Summary Format  Send Blanks  Cancel Help	

#### • W-Bit for S6:

This option specifies whether S5 Alarm messages are to be sent to the Host with the **Wait Bit** set to **0** or **1**. (See *Figure 13.20*.)

#### **Terminal Options**



GEM Configuration	X	
Communication Init. Comm. State: Enable: Poll Delay 20 Estab. Comm. Delay: 20	Control States Init. Control State: Online Online Failed State: Equipment Offline	
Spooling Spooling Enabled Overwrite Spool Max. Spool Transmit. 0 Max Spool File Size. 10000	Event Reports Annotated Reports (S6F13) WeBit for S6 Alarms WeBit for S5	Terminal options.
Equipment Identification Model (MDLN): P15 Rev. 6.3 Device Name: P-15 PROFILE	Terminal ▼ W-Bit for S10 ■ Buffer TTY Msgs Summary Format ■ Send Blanks	
ОК	Cancel Help	

• W-Bit for S10:

This option specifies whether S10 messages are to be sent to the Host with the Wait Bit set to 0 or 1. An X in the check box indicates that the wait bit is set to 1. (See *Figure 13.21.*)

• Buffer TTY Msgs:

With this option enabled, the system does not display the messages. (See *Figure 13.21*.)

### **Trace Configuration**

This option is designed to limit which messages are stored in the Status (Log) File on the disk. The divisions are set by message priority. Each message generated by the system carries with it a priority rating. By choosing one of the options, only the desired messages are saved to the Status (Log) File.

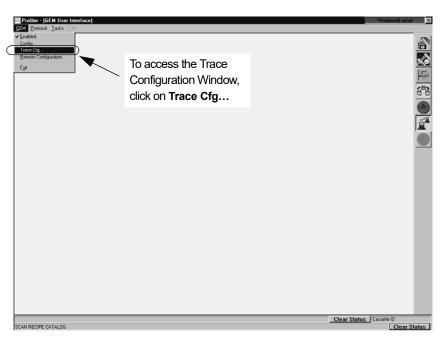


Figure 13.22 GEM User Interface Screen - Trace Configuration

1. To access the Trace Configuration dialog box from the GEM/SECS window, click on **Trace Cfg...** from the **GEM** drop-down menu. (See *Figure 13.22*.)

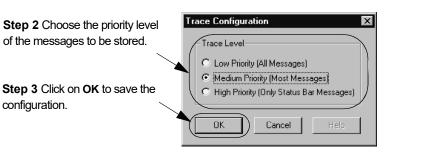


Figure 13.23 Trace Configuration Dialog Box

- 2. Choose the priority level of the messages to be stored by clicking in the radio button of the selection. (See *Figure 13.23*.)
- Low Priority (All Messages)

This option prescribes saving all messages to the Status (log) file.

Medium Priority (Most Messages)

This option prescribes saving to the Status (log) file, most generated messages, generally omitting those messages used only for communication.

High Priority (Only Status Bar Messages)

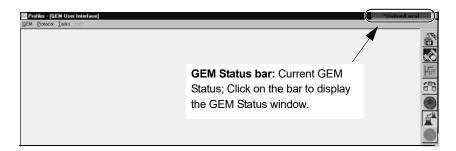
This option prescribes saving only the most important messages, those that are typically displayed in the Status Bar Messages box.

3. Click on **OK** in the Trace Configuration dialog box to save the configuration.

# **GEM STATUS WINDOW**

When the GEM option is installed in a system, the GEM status window can be accessed through the Status Bar at the top right of all screens operating in the system environment.





# **Current GEM Status Information**

1. To access the **GEM Status** window, click on the **Status Bar** at the top right of the screen (circled in *Figure 13.24*, where it appears in every screen.)

Figure 13.25 GEM Status Window

	GEM Status	×
GEM Status: Current general communication information status. Read-Only.	Link State: Control State: Online Substate: Spool State: Prev. Proc. State: Process State: Send TTY Ms View and ACK H	

- 2. The GEM Status window displays the **current** GEM communication status in the system. This window can be helpful for troubleshooting purposes.
  - Link State: The Link State has two possibilities:

**Enabled:** This means that the communication link between the system and the Host is established. In this mode, the system and Host might be either Communicating or Not Communicating. Note: Not Communicating can also mean that it is "active until communications are formally established" (S1F13 and S1F14).

**Disabled:** This means that the communication link between the system and the Host has been disabled so no link is possible in this state.

• Control State: The Control State has two possibilities:

**Online:** This means that the system is in operating mode. In this state, control of the system can be from: **Host** (Host computer controlling the processing); or **Local** (the system controlling its own activity).

**Host Offline:** This means that the Host is not sending or responding to messages from the system. In this case, if the control state is set to Local, the system continues to process wafers. If the system is set to Host control, the system has limited functionality.

**Offline:** This means the system is not sending or responding to messages from the Host. In this case, the system can only operate under Local control.

- Online Substrate: This is the status of the communication link. The Online status could either be Online/Remote (Host control) or Online/Local (system control).
- **Spool State:** This is the status of the spooling activity between the system and the Host if the system is set to spool and the communication link is active. If the system is set to spool information, then the spooling activity is either **Active** or **Inactive**. During a communication interruption, the system spools messages to a queue. When communication is restored, the Host can send an S6F23 message requesting that the stored messages be sent to the Host.
- **Prev. Proc. State:** This indicates which processing state the system was last in, immediately prior to the current processing status. For more information on the process states see the **KLA-Tencor Profiler SECS Interface** manual.
- **Process State:** This indicates which processing state the system is currently operating in. For more information on the process states see the **KLA-Tencor Profiler GEM/SECS Interface** manual.

# **GEM TTY Messages: Sending and Receiving**

It is possible to send and receive TTY messages using GEM. The messages dealt with in this screen are strictly text communications between the system and the Host. These are not commands that the Host computer can respond to.

	Figure 13.26 (	JEM Status Window
	GEM Status	×
	Link State: Control State: Online Substate:	Enabled/Not Communicating Online/Local Local Control
<b>Step 1</b> To open the interactive window for sending TTY messages, click here.	Spool State: Prev. Proc. State: Process State:	Active INIT IDLE
	Send TTY Ms	

#### Sending TTY Messages to the Host

1. To open the dialog box for sending TTY messages, click on the  ${\bf Send}\ {\bf TTY}\ {\bf Msg}\ {\bf to}$ Host button. (See Figure 13.26.)

Figure 13.27 Send TTY Message Window

	Send TTY Message	х
Step 2 Click in the message	Enter text message to send to host:	
box to activate cursor, then type the message.		
	OK Cancel Help	

2. Type in the message that is to be sent to the Host screen. When satisfied with the message content, click on the OK button to send it to the Host. (See *Figure 13.27.*)

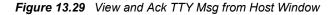
#### View and Acknowledge TTY Message From the Host

When a message comes from the Host, it can be viewed in the View and Ack Tty Msg from Host window. To enter the window, click on the View and ACK Host TTY Msg button (circled in Figure 13.28 below). If a message arrives from the Host during normal processing, an indicator appears (the letters TTY) at the upper right corner of the screen, in the status bar. Click on the Status Bar to display the GEM Status box.

	GEM Status	×
	Link State:	Enabled/Not Communicating
	Control State:	Online/Local
	Online Substate:	Local Control
	Spool State:	Active
View and Acknowledge	Prev. Proc. State:	INIT
Host TTY Message button.	Process State:	IDLE
	Send TTY Ms View and ACK H	

Figure 13.28 GEM Status - View and Ack Host TTY Msg Window

The Host might require a response from the system signalling that the message delivered to the system was read. To acknowledge receipt of the message click on the **ACK HOST MSG** (Acknowledge Host Message) button (circled in *Figure 13.29*).



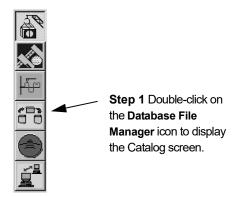
	View and Ack Tty Msg from Host	×
Text from Host message		
appears here		<u> </u>
Click on the ACK HOST	at .	<b>T</b>
MSG to acknowledge receipt of the message.		elp

# **Uploading Recipes to the Host**

Using GEM/SECS, process recipes can be uploaded (exported) to the Host computer. If the information has been stored in one of the files in the Database File Manager, it can be uploaded using the following procedure. (Note: the Host can also initiate the upload.)

1. From any top level screen, click on the **Database File Manager** icon.

Figure 13.30 Database File Manager Icon Choice



 The Database Catalog screen is displayed. This screen provides access to: Scan Recipes; Scan Data; Sequence Recipes; Sequence Data. (See the access buttons, circled in *Figure 13.31*. Only the Recipe screens are used in this procedure.)

	Profiler - [Cata	uter Diagnostic Tasks Help						Online	:/Local ×
	Fie For Fulla	x ⊕ 0+ 0+ 2D 30	d.						5%
			Scan Recipe Name:						<u> </u>
	(Scan Recipe		DRMMD						×2
Step 3 Only the	Hecipe	Recipe Path:	Recipe Name	Length (µm)	Sampling Bate (Hz)	Speed (µm/s)	Creation Date (yyyy-mm-dd)	Time	파
Scan Recipe and the Sequence Recipe catalogs are used in this procedure.	Scan Data Sequence Recipe Data	SCANRCP	ORIGA OPFISO OFFISO STEPHIN STEPHIN TIPCTRL RIST	10 5 200 500 1600 500 500 500 500 500	200 200 50 50 50 50 50 200	H00 100 50 50 50 2 100	2001-01-14 2001-02-14 2001-02-14 2001-02-27 2001-02-27 2001-02-27 2000-12-18 2000-03-14 2000-03-14 2000-03-14 2000-03-14	08:35 09:00 09:01 08:36 22:50	
	SCAN RECIPE CAT		ejete Piirz	New	View	Hodiy	Egport		Clear Status

Figure 13.31 Database Catalog Screen.

- **3**. Either **Scan Recipe** or **Sequence Recipe** can be chosen. The window then displays a list of related recipes. (See *Figure 13.31*.)
- 4. In the chosen window, move the cursor over the desired item in the list and click on it. This highlights the specific file/recipe that is to be uploaded. (The screens are presented below.)

	Profiler Cara							*Online	/Local ×
Step 5 To upload (export) a	Ele Ed PPTress	Diag etic Tasks Help B							and the second s
recipe, click on <b>PPTransfer</b>	Down		Scan Recipe Name:						<u> </u>
then on <b>Upload</b> .	Scan		DRMMD					_	~
	Recipe	Recipe Path:	Recipe Name	Length (µm)	Sampling Rate (Hz)	Speed (µm/s)	Creation Date (yyyy-mm-dd)	Time	1000 1000 1000 1000
	Scan Data Sequence Recipe Sequence Data	Sequence Recipe	BSWD DRHSH OFF150 OFF500 STEPHTH STEPHTH TIECTRL HIST	1005 200 1600 500 500 500 12 500	200 200 50 50 50 50 50 50 500 200	100 100 50 50 50 50 2 100	2000-06-27 2001-02-14 2001-02-14 2001-02-27 20001-02-27 2000-12-18 2002-04-14 2000-04-14 2000-04-14 2000-09-14 2000-09-14	08:35 09:00 09:01 08:36 22:50 14:23 14:35	
		Generated by DRM	te Pint	<u>N</u> ew	View/	Modiy	Egpot.	import	
	SCAN RECIPE CATA	LOG						IS Catterie ID	lear Status

Figure 13.32 Scan and Sequence Recipe Windows

Scan Recipe Window



Efe (get PPTranter Deported Table 1990)         Scan         Scance         Delete         Pirz         Her         Vere         Man         Vere	Profiler - [Cata				*Online	e/Local ×
Scan Recce Scan Scan Scan Bata Sequence Patr: Sequence Sequence Patr: Sequence Ceated By Ceated By Ceated By Cost 500 Cost 5	Fie For Fullar		30			5%
Seguence Bata						<u> </u>
Seguence Bata	Scan		CORS_SEC			*
Seguence Bata	Hecipe	Sequence Path:	Sequence	Created By	Creation Date Time [yssymmedd]	⊸
Seguence Bata	Scan Data	SEQRCP	CORS_SEQ		2001-02-13 15:54	80
Seguence Bata						
Seguence Bata						
Seguence Bata	Sequence Recipe					-
Data						
Delete Pirz New View/Modey Egot import	Sequence Data					
Delete Pirz New View/Modey Egot import						
Delete Pirz New View/Modey Egot import						
Delete Pirz New View/Modey Egot import						
Delete Pirz New View/Modey Egot import						
Delete Pirz New View/Modey Egot import						
Dejene Pirz New View/Acd8y Egost jmpost					-	
Clear Status Correction		1				
			Dejete Print	New View/Modily	Egport [mport	
	CEOUENCE DE CO	C C171100				

5. In the **Screen Menu** bar, click on **PPTransfer** to display the PPT drop-down menu. Click on **Upload**. (It is available in all four screens. See circled display in the **Scan Recipe Window** in *Figure 13.32*.)

- 6. This displays the **Upload** dialog box. (See *Figure 13.33*.) Check the file name presented in the dialog box and compare it against the file highlighted in the database catalog window. They should be the same.
- 7. If they are the same, click on **OK**. It is then transferred to the Host.

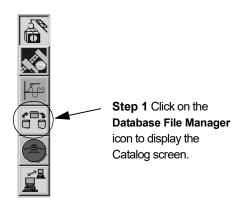
#### Figure 13.33 Upload Window



### **Downloading Recipes from the Host**

Using GEM/SECS, process recipes can be downloaded (imported) from the Host computer. To download a recipe from the Host, use the following procedure.

1. From any top level screen, double-click on the **Database File Manager** icon.(See *Figure 13.34*.)





2. When the Database File Manager opens, click on the 2D or 3D icons in the tool bar so the system displays the required recipe type. (See *Figure 13.35*.)

3. From the **Catalog** (database) screen click on **PPTransfer** (Process Program Transfer) in the Screen menu bar to display the PPT menu. Click on **Download** to display the **PPid** (Process Program identification) window. (Download is circled in *Figure 13.35.*)

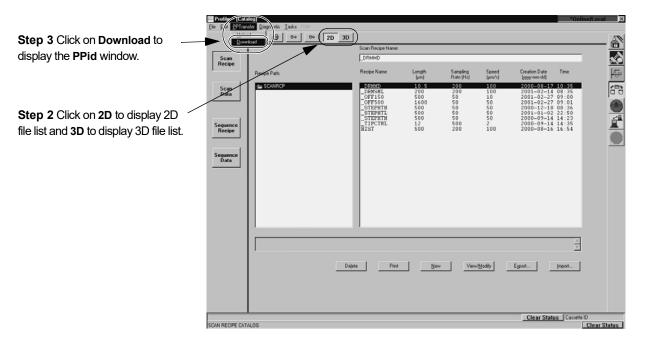


Figure 13.35 Database Screen - PPTransfer Menu

- 4. In the **PPid**: box, type in the exact name of the recipe that is to be downloaded. (See *Figure 13.36*.)
- 5. Click **OK** to begin the Download process. (See *Figure 13.36*.)

#### Figure 13.36 PPid Window

Step 5 When the recipe name is in the PPid field, click OK to start the download.	PPId X	<b>Step 4</b> Enter the exact name of the Recipe to be downloaded from the Host.

6. When the download is complete, the recipe appears in either the **Scan Recipe** file (2D or 3D) or the **Sequence Recipe** file (2D or 3D), depending on which type of recipe it is. GEM/SECS directs the recipe to the proper file. The downloaded recipe can now be accessed.

# WAFER STRESS APPLICATION OPTION

# INTRODUCTION

Stress can be generated in the film and wafer as a result of thin film deposition. The deformation of the thin film can create bending and compressing, or expansion of the substrate surface. The result is a slight concave or convex curvature of the wafer. Careful monitoring of the thin film stress data is useful for reducing process variation.

The KLA-Tencor Wafer Stress application option provides a tool for measuring the wafer curvature at the wafer surface so calculations can be made regarding the stress generated by a deposited film. This is accomplished by creating a reference scan before deposition, and comparing it with the post deposition scan of the same wafer, in the same position, using the same scan recipe.

The KLA-Tencor Profiler software calibrates the following stress values:

- Average Stress derived from a polynomial fit of the entire profile, excluding 5% of the fit data on either end.
- Maximum Stress the maximum absolute stress value.
- Center Stress stress at the midpoint of the profile data.

### **Chapter Contents**

This chapter describes:

- Data Collection on page 14-4
- Loading Wafers on page 14-5
- The Stress Application Window on page 14-7
- Selecting, Creating, and Modifying a Stress Recipe on page 14-12
- Saving a Stress Recipe on page 14-20
- Printing a Stress Recipe on page 14-22
- Creating Stress Data on page 14-22
- Analyzing Stress Scan Results on page 14-26

### **Stoney Equation**

The Stoney equation for stress in a thin-film layer deposited on a substrate is as follows:

$$\sigma = \frac{1}{6R} \frac{E}{(1-\nu)} \frac{t_s^2}{t_f}$$

where

$$\frac{E}{(1-v)}$$
 = wafer elastic constant

 $\sigma = {\rm stress}$ 

#### $t_s$ = wafer thickness

 $t_f = \text{film thickness}$ 

R = radius of curvature

E = Young's Modulus for the wafer (substrate)

v = Poisson's Ratio

As a profile is taken, the height of the wafer is being measured as a function of position:

$$y = f(x)$$

where

$$R(x) = \frac{\left[1 + (dy/dx)^2\right]^{3/2}}{d^2 y/dx^2}$$

with y = Z-axis.

Two methods are available to obtain **y** (which relates to the Z-axis) from the profile. These are the two methods of calculation that exist for determining the stress: the least square fit (13 Point Least Square Fit), and the polynomial fit (Polynomial Fit). The recommended algorithm is the Polynomial Fit. It is chosen in the Stress recipe editor, at the bottom of the screen. This algorithm produces the best repeatability of the two available methods. The calculation provides three polynomial order options, 5th, 6th, and 7th order. For the best repeatable results, use the 5th order polynomial fit (see *Choosing the Stress Calculation Method* on page 14-19).

#### **Polynomial Fit**

The Polynomial Fit uses the entire data set. It is important to note that higher order polynomials (6th and 7th) might result in fitting data to local irregularities. The polynomial fitting procedure is as follows:

A function y = f(x) can be expressed in terms of a polynomial order n as [3] [4] [5],

 $\mathbf{y} = \mathbf{c}_0 + \mathbf{c}_1 \mathbf{x} + \mathbf{c}_2 \mathbf{x}^2 + \dots + \mathbf{c}_n \mathbf{x}^n$ 

As illustrated above, n + 1 coefficients exist for polynomial n. After the value of the coefficients are computed, the new y values for different values of x can be computed.

#### **EXAMPLE:**

In the actual polynomial fit algorithm, a 5th, 6th, or 7th order polynomial is used for the calculation. In this example, a 3rd order polynomial is going to be used for the purpose of illustrating the process of fitting a polynomial.

The general equation for a 3rd order polynomial is:

 $y = c_0 + c_1 x + c_2 x^2 + c_3 x^3$ 

To compute the coefficients 4 equations are required to compute the 4 unknowns. The 4 equations are generated by multiplying the above equation by the coefficients of  $c_3$ ,  $c_2$ ,  $c_1$ , and  $c_0$ .

```
x^{3}y = c_{0}x^{3} + c_{1}x^{4} + c_{2}x^{5} + c_{3}x^{6}
x^{2}y = c_{0}x^{2} + c_{1}x^{3} + c_{2}x^{4} + c_{3}x^{5}
xy = c_{0}x + c_{1}x^{2} + c_{2}x^{3} + c_{3}x^{4}
y = c_{0} + c_{1}x + c_{2}x^{2} + c_{3}x^{3}
```

The next step is to solve this set of simultaneous equations to find the values of  $c_3$ ,  $c_2$ ,  $c_1$ , and  $c_0$ . Crout's method [3] [4] is used here to solve this.

When the coefficients have been calculated, the new values for y are computed for different values of x. The radius of curvature is calculated for any value of x using the following formula:

$$R(x) = \frac{\left[1 + (dy/dx)^2\right]^{3/2}}{d^2 y/dx^2}$$

where,

$$dy/dx = 3c_3x^2 + 2c_2x + c_1$$
 and  $d^2y/dx^2 = 6c_3x = 2c_2$ 

The results are then used to calculate stress using the stress formula presented at the beginning of this section.

#### Least Square Fit

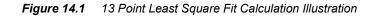
The Least Square Fit method is more complicated than the Polynomial Fit method. It consists of fitting local sections of data to circular arcs and computing the mean radius from the local radius of curvature. This is more susceptible to noise variations and fine surface geometries, making it less robust.

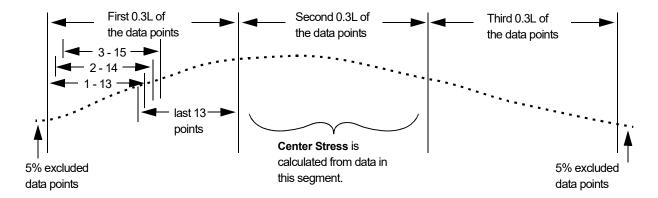


**NOTE:** The Least Square Fit method is provided so that users can correlate stress results with old generation profilers where it was the default algorithm used for stress.

Explanation: The **13 Point Least Square Fit** algorithm immediately disregards the beginning and ending 5% of the data points. It then divides the remaining scan length into three identical lengths of 0.3L (L equals the scan length). (See *Figure 14.1*.)

Within each 0.3L section, the local radius of curvature is calculated for each set of 13 data points in the section. Starting with the first data point, it calculates the local radius for the first 13 points (1-13). Then the calculation is made for the second set of 13 points (2-14). (See *Figure 14.1*.) This continues until data point N-12 of the section where it calculates the last point (N = total data points in the section).





The average radius of each 0.3L segment is the mean of the local radii. The stress is calculated for each 0.3L segment based on the mean radius of that section. The Average Stress and the Max Stress reflect the mean and maximum stress of all the segment stress calculations. The Center Stress is the stress calculated from the mean radius of the center 0.3L segment. (See *Figure 14.1*.)

# DATA COLLECTION

Use the Wafer Stress application to compare pre- and post-processing traces. This comparison calculates the curvature caused solely by the process-induced stress.

Only the pre- and post-deposition traces, along with their summaries, are saved. Stress values are not saved but are recalculated each time for the raw traces. To calculate the stress values, both the pre- and post-deposition traces must be present in the Scan Data catalog.

### Scan Data Identification

To compute and display a difference measurement, both pre- and post-deposition raw data must be saved. Saving the raw and summary data allows for the recalculation of stress values using different parameters.

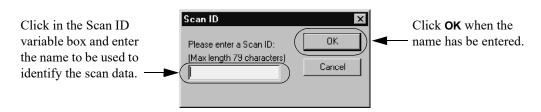
In order to save and store data for retrieval and use in the stress application, each data set must be given a name. The name must contain 79 characters or less and should be designed to help the user identify it as a pre- or post-processing scan. Ideally the scan name also includes other information such as a reference to the substrate composition. However, it is up to the user to come up with a suitable name. The name is entered in the dialog box shown in *Figure 14.2*.

#### Naming Scan Data Procedure

When a scan is initiated in the Stress application, this dialog box appears.

- 1. Enter the scan data name in the variable box.
- 2. Click **OK** to accept the name. This initiates the scan.

#### Figure 14.2 Stress Recipe Name Assignment Dialog Box



# LOADING WAFERS

In the P-15 system, the manual load procedure is used. For general information on installing a precision locator, see *Installing the Precision Locator:* on page 11-47. See *Optional Stress Precision Locators* on page 11-55 for graphic representations of some of the stress locators.

The system might come with a stress locators. Use the manual load procedure. (See also *Figure 14.4*.)

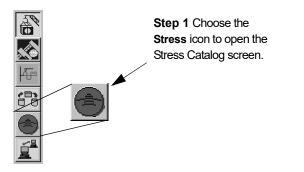
The stress measurement procedure depends on a pre-processing scan of the same wafer that is subsequently measured after processing. The two scans are then compared and a stress calculation is performed by the system. For the results to be meaningful, the scan must be taken of the identical location on the same wafer, before and after processing. Use the following procedure to create the first scan.

This procedure assumes that the precision locator is in place on the sample stage.

### Load Wafer - Manual Procedure

Begin: (Manual) Load Wafer Procedure 1. From the **Catalog** screen, click on the **Stress** icon. This opens the Stress catalog screen displaying the Stress Recipe list. (See *Figure 14.3*.)

Figure 14.3 Catalog Screen – Choosing the Stress Application



2. In the Stress screen, click Substrate to display its menu. (See Figure 14.4.)

Figure 14.4 Stress Screen with Substrate Menu

Step 2 Click on Substrate to	Profiler - [S Becipe Substra	t <b>ress]</b> ite <u>V</u> acuum <u>V</u> i	ew <u>S</u> tress <u>1</u>	asks <u>H</u> elp					×
display its menu.	NCM -	ial Load	95	LEVEL ST	ART 🛞 🕀	) ? N	?		I and the second
	Stre: Init H Reci	/Unload andler	ame:						
	Catal SMIF	Load/Unload MIF	me				Date	Time	
<u>Substrate</u> <u>V</u> acuum <u>V</u> ie	Scan Data								
( <u>Manual Load</u> )	Catalog								60
Load/Unload		Í							
/ <u>I</u> nit Handler									
<u>S</u> MIF Load/Unload Init SMIF									_
Step 3 Click on Manual Load to									
move the stage to the door.									
Step 7 After the wafer has been									
placed on the stage, click on									
Substrate.									
Step 8 Click on Manual Load.			_	<u>P</u> rint	<u>V</u> iew/Modify	<u>S</u> tart		Delete	
The stage moves back under	SCAN DATA CAT	4106						Empty	Clear Status
the stylus.		11200						) =···e 0	oroar blatas

**3**. From the **Substrate** menu choose **Manual Load**. (See *Figure 14.4*.) This moves the sample stage to the stage door. Do not open the stage door until the stage stops.



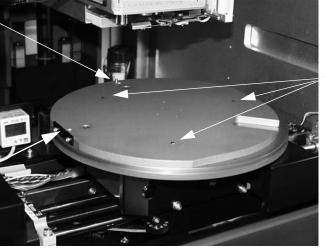
**CAUTION:** Do not operate the stage or elevator with the stage door open. If the stage or elevator is activated with the stage door open, the system door interlock causes the system to cut power to all motors.

**Step 5** Place the wafer on the stage with the stage pin in the

notch.

4. Open the stage door.

Figure 14.5 Precision Locator on the Stage



Three points on which the wafer rests.

that it rests against the **positioning plate**.

Step 5 Position the wafer so

5. Place the wafer on the stress precision locator, with the locator pin firmly in the wafer notch, and the left side of the wafer against the positioning plate. (See *Figure 14.5.*)

The wafer rests on three precision points. (See *Figure 14.5*.)

- 6. Close the stage door.
- 7. Click Substrate, in the menu bar, to display its menu.
- 8. From the menu, choose **Manual Load**. This moves the sample stage back under the stylus. (See *Figure 14.4*.)
- 9. Leave the Stress screen open for the next procedure.

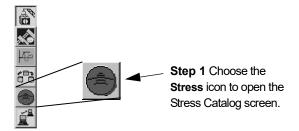
# THE STRESS APPLICATION WINDOW

### **Stress Recipe Catalog**

This section describes the various parts of the Stress Recipe Catalog screen and the function of the stress recipe related buttons.

1. Click the Stress icon in the Catalog screen. (See Figure 14.6.)

Figure 14.6 Catalog Screen – Choosing the Stress Application



End: (Manual) Load Wafer Procedure 2. This displays the **Stress** application screen. If the Recipe catalog is not displayed, click on **Stress Recipe Catalog** to view the currently saved and available stress recipes. (See *Figure 14.7.*)

Figure 14.7 Stress Application Screen

Otara Olfrastalus altr	🐺 Profiler - [Stre						X
Step 2 If not already		<u>V</u> acuum <u>V</u> iew <u>S</u> t			- 1		
highlighted, click on Stress	NEW 🔡 🤅		EVEL START	<b>⊗</b> ⊕ ? K	?		<u> </u>
Recipe Catalog to display	Stress	Stress Recipe Name:	STRESS_GAL				
the current list of stress	Recipe Catalog	Stress Recipe Name	,		Date	Time	
related scan recipes.		1000_50 5000 200			10/27/1998	09:21:34 AM 10:39:11 AM	푸
	Data	MARCUS STRESS_GAL			10/27/1998 05/11/1999 05/12/1999	02:19:05 PM 04:08:54 PM	
					00/12/1000	04.00.04 111	
Recipe list area. See							
Figure 14.8.							
-							
Recipe functions. See 🔍							
Figure 14.9.	$\langle   $						
				w/Modiły <u>S</u> tart		Delete	)
	SCAN DATA CATAL	.0G				Empty	Ciear Status

**3**. Choose a Recipe to use for a stress scan by clicking on the recipe to highlight it. If the name is long, it might be truncated in the list area, making it difficult to distinguish between similar names. When highlighted, the recipe names appear in its entirety in the **Stress Recipe Name** box. (See *Figure 14.8.*)

Figure 14.8 Stress Recipe List Area

The Stress Recipe Name. When a recipe is selected, its	Stress Recipe Name: STRESS_GAL	Date	Time
name appears in full in the			)
Stress Recipe Name box.	1000_50 5000_200 MARCUS STRESS_GAL	10/27/1998 10/27/1998 05/11/1999 05/12/1999	09:21:34 AM 10:39:11 AM 02:19:05 PM 04:08:54 PM
List of currently available	Dates and times that the corresponding		
Stress Recipes.	recipes were created.		

The **Stress Recipe Name** list contains all the currently defined and saved Stress Recipes. Each recipe is presented with its creation date and time. (See *Figure 14.8.*)

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14-8

4. Four function buttons are positioned at the bottom of the recipe list area. (See *Figure 14.7.*) These are all duplicated functions, residing originally in the menu bar menus for use in conjunction with the listed recipes. (See descriptions in *Figure 14.9.*)

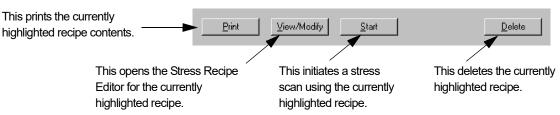


Figure 14.9 Function Buttons in the Stress Recipe Screen

- Click **Print** to print the currently highlighted recipe.
- Click View/Modify to open the Stress Recipe Editor for the currently highlighted recipe.
- Click **Start** to initiate a stress scan using the currently highlighted recipe.
- Click **Delete** to delete the currently highlighted recipe from the recipe list.

# Stress Scan Data File Catalog

This section describes the various parts of the Stress Data Catalog screen and the function of the data file related buttons.

1. To access the available stress data files, click on **Scan Data Catalog**. This displays the list of data files from scans that have been performed using a Stress Recipe for use with the Calculation function. (See *Figure 14.10*.)

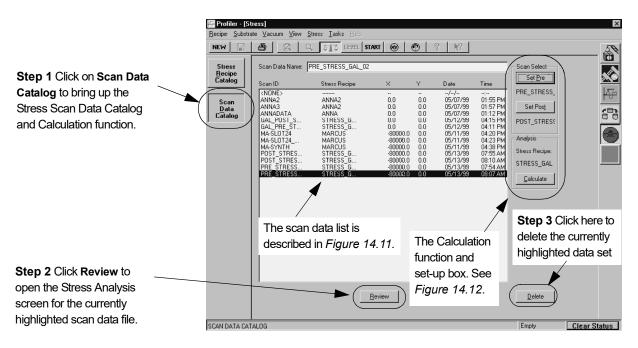


Figure 14.10 Stress Screen with the Scan Data Catalog Displayed

The **Scan Data Catalog** contains the scan data files that were collected from scans that used stress recipes. Each data file listing contains six items. See *Figure 14.11* for details.

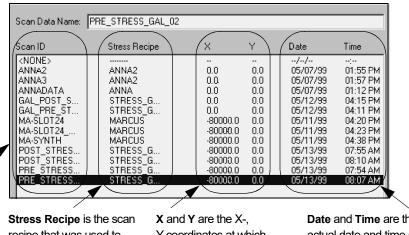


Figure 14.11 Scan Data Information in the Stress Data Catalog

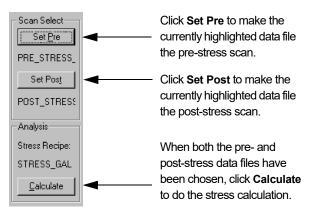
Scan ID is the name the scan data was given when the scan was taken.

recipe that was used to perform the scan. X and Y are the X-, Y-coordinates at which the scan began. Date and Time are the actual date and time at which the scan was run.

- Scan ID is the name given the data file when a scan was performed.
- **Stress Recipe** is the name of the recipe that was used to create the scan.

- X and Y are the actual coordinates on the wafer where the scan began.
- Date and Time are the actual date and time that the scan was created.
- 2. Click **Review** to open the Stress Analysis screen to view the data in the highlighted data file.
- 3. Click **Delete** to delete the currently highlighted stress data set.
- 4. The Calculation function and setup is configured and executed in this screen. (See *Figure 14.12.*)

Figure 14.12	Stress Calculation Function and Set-Up	1
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- Click Set Pre to make the currently highlighted data file the pre-stress scan.
- Click **Set Post** to make the currently highlighted data file the post-stress scan.
- With both pre- and post-stress data files chosen, click **Calculation** to perform the stress calculation.



**NOTE:** This step requires that the appropriate recipe has already been chosen in the Stress Recipe Catalog. (See *Stress Scan Analysis Procedure*, Step 2. *on page 14-28*.)

### The Stress Screen Tool Bar

The Stress Screen has a tool bar that contains six active icons. These icons present quick access to six functions that also reside in the individual menu bar items.

Table 14.1 Tool Bar Icons

Button	Action
NEW	Invokes the Stress Recipe Editor to add a new stress recipe.
	This icon is only active if there is a change in a recipe or for saving a new recipe. It saves changes to the current file.

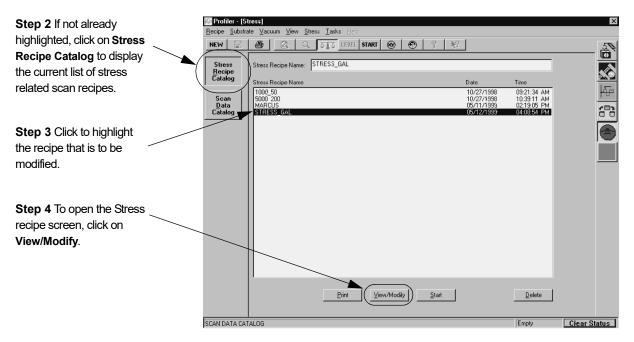
<b>Table 14.1</b> T	ool Bar Icons
Button	Action
<b>e</b>	Displays the Print dialog box for printing data on the current screen.
START	Starts a scan using the current stress recipe.
8	Toggles to the XY View screen.
	Switches to the Theta view window.

# SELECTING, CREATING, AND MODIFYING A STRESS RECIPE

### Select and Open a Stress Recipe

- 1. From any top level screen, click the **Stress** icon in the process icon bar. This opens the Stress application screen.
- 2. This displays the **Stress** application screen. Click on **Stress Recipe Catalog** to view the currently saved and available stress recipes. (See *Figure 14.13*.)

Figure 14.13 Stress Application Screen

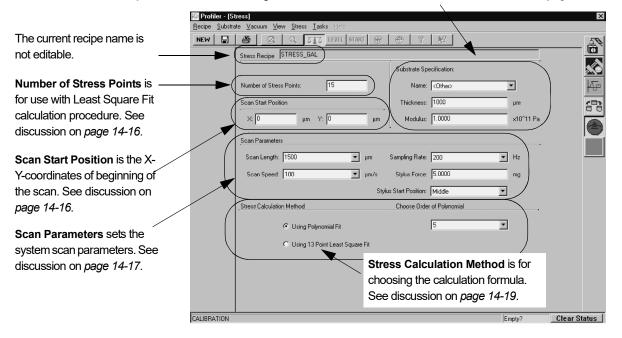


3. Click on the recipe that is to be viewed or modified. (See Figure 14.13.)

4. Click View/Modify (see *Figure 14.13*.) to open the Stress recipe editor.

Figure 14.14 Stress Recipe Editor Window

Substrate Specification is for choosing the substrate modulus and thickness. See discussion on page 14-18.



### **Creating a New Stress Recipe**

1. To open the Stress application, double-click the **Stress** icon in the **Catalog** screen. (See *Figure 14.15*.) This opens the Stress Catalog screen.

Figure 14.15 Catalog Screen – Choosing the Stress Application

🕀 Profiler - [Cal	alog]					×	
<u>Eile E</u> dit <u>S</u> ampl	e ⊻acuum <u>H</u> ost <u>D</u> iagnostic j	Lasks Help					
	📇 START 🛞 🕀	🕼 🛞 2D	3D			92	
		Scan Data Name	c				
Scan		SCAN1					
Recipe	Scan Dala Path:	Scan Data	Recipe ID	Length Y (um) (u	Size Creation D m) (yyyy-mm	ale Iz-	
Scan	SCAN DATA	scen1	SC300	1 1	2000-0		
Data	≥ \$C300	_					
Sequence Recipe							T
Sequence							1
Data							I I
							Step 1 Choose
							-
							the Stress icon to
	Drive:						open the Stress
	<b>a</b> c	-					
							Catalog screen.
	Ihur	nbrials <u>B</u> eview					5
SCAN DATA CATA	LOG				Empty	Clear Status	

2. This displays the **Stress** application screen. If it is not currently active, click on **Stress Recipe Catalog** to view the available stress recipes. (See *Figure 14.16*.)

Figure 14.16 Stress Application Scree
---------------------------------------

Step 4 Click NEW to open	Recipe Substra	strate Vacuum View Stress Iasks Help	
the recipe editor for	( NEW ) 🔛	🖉 🖉 Q. Tris Level Start 🛞 🔊 ? 🕅	<i>2</i> , <i>b</i>
creating a new recipe.	Stress Recipe Catalog	Stress Recipe Name: STRESS_GAL Stress Recipe Name Date Time	
Step 2 If not already	Scan	10/02/50 5000 200 10/27/1998 09:21:34 AM 10/27/1998 10:39:11 AM	- <del>L</del>
chosen, click on Stress	Data Catalog	MARCUS 05/11/1999 02:19:05 PM STRESS_GAL 05/12/1999 04:08:54 PM	80
Recipe Catalog to display			
the current list of stress			
related scan recipes.			
Step 3 Click to highlight			
the recipe that is to be used			
to create the new recipe.			
		Print View/Modify Start Delete	
	SCAN DATA CAT	ATALOG Emply Clear	Status

- **3**. If there is a recipe that has parameters closest to those required in the new recipe, highlight it.
- 4. Click **NEW**. This brings up a dialog box for naming the new recipe.
- 5. Enter the name of new stress recipe.

Figure 14.17 Stress Recipe Name Dialog Box.

Step 5 Enter the recipe name in the box provided.	Stress Recipe Name Please enter new Stress Recipe Name: (Max length 79 characters) [stress_ga!	OK Cancel	Step 6 When the
	stress_gal		Step 6 When the name is correctly entered, click <b>OK</b> .

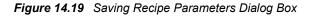
Ą

6. Click **OK** to accept the name, and the Stress Recipe Editor opens, ready for entering new parameters to form a new stress recipe. (See *Figure 14.17*.)

0 0 10				
Profiler - [St lecipe Substra	1 <b>2333)</b> te <u>V</u> acuum <u>V</u> iew <u>S</u> tress <u>I</u> asks Help			×
NEW   🔛	🖀 🙆 Q. TIT LEVEL START 🛞	⊕ ? №		50
	Stress Recipe STRESS_GAL			<u> </u>
		Substrate Specification:	,	
	Number of Stress Points: 15	Name: <0ther>	•	구
	Scan Start Position	Thickness: 1000	μm	8
	X: 0 μm Y: 0 μm	Modulus: 1.0000	x10^11 Pa	
	Scan Parameters		,	
	Scan Length: 1500 💌 μm	Sampling Rate: 200	] Hz	
	Scan Speed: 100 💌 µm/s	Stylus Force: 5.0000	mg	
	Stylu	s Start Position: Middle	]	
	Stress Calculation Method	Choose Order of Polynomial	<i>.</i>	
	<ul> <li>Using Polynomial Fit</li> </ul>	5	]	
	C Using 13 Point Least Square Fit			
ALIBRATION		E	Empty?	Clear Status

Figure 14.18 Stress Screen with Stress Recipe Editor Open

- 7. Make the necessary changes to the parameters. (See *Modifying a Stress Recipe* on page 14-15.)
- 8. If the user attempts to start a scan using this recipe before saving the new parameters, a dialog box appears stating that the recipe parameters have changed and request a decision as to whether to save the new parameters or not. It is important to save the new parameters if the recipe is to be used again to run comparative scans.



Saving R	lecipe X
٢	Data for this Stress Recipe have changed. Save the changes?
	Cancel

Click **OK** to save the new parameters.

### Modifying a Stress Recipe

Once a recipe has been chosen and the Stress recipe editor opened, the recipe parameters can be modified.

#### **Recipe Name**

This part of the recipe cannot be modified. The current recipe name is listed at the top left of the screen. (See *Figure 14.14* and *Figure 14.20*.) (If a new recipe is required with parameters like those of the current recipe, click **NEW** at the left end of the tool bar. This creates a new recipe with the same attributes at the original recipe.)

Figure 14.20 Stress Recipe Name

Stress Recipe: STRESS\_GAL

#### **Number of Stress Points**

This number was used with the **Least Square Fit** calculation procedure. (See *Choosing the Stress Calculation Method* on page 14-19.) The calculations related to this procedure are described in the introduction to this chapter. (See *Figure 14.14* and *Figure 14.21*.) This number belongs to legacy software and has no effect on any calculation. Ignore this number.

Figure 14.21 Number of Stress Points

This number is only active with the **13 Point Least Square Fit**.

Number of Stress Points: 15

#### **Scan Start Position**

This is the start position on the wafer for each comparative scan, described in X-, Y-coordinates. If the proper procedure was used for wafer placement on the stress locator, this setting should ensure that the pre- and post-processing scans are performed at the same location on the wafer. (See *Figure 14.14* and *Figure 14.22*.)

For general purposes, the longer the scan, the more accurate are the results. The amount of time required to complete the scan must be balanced against the need for accurate data. KLA-Tencor recommends scanning 80% of the wafer diameter to determine the stress.

#### **EXAMPLE:**

When scanning across the diameter of an eight inch wafer (200000  $\mu$ m), the scan should be 160000  $\mu$ m long. This means that the scan should begin at X = -80000, Y = 0. It should end at X = 80000, Y = 0. (See *Figure 14.22*.)

To change the coordinates:

- 1. Highlight the current X-coordinate number and enter the new one.
- 2. Highlight the current Y-coordinate number and enter the new one.



**NOTE:** If the wafer needs to be rotated, enter the XY View screen, rotate the wafer, exit the XY View screen, then enter new coordinates.

OR

- 1. ALTERNATIVE Step 1: An alternative is to click on the XY icon in the tool bar to open the XY View screen.
- 2. ALTERNATIVE Step 2: Move the video image until finding the target area, then click on the desired start position. (In scans of specific attributes this can prove to provide easier positioning of the scan start, but in general, it is repeatability is less accurate.)
- 3. ALTERNATIVE Step 3: Click **OK** to accept the start position.

Figure 14.22 Scan Start Position

Scan Start Position			
X: -80000	μm	Y: 0	μm

#### **Scan Parameters**

The Scan Parameters allow the user to set the scan length, speed, sampling rate and applied force. Each of these parameters affects the outcome of the stress calculation. (See *Figure 14.14* and *Figure 14.23*.)

#### Figure 14.23 Scan Parameters

Scan Length: 1500	•	μm	Sampling Rate:	200	Hz
Scan Speed: 100	•	µm/s	Stylus Force:	5.0000	mg
		Style	us Start Position:	Middle	

**Scan Length**: For best results, the scan length should be 80% of the diameter of the wafer being measured for stress. The longer the scan, the more accurate the results.

**Scan Speed**: Scan speed often works in concert with Applied Force. If the speed is too high with a very light Applied Force, the results could be inaccurate. (See Stylus Force below.) For long stress scans, it is recommended that the scan speed be 10000  $\mu$ m/s or less, with 2000  $\mu$ m/s - 5000  $\mu$ m/s being optimum.

**Sampling Rate**: This is the number of data points collected as a function of time. For a set sampling rate, as the scan speed increases, the data points become further apart.

**Stylus Force (Applied Force)**: Applied Force is the force exerted on the sample surface by the stylus tip. As the force goes up on a smaller tip, the greater the potential for damage to the sample surface and the to the tip itself. For this reason, it is recommended that at least a 2  $\mu$ m tip be used for this type of scan over a long distance (12.5  $\mu$ m or even 25  $\mu$ m is acceptable). The larger tip allows for a greater Applied Force and a faster scan speed without danger to the tip or sample surface. The recommended force setting for a long fast scan using a 2  $\mu$ m stylus is 5 mg.

**Stylus Start Position**: This allows the user to choose which profile type is used in the scan. Three choices are presented: Middle  $\neg$ , Top  $\Box$ , and Bottom

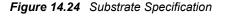
. These profile types correspond to the stylus movement limits as described in *Profile Type:* Available choices for each range and the resultant scan traces on page 3-42.

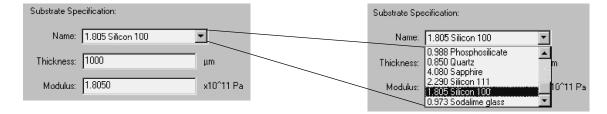
KLA-Tencor recommends using the **Middle** option first. If the Middle option limits out, observe the direction of the limit and choose the corresponding profile type.

#### **Substrate Specification**

The Substrate settings refer to the wafer composition and thickness. Each type of substrate has an elasticity constant that is important in the calculation. The software is programmed to provide the constant (**Modulus**) for each listed substrate type. (See *Figure 14.14* and *Figure 14.24*.) Click on the menu-arrow next to the substrate **Name** variable box and scroll through the list and choose the substrate being used. Choosing the substrate automatically sets the **Modulus**. The operator must set the substrate **Thickness** by double-clicking in the variable box and entering the new thickness in microns ( $\mu$ m). (See *Figure 14.24*.) It is important to note that the user is given another chance to enter the thickness each time the scan is started. This way, a sample can be tested numerous times using the same material in different thicknesses without having to go into the recipe each time to change this parameter.

If the user is measuring a substrate that is not listed, the user can choose **None** from the list of substrates and enter the modulus and thickness. Like the other substrates, the user is given the opportunity to change the thickness each time a scan is run using this recipe.





The following is a list of common substrates and their corresponding elastic constants. The Orientation is the crystalline orientation of the substrate being tested.

Substrate Material	Orientation	Elastic Constants (10 <sup>11</sup> Pa)
Aluminum	*	1.030
Aluminum Oxide (Al <sub>2</sub> O <sub>3</sub> )	+	3.835
Aluminum Oxide (Al <sub>2</sub> O <sub>3</sub> )	+	4.895
Aluminum Nitride (AIN)	+	4.367
Beryllium Oxide (BeO)	+	4.367
Borophosphosilicate (BPSG) Glass	+	1.500
Gallium Arsenide (GaAs)	111	1.741
Gallium Arsenide (GaAs)	100	1.239
Germanium (Ge)	111	1.837
Germanium (Ge)	100	1.420
Phosphosilicate (PSG) Glass	+	0.988
Quartz	+	0.850
Sapphire	+	4.080
Silicon	111	2.290
Silicon	100	1.805
Sodalime glass (Corning microsheet 0211)	+	0.973

 Table 14.2
 Elastic Constant of Substrates

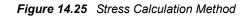
(+ = amorphous structure)

#### **Choosing the Stress Calculation Method**

 The stress can be calculated using either of two methods. The first, Polynomial Fit, is the recommended method. This method gives the best repeatability. The Using Polynomial Fit option gives the opportunity to choose from three polynomial orders, 5th, 6th, and 7th. The best results come from the 5th order polynomial. The higher the order, the higher the possibility that smaller sample surface features could be included in the calculation.

To choose the order, click on the menu-arrow next to the variable box and click on the order to be used. (See *Figure 14.25*.)

2. The second method is the **13 Point Least Square Fit** method, described in the introduction to this chapter. **13 Point Least Square Fit** calibration is a legacy formula that does not provide the best calculation results for stress. Its repeatability is not as good as the Polynomial Fit procedure. It is still present in the software for use by those who wish to compare the results of current scans with older scans that used the **13 Point Least Square Fit** calibration for stress calculations before the new Polynomial Fit formula was available. This method should not be used unless it is well understood and conducted for specifically defined results. (See *Figure 14.25*.)



 Step 1 Click in the empty radio button to choose it. The dot indicates that it is chosen.
 Stress Calculation Method
 Choose Order of Polynomial

 The 13 Point Least Square Fit option (does not provide the best reproducible results).
 Stress Calculation Method
 5
 Image: Click on the menu-arrow to view the menu. Choose the desired polynomial order. 5 is generally acceptable for most stress applications.

# SAVING A STRESS RECIPE

It is necessary to save a current recipe if any of the following circumstances occur:

- If any of the parameters in a current recipe have been changed and the changes need to be preserved.
- If any of the parameters in a current recipe have been changed and the changes need to be preserved, but the old recipe also needs to be saved. In this case it is necessary to perform a **Save As** procedure.
- If a new recipe has been created and used but not saved, and there is a need to preserve the recipe for future use.

# **Saving Recipe Parameters**

When the parameters in a current recipe have changed and those changes need to preserved in the current recipe, use the following procedure.

- 1. From the Stress Recipe screen, click **Recipe** in the Menu Bar. This displays its **menu**.
- 2. Click Save.

# Saving Recipe Parameters as a New Recipe

If the user changes parameters in a recipe and needs to keep the old recipe in tact while preserving the changes, a new recipe can be created from the original.

1. When the parameters have been changed in a recipe, and before the changes have been saved as part of the original recipe, click Recipe at the far left end of the Menu Bar to display its menu.



	Profiler - [St							x
-		te ⊻acuum ⊻iew						
Click <b>Recipe</b> to display its	New Save Stress Be	Ctrl+N scine Ctrl+S	Q SIS LEVEL	START 🛞	+ ?	N?		🔂
menu.	Save Stress Re	ecipe <u>A</u> s	RESS_TEST_01					
	<u>P</u> rint Print Pre⊻iew	Ctrl+P			Substrate Spe	ecification:		
	Print Setup		pints: 15	_	Name:	<other></other>	•	파 68
Click Save As to open the	E <u>x</u> it		_		Thickness:	1000	μm	· · · · · · · · · · · · · · · · · · ·
Stress Recipe Name dialog			 μm Υ: Ο	, μm	Modulus:		x10^11 Pa	
box. (See Figure 14.27.)		n p	pun r. lo	- Fun		1.0000	210 1110	
		Scan Parameters						
		Scan Length: 1	500	Ψ μm	Sampling Rate:	200 💌	Hz	
		Scan Speed: 1	00	▼ µm/s	Stylus Force:	5.0000	mg	
				Stylu	us Start Position:	Middle		
		Stress Calculation 1	Method		Choose Order	of Polynomial	,	
			Using Polynomial Fit			5		
			Using 13 Point Least S	autro Eit				
			- Using 131'Offic Lease 3	quare nit				
	CALIBRATION					E	mpty?	Clear Status

2. Choose Save As to display the Stress Recipe Name dialog box.

Figure 14.27 Stress Recipe Name Dialog Box.

Stress Recipe Name	×
Pleace enter new Stress Recipe Name: (Max length 79 characters) stress_gal	OK Cancel

- **3**. Enter the name of the new recipe name in the provided space. The name should help the user quickly identify the specific use for the recipe.
- 4. Click **OK** to establish the new recipe using the parameters displayed in the original one.

# PRINTING A STRESS RECIPE

With the Stress Recipe Editor open, click on the printer icon. This prints the currently displayed stress recipe.

Figure 14.28 Printer Icon in Tool Bar

Click the printer icon to print the list of stress recipe parameters for the current recipe.		Vacuum         View         Stress         Lasks         Help           Image: Construction         Construction         Image: C	Constraint Specification:     Name: <01ther>     Thickness: 1000     Modulus: 1.0000  Sampling Rate: 200     Stylus Force: 5.0000 us Start Position: Middle     Choose Order of Polynomial 5	μm μm x10 <sup>-11</sup> Pa	
	CALIBRATION	<ul> <li>Using Polynomial Fit</li> </ul>		T Emply?	_Clear Status

# **CREATING STRESS DATA**

# Taking a Single Pre-Stress Scan

In order to create stress data that is accurate and usable, the following must be observed:

- The same wafer must be used for the pre- and post-stress scans.
- The wafer must be positioned in exactly the same place on the stage for both pre- and post-stress scans. This is accomplished through the use of a stress precision locator.
- The pre- and post-stress scans must be performed using the same recipe.

#### Load a Wafer on the Stress Locator

It is essential that the wafer be placed in the same place, in the same orientation on the stage, for both the pre- and post-stress scans. It is also very important that the wafer be supported on three points. If the wafer rests flat on the stage, its weight could create deformation that could distort the stress data. For these reasons it is essential that the stage be equipped with a stress precision locator.

- 1. If the stress precision locator is not in place on the stage, attach it using the procedure described in *Installing a Precision Locator* on page 11-47, with additional reference to *Optional Precision Locators* on page 11-58.
- 2. Load the wafer using the Load Wafer Manual Procedure on page 14-6.

#### **Choosing a Stress Recipe**

Choose the stress recipe that is to be used for both the pre- and post-stress scans using the following procedure.

- 1. To open the Stress application, click the **Stress** icon Stress Catalog screen.
- 2. This displays the **Stress** application screen. If the Recipe catalog is not displayed, click on **Stress Recipe Catalog** to view the currently saved and available stress recipes. (See *Figure 14.29*.)

Figure 14.29 Stress Application Screen

Step 2 If not already highlighted, click on Stress	Profiler - [SI <u>B</u> ecipe <u>S</u> ubstra NEW	ress) Re Vacuum View Stress Iasks Help 🚳 📿 🔍 🐨 teven start 🛞 🤅	) ? N?	×
Recipe Catalog to display the current list of stress related scan recipes.	Stress Recipe Catalog Scan Data Catalog	Stress Recipe Name: STRESS_GAL Stress Recipe Name 1000,50 5000 200 MARCUS STRESS_GAL	Date         Time           10/27/1988         09:21:34 AM           10/27/1988         10:33 11 AM           05/11/1999         02:13:05 PM           05/12/1393         04:108:54 PM	
Recipe list area. See <i>Figure 14.30</i> .		<b>Step 4</b> To change recipe parameters click <b>View/Modify</b> .	<b>Step 7</b> To start the scan using the highlighted recipe, click <b>Start</b> .	
	SCAN DATA CAT	<u>Print</u>	<u>Start</u> Delete Empty	Cicar Status

**3**. Choose a Recipe to use for a pre-stress scan by clicking on the recipe to highlight it. When highlighted, the recipe name appears in its entirety in the **Stress Recipe Name** box. (See *Figure 14.30*.)

If no changes are required to the current recipe before it is run, skip to Step 7.

If recipe parameter modifications are required before running the scan, continue.

Figure 14.30 Stress Recipe List Area

	Stress Recipe Name:	STRESS_GAL		
When a recipe is selected, its				
name appears in full in the	Stress Recipe Name		Date	Time
	1000 50		10/27/1998	09:21:34 AM
Stress Recipe Name box.	5000 200		10/27/1998	10:39:11 AM
	MARCUS		05/11/1999	02:19:05 PM
List of ourraptly available	STRESS_GAL		05/12/1999	04:08:54 PM
List of currently available				
Stress Recipes.				

If the Stress Recipe must be Modified:

Starting the Pre-stress

Scan

- 4. If the recipe requires modification of parameters before the scans can be run, click View/Modify at the bottom center of the screen. (See *Figure 14.29*.)
- 5. The Stress Recipe window opens. Change the parameters requiring adjustment. (For information of parameters see *Modifying a Stress Recipe* on page 14-15.)
- 6. To save the recipe changes either directly to the recipe or create a new recipe, see *Saving Recipe Parameters* on page 14-20 or *Saving Recipe Parameters as a New Recipe* on page 14-20.
- 7. From either the Stress catalog screen or the Stress recipe editor, click the **START** button to initiate the pre-stress scan.

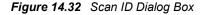
Figure 14.31 Stress Recipe Catalog Screen

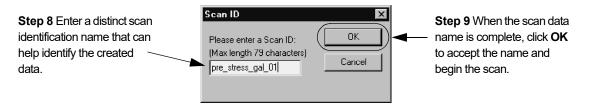
🐺 Profiler - [St	ess		×
<u>R</u> ecipe <u>S</u> ubstra	e <u>V</u> acuum <u>V</u> iew <u>S</u> tress <u>I</u> asks <u>Help</u>		
NEW	🛎 🙆 a TTT LEVE START 🔊 😁	? N?	
Stress Recipe	Stress Recipe Name: STRESS_GAL		
Catalog	Stress Recipe Name	Date Time	
Scan	1000_50 5000_200	10/27/1998 09:21:34 10/27/1998 10:39:11	AM I U
<u>D</u> ata Catalog	MARCUS STRESS_GAL	05/11/1999 02:19:05 05/12/1999 04:08:54	
	Step 7 With the stress		
	recipe chosen, click		
	START to initiate the		
	pre-stress scan, using		
	the highlighted recipe.		
	1		
	<u>P</u> rint <u>V</u> iew/Modiły	<u>S</u> tart <u>D</u> elete	;
SCAN DATA CAT	ALOG	Empty	Clear Status

8. This displays the **Scan ID** dialog box. Enter a scan data identification name that allows the user to clearly isolate it from other data.

#### EXAMPLE:

In *Figure 14.32*, **pre\_** refers to pre-stress, **stress\_** identifies the scan as stress related, **gal\_** indicates that it is a gallium arsenide substrate, and **01** is the scan number.





9. When the name has been entered, click **OK** to accept the scan data name and begin the scan. (See *Figure 14.33*.)

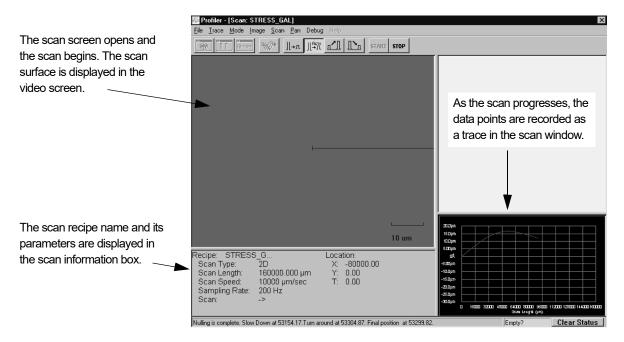


Figure 14.33 Scan Screen with Real Time Scan Trace

10. When the scan is complete, the data is automatically saved and the Scan Analysis screen opens. (See *Figure 14.34*.)

To close the analysis screen, click on the control button at the top left corner of the screen and choose **Close** from its menu. (See *Figure 14.34*.)

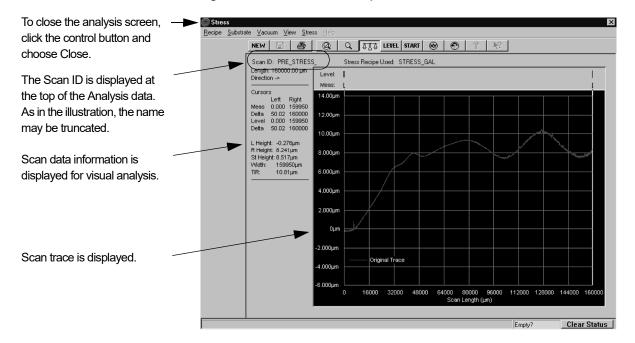


Figure 14.34 Stress Scan Analysis Screen

To close the analysis screen, click on the control button at the top left corner of the screen and choose **Close** from its menu. (See *Figure 14.34*.)

## Taking a Single Post-Stress Scan

Use the same procedure detailed in Taking a Single Pre-Stress Scan. Be sure to name the scan in such a way that it can be distinguished clearly from other scans in regards to pre- or post-stress, substrate, and any other pertinent information.

The scan should:

- Have the same recipe as the pre-stress scan
- Be made with the wafer placed on the stress locator
- Be made with wafer in the same orientation on the locator as in the pre-stress scan

# **ANALYZING STRESS SCAN RESULTS**

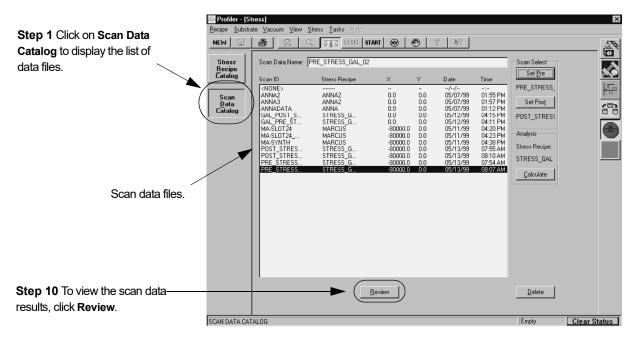
Stress analysis is accomplished through the comparison of a pre-stress scan and a post-stress scan. The analysis is not saved, but is instead generated each time the calculations are performed.

## **Viewing Stress Scan Results**

1. From the Stress screen, click on **Scan Data Catalog**. This displays the names of the scan data files. (See *Figure 14.35*.)

Notice that the catalog list has information regarding the ID (name) of the data file, the stress recipe used to collect the data, the X- and Y-coordinates at which the scan started, the date the data was collected, and the time it was collected.

Figure 14.35 Stress Screen with Scan Data Catalog Displayed



2. Click to highlight the data file that is to be viewed. Click **Review** at the bottom center of the screen to open the data file. (See *Figure 14.35*.)

Figure 14.36 Stress Screen with Stress Data File

Stress X Recipe Substrate Vacuum View Str If only partial scan data is visible, Q |) 🔍 🚺 🕹 LEVEL START 🛞 🕐 🤗 🐙 NEW click on the cancel zoom icon to Scan ID: PRE\_STRESS Length: 160000.00 µm Direction -> Stress Recipe Used: STRESS\_GAL display the entire graphic. Level: Meas Cursors rs Left Right 0.000 159950 50.02 160000 0.000 159950 50.02 160000 4.00ur Meas Delta Level Delta 12.00µ 10.00µm -0.276µm eight: 8.241µm eight: 8.517µm h: 159950µm 10.81µm 8.000µm Width: TIR: 6.000µm 4.000um 2.000µm Our 2.000um riginal 1.000µn 6.000µn 112000 128000 144000 16000 32000 48000 64000 80000 96000 1600

- 3. If the data is not fully displayed, click the cancel zoom icon. (See Figure 14.36.)
- 4. To return to the Stress catalog screen, press the **Esc** key.

## **Stress Scan Analysis Procedure**

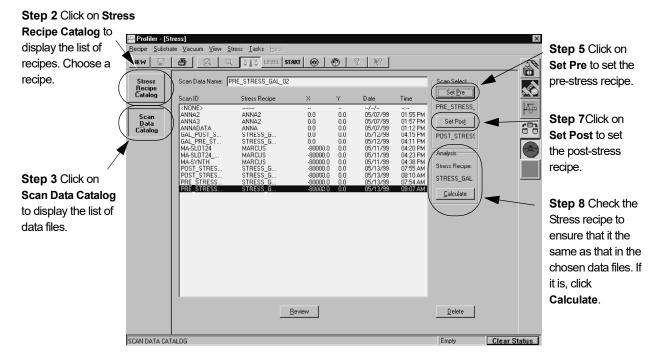
Analysis can be made by comparing a pre-stress single trace with a post-stress single trace of the same wafer at the same location using the same stress recipe.

- 1. To open the Stress application, click the **Stress** icon Stress Catalog screen.
- 2. With the **Stress Recipe Catalog** chosen, click on the recipe that is to be used for the calculation. A chosen recipe is highlighted. (See *Figure 14.37*.)

Clear Status

Empty?

- 3. After the recipe is chosen, click Scan Data Catalog. (See Figure 14.37.)
  - Figure 14.37 Stress Screen with Scan Data Catalog Displayed

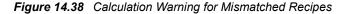


4. Highlight the data file that is to be used as the pre-stress scan.

The Scan ID names might be difficult to tell apart if they are truncated. However, when a data file is highlighted, its entire name is displayed above the scan data file list, in the box titled **Scan Data Name**.

- 5. With the data file highlighted in the Stress Scan Data Catalog, click **Set Pre** to choose the highlighted file for use as the pre-stress scan data file in the calculation. (See *Figure 14.37*.)
- 6. Highlight the data file that is to be used as the post-stress scan.
- 7. Click **Set Post** to choose the highlighted file for use as the post-stress scan data file in the calculation. (See *Figure 14.37*.)
- 8. When both pre- and post-stress data files are chosen, the **Calculate** button is enabled. Check the recipe in the Analysis box and if correct for the pre- and post-stress data files, click on **Calculate** to perform the stress analysis. (See *Figure 14.37.*)

If an incorrect match is made of recipes between the pre- and post-stress data files, and the chosen recipe, a warning box appears. (See *Figure 14.38.*) Click OK to abort the calculation. Start again by choosing the stress recipe in the recipe catalog and again choose the pre- and post-stress scan data files.





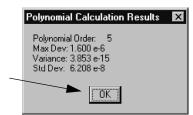
- 10. If the data files are accepted for calculation, the **Film Thickness** dialog box appears. (See *Figure 14.39*.) Enter the film thickness, in microns ( $\mu$ m) in the variable box.
- 11. Click **OK** when the thickness has been entered. (See *Figure 14.39*.)

Figure 14.39 Film Thickness Dialog Box

Step 10 Double-click in the variable field to highlight the current value and enter the correct film thickness in microns.

12. The calculation is performed by the system and the calculation results message box titled, **Polynomial Calculation Results**, appears. (See *Figure 14.40*.) Click **OK** to continue.





Step 11 Click OK to continue.

**13**. The Stress calculation analysis screen opens for reviewing the result of the calculation. (See *Figure 14.41* and *Choosing the Stress Calculation Method* on page 14-19.)

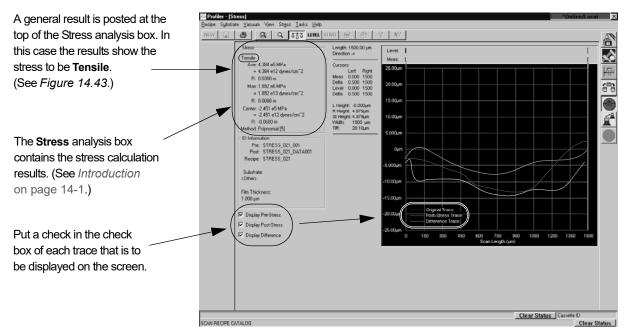


Figure 14.41 Stress Calculation Analysis Screen

NOTE: The data and traces are fictitious and created only to show the position of data reports.

# Analyzing the Results

The calculation results are displayed in the Polynomial Calculation Results message box immediately after the scan is complete. See *Table 14.3* for an explanation of the individual results. Click **OK** to continue with the analysis display.



	Polynomial Calculation Results	×
	Polynomial Order: 5 Max Dev: 1.600 e-6 Variance: 3.853 e-15 Std Dev: 6.208 e-8	
Je. ———		

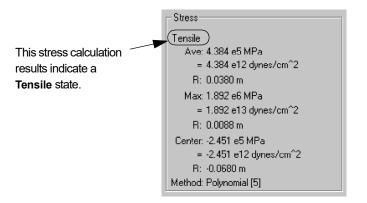
Click OK to continue.

Result	Explanation
Polynomial Order	Chosen as part of the Recipe. (See Choosing the Stress Calculation Method on page 14-19.)
Max. Dev.	Maximum Deviation of the fit polynomial from the original profile
Variance	Variance = (Standard Deviation) <sup>2</sup>
Std. Dev.	Standard Deviation from the Mean

 Table 14.3
 Polynomial Calculation Results Message Box

After the Polynomial Calculation Results message box is closed, the Stress Analysis screen is displayed. The Stress box in the upper left portion of the screen (see *Figure 14.43*) displays the results of the calculation. The computative analysis is characterized at the top of the box as either compressive or tensile. (See *Table 14.4* for an explanation of the box contents.)





The results in each category are displayed in MPa and dynes/cm<sup>2</sup>. In addition, the **R**: in each set of data represents the Radius of Curvature. The Radius of Curvature is the average radius used in calculating stress per the definitions in the Introduction.

Result	Explanation
Stress Designation	Compressive
	Positive value average stress (Ave.) Positive value polynomial
	Tensile
	Negative value average stress (Ave.) Negative value polynomial
Ave.	Average stress over the entire scan, derived from the polynomial fit of the entire profile minus 5% on either end.
Max.	Maximum absolute stress over the entire profile
Center	Stress at the center of the profile
Method	Polynomial Fit or 13 Point Least Square Fit

 Table 14.4
 Stress Calculation Results Box Contents

# **CMP ANALYSIS ALGORITHMS**

# INTRODUCTION

CMP (Chemical Mechanical Polishing) processes are used on a variety of different surface compositions. In general, the analysis of CMP surface scans centers around three structures: arrays, lines, and pads. Each of these structures requires its own unique method of analysis. The analysis can be performed on scans in 2D or 3D scans. In the P-15 systems, the analysis is integrated into the system software. Each basic structure is discussed in its own section. The CMP Analysis chapter contains the following sections:

- Arrays on page 15-2
- Lines on page 15-3
- Pads on page 15-5
- Setup for Analysis on page 15-6
- Analysis Application on page 15-8

# ARRAYS

For the purposes of this analysis, "array" is defined as an array of circular contacts or vias (plug). The contacts or vias are usually a metal like tungsten or copper which typically have polish rates higher than that of the surrounding array oxide. The basic composition of a sample array is illustrated in *Figure 15.1*.

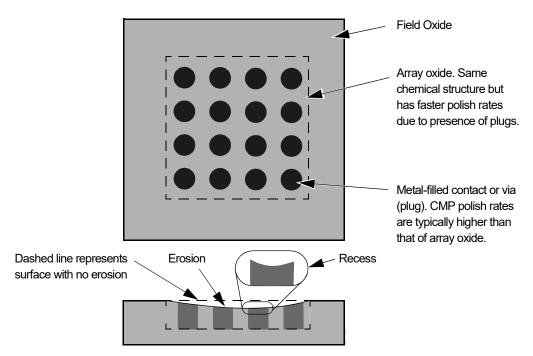


Figure 15.1 Sample Array

## Using the ARRAY Analysis Routine

This routine is designed to perform analysis on both 2D and 3D Profiler data. The same set of input parameters are used for 2D and 3D data belonging to a single recipe, e.g., 2D slices from a 3D data set. The routine is intended for use with array profiles that have negligible recess and considerable erosion. It calculates both erosion and recession.

## Analysis Process

The analysis is performed on Normal data as described in the following sequence:

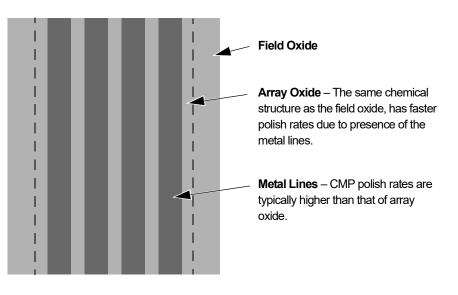
- 1. The data is smoothed using a median filter with a kernel (smoothing window) of five data points.
- 2. The "erosion region" (ER) is found by determining the minimum and maximum slopes in the profile. The slope of each point is defined to be the average slope with respect to the ten nearest neighbors.

- **3**. The "calculations region" (CR) is defined as some fraction of the ER. By default this fraction is set to 1/2 (50%).
- 4. Determine the local maxima within the CR using a window of 5 data points.
- 5. Determine the local minima within the CR using a window of 5 data points.
- 6. Using the local maxima, interpolate to obtain a curve that fits those points (curve A).
- 7. Using the local minima, interpolate to obtain a curve that fits those points (curve B).
- 8. Calculate the average of curve A. This is the erosion value.
- 9. Calculate the average of curve B. Subtract the erosion value from this average to obtain the recess value.

## Lines

For the purposes of this analysis, "lines" is defined as an intermittent distribution of metal and oxide lines. The metal line are usually a soft metal like aluminum or copper which typically have polish rates higher than that of the surrounding array oxide. The basic composition of a sample set of line is illustrated in *Figure 15.2*.





#### **Using the LINES Analysis Routine**

The LINES routine assumes that the lines are running parallel to each other. The scan path must be perpendicular to the lines. This routine is designed to perform analysis on both 2D and 3D Profiler data. The same set of input parameters are used for 2D and 3D data belonging to a single recipe, e.g., 2D slices from a 3D data set. The analysis is intended for profiles exhibiting both recess and erosion. It calculates both erosion and recession.

## Analysis Process

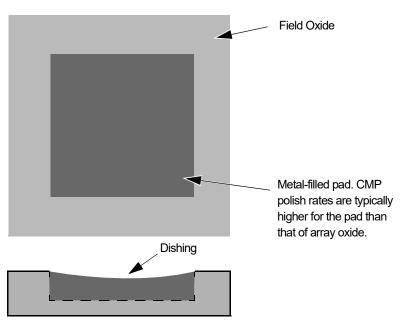
The analysis is performed on Normal data as described in the following sequence:

- 1. The data is smoothed using a median filter with a kernel (smoothing window) of five data points.
- 2. The "erosion region" (ER) is found by determining the minimum and maximum slopes in the profile. The slope at each point is defined to be the average slope with respect to the ten nearest neighbors.
- **3**. The "calculations region" (CR) is defined as some fraction of the ER. By default, this fraction is set to 1/2 (50%).
- 4. Determine the vertical range of data within the CR. Define Tolerance to be 1/2 of the vertical range.
- 5. Determine the local maxima within the CR using a window of variable size. The size of the window is roughly equivalent to the pitch of the lines. The Tolerance is used to calculate the size of this window for each individual data point.
- 6. Determine the local minima within the CR using a window of variable size. The size of the window is roughly equivalent to the pitch of the lines. The Tolerance is used to calculate the size of this window for each individual data point.
- 7. Using the local maxima, interpolate to obtain a curve that fits those points (curve A).
- 8. Using the local minima, interpolate to obtain a curve that fits those points (curve B).
- 9. Calculate the average of curve A. This is the erosion value.
- 10. Calculate the average of curve B. Subtract the erosion value from this average to obtain the recess value.

## Pads

For the purposes of this analysis, "pads" is defined as a larger region of metal surrounded by an oxide. The pads are usually a soft metal like which typically has a polish rate higher than that of the surrounding oxide. The basic composition of a sample pad is illustrated in *Figure 15.3*.





#### **Using the PADS Analysis Routine**

This routine is designed to perform analysis on both 2D and 3D Profiler data. The same set of input parameters are used for 2D and 3D data belonging to a single recipe, e.g., 2D slices from a 3D data set. The routine is intended for use with pad profiles to calculate dishing.

#### **Analysis Process**

The analysis is performed on Normal data as described in the following sequence:

- 1. The data is smoothed using a median filter with a kernel (smoothing window) of five data points.
- 2. Find the "erosion region" ER by finding the minimum and maximum slopes in the profile. The slope at each point is defined to be the average slope with respect to the ten nearest neighbors.
- 3. The "calculations region" (CR) is defined as some fraction of the ER. By default, this fraction is set to 1/2 (50%).
- 4. Calculate the average of all data points within the calculation region. This will be the dishing value.

## **Setup for Analysis**

## Introduction

A scan can be programmed to include any of the three types of analysis, erosion, recess, and dishing, using the scan recipe. The scan data is processed to present erosion and recess, or dishing values to the Analysis screen. In addition, the 6.x software saves the data from each scan so that the erosion, recess, or dishing values can be calculated later by changing the recipe parameters used to create the original scan.

## Setup for Erosion and Recess Analysis

- 1. From the Catalog screen choose Scan Recipe.
- 2. Double-click on the required recipe to open the Recipe Editor for that recipe. (Or click to highlight the required recipe, then click on **View/Modify** at the bottom of the screen.)
- **3**. From the Recipe Editor screen choose **Setup Analysis Tools**. This displays the Setup Analysis Tools dialog box. (See *Figure 15.4*.)
- 4. Click on the CMP Analysis Setup tab to display its page. (See Figure 15.4.)

Figure 15.4Setup Analysis Tools Dialog Box

	🔛 Profiler - [Recipe Ed			*Online/Local ×
	Recipe Options Sample			
		3 🗠 🖄 START 🛞 🕙 🔩 🕾		
Step 4 Click on the CMP Analysis Setup	Scan Parameter Definition Feature	⊂20 Scan X Scan Size (µm). 100.000 ▼		
tab to display its page.		Setup Analysis Tools	×	
tab to display its page.	Filters Cursors	Scan Speed (ur Deprin Analytis CMP Analytis Setup	)	
	Unit Output	Sampling Rate I Multi-Scan Aver	Condition for User Defined Input Parameters: Scan Length > Anay Wath > Pitch > Wath > 0.0	
	General Parameters	Scan Direction:	Current Scan Length 100 µm	
	Roughness	Johnsteine	Array Width Information	
	Waviness	Scan Time:	C Unknown	
	Bearing Ratio Cutting Depth	Individual Trace Select Parameters to Calculate	C UserDefined	
Step 3 Click on Setup	High Spot Count	Approx. Total (* - Stylus: Erosion	Pitch Information	
• •	Peak Count	Applied Force (r	@ Unknown	
Analysis Tools to open	Setup Analysis Tools	Stylus Radius ().	C User Defined	
its dialog box.		Vertical Rangin Range/Resolut	Width Information  C Unknown	
		Profile Type : Dishing	C UserDefined	
			OK Cancel	
	SEQUENCE RECIPE CATA	106	Clear	Status Cassette ID Empty? Clear Status
	DEQUENCE NEUPE CATA	50V		

5. From the Select CMP Application drop-down menu select either Array or Lines. Both of these selection enable the Erosion and Recess analysis checkboxes in the Select Parameters to Calculate field. Both choices open with a check in their checkbox. (See *Figure 15.5.*) This indicates that they are enabled and will be calculated, with the results displayed in the Analysis screen's Statistics window.

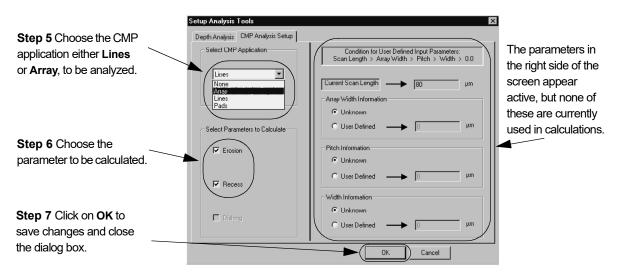


Figure 15.5 CMP Analysis Setup Page

6. With either Lines or Arrays chosen, with the selected application displayed in the Setup CMP Application drop-down menu field, choose the parameters (Erosion, or Recess) to be calculated. The default is, both Erosion and Recess are enabled. (See *Figure 15.5.*) To enable or disable a parameter, click in the checkbox to toggle the check in and out of the field.

Notice the parameters on the right side of the screen appear to be active. Values can be entered in the User Defined fields, but they are not currently used in the calculations. These parameters are part of an upcoming capability enhancement to the current algorithm.

- 7. Click **OK** when all the changes are complete. This closes the Setup analysis Tools dialog box.
- 8. The recipe must be saved after the recipe changes are complete if they are to be preserved in the recipe. (See *Figure 15.5.*)

#### **Setup for Dishing Analysis**

The dishing analysis is performed on Pads. When the Pads application is chosen, the only parameter that is active is Dishing. Erosion and Recess are inactive.

1. In the CMP Analysis Setup page, choose **Pads** from the **Select CMP Application** drop-down menu.

The **Select Parameters to Calculate** field changes to reflect the **Dishing** parameter active and enabled. If left as it is, the Dishing analysis takes place and the results are displayed in the Analysis screen's Statistics window.

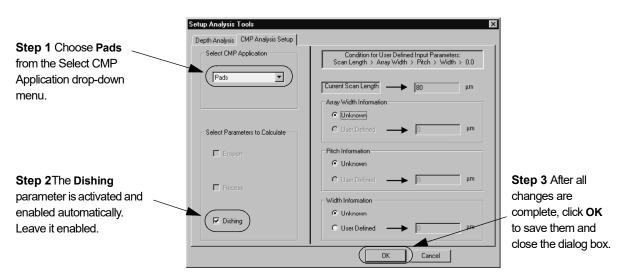


Figure 15.6 CMP Analysis Setup for Pads Analysis

- 2. The Dishing parameter should be active and have a check in the checkbox (enabled). Leave it that way. If no check is present, click in the checkbox to place the check in the box. (See *Figure 15.6.*)
- **3**. After all changes are complete, click on **OK** to save the changes and close the dialog box. (See *Figure 15.6*.)

## **Analysis Application**

During the analysis of data following a scan, the chosen parameters are calculated and displayed in the Statistics window of the Analysis screen. For data gathered from scans that used recipes from previous software versions, the data can be recalculated by changing parameters in the recipe originally used to create that data. this means that data which was originally processed without the erosion, recess, or dishing calculations can be recalculated by activating these applications and parameters in the original recipe.

## Analysis of New Data

When a scan or sequence of scans are run using one or more recipes containing the CMP Analysis Algorithm, the results are displayed in the Analysis screen immediately following the scan.

- 1. Set up the recipe to be used according to the procedures described in the section titled *Setup for Analysis* on page 15-6.
- 2. If the recipe, or a series of related recipes, is to be used in a sequence, follow the procedure for establishing a sequence described in *Creating a Sequence Recipe* on page 7-13.

## Starting a Sequence Containing CMP Analysis

The following procedure assumes that the recipes used in the sequence have already been set up to perform the CMP analysis.

- 1. In the Catalog screen, choose **Sequence Recipe**. This displays the available sequence recipes in the List window. (See *Figure 15.7*.)
- 2. In the Sequence Scan List window, click on to highlight the sequence recipe to be used. (See *Figure 15.7.*)
- 3. Click **START** to initiate the scan sequence. (See *Figure 15.7.*)

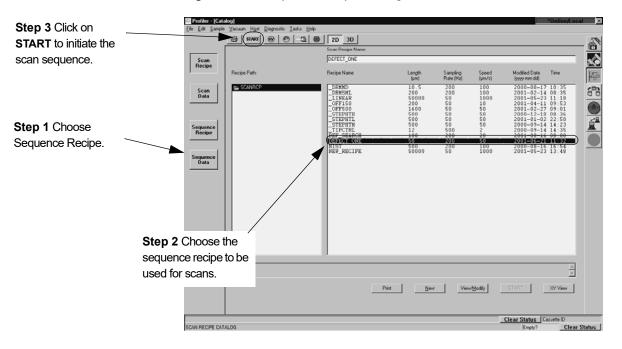


Figure 15.7 Sequence Recipe Catalog Screen

4. Click on **START** in the tool bar to initiate the scan sequence. (See *Figure 15.7.*) The screen changes to the View Scan screen and scan sequence begins. The procedure continues until all the scans at all the designated sites are complete. When the sequence ends the system performs all the required calculations. The Analysis screen is then displayed.

#### Analysis Screen for Sequences Running the CMP Analysis

The Analysis screen is composed of two major windows, the Analysis Trace and the Statistics. For more information on 3D the Analysis screen functions see 3D Analysis Screen Features on page 9-3, and for 2D see 2D Analysis Window Features on page 8-5.

Once the screen is open, the results of the CMP Analysis calculations are visible in the Statistics window. (See *Figure 15.8*.)

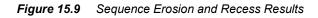
The sequence in *Figure 15.8* contains scans from each wafer in a cassette. The same sites were scanned on each wafer. One scan is performed on each different site on the wafer. Each site scan is performed using a different recipe. Each identical scan site on all the wafers is processed using the same recipe. E.g., all #3 scan sites use the same recipe. This makes it possible to correlate the results and view them all together in one place.

1. To view the trace of the statistics set in the Statistics window, click on the site number below the cassette wafer slot. (See *Figure 15.8*.)

it: 1-F-931	E50-5			is <u>W</u> indow <u>H</u>	100.0			- 8					
J.	III Seque	CT Parame	ter Data										- 10
eskew Sample	Lot: 1-F-93 Op:	1	Se Re	quence: 1-F-931 cipe: E50-5									
Site 3	Deskew	Sample	Stat	Analyze	Xoffset	Yoffset	Depth 1	S.D. 1	Depth 2	S.D. 2	Erosion	Recess	
Passed Slot 5	Passed	Sile 3 Slot 5		Inc	2.31 µm	2.00 µm	-612.0Å	48.1 Å	137.6 Å	42.0 Å	-399.1 Å	-161.6 Å	
Site 3		Site 3		Inc	2.31 µm	2.00 µm	-267.6 Å	10.5 Å	63.6 Å	15.7 Å	-199.2 Å	-66.1 Å	
assed Slot 6	Passed	Slot 6 Site 3		Inc	2.31 µm	2.00 µm	-233.3 Å	32.1 Å	51.4 Å	12.5 Å	-233.7 Å	-65.9 Å	
	Passed	Silot 7 Silte 3		Inc	2.31 µm	2.00 µm	-328.4 Å	33.2 Å	14.5 Å	28.4 Å	-183.6 Å	-172.2Å	
Site 3	Passed	Slot 8		Inc						20.4 A			
	Passed	Sile 3 Slot 9		Inc	2.31 µm	2.00 µm	-247.2 Å	34.8 Å	114.6 Å	28 1 Å	-328.2 Å	68.4 Å	
<b>A</b>		Site 3		Inc	2.31 µm	2.00 µm	-247.3 Å	10.7 Å	83.7 Å	23.0 Å	-106.1 Å	-91.4 Å	
	Passed	Slot 10 Site 3		Inc	2.31 µm	2.00 µm	-283.3 Å	17.4Å	115.9Å	19.1 Å	-127.6Å	-81.8 Å	
	Passed <	Slot 11	_										
<b>p 1</b> Click on the		ata: Slot f	Cite III	2									Ē
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	E50-5 Length: 350	0.00 µm	Meas:	U									
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	R Height: 0 St Height: 2	5A 390A	-400Å	,	150 700	1050	1400	1750	2100	2450	2900	3150	
	Vykatric 1												

Figure 15.8 Analysis Screen for Sequence with CMP Analysis

The Erosion and Recess calculation results are displayed in their respective columns in the Statistics window. (See *Figure 15.9.*) If one of the calculations shows a result that is questionable, the trace can be viewed and the data recalculated after adjusting parameters, like applying a filter or cursor placement.



	uuuo -		Data Set: A-1-TO-23	lp							*Online/Local
	E50-5						- 8				
(	<b>#</b> Sequer	nce Paramete	er Data								_ 🗆
(	Lot: 1-F-93 Op:	1	Sequence: 1-F-931 Recipe: E50-5								
	Deskew	Sample	Stat Analyze	Xoffset	Yoffset	Depth 1	S.D. 1	Depth 2	S.D. 2	Erosion	Recess
$\checkmark$		Site 3	Inc	2.31 μm	2.00 μm	-612.0 Å	48.1 Å	137.5 Å	42.0 Å	-161.6 Å	-399.1 Å
	Passed	Slot 5					10.51		10.0	100.01	
Sequence 🔶	Passed	Site 3 Slot 6	Inc	2.31 μm	2.00 μm	-267.6 Å	10.5 Å	63.6 Å	15.7Å	-199.2 Å	-66.1 Å
dentification	F dsseu	Site 3	Inc	2.31 µm	2.00 μm	-233.3 Å	32.1 Å	0.0 Å	0.0 Å	-55.9 Å	-233.7 Å
denuncation	Passed	Slot 7									
nformation.		Site 3	Inc	2.31 μm	2.00 μm	-328.4 Å	33.2 Å	0.0 Å	0.0 Å	-172.2 Å	-183.6 Å
normation.	Passed	Slot 8									
		Site 3	Inc	2.31 μm	2.00 μm	-247.2 Å	34.8 Å	114.6 Å	28 1 Å	68.4 Å	-328.2 Å
	Passed	Slot 9									
		Site 3	Inc	2.31 µm	2.00 µm	-247.3 Å	10.7 Å	83.7 Å	23.8 Å	-91.4 Å	-186.1 Å
	Passed	Slot 10		2.01	2.00	202.2.8	17.4.8	115.0.8	101.8	107.0 \$	01.0.8
	Derrord	Site 3 Slot 11	Inc	2.31 μm	2.00 μm	-283.3 Å	17.4 Å	115.9 Å	19.1 Å	-127.6 Å	-81.8 Å
	Passed ◀	510(11									

Erosion and Recess calculation results for the scan of site #3 on some of the wafers in Lot 1-F-931.

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