6

VIEW SCAN WINDOW

INTRODUCTION

This chapter describes:

2D SCREEN FUNCTION

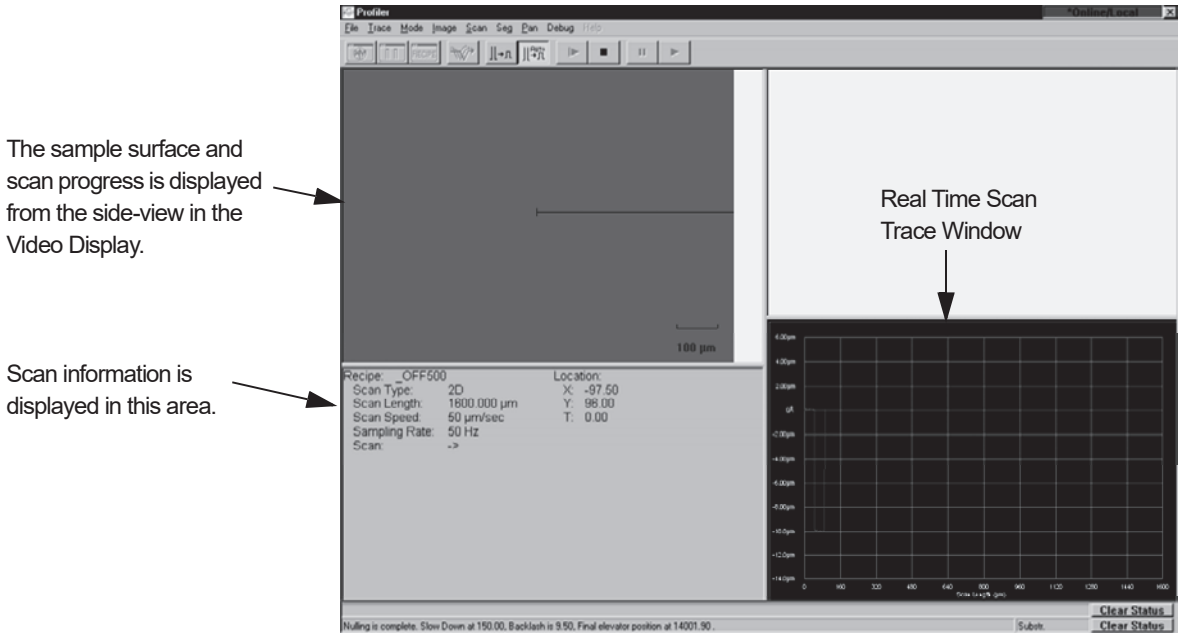
The **View Scan Window** appears while a scan is being run. It allows the user to observe the progress of the scan and to adjust scan parameters in the various screens for optimum scan results. The scan can be started once the recipe has been chosen and the sample loaded onto the sample stage. The scan 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*.)

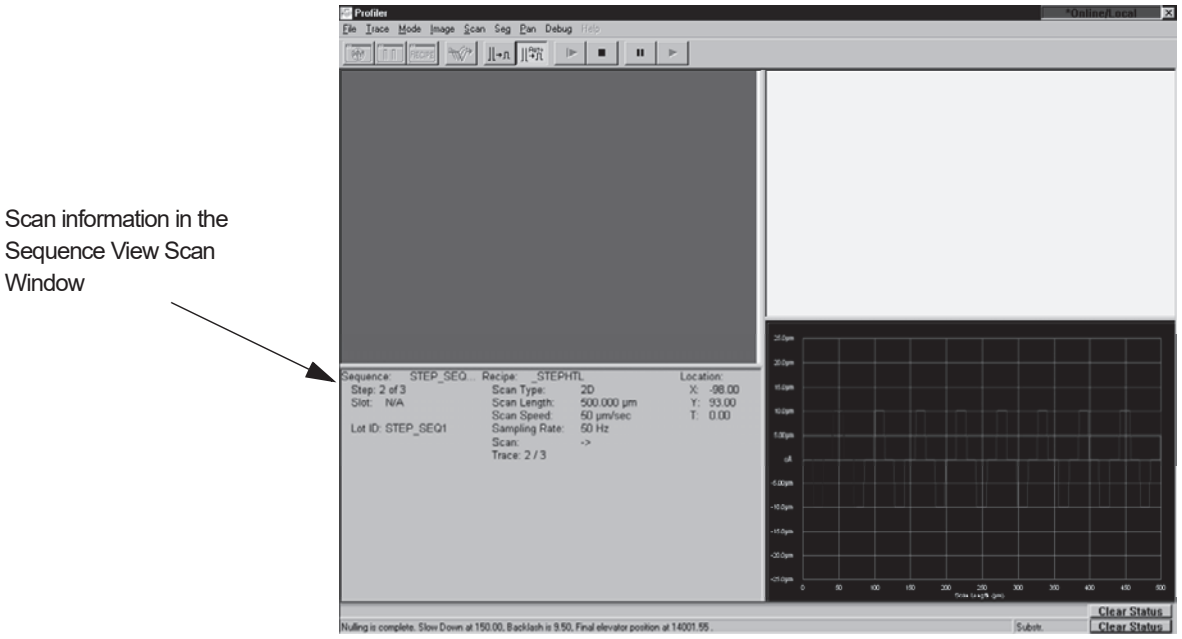
The head lowers bringing the stylus into contact with the sample at the start-of-scan position. The scan begins, first briefly traveling *opposite* the scan direction, then reversing. This allows the mechanical instruments to settle down and the stage to reach the programmed scan speed before data collection 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*



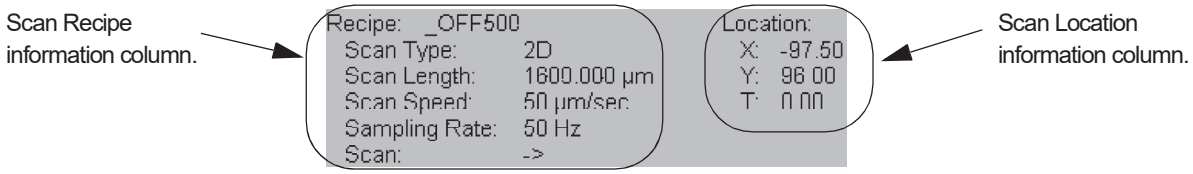
Two columns of information are presented in the lower left quadrant of the 2D scan screen (*Figure 6.1*) and three columns in the 2D sequence screen (*Figure 6.2*).

Figure 6.2 *2D Sequence View Scan Window*



2D Scan Information Field

Figure 6.3 *2D Scan Window - 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

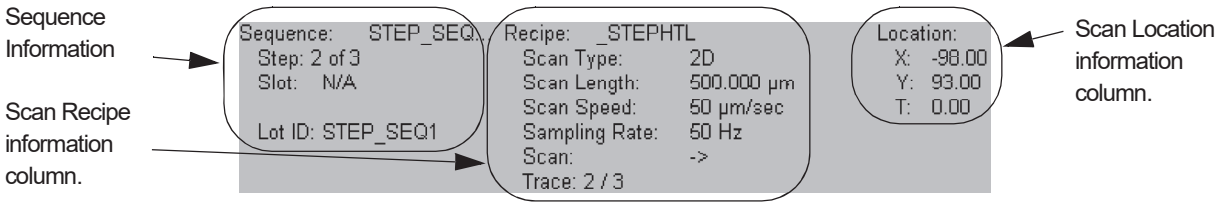
The second column in the Scan Information field is the Location column. It contains the coordinates and orientation of the scan starting point. *Table 6.2* presents a brief description of each parameter.

Table 6.2 *View Scan Screen - 2D Location Information Column*

Parameter	Description
X	The X coordinate of the scan origination point
Y	The Y coordinate of the scan origination point
T	The rotational value of the sample at the scan origination point.

Scan Information Field - 2D Sequence Recipe Column

Figure 6.4 *2D Scan Window - Scan Information Field*



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 *Table 7.7 on page 7-11*.)

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.

Table 6.4 *Scan Screen - Recipe Information Column*

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.

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.
T	The rotational value of the sample at the scan origination point for the current scan in the sequence.

Video Image

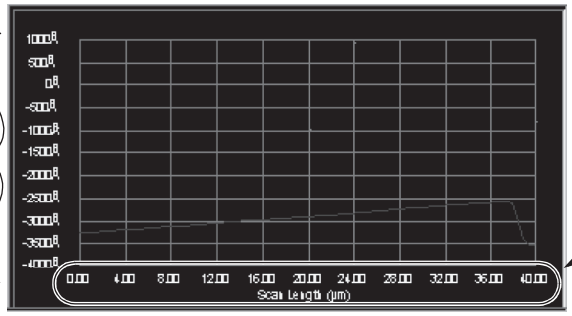
The upper left quadrant of the screen displays a side-view of the scan as it progresses across the sample surface. A trace arrow in the top-down view, visible with its origin at the crosshair of image, marks the course of the scan. (See *Figure 6.1 on page 6-2*.)

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.

Figure 6.5 *Scan screen - real time Trace Window*

This is the Y axis of the scan graph. It is set by system to capture the height and depth of sample surface features.



This is the X axis of the scan graph. It is determined by the **Scan Length** setting in the recipe.

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.

Table 6.6 *2D View Scan Window Tool Bar Buttons*

Button	Description
	**XY View Screen Icon** – Changes to view the XY View screen.
	**Analysis Screen Icon** – Changes screens to view the Analysis screen.
	**Recipe Editor Screen Icon** – Changes screens to view the Recipe Editor Screen
	**Manual Scaling** – Resizes the trace to fit in the graph. Requires operator initiation.
	**Auto Scaling** – Automatically resizes the trace after each scan.
	**START SCAN** – Starts a stopped scan. The scan that was stopped begins again from the start, the prior partial scan is not retained.
	**STOP SCAN** – 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.
	**PAUSE SEQUENCE** – N/A for single scans.
	**START/RESUME SEQUENCE** – N/A for single scans.

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.

Figure 6.6 *2D View Scan Screen Menu Bar*

Table 6.7 *2D View Scan Screen - File Menu*

File Menu	Description of Menu Items
	**Oscilloscope** – Not available with P-series systems.
	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.
	Analysis – Returns to the Analysis screen with the current data displayed. ◆ If the scan is stopped by the user, the user can toggle to the Analysis screen by using the File/Analysis menu item. ◆ 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.
	Edit Recipe – Opens the Recipe screen for the current scan. ◆ 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.
	Exit Scan – Closes the current screen.

Table 6.8 *2D View Scan Screen - Trace Menu*

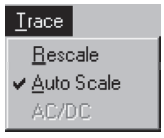
Trace Menu	Description of Menu Items
	**Rescale** – Resizes the trace to fit in the graph. Requires operator initiation.
	Auto Scale – Scales the trace as it is being created.
	AC/DC – Grayed out - Not available.

Table 6.9 *2D View Scan Screen - Mode Menu*

Mode Menu	Description of Menu Items
	**Background Subtraction** – appears active but is not available for use with the P-15 system.

Table 6.10 *2D View Scan Screen - Image Menu*

Image Menu	Description of Menu Items
	**Zoom In** – Not available in the P-series systems.
	Center Anchor – Not available for single 2D scans.
	Corner Anchor – Not available for single 2D scans.
	Edit Scan Parameters… – Use the **File/Recipe** menu item for this function.

Table 6.11 *2D View Scan Screen - Scan Menu*

Scan Menu	Description of Menu Items
	**Start** – 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.
	Stop – 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.

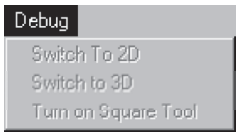
Table 6.12 *2D View Scan Screen - Sequence Menu*

Sequence Menu	Description of Menu Items
	**Pause** – Used in Scan Sequences only.
	Resume – Used in Scan Sequences only.

Table 6.13 *2D View Scan Screen - Pan Menu*

Pan Menu	Description of Menu Items
	**Slow** – Small size stage movement increments. The Slow movement is defined in the Move Speeds dialog box.
	Medium – Medium size stage movement increments. The Medium movement is defined in the Move Speeds dialog box.
	Fast – Large size stage movement increments. The Fast movement is defined in the Move Speeds dialog box.
	Move Speeds… – 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.
	Up – Not Available in the P-Series systems.
	Down – Not Available in the P-Series systems.

Table 6.14 *2D View Scan Screen - Debug Menu*

Debug Menu	Description of Menu Items
	**Switch to 2D** – unavailable for this application
	Switch to 3D – unavailable for this application
	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.

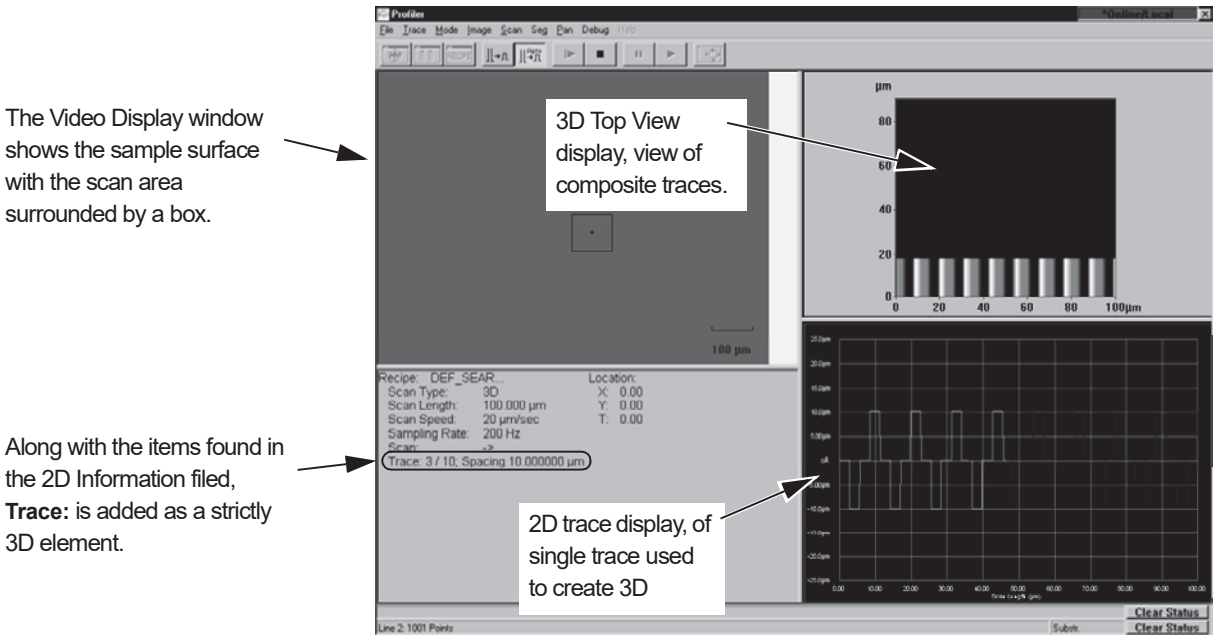
The **View Scan Window** for 3D scans appears while a scan is being run. It allows the user to observe the progress of the scan and to adjust scan parameters in the various screens for optimum scan results. The scan can be started once the recipe has been chosen and the sample loaded onto the sample 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.

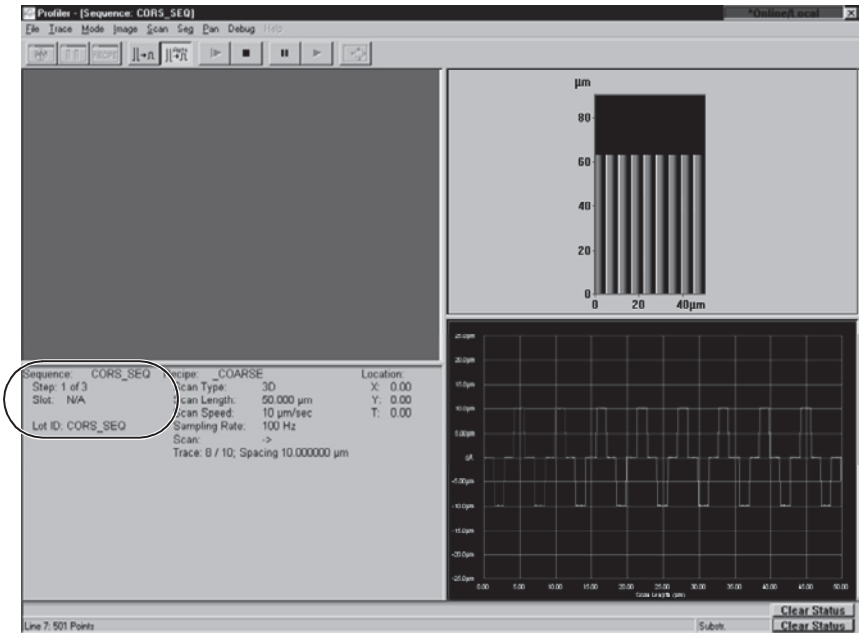
Figure 6.7 *3D View Scan Screen During a Single Scan*



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*

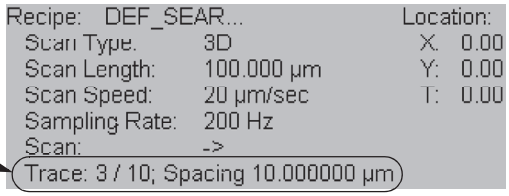
When performing a sequence, the Sequence information is added to the information set.



3D Scan Information Field

Figure 6.9 *3D Scan Window - Scan Information Field*

The only parameter in this field that is different from the 2D field is **Trace:**



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

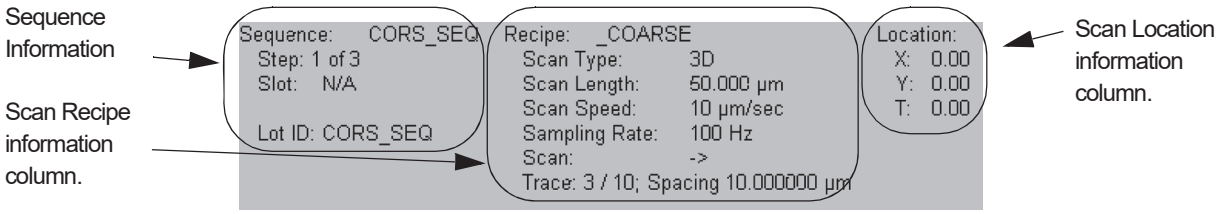
The second column in the Scan Information field is the Location column. It contains the coordinates and orientation of the scan starting point. *Table 6.16* presents a brief description of each parameter. This information is identical with that for 2D scans.

Table 6.16 *View Scan Screen - 3D Location Information Column*

Parameter	Description
X	The X coordinate of the scan origination point
Y	The Y coordinate of the scan origination point
T	The rotational value of the sample at the scan origination point.

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 Column*

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 *Table 7.7 on page 7-11*.)

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.

Table 6.18 Scan Screen - Recipe Information Column

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.

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.
T	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.

Table 6.20 *3D View Scan Window Tool Bar Buttons*

Button	Description
	**XY View Screen Icon** – Disabled for this process.
	**Analysis Screen Icon** – Disabled for this process.
	**Recipe Editor Screen Icon** – Disabled for this process.
	**Manual Scaling** – Resizes the trace to fit in the graph. Requires operator initiation.
	**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. **Single Scans**: 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.
	**STOP SCAN** – **Sequences**: Stops a scan sequence that is in process and returns to the Scan Catalog screen. **Single Scans**: Stop a scan that is in progress and returns to the Scan Catalog screen.
	**PAUSE SEQUENCE** – 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.
	**START/RESUME SEQUENCE** – Starts a sequence or resumes a paused sequence. Resuming a sequence starts it from the beginning of the interrupted scan.
	**PAN AND ZOOM** – This icon is not applicable for the P-15 system.

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*

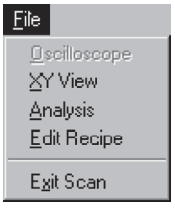
File Menu	Description of Menu Items
	**Oscilloscope** – Not available with P-series systems.
	XY View – Disabled for 3D scans
	Analysis – Disabled for 3D scans
	Edit Recipe – Disabled for 3D scans
	Exit Scan – Disabled for 3D scans

Table 6.22 *3D View Scan Screen - Trace Menu*

Trace Menu	Description of Menu Items
	**Rescale** – 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*

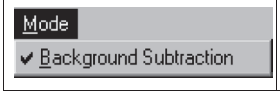
Mode Menu	Description of Menu Items
	**Background Subtraction** – appears active but is not available for use with the P-15 system.

Table 6.24 *3D View Scan Screen - Image Menu*

Image Menu	Description of Menu Items
	**Zoom In** – Not available in P-15 systems.
	Center Anchor – Not available in P-15 systems.
	Corner Anchor – Not available in P-15 systems.
	Edit Scan Parameters… – Use the File/Edit Recipe menu items to perform this function.

Table 6.25 *3D View Scan Screen - Scan Menu*

Scan Menu	Description of Menu Items
	**Start** – **Sequences**: The sequence is terminated when the STOP button is clicked. There is no opportunity to use this menu item. **Single Scans**: 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*

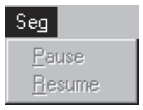
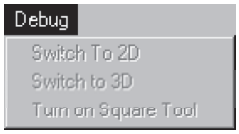
Sequence Menu	Description of Menu Items
	**Pause** – Pauses the scan sequence. The current scan is abandoned and will be started over when the Resume icon or menu item is clicked.
	Resume – Resumes the sequence again, initiating it at the beginning of the scan that was interrupted.

Table 6.27 *3D View Scan Screen - Pan Menu*

Pan Menu	Description of Menu Items
	**Slow** – Might appear active but is non functional.
	Medium – Might appear active but is non functional.
	Fast – Might appear active but is non functional.
	Move Speeds… – Might appear active but is non functional.
	Left – Not Available in the P-Series systems.
	Right – Not Available in the P-Series systems.
	Up – Not Available in the P-Series systems.
	Down – Not Available in the P-Series systems.

Table 6.28 *3D View Scan Screen - Debug Menu*

Debug Menu	Description of Menu Items
	**Switch to 2D** – unavailable for this application
	Switch to 3D – unavailable for this application
	Turn on Square Tool – unavailable for this application

Video Image

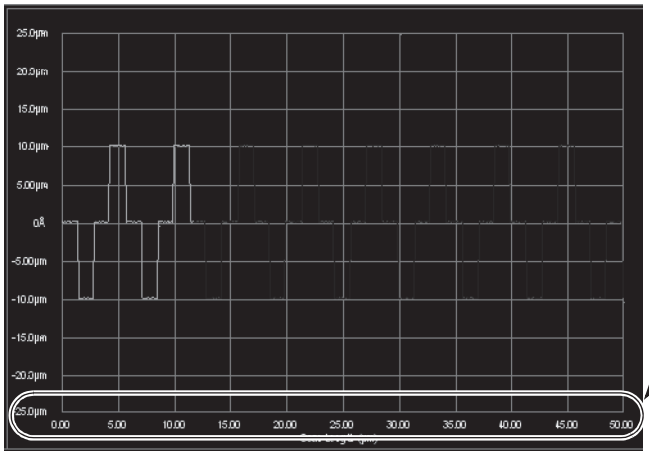
The upper left section of the screen displays scan image on the sample surface. (See *Figure 6.8*.) Prior to the scan, a scan boundary box surrounds the scan area in the image.

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 **Y**axis 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.

Figure 6.12 *Scan screen - real time Trace Window*

This is the Y-axis of the scan graph. It is set by system to capture the height and depth of sample surface features.

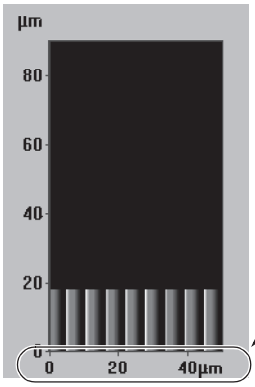


This is the X-axis of the scan graph. It is determined by the **Scan Length** setting in the recipe.

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.

Figure 6.13 *Top View Image of the 3D Scan In Progress*

The height of the scan image is defined by the Y distance in the Recipe Editor for the recipe being used.



the width of the scan image is defined by the X distance in the Recipe Editor for the recipe being used.

SHOW MEASUREMENT SITE DURING SEQUENCE RUN

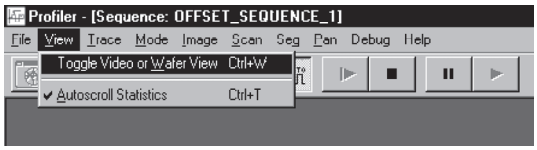
Introduction

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)*



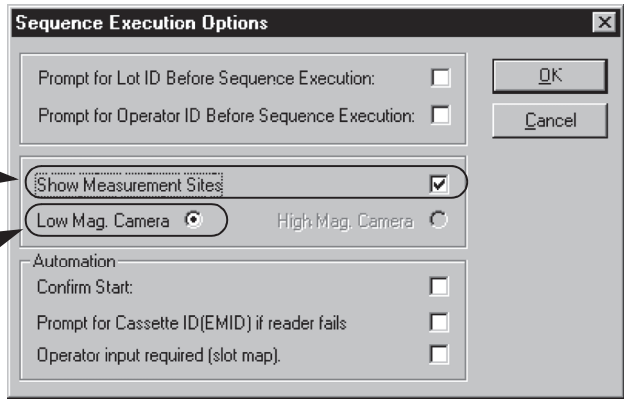
Configuration

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 causes the starting point of the scan site to be displayed in the video screen.

Low Mag. Camera is chosen by default to view the scan site in the video image.



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.

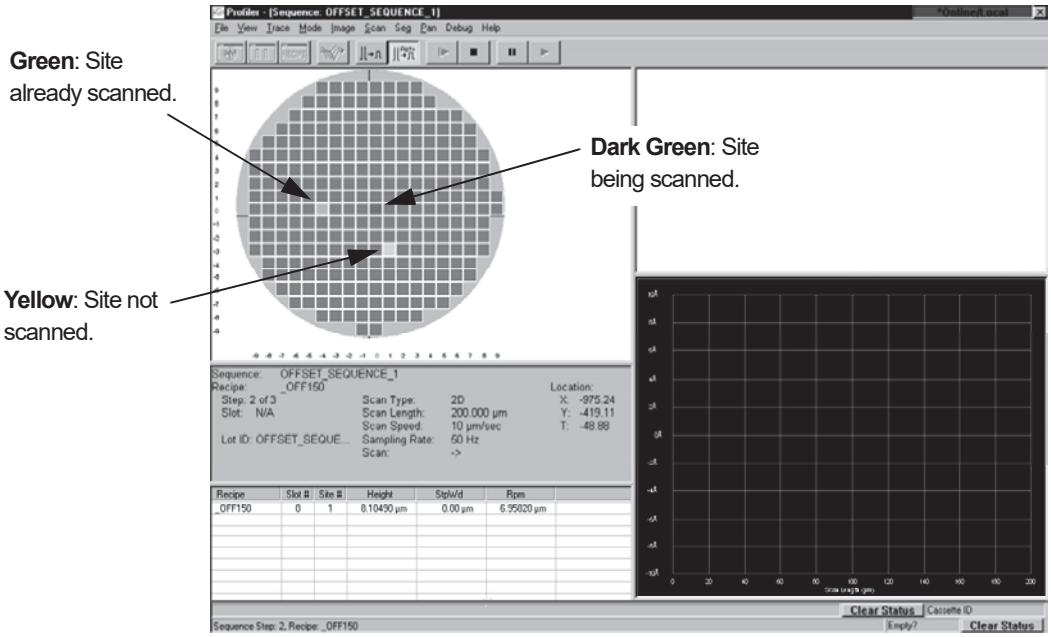
Wafer Image Display

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.

7

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:

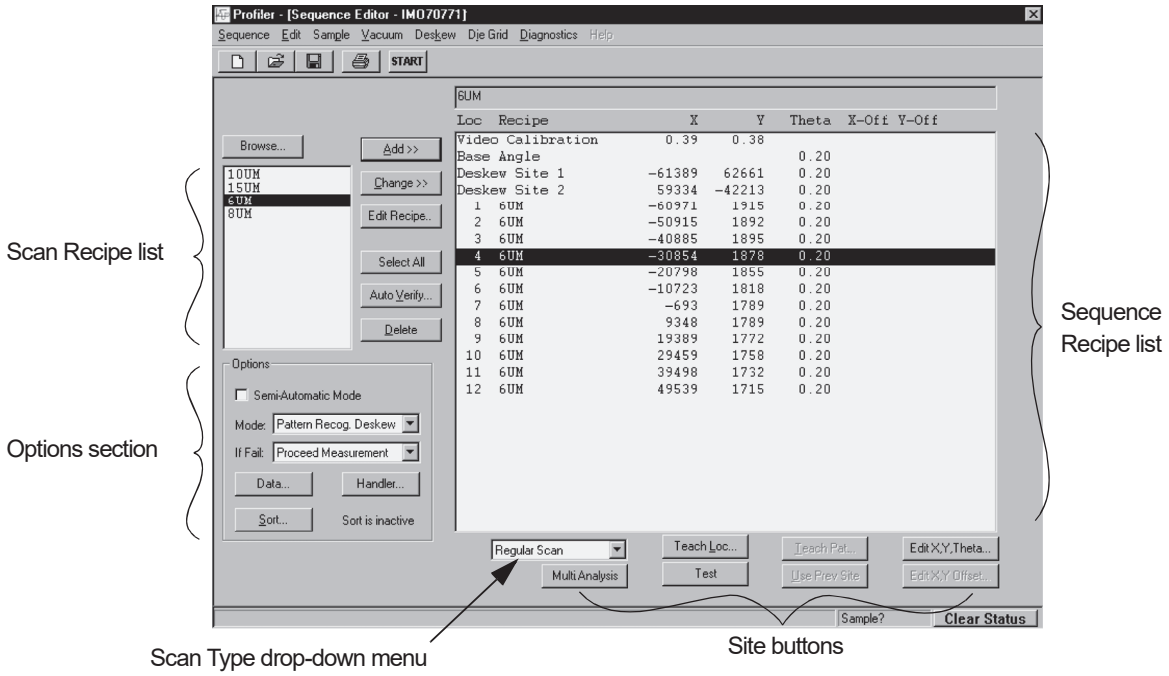
STARTING THE SEQUENCE EDITOR APPLICATION

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.
	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 **Save Sequence As** dialog box first.
	Prints the selected Sequence recipe.
	Starts a scan using the current Sequence recipe.

Table 7.2 *Sequence List Buttons*

Button	Description
	Adds the selected Scan recipe into the sequence.
	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.
	Displays the Scan Recipe Editor, open to the recipe selected in the Scan recipe Catalog (the field to the left of the **Edit Recipe…** button.)
	This selects all the recipes in the current Sequence Recipe.
	This goes to the XY View screen and locates the current scan location in the video screen for verification.
	Deletes the selected site from the sequence.

Table 7.3 *Options Buttons*

Button	Description
Data...	Displays the Data Saving Options dialog box where sequence data can be automatically saved, exported, or printed.
Sort...	Displays the dialog box for the sort software option.
Handler...	Displays the **Handler** dialog box. The P-15 has no handler so the only option available is **Manual Load**.

Table 7.4 *Site Buttons*

Button	Description
Teach Loc...	Goes to the XY view so a measurement site can be chosen based on a location observed on the screen.
Teach 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

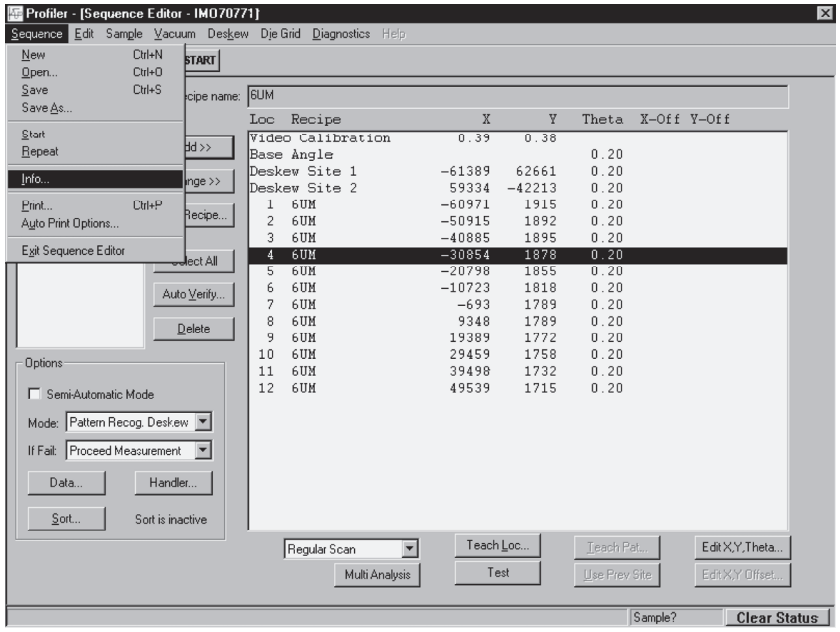
The Sequence Information dialog box displays the title, author, date and time of creation (or modification) of the sequence. It also provides a text box for annotations.

1. In the Sequence Editor, click the **Sequence** menu to display its menu. (See *Figure 7.2*).

Figure 7.2 *Sequence Editor – Sequence Menu*

Step 1 Click on **Sequence** to display its menu.

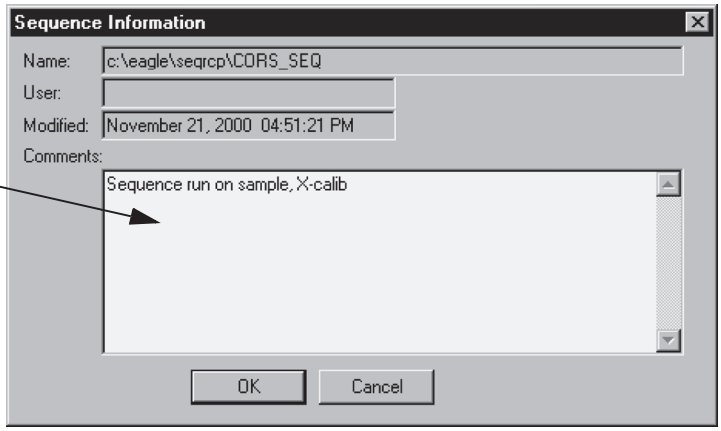
Step 2 Click **Info…** to display its dialog box.



2. From the Sequence Menu, select **Info…** (See *Figure 7.2*)

Figure 7.3 *Sequence Information Dialog Box*

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.



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.

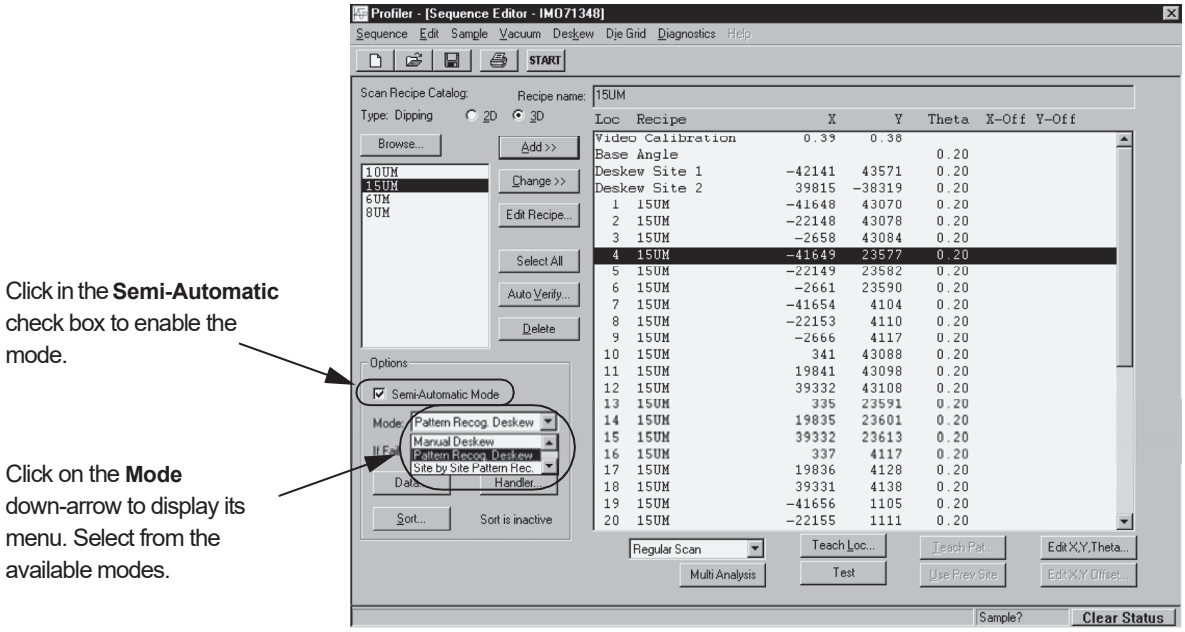
Semi-Automatic

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*

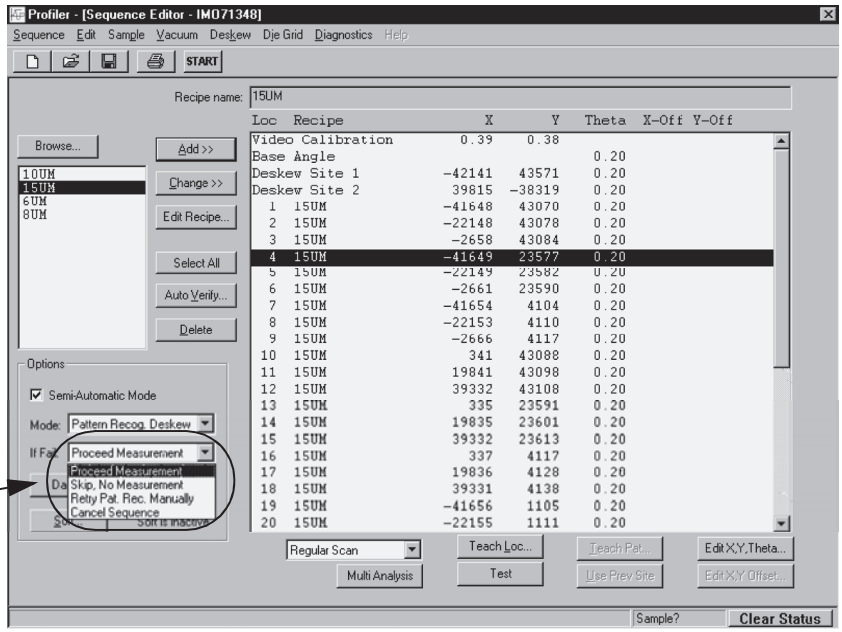
Mode	Description
No Deskew	The sequence contains no deskew points for alignment.
Manual Deskew	Deskew points are set and must be confirmed manually by the operator.
Pattern Rec. Deskew	Deskew points are set using the Pattern Recognition option.
Site-by-Site Pattern Recognition	Scan sites are set relative 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*.)

Figure 7.5 *Sequence Editor – If Fail Menu*



Step 1 Click on the **If Fail** down-arrow to display its menu. Select from the available modes.

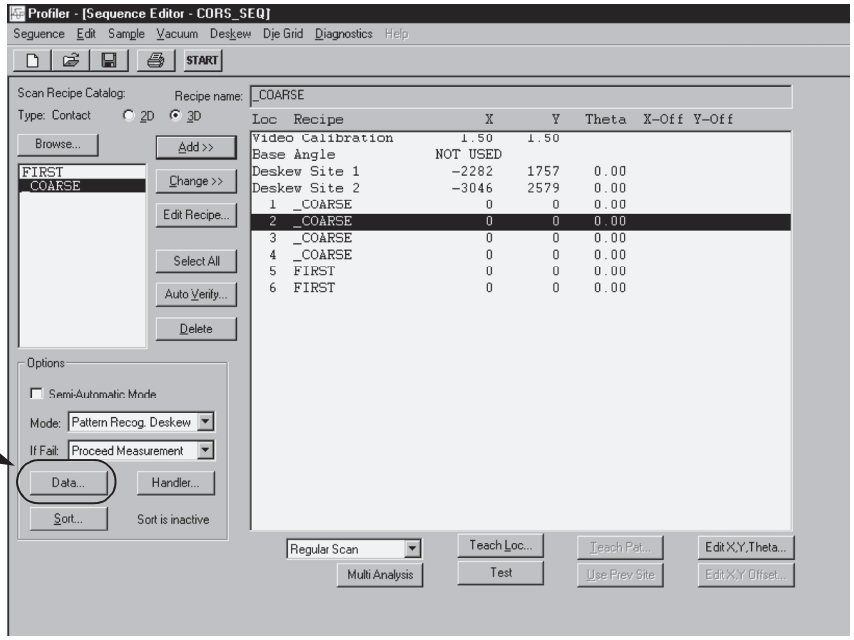
Table 7.6 *If Fail Drop-down Menu*

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 **OK** to continue with scan without pattern recognition confirmation.
Cancel Sequence	Sequence is suspended. User must restart the sequence.

Begin: Set Data Options

2. Click the **Data** button to choose options for data collection that automatically execute upon sequence completion.

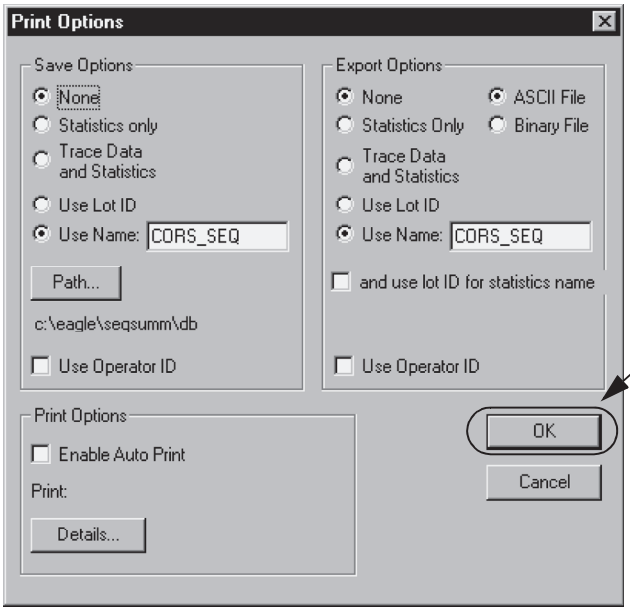
Figure 7.6 *Sequence Editor*



Step 2 Click the Data button to open 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 7.7 *Data Options*



Step 1 When the options have been chosen, click **OK**.

3. Choose an option from the Save, Export, and Print options. (See *Table 7.7*.)

Table 7.7 *Save and Export Options*

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 **Use Name**.

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 **Details...** button to open a standard print dialog box and set print options.

End: Set Data Options

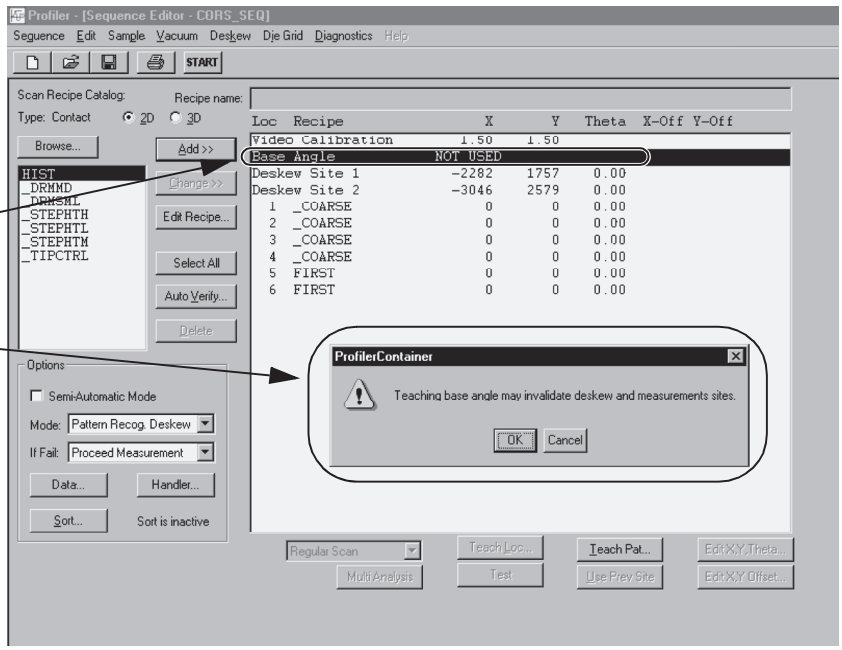
4. Click **OK** to set the options.

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.

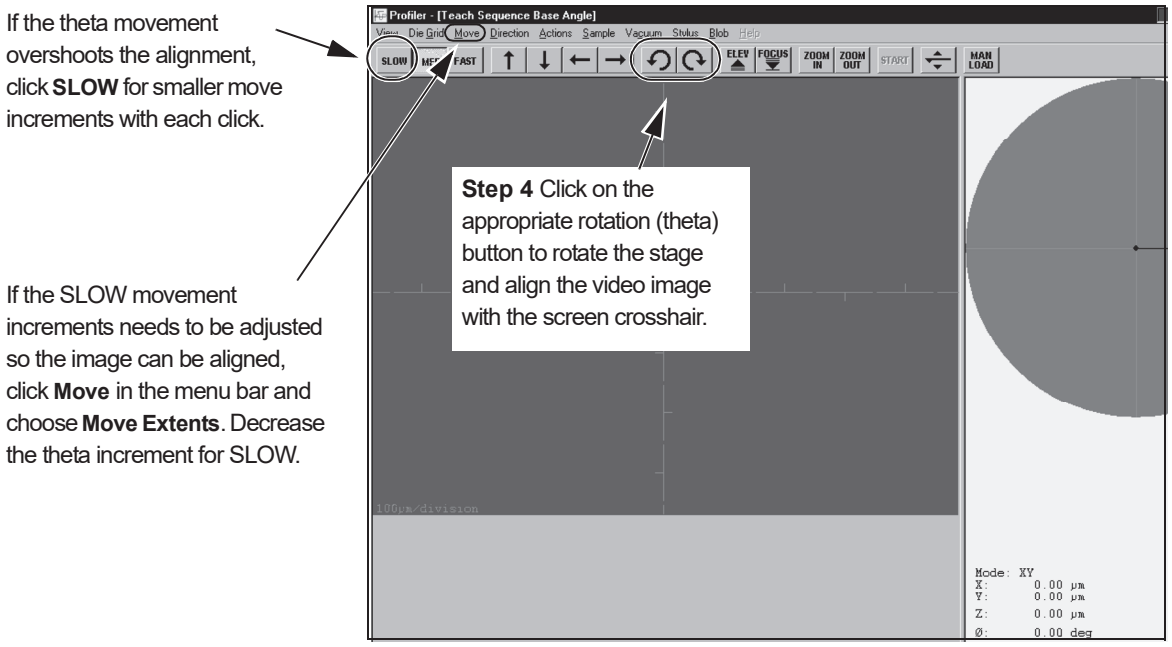
Figure 7.8 *Sequence Editor*



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

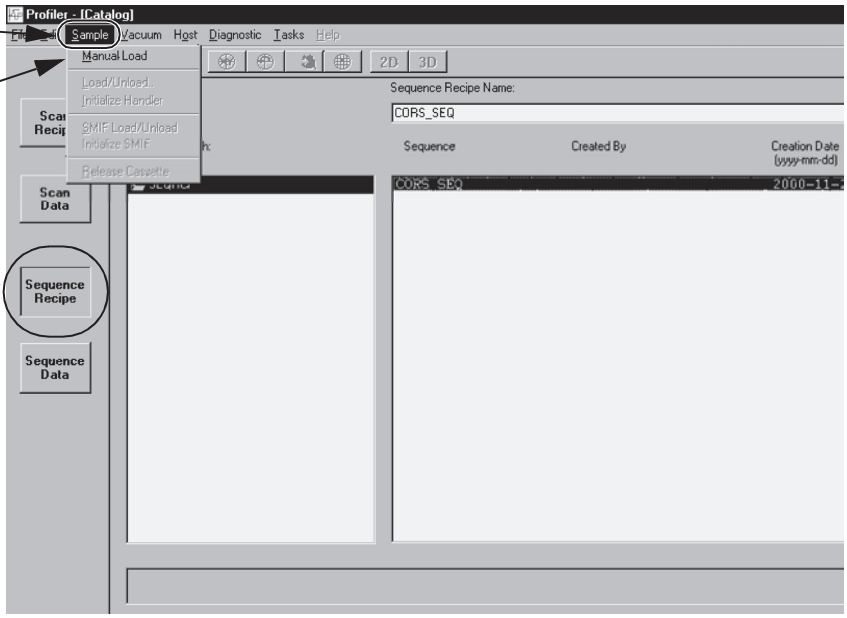
1. From the Catalog screen, click on the **Sequence Recipe** button to display scan recipes in the Information Display Window.

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 the menu bar to display its menu.
Step 3 Click on **Manual Load** to bring the stage to the stage door.

Step 1 Click on the **Sequence Recipe** button to display the Scan Recipe Catalog screen.



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.

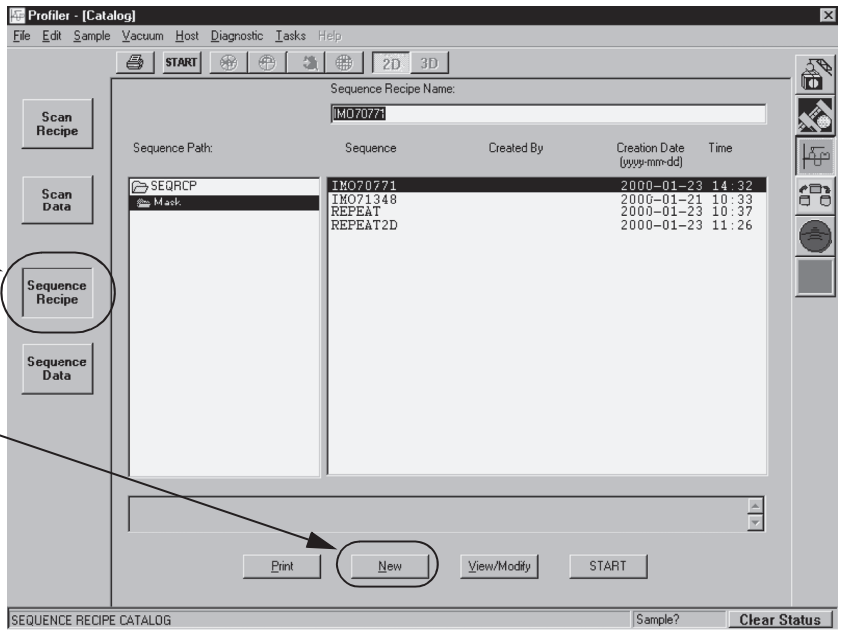
End: OPTIONAL Manual Wafer Load Procedure

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*

Step 9 Click on the Sequence Recipe button to display the Sequence list in the display window.

Step 10 To open the Sequence Editor for a new recipe, click on the **NEW** button at the bottom of the screen.

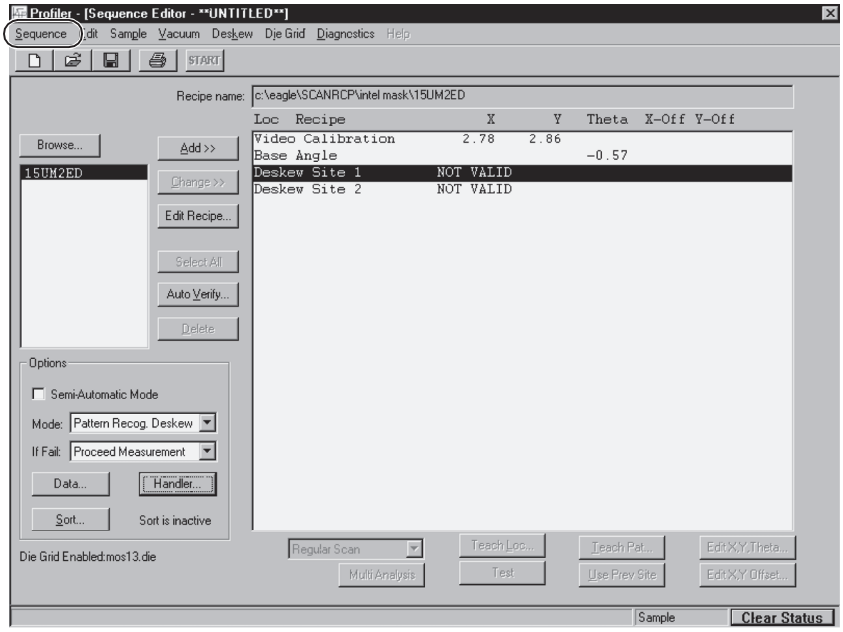


9. Click on the **Sequence Recipe** button to change to the Sequence catalog list. (See *Figure 7.11*.)
10. From the **Sequence** catalog, open a new sequence by clicking on the **NEW** button at the bottom of the screen. (See *Figure 7.11*.)

    The Sequence Editor opens, formatted to create a new sequence recipe. (See *Figure 7.12*.)

Figure 7.12 *Sequence Editor for NEW Recipe with Pattern Recognition*

Step 11 Click on **Sequence** and then on **Save** or **Save As** to display the dialog box for saving and naming the sequence.



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.

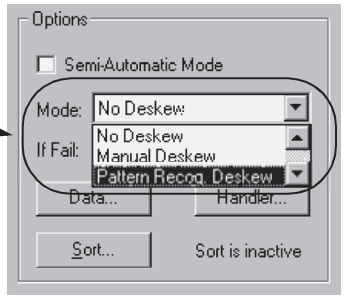
1. To use a die grid, Pattern Recognition Deskew must be in place. To tie the deskew process to pattern recognition, use the following procedure. In the **Options** box located in the lower left corner of the Sequence Editor, click on the menu arrow next to the **Mode** field.

2. Click on **Pattern Recog. Deskew…** (See *Figure 7.13*.)

Figure 7.13 *Options Section in the Sequence Editor*

Step 1 Click on the menu arrow for its menu.

Step 2 Choose **Pattern Recog. Deskew**.



Begin: Load Die Grid

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.

   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.

   For additional information about the use of Die Grid Navigation, see *Using Die Grid Navigation* on page 5-19.

NOTE: Whenever possible, load a die grid before teaching any sites; because it invalidates all currently taught positions.

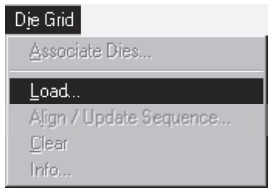
   Ensure that the wafer on the stage has the same pattern as that of the die grid being loaded.

CAUTION: 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 system, it is best to use a precision locator to place the wafer in the proper orientation.

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.

Figure 7.14 *Die Grid Menu*

Step 4 Click on **Die Grid** in the menu bar to display its menu.

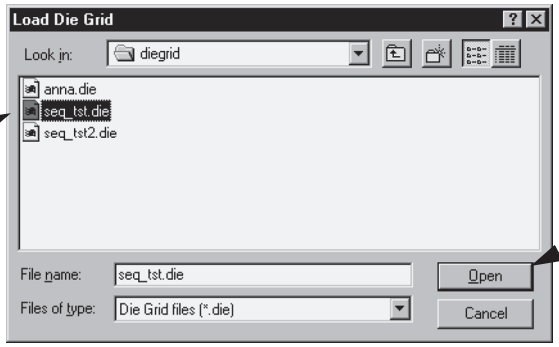


Step 5 Click on **Load...** to display the Load Die Grid dialog box overlay on the XY View screen.

5. Click on **Load...** (See *Figure 7.14*.)

Figure 7.15 *Load Die Grid Dialog Box*

Step 6 Double-click on the name of the die grid to be used.



Step 7 Click on **Open** to open the die grid.

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*.)

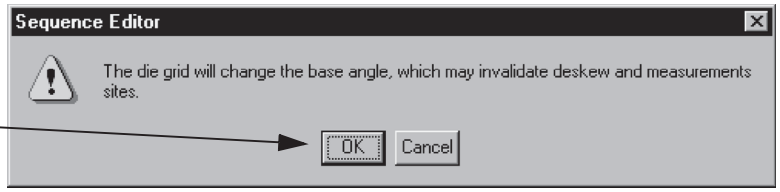
   The system nulls the stylus and begin to search for the pattern that is displayed in the sample navigation window. After it successfully locates the test pattern, the die grid is loaded.

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*

Step 8 Read the warning and click **OK** to close it.



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 Pattern Recognition Sites

10. This procedure is designed to set up the pattern recognition that allows the 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*.)

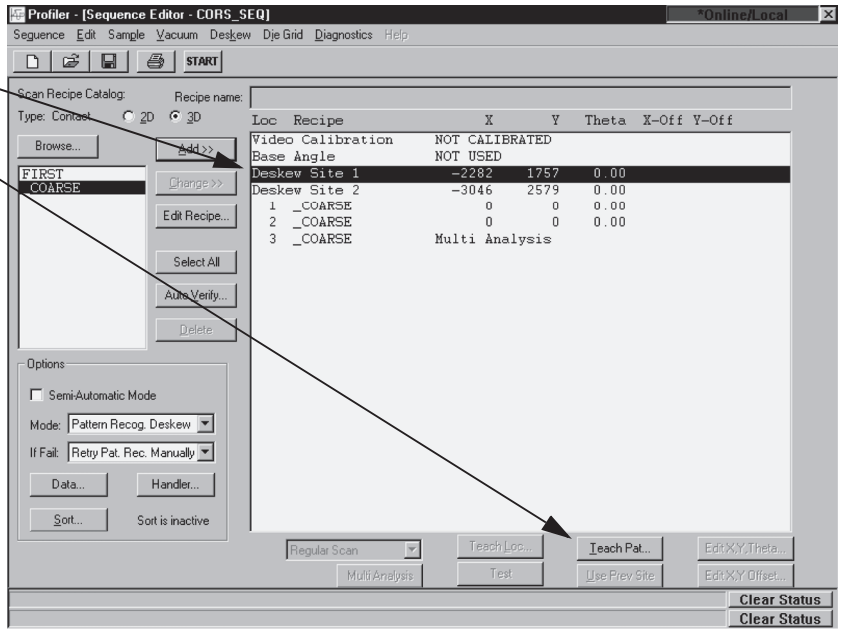
11. The **Teach Pattern** button at the bottom of the screen becomes active. (See *Figure 7.17*.) Click the button to begin the Teach Pattern procedure for Site #1.

Figure 7.17 *Sequence Editor*

Step 10 Click on **Deskew Site 1**.

Step 11 Click on **Teach Pattern**.

After the pattern is taught, repeat the procedure for Site 2.

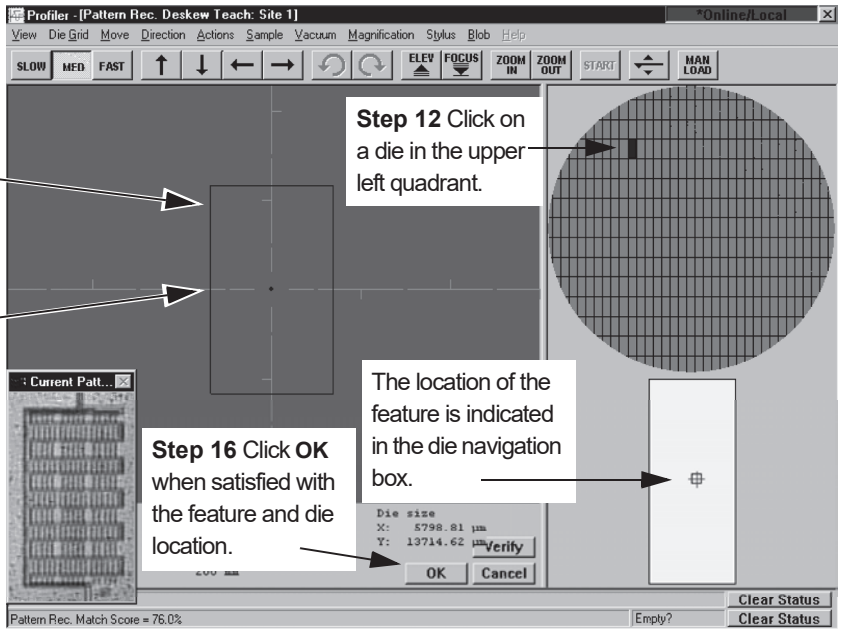


12. The **Pattern Rec. Deskew Teach: Site 1** screen is displayed. Click on a die in the upper left quadrant of the sample navigation grid. the dark (blue on the screen) rectangle has been chosen in *Figure 7.18*.

Figure 7.18 *Pattern Rec. Deskew Teach: Site 1 Screen*

Step 15 Use the click-and-drag process to draw a box around the feature to be used for pattern recognition deskew.

(The video image is not visible in this illustration but would be present on the actual screen.) The box is drawn around the feature that is displayed in the **Current Patt...** box.



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**.

End: Teach Global Pattern Recognition Sites

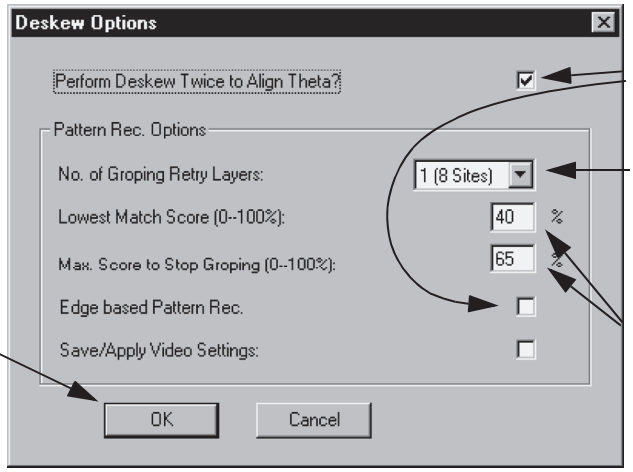
17. Repeat **Step 10** through **Step 16** for **Site 2**. For a location, choose the lower right quadrant, at approximately the opposite die position, at an approximate 45° angle through the center of the die grid from the first die.

Begin: Setting Deskew Options

18. 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*.)

Figure 7.19 *Deskew Options Dialog Box*



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*.)

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*.)

End: Set Deskew Options

25. Click on **OK** when all the parameters have been set.

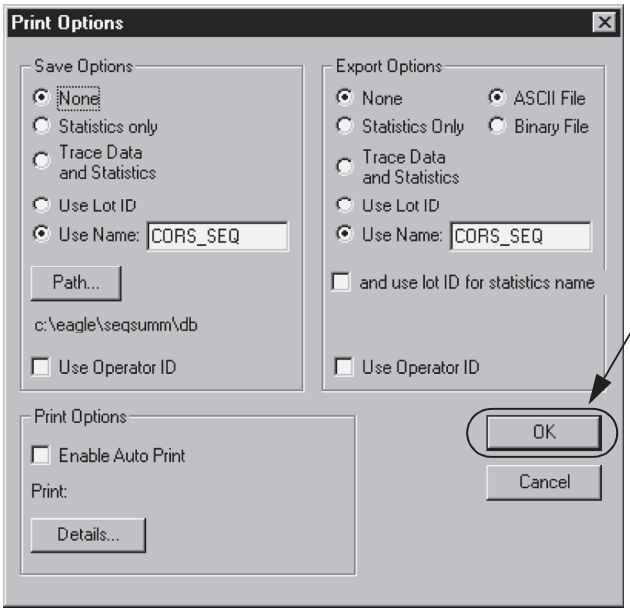
Begin: Set Data Options

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*



Step 28 When the options have been chosen, click **OK**.

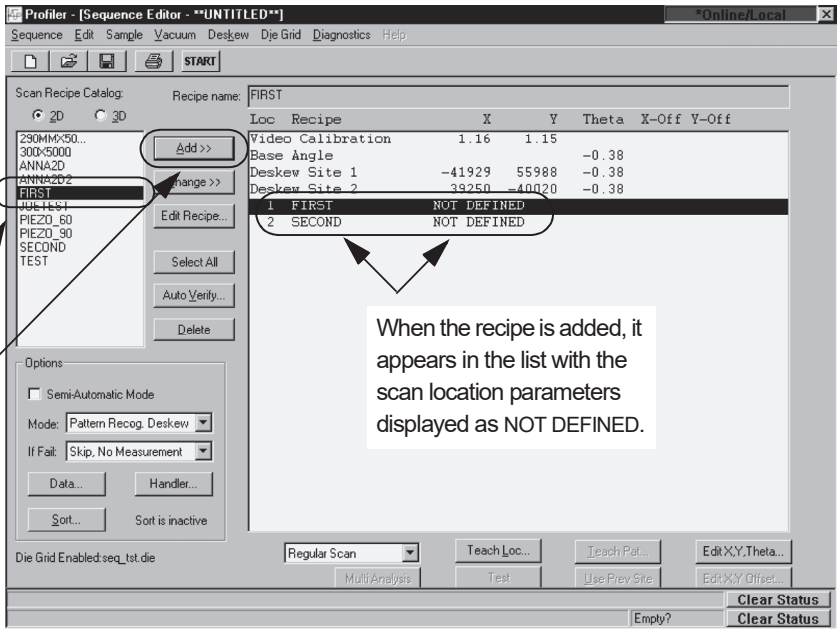
27. Set the options according to the scan sequence requirements. (See Step 2 on page -10 through Step 4 on page -11, in *Editing the Options Field in the Sequence Editor*.)

End: Set Data Options

28. Click on **OK** when options have be set.

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*



The Sequence Editor comes up with no recipes listed. Use **Step 30** to create a sequence of recipes:

1. Highlight a scan recipe.
2. Click on the Add button.
3. Repeat Steps 1 and 2 for each additional recipe.

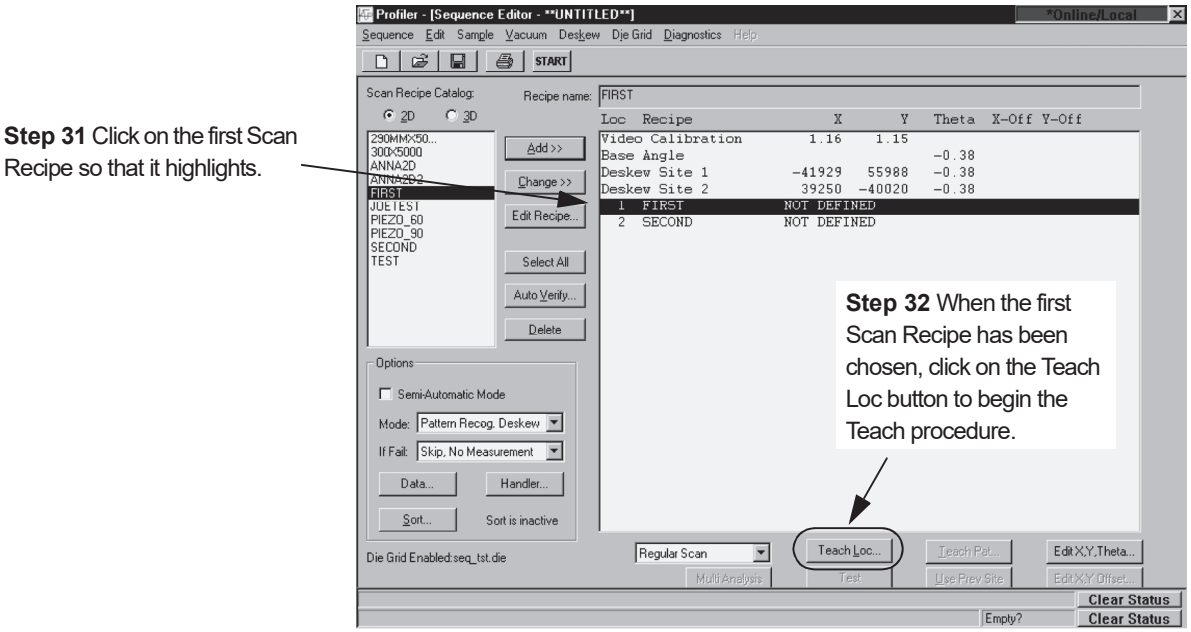
Adding Scan Recipes

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*.)

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

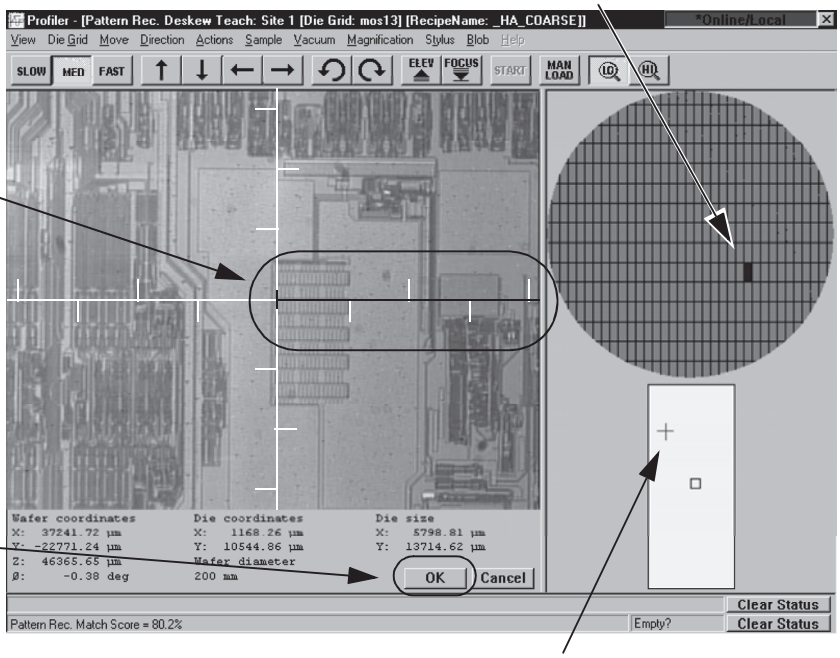
Figure 7.23 *Teach Location for First Recipe Scan*

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.

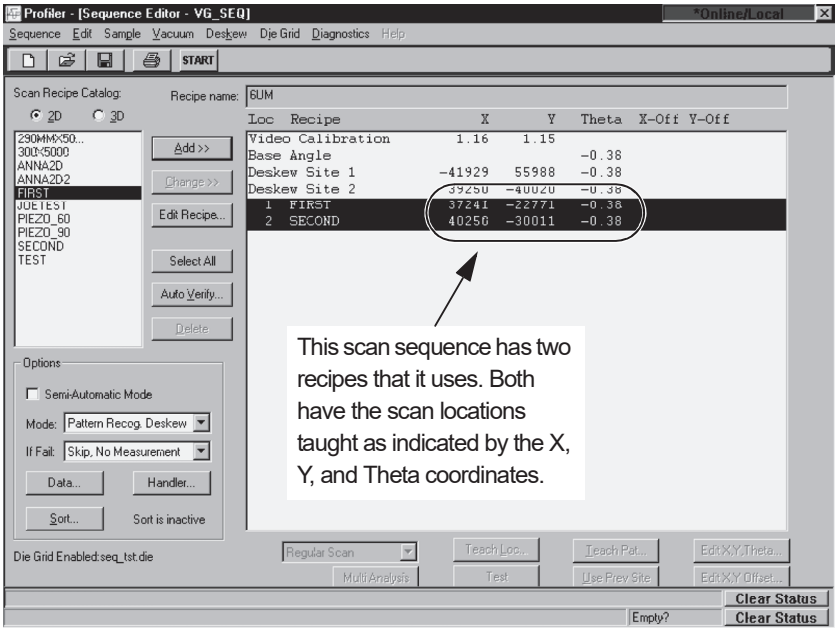


The die navigation box can be used to position the scan for the recipe. Click on the place in the die where the scan feature resides. The video image displays that position.

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*.)

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.

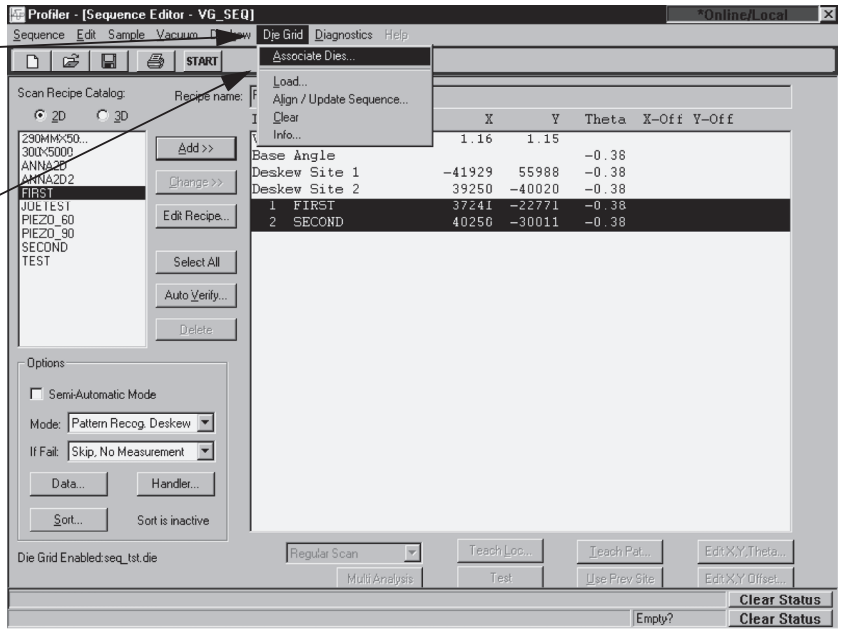
1. Ensure that the procedure in *Linking a Die Grid with a Sequence* on page 7-16 has been completed for the sequence being used.
2. From the Sequence Editor highlight the recipe that is to have additional dies associated with.
3. Click on **Die Grid** in the menu bar. (See *Figure 7.25*.)

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 menu bar to display its menu.

Step 4 Click on **Associate Dies...** to begin the process of choosing new scan sites.

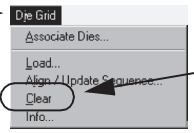


This displays XY screen titled "**Associate Dies With Sequence Scan Sites**," with a graphic display of the die grid configuration, visible to the right of the video display area. (See *Figure 7.27*.)

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 5 In the menu bar, click on **Die Grid** to display its menu.

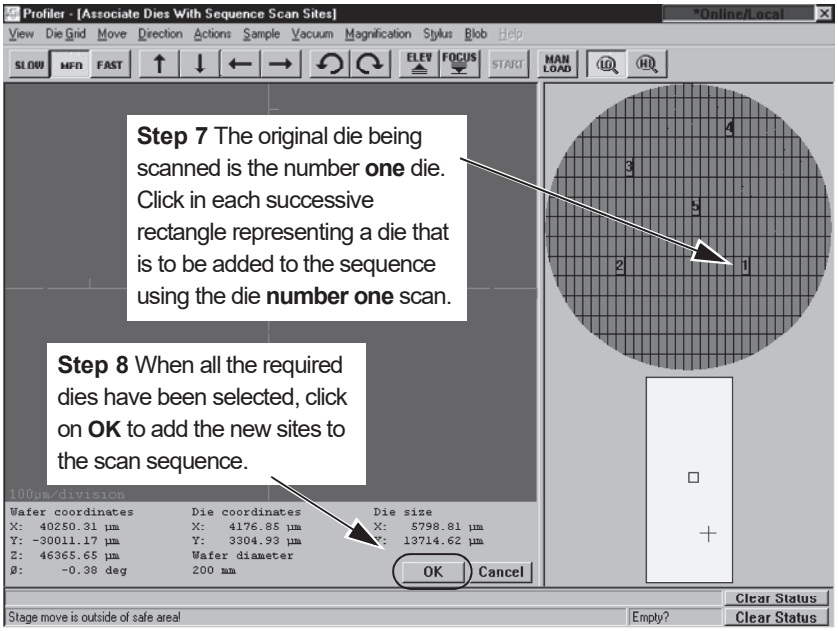


Step 6 Click on **Clear** to remove the unwanted dies from the die grid.

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*



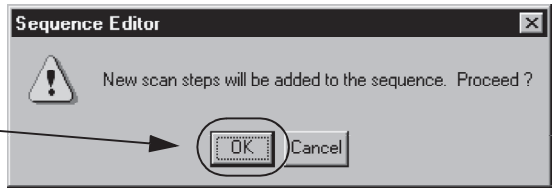
NOTE: Dies can be selected or deselected by clicking or them.

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 **OK** to continue or **Cancel** to abort the addition of the sites to the sequence.

Figure 7.28 *Sequence Editor Message Box*

Step 9 Click on **OK** to add the additional selected sites to the scan sequence.



When **OK** is clicked, the Sequence Editor is displayed with the additional sites in the Sequence Recipe.

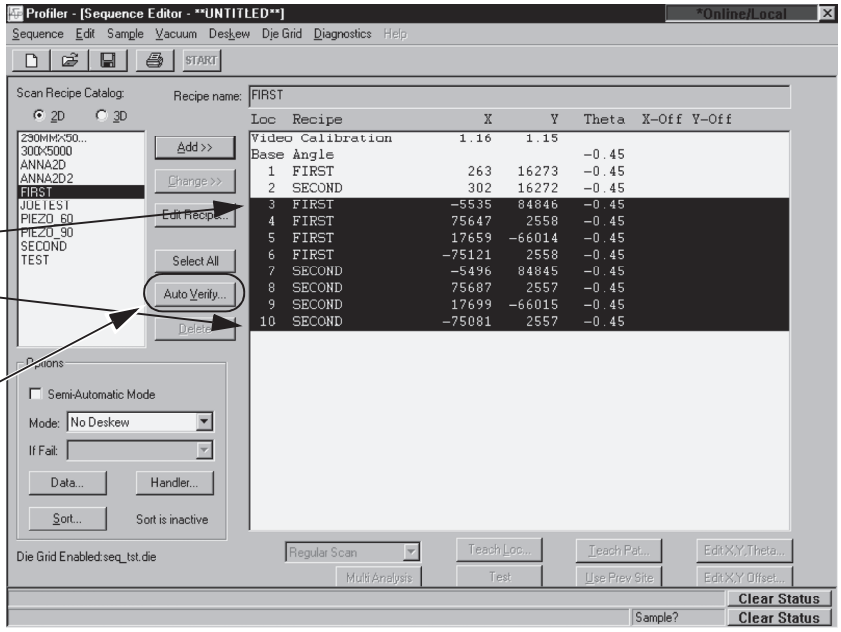
Notice that each new site has the coordinates of the scan location for that die. In the illustration *Figure 7.29*, two sets of new sites have been added, one for additional dies using the scan named FIRST, and one for dies using the scan named SECOND.

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*

Step 10 The new scan sites are presented below the original ones in the recipe list. Each has its own scan position coordinates listed. Highlight the entire group of new scan locations by clicking on the first one, then hold down the shift key and click on the last one.

Step 11 After all the new recipes are highlighted, click on the **Auto Verify** button.



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 Verify

d. 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.

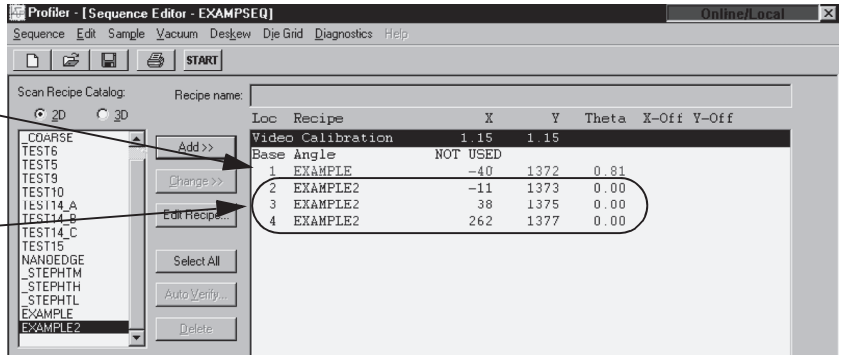
6. Designate the other sub-scans (usually 100 µm or less) as done for the long scan, using the **Scan Type** list to select **Correlation Sub-scan**.

   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*

The first recipe, the parent long scan, is in red.

The subscan recipes, the correlation subscans, are in blue.



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.

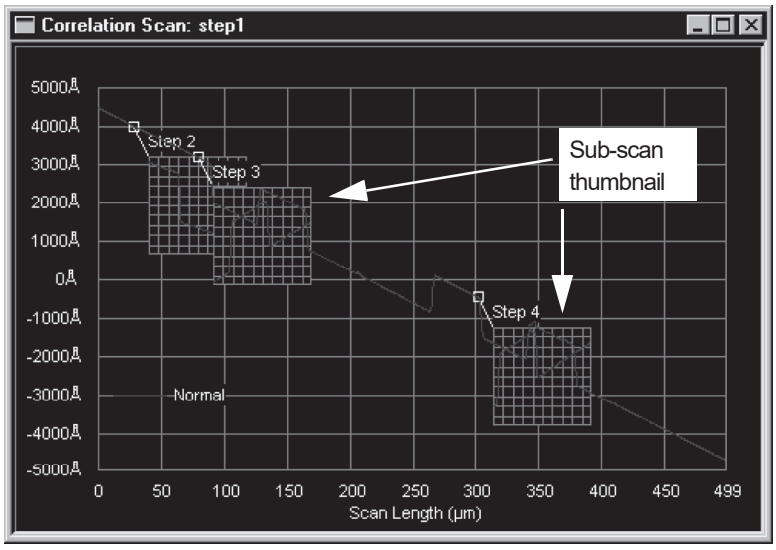
2. Click the **File** menu, and select **Correlation Scan**.

   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*



5. 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

1. 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 5***b*.

      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.

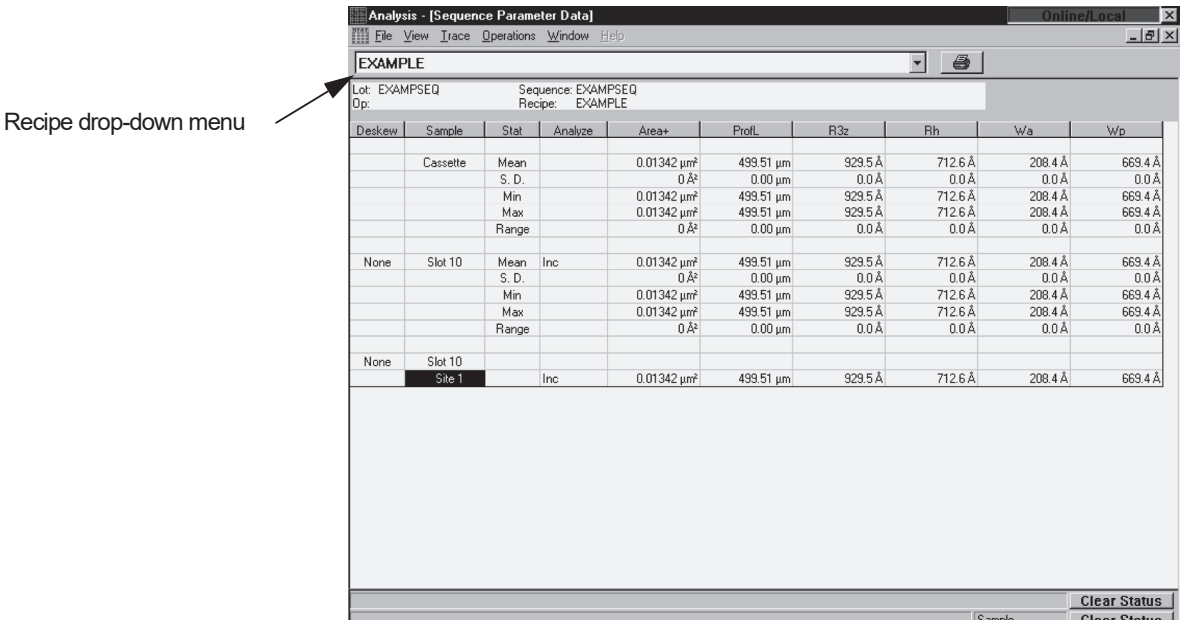
VIEWING SEQUENCE DATA

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*



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.

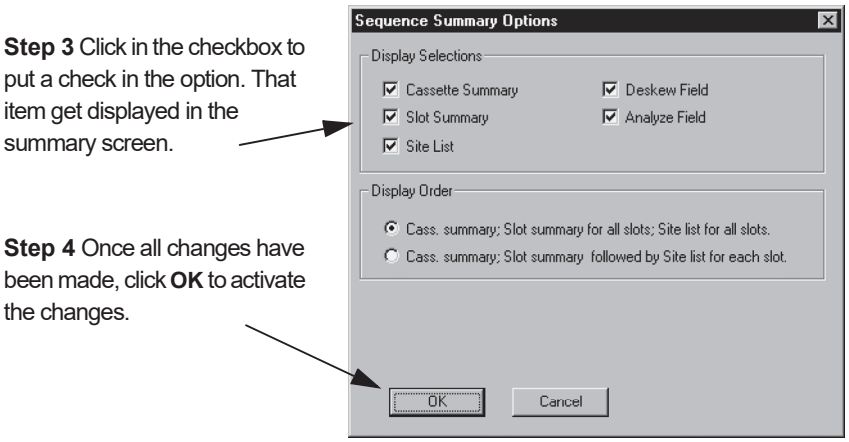
Sequence Summary Options

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*.)

Figure 7.33 *Sequence Summary Options Dialog Box*



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.

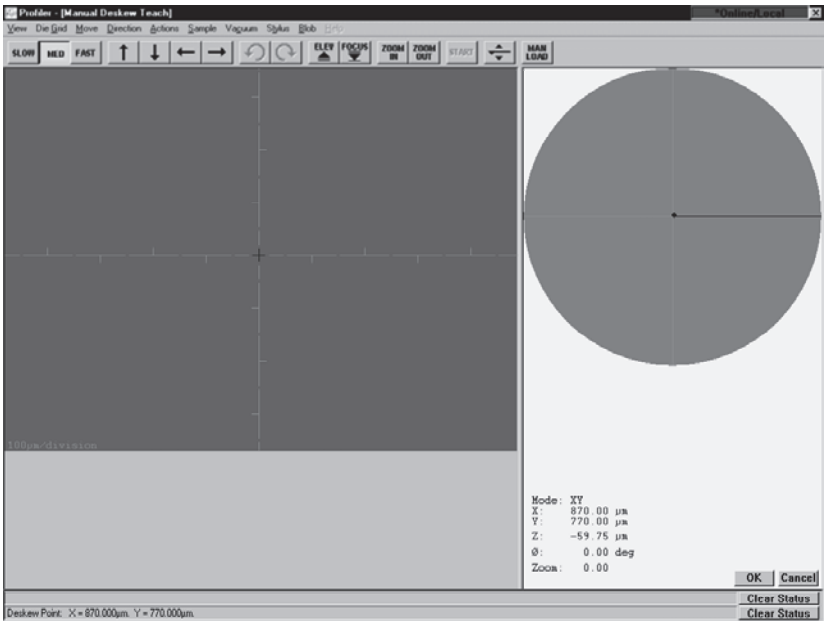
1. Create a new sequence.
2. When ready to set up manual deskew, proceed with the following steps.
3. Set the deskew mode to **Manual Deskew**.

   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.

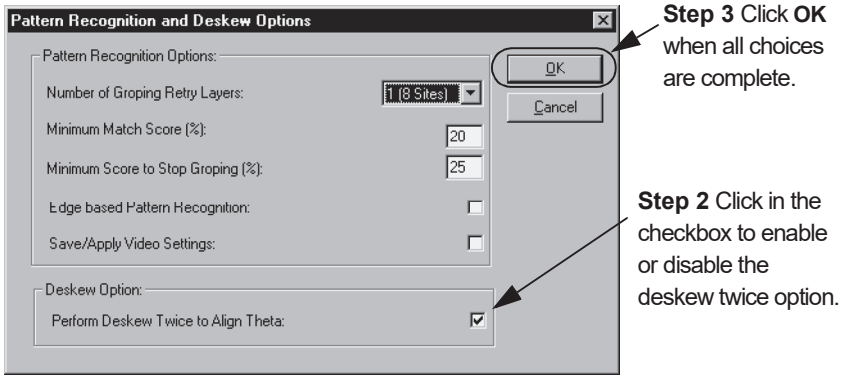
14. Repeat **Step 11** through **Step 13** for deskew site #2.
    The tool then proceeds with the measurement sites.

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*



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 ◆ Other polygon shapes
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*

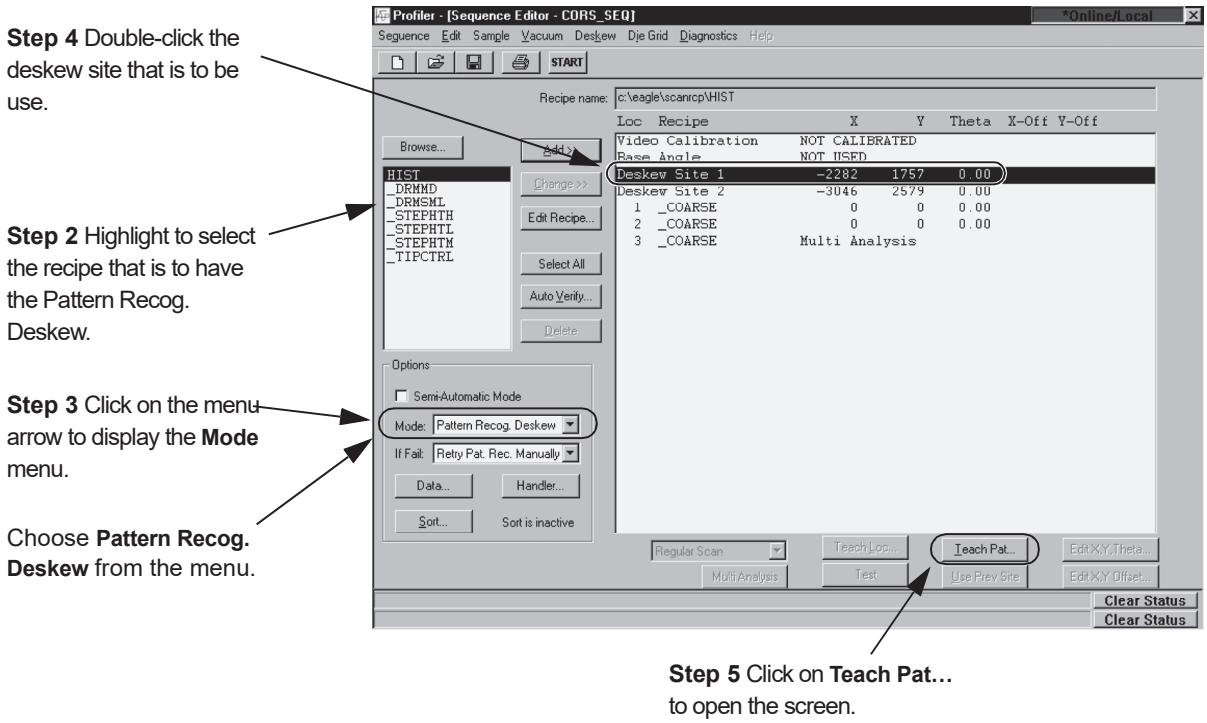
Search Criteria	Description
Search time depends on pattern size.	The larger the pattern, the faster the system can recognize the pattern. However, larger patterns require more accurate initial positioning within the camera's field of view because the search area is reduced. Also, Pattern Recognition options can be set so that the system performs a pattern search if the pattern is not found within the field of view. See *Using Groping with Pattern Recognition* 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*

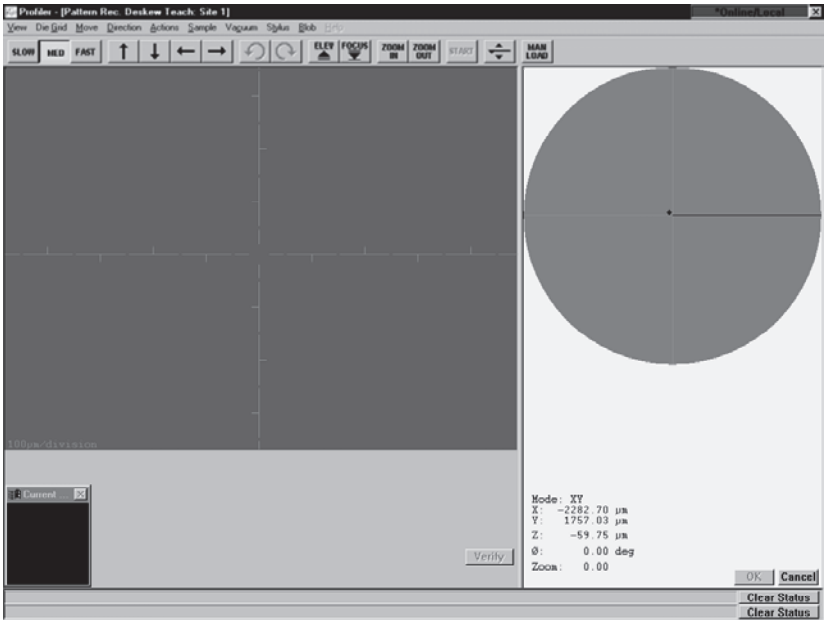


4. Double-click the **Deskew Site 1** entry near the top of the sequence list or highlight the **Deskew Site 1** entry. (See *Figure 7.36*.)

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.

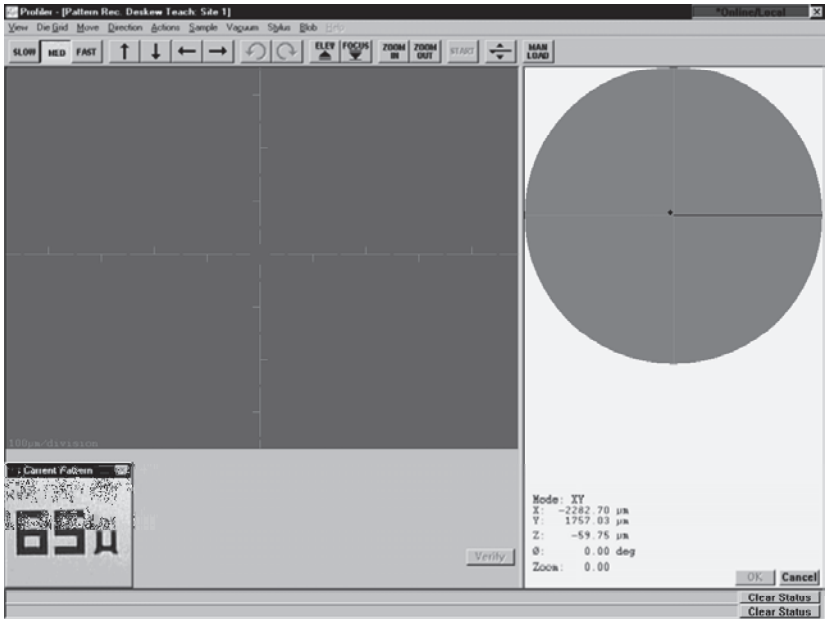
      The system processes the image information defined by the rectangle.

   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.

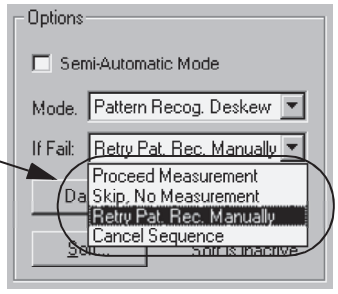
    A box is drawn around the feature when it is found.
11. If recognition fails, select another pattern and retry.
12. Click **OK** to accept the new pattern.
13. Repeat **Step 2** to **Step 9** for **Deskew Site 2** to establish the second deskew point.
14. Once the deskew sites have been successfully 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*

Step 16 Choose on of the four **If Fail** options to guide the system performance when pattern recognition fails.



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.*

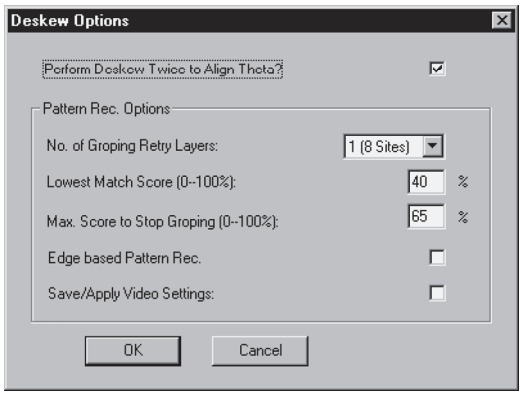
The three groping parameters are described in *Table 7.12*.

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*



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 *Groping Parameters*

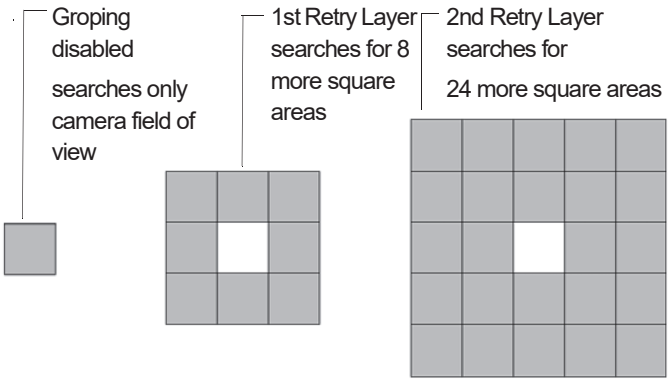
Parameter	Description
Number of Groping Retry Layers	This parameter controls how much of the area around the deskew site is searched for the pattern. Each layer consists of a square area constructed by evenly surrounding the deskew site with squares the size of the camera field of view. (See *Figure 7.41*). ***Figure 7.41*** *Groping Retry Layers*  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.

Table 7.12 *Groping Parameters (Continued)*

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 **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 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. **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.

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 **Save/Apply Video Settings** 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 **Pattern Recognition and Deskew Options** dialog box, a second deskew is performed to compensate for this error. This allows accurate sample rotations within a sequence.

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
@ at sign	**_** underscore
# number sign	**-** hyphen
$ dollar sign	**{** left brace
% percent sign	**}** right brace
^ caret	**‘** single quotation mark
& ampersand	**'** apostrophe

3. Click **OK**.

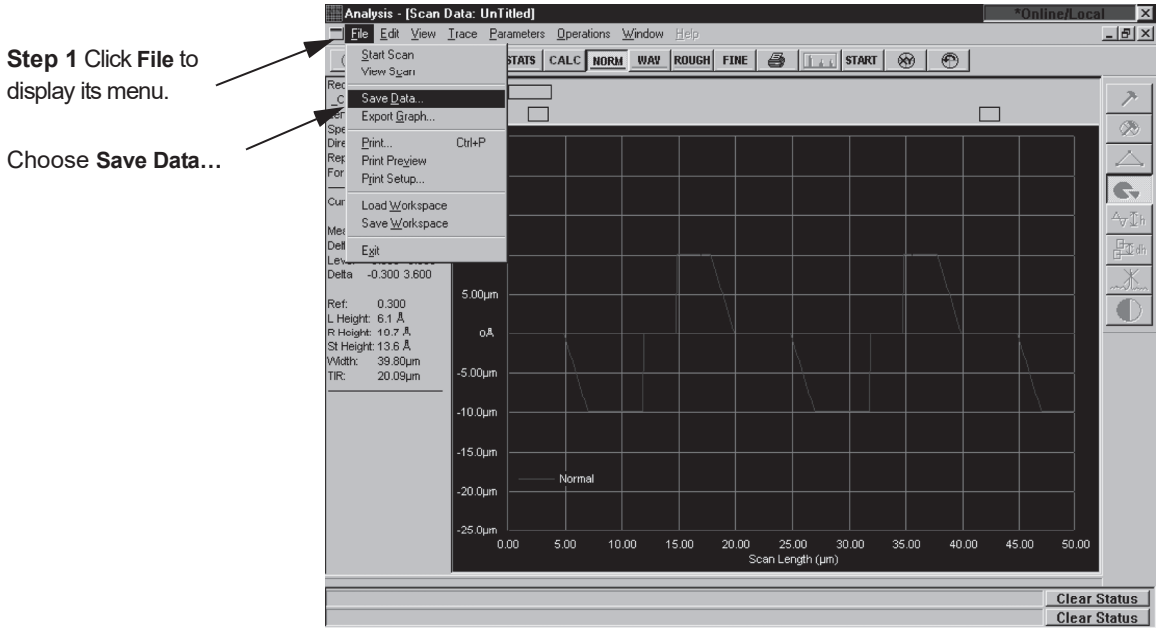
SAVING THE SEQUENCE DATA

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*.)

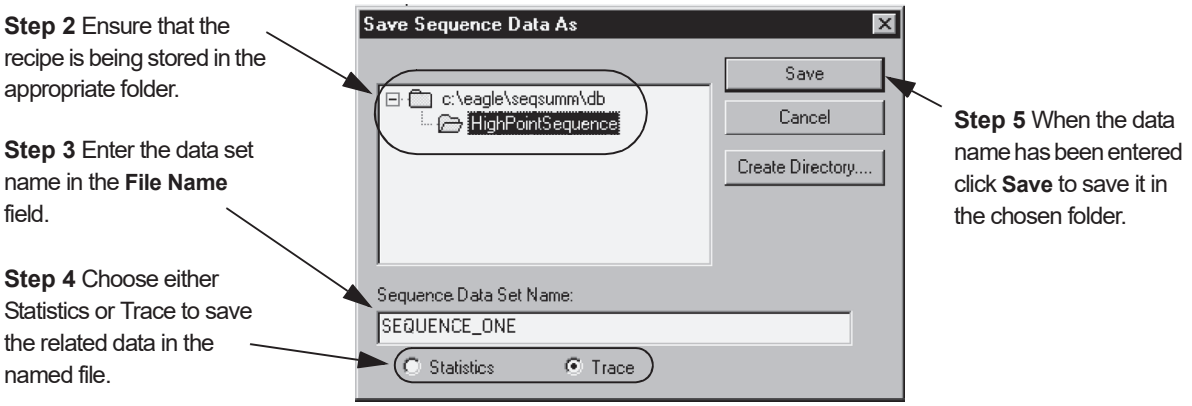
Figure 7.42 *Analysis Screen with File Menu*



2. Ensure that the data is being saved into the correct folder. (See *Figure 7.43*.)
3. 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*.)

Figure 7.43 *Save Data Set Dialog Box*



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.

5. 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.

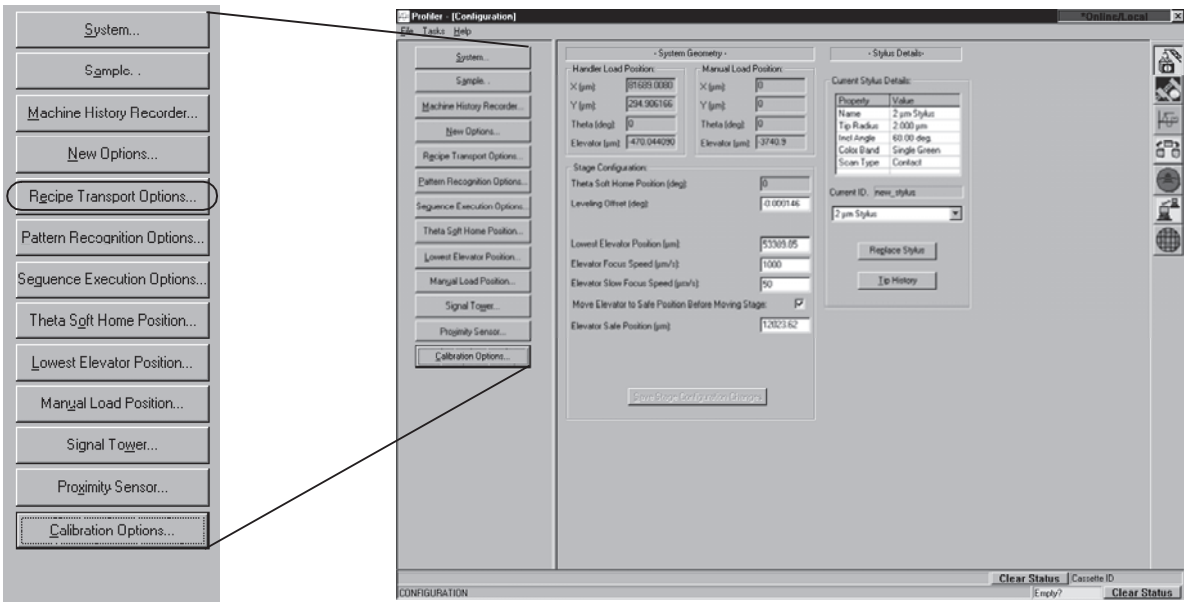
Sequence Transport Configuration

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*

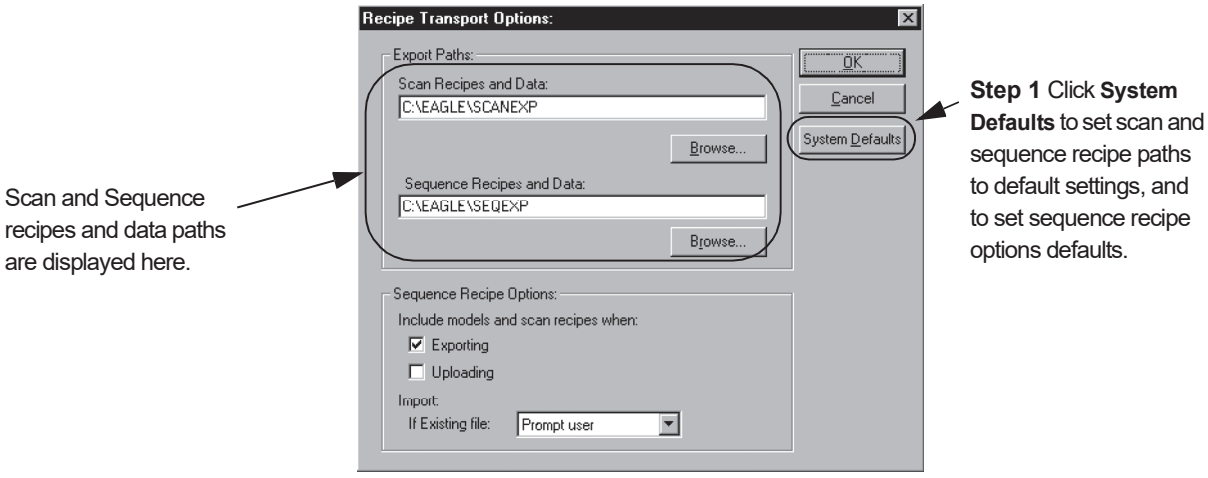


Export Paths

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*.

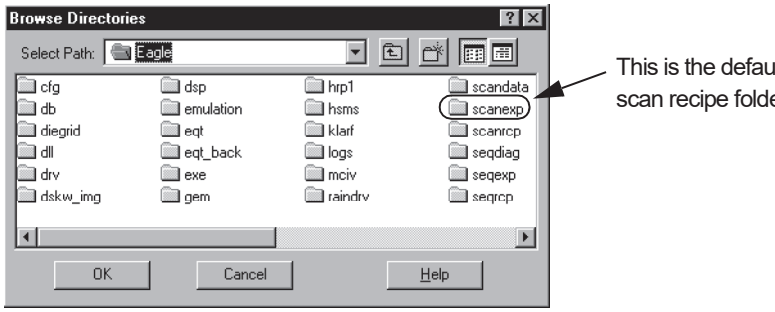
1. To change back to the default scan and sequence recipes, sequence recipe option defaults, and data paths (C:\EAGLE\SCANEXP and C:\EAGLE\SEQEXP), click on the **System Defaults** button.

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 7.46 *Browse Directories Dialog Box*



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.

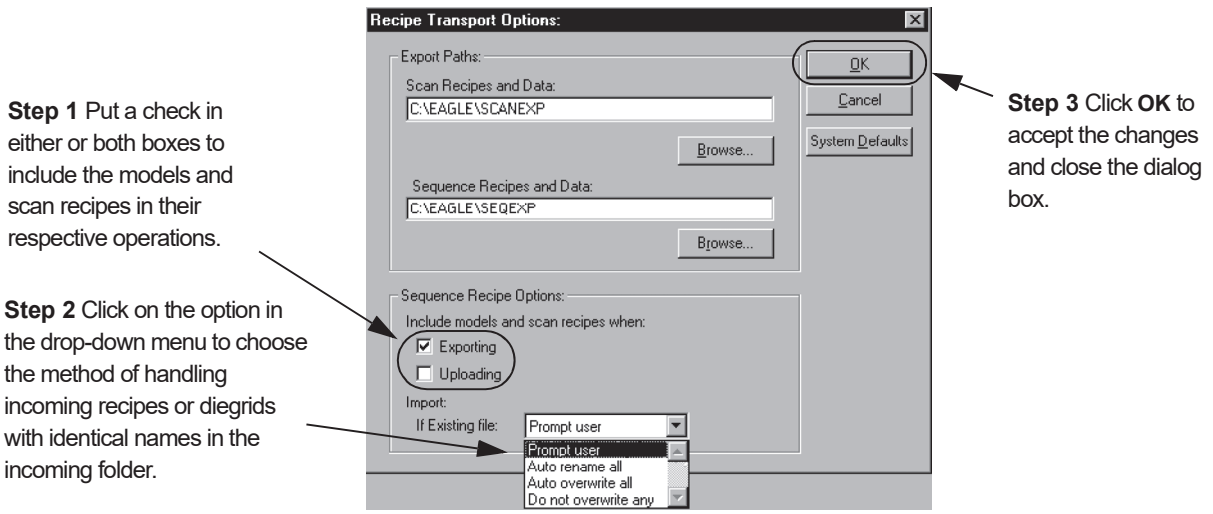
The **Upload** option, when checked, accepts the models and scan recipes when uploading the sequence recipe. If unchecked, the models and scan recipes are not included with basic sequence, deskew, and site by site model.

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*



2. 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.

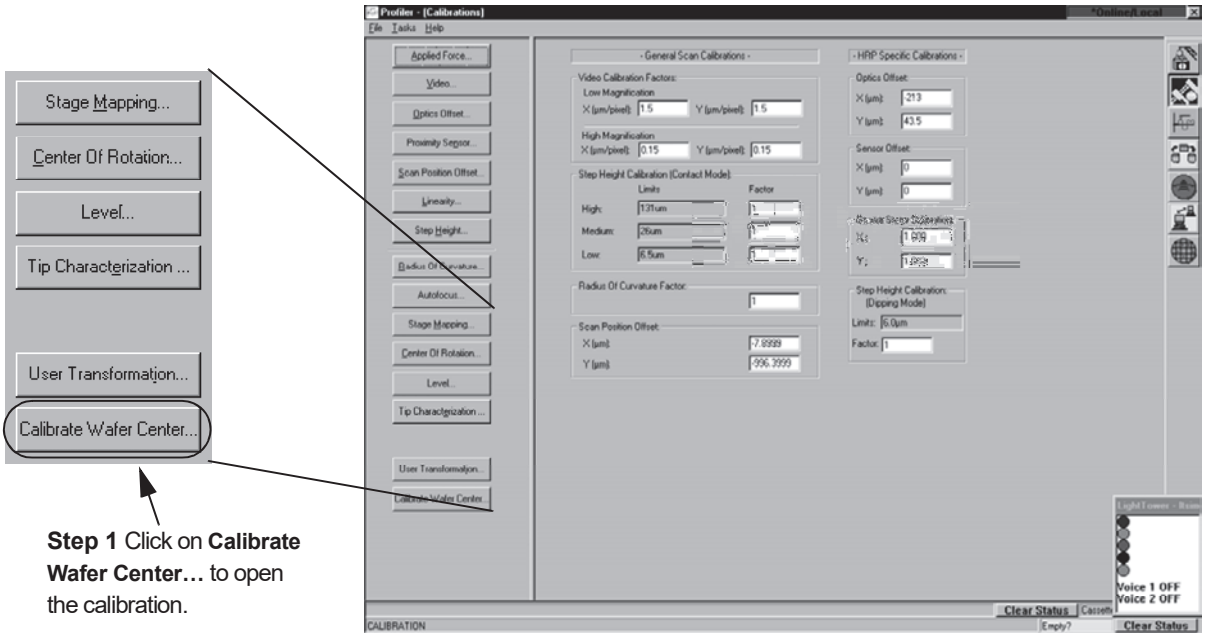
Calibration Procedure

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.

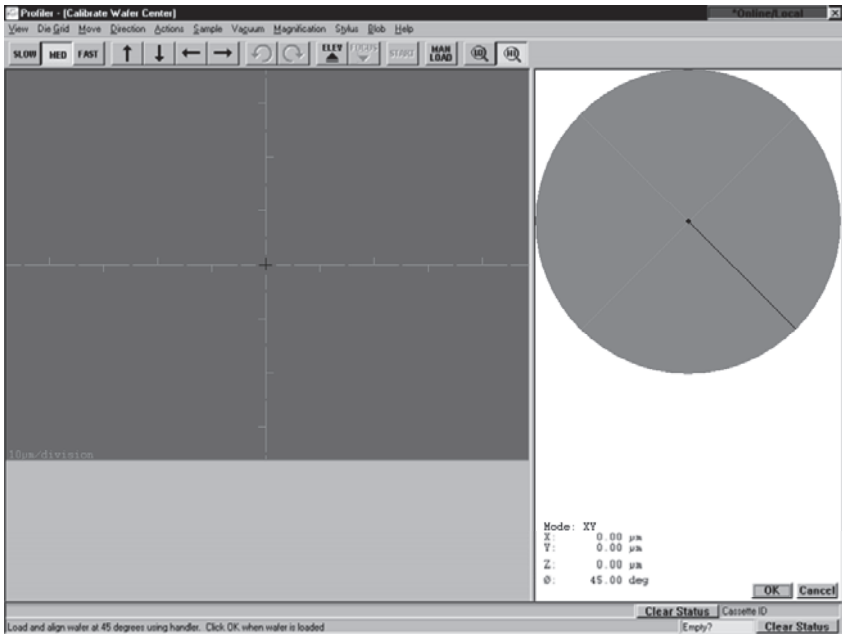
NOTE: The user must be logged in under the proper security level to access the **Calibrate Wafer Center** calibration. Without the correct level, the calibration might be missing from the menu or grayed out.

Figure 7.48 *Calibration Screen*



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°.

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

1. From Windows Explorer, run
   `<Drive where Eagle is located>:\eagle\exe\StagetoWafer.exe`
2. 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

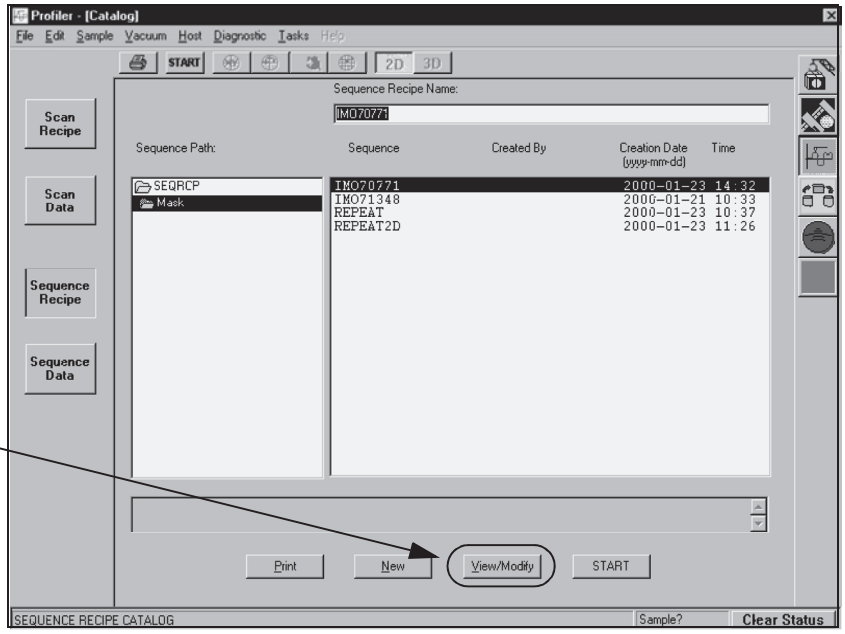
The P-15 does not have a handler. **Manual Load/Unload** is the only active feature in this dialog box, and is available for use in the P-15 system.

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*

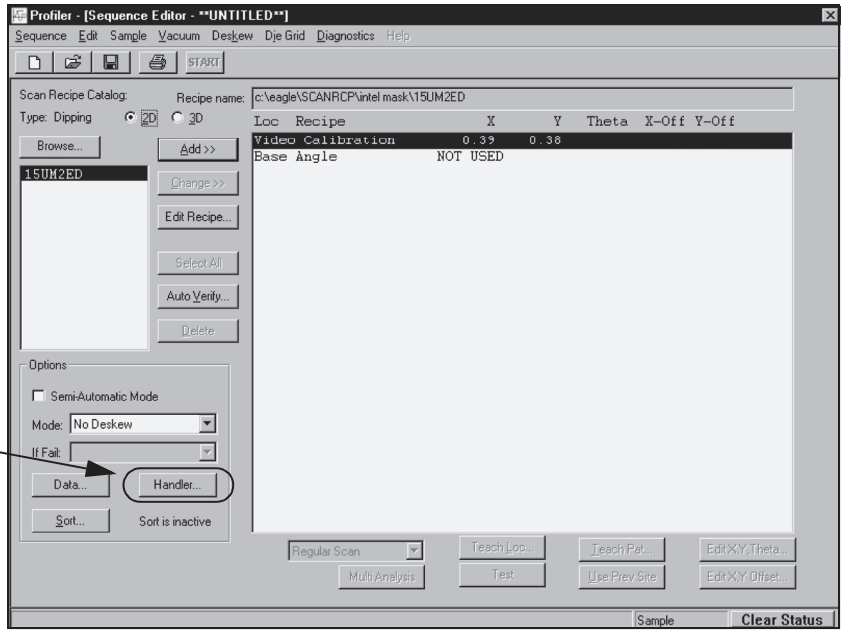


Step 1 To display the **Sequence Editor**, click on **View/Modify**.

2. Click on the **Handler…** button (see *Figure 7.51*) to display the **Handler Options** dialog box. (See *Figure 7.52*.)

Figure 7.51 *Sequence Editor*

Step 2 Click on **Handler** to display the **Handler Options** dialog box.



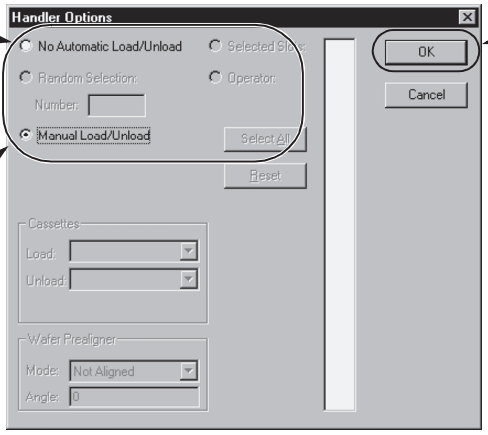
Using Handler Options to Set the Sample Selection Procedure

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*

Click on the **No Automatic Load/Unload** radio button to set manually loaded single sample sequence scans.

Sample loading Options



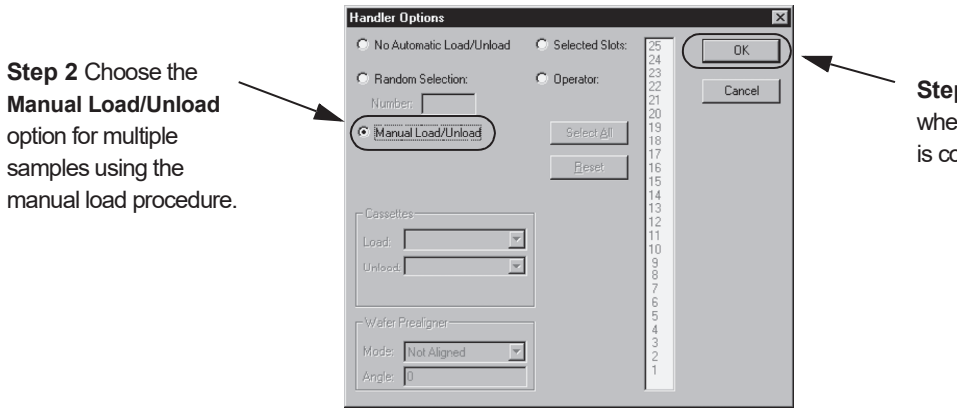
Click on **OK** after all the desired changes have been made.

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.

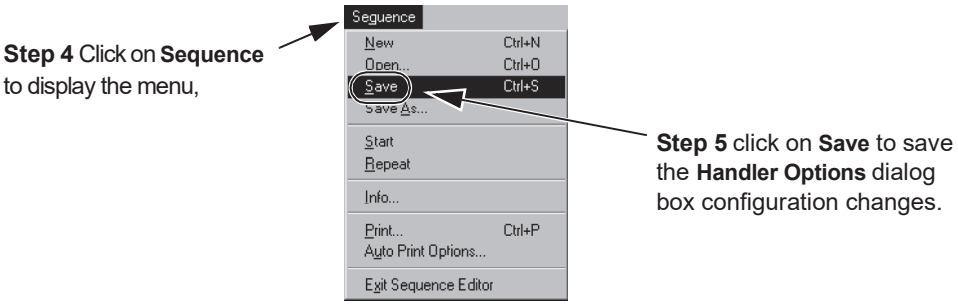
1. In the Sequence Editor click on the **Handler…** button. This displays the Handler Options dialog box. (See *Figure 7.53*.)

Figure 7.53 *Handler Options Dialog Box - Manual Load/Unload Option*



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*.)
3. 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*



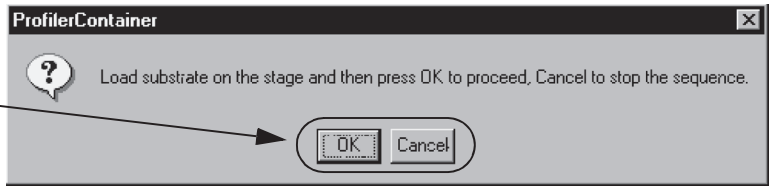
6. When the sequence containing the Manual Load/Unload option is started, a message box appears telling the user to load a sample (substrate) then click **OK** to continue or **Cancel** to stop the sequence. (See *Figure 7.55*.)

   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 stage and click **OK** to continue.

Step 8 Click **Cancel** 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*.)

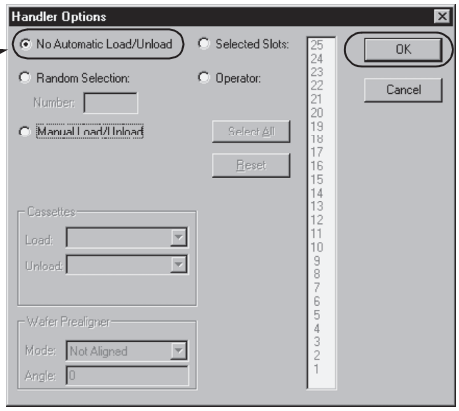
No Automatic Load/Unload

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*

Step 2 Choose the **No Automatic Load/Unload** option for single or random sequence execution.

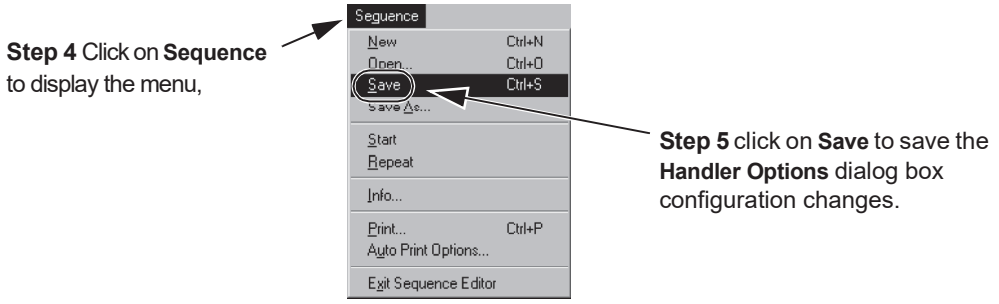


Step 3 Click **OK** when the selection is complete.

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.

5. Click on **Save** to save the changes in the sequence. (See *Figure 7.54*.)

Figure 7.57 *The Sequence Menu*



8

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

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:

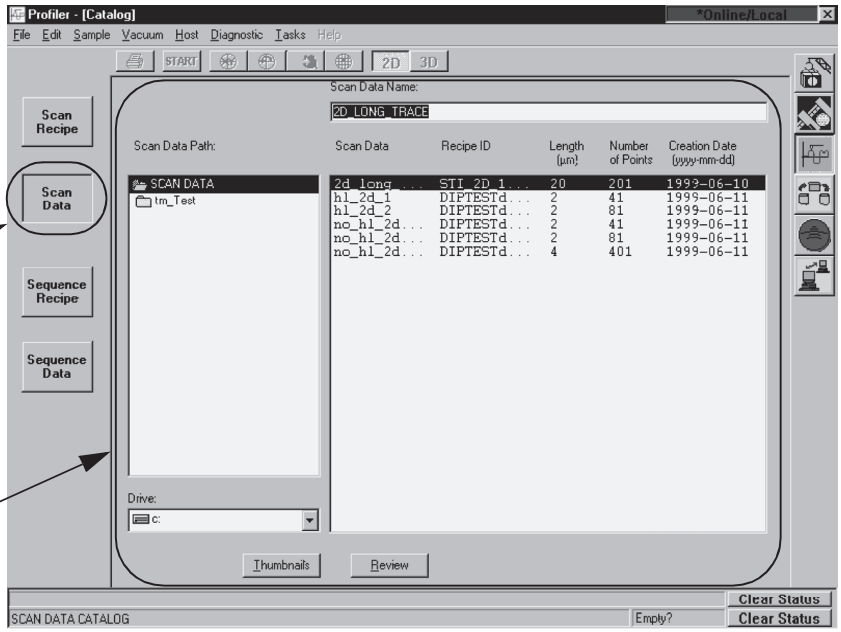
- Its name appears in the Scan or Sequence Data (if it was save to that location).
- It must be opened through the Analysis screen in order to view or reanalyze it.
- It can be reanalyzed by changing the scan recipe parameters.

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*



Step 1 To display the **Scan Data** Catalog in the Scan screen, click on the **Scan Data** button.

Information display Window

2. Click the **2D** button at the top of the screen to display the 2D Scan Data sets. (See *Figure 8.2*.)

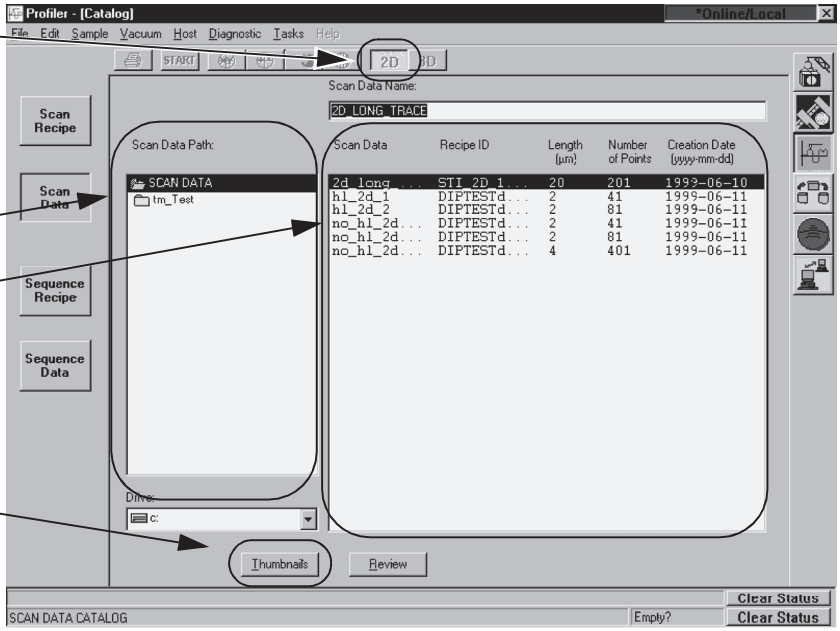
Figure 8.2 *Scan Data Catalog*

Step 2 Click on 2D to display 2D scan data sets in the catalog.

The Information Display window portion of the catalog screen contains:

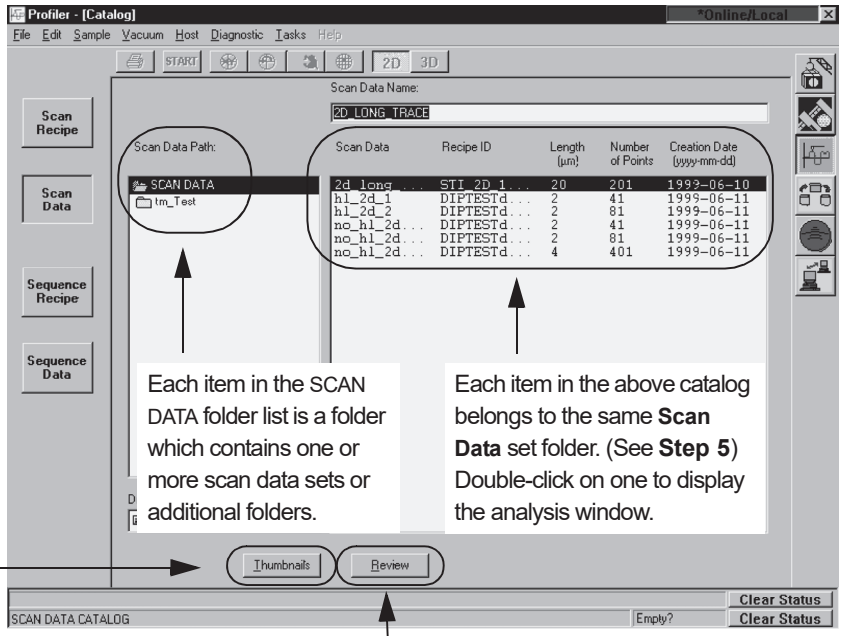
- The list of folders
- Displays the scan data list, the contents of the selected folder. (See *Figure 8.3*.)

Step 4 After clicking on the desired folder, click the **Thumbnail** button to display thumbnails of all data sets in the folder. (See *Figure 8.4*.)



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*



Step 4 Click on **Thumbnails** to display a set of small graphic presentations of the individual scan traces. (See *Figure 8.4*.)

Step 5 Click on a **Scan Data** set, then click on **Review** to display the analysis screen.

Figure 8.4 *Thumbnail Display of Data Traces*

When the **Thumbnail** button is clicked on, the **Thumbnail** dialog box appears containing thumbnail traces of all data in the folder.

(See **Step 5**) To access the **Analysis** screen for any one of the thumbnails, double-click on the thumbnail.
Alternative: See *Figure 8.5*.

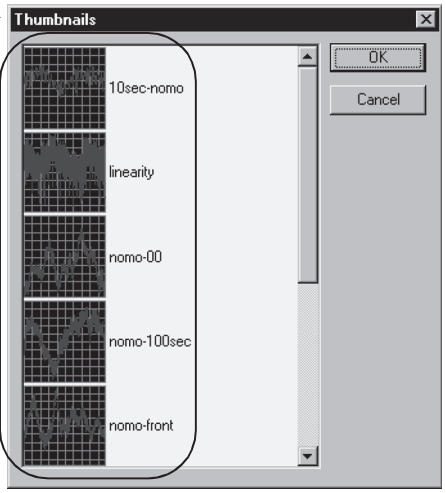
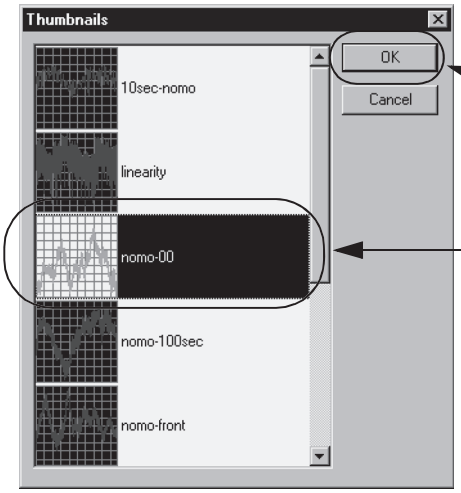


Figure 8.5 *Thumbnail Display of Data Traces*



Alternative: To access the Analysis screen using a thumbnail:

(See **Step 5**) Second, Then click **OK**.

(See **Step 5**) First, click on the thumbnail;

2D Analysis Window Features

The Analysis toolbar contains buttons that provide access to commonly used functions. (See *Table 8.1*.)

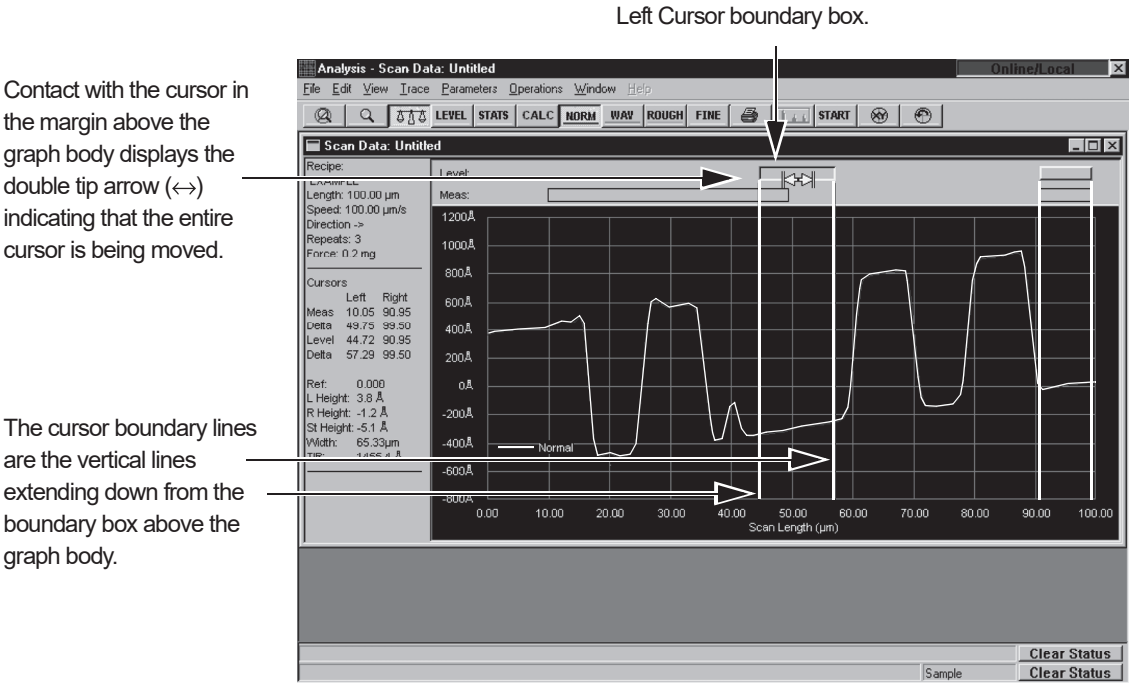
Table 8.1 *2D Analysis toolbar*

Button	Description
	Displays the graph view in the original view size.
	Activates the zoom capability. To focus on a certain part of the graph, use the cursor boundaries to define the zoom-in area.
	Turns the Auto Scale Function for the zoom capability on and off.
	First click activates the LEVEL cursors. Second click levels the trace according to cursor settings and activates the Measurement cursors.
	Opens the Surface Parameter Summary window. If the Surface Parameter Summary window is currently minimized, it appears maximized upon clicking this button.
	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.
	Toggles, ON/OFF, the normal trace graph.
	Toggles, ON/OFF, the waviness trace graph.
	Toggles, ON/OFF, the roughness trace graph.
	Activates Fine Cursor Movement mode of measurement and leveling cursors.
	Prints the Analysis graph and the surface parameter summary.
	Show/Hide Major Modes for the Histogram.

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.

Figure 8.6 *Data Before Leveling, with Leveling Cursors Visible*



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.

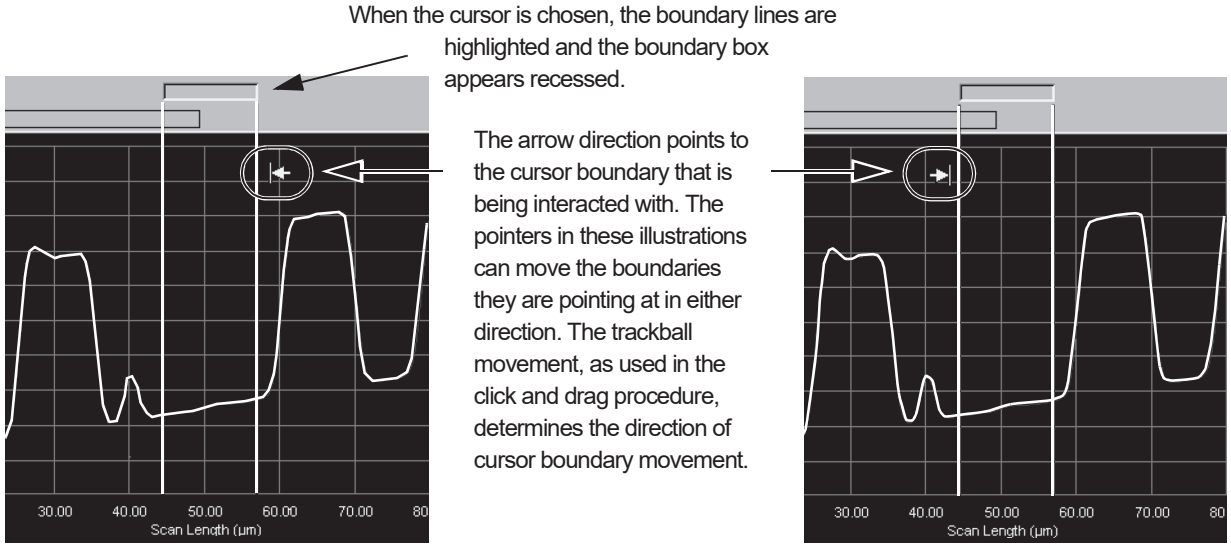
In the following discussion the screen's arrow cursor is called the *pointer*. The word *cursor* is used to describe the vertical boundary lines used to manipulate screen data.

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*.)

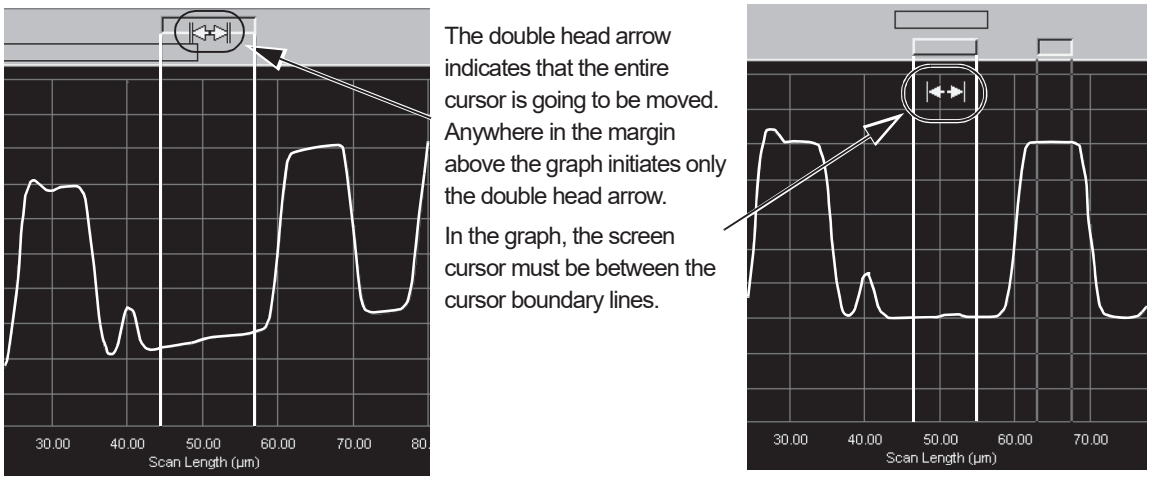
Figure 8.7 *Screen Cursor Positioning*



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. The pointer in the right illustration only moves the left 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.

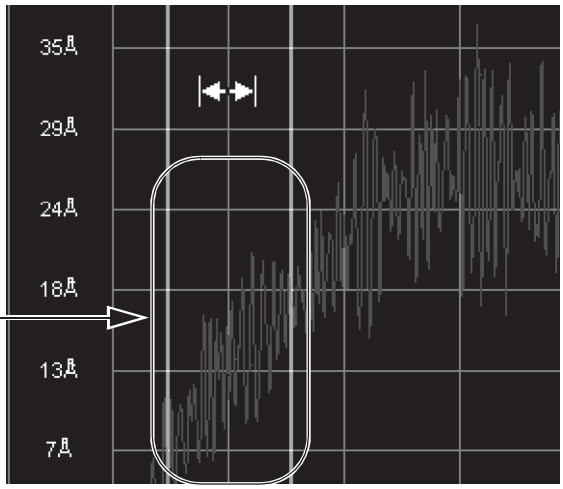
Once the desired cursor is highlighted (or both cursors are highlighted) use the up or down arrow keys to spread or reduce the cursor(s) size. Notice that the cursor boundaries move outward (up arrow) or inward (down arrow) a small consistent distance each time the arrow key is clicked.

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*.

Figure 8.9 *Delta Mode - Cursor Spread on a Scan Trace*

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).

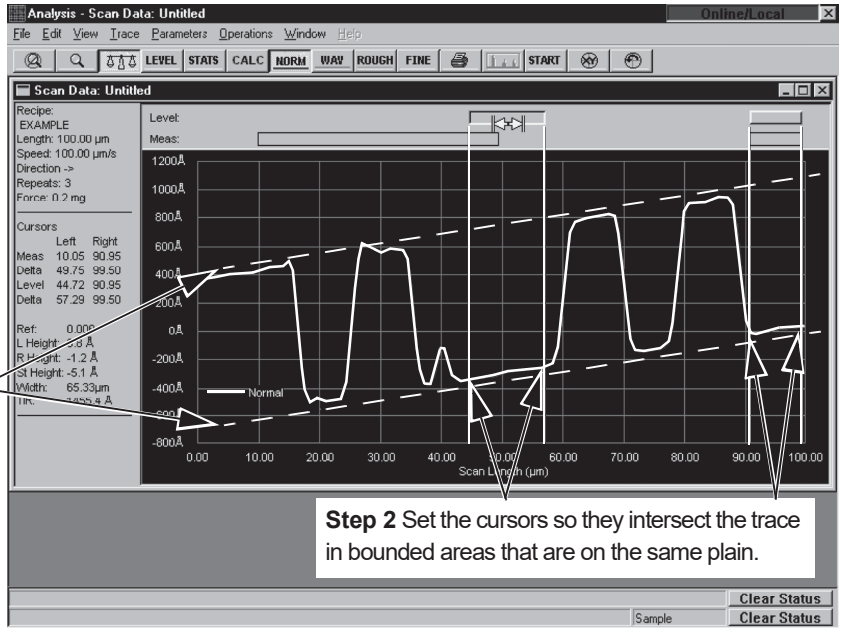
Figure 8.10 *Analysis Screen with Unleveled Trace and Level Cursors*

The **LEVEL** button is used two times:

Step 1 The first click activates the Leveling Cursors.

Step 3 The second click levels the trace and activates the Measurement Cursors.

The dashed lines are not in the actual screen but are used here to show two planes which can be used in this trace for setting leveling cursors.



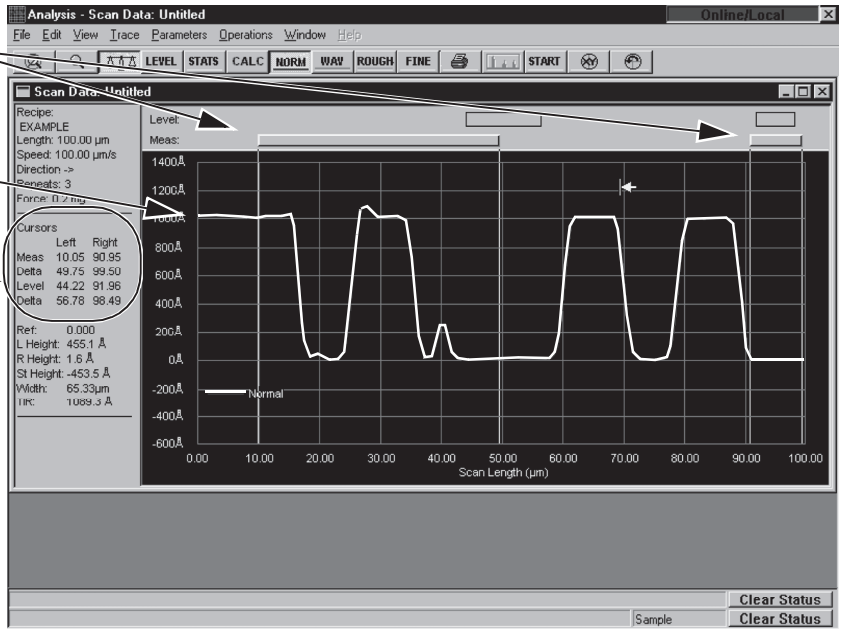
2. To set the cursors so that the trace is accurately leveled, it is important to find two areas on the trace that are on the same plain. Set the cursors to the desired positions. (For help moving cursors, see *Using Cursors* on page 8-6.)

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*

After the **LEVEL** button is clicked on the second time, the Measurement Cursors are activated and the trace appears leveled out.

As the cursors are moved in the Analysis screen, the Cursors limits adjust automatically to reflect the new positions. (See *Figure 8.12*.)



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.

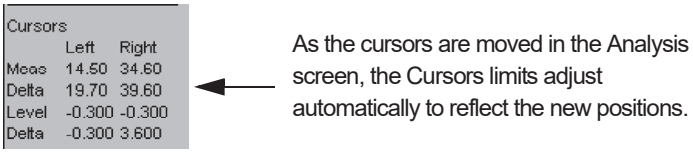
2. To determine the area in a peak or valley region, the Measurement Cursors can be moved (or adjusted if they were partially out of position) to accurately enclose those regions and the area calculated or recalculated.

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.

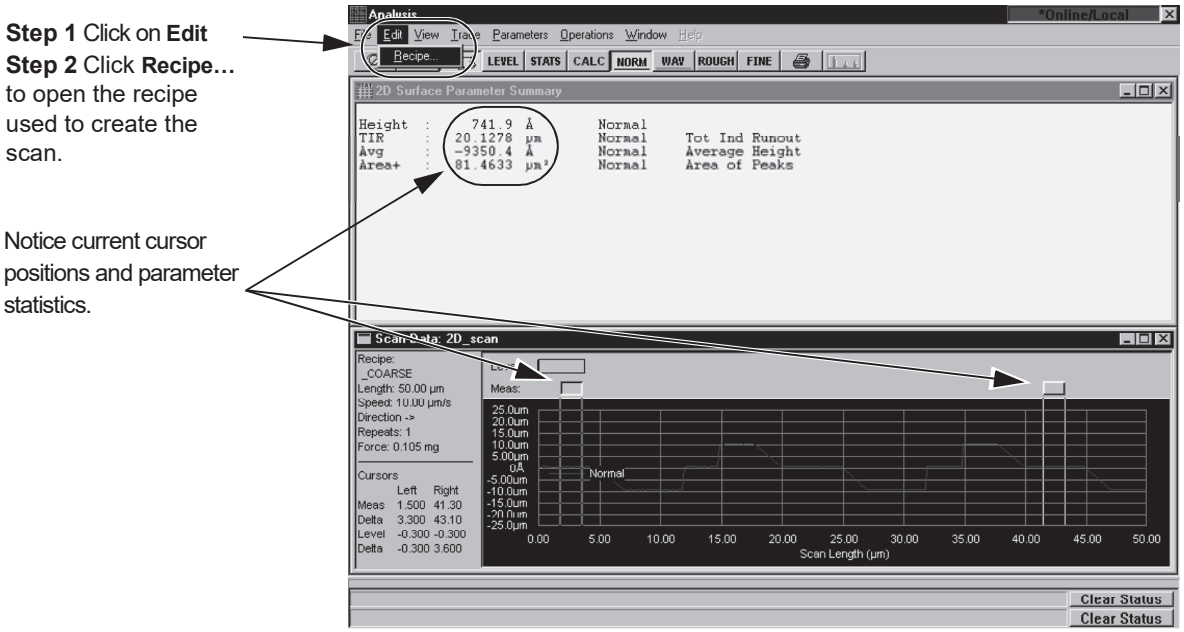
Figure 8.12 *Analysis Screen's Cursors Settings*



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*

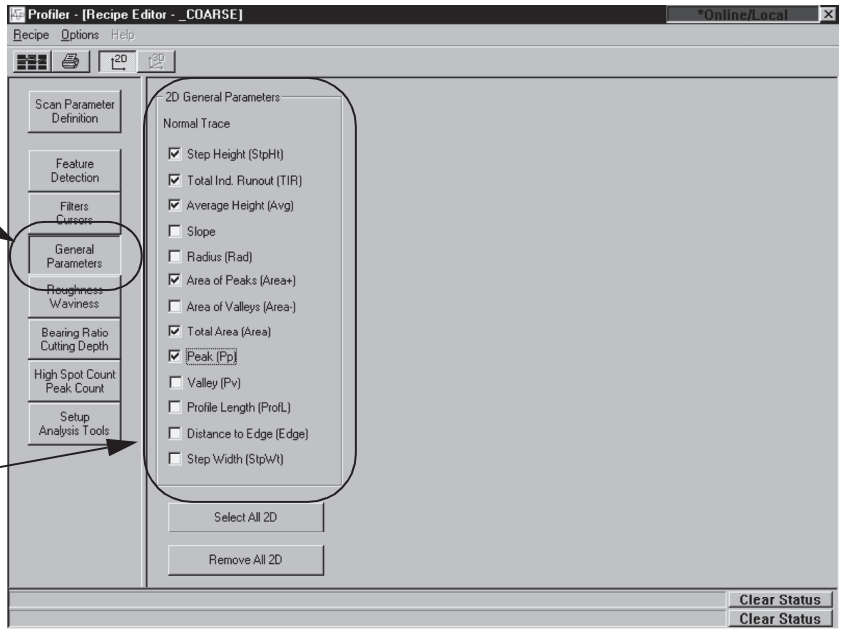


This displays the scan recipe screen from which parameters can be added or removed. In *Figure 8.14* the **General Parameters** window of the Recipe screen has been opened to change the parameter set to be calculated with the next cursor adjustment. (This procedure can be used with both live and saved data.)

Figure 8.14 *Recipe Screen - General Parameters Window*

The General Parameters button has been chosen and its contents displayed.

Parameters have been chosen that reflect the needs relating to the pending cursor change.

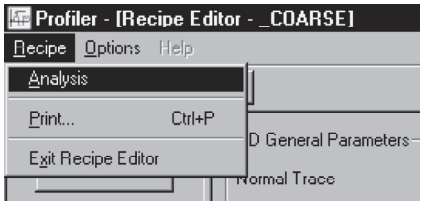


3. When the parameters have been chosen, click on **Recipe** to display its menu. (See *Figure 8.15*.)
4. Choose **Analysis** to return to the Analysis screen. The system calculated the parameter values for the chosen parameters using the current cursor settings and displays them in the **Surface Parameter Summary** window. (See *Figure 8.15*.)

Figure 8.15 *Exit Recipe Editor to Return to Analysis Screen*

Step 3 Click on **Recipe** to display its menu.

Step 4 Choose **Analysis** to return to the Analysis screen.



After repositioning the cursors, to recalculate the parameters in the **Surface Parameter Summary** window, use the following procedure:

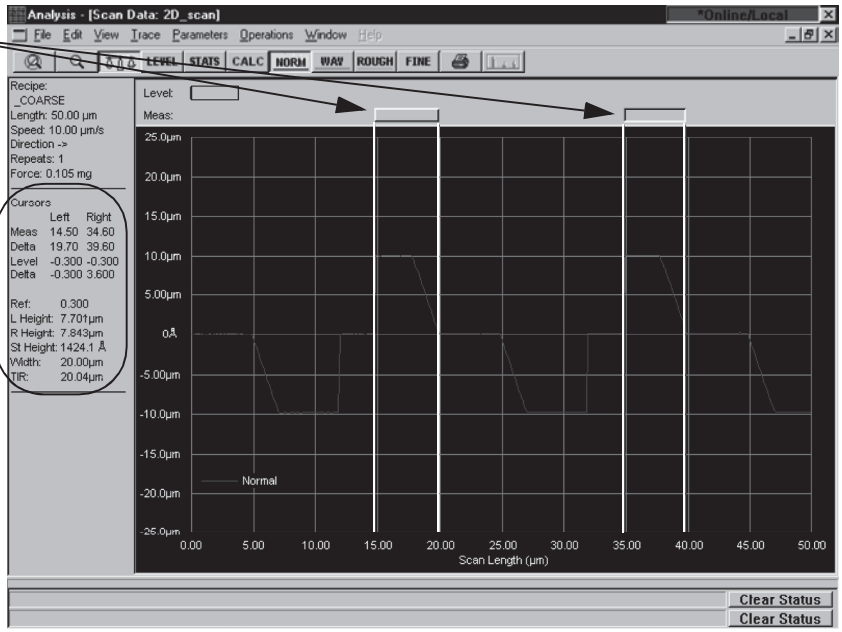
5. Set the Measurement Cursor positions. (For help positioning the cursors, see *Using Cursors* on page 8-6.)

   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*.)

Figure 8.16 *Analysis screen with Repositioned Cursors*

Step 5 The cursors are moved to a new position. In this illustration they are positioned to find the area under the two high features on the graph.

The cursor positions and related height, width and step parameters are automatically updated as the cursors are moved.

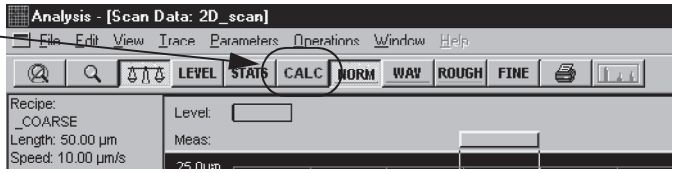


6. After positioning the measurement cursors, the parameters in the **Surface Parameter Summary** window are ready to be updated:

   Click the **CALC** button to perform the recalculation. (See *Figure 8.17*.)

Figure 8.17 *CALC Button in Analysis Screen*

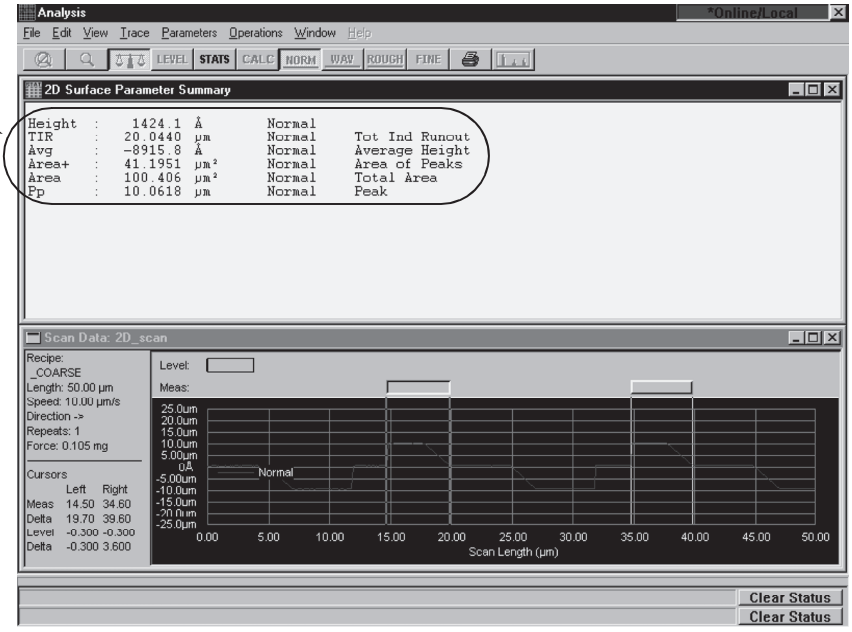
Step 6 Click **CALC** to recalculate the parameters using the new cursor positions.



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.

Figure 8.18 *Surface Parameter Summary Window*

When the recalculation procedure is performed, only the parameters chosen in the scan recipe are visible and only those are changed.

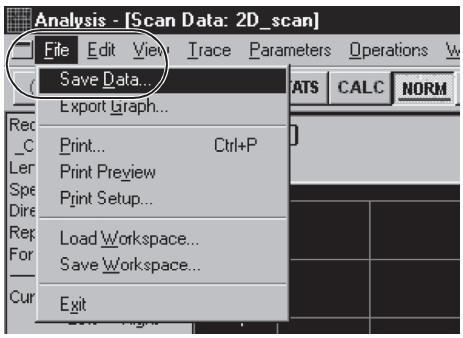


7. To retain the newly calculated values in a data file and the new cursor positions in the recipe, the data must be saved. Click **File** to open its menu. (See *Figure 8.19*.)
8. Choose **Save Data…** from the File menu to open its dialog box. (See *Figure 8.19*.)

Figure 8.19 *File Menu in Analysis Screen*

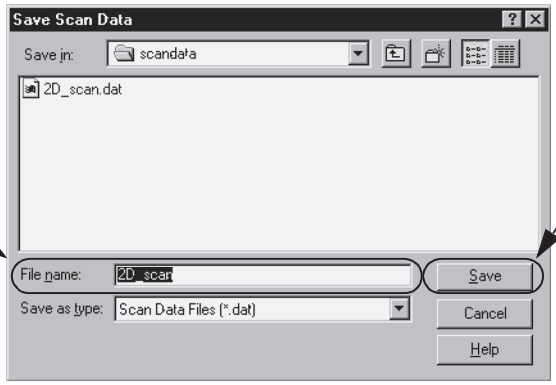
Step 7 To save data, click **File** to display its menu.

Step 8 Choose **Save Data…** from the File menu.



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*.)

Figure 8.20 *Save Scan Data Dialog Box*



Step 9 Enter the file name.

Step 10 After the name is entered click **Save** to save the data to the file.

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

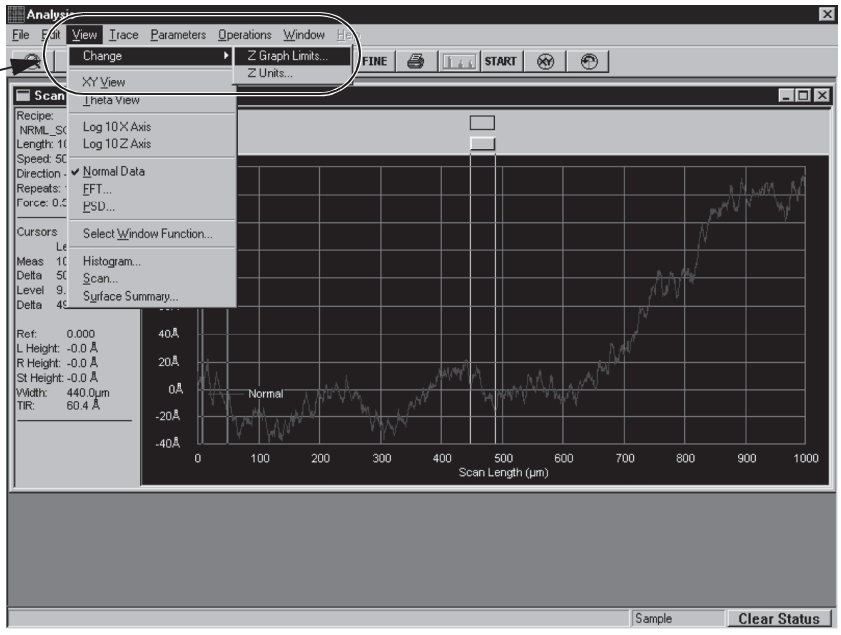
Changing the Z Limits Display allows the user to set the scale on the graph.

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

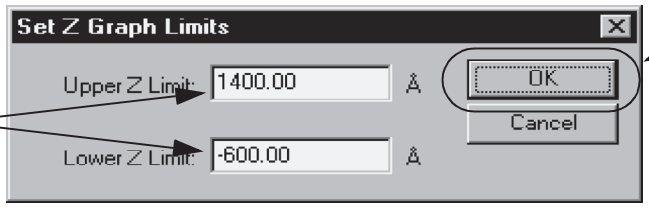
- **Step 1** Click **View** to display the menu.
- **Step 2** Choose **Change**
- **Step 3** Choose **Z Graph Limits**



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*).

Figure 8.22 *Setting Z Graph Limits*

Step 4 To change the limits, double-click on the current limit to highlight it. Enter the new limit.



Step 5 Click on **OK** to save the changes to the limits.

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

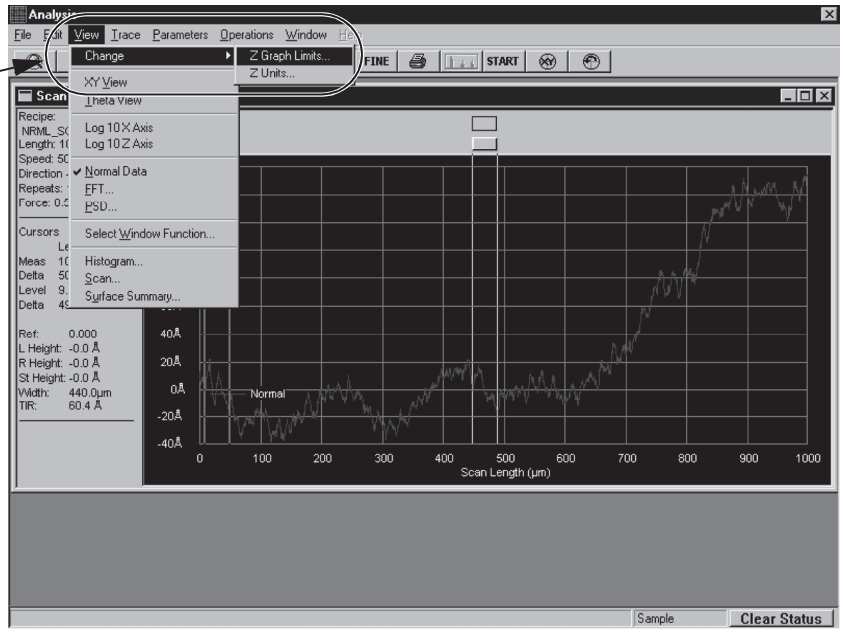
The Profiler plots the data in µm, nm, Å, or both µm and Å with a crossover value that is set by the user.

1. Click the **View** menu to display its menu. (See *Figure 8.23*.)

Figure 8.23 *Analysis Screen with View Menu*

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**



2. Choose **Change** from the View menu. (See *Figure 8.23*.)

3. Select **Z Units**. (See *Figure 8.23*.)
   The **Set Z Units** dialog box appears (see *Figure 8.24*).

Figure 8.24 *Set Z Units Dialog Box*

Step 4 Choose the desired units by clicking in the appropriate radio button.

For the bottom choice, after clicking in the radio button, enter a distance at which it changes between microns and angstroms.

Step 5 Click on **OK** to apply the settings to the displayed data.

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 (µm) to angstroms (Å) or from Å to µm. 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).

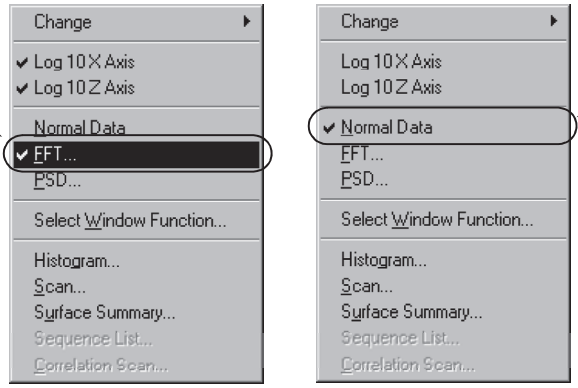
A choice of window functions is available to apply to the endpoints of the FFT data.

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*

Step 2 To choose Fast Fourier Transform, click FFT. A check next to FFT indicates that it is chosen.



Step 4 To return to the normal data presentation, click on Normal Data. A check next to Normal Data indicates that it is 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*

Step 1 Click on **View** to display its menu. See the menu in *Figure 8.25*. Choose **Normal Trace**.

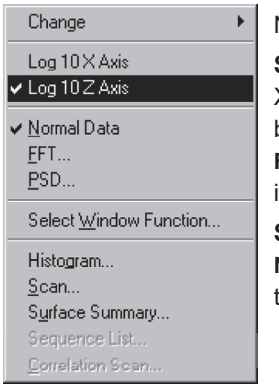
A Normal Trace without logarithmic scaling.

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.

Figure 8.27 *View Menu*

EXAMPLE:

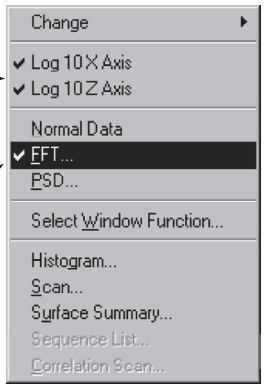
With Normal Data chosen, click on Log 10 Z Axis to display the Normal data in Z Axis logarithmic scaling. For result see *Figure 8.28*.



Normal Application.

Step 3 Click on Log 10 X Axis, Log Z Axis, or both to display **F**ast **F**ourier **T**ransform data in logarithmic scaling.

Step 2 Click on **Normal Data** or **FFT**. In this example, **FFT**.

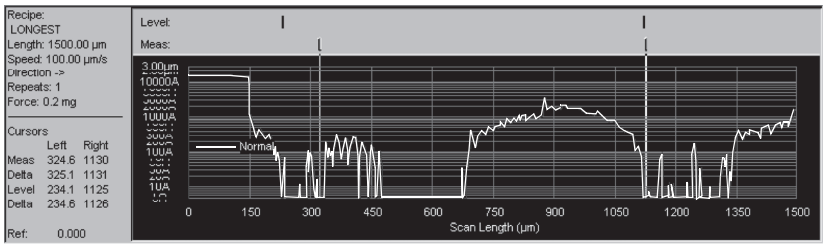


A check appears beside the menu selection and the instrument replots the data for the chosen axis.

Figure 8.28 *Normal Trace and Z Axis Logarithmic Scaling*

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.



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.

Zoom Procedure

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  toggles the scale function on and off.
2. Click on the **Zoom-in** icon to activate the zoom function. (See *Figure 8.29*.)

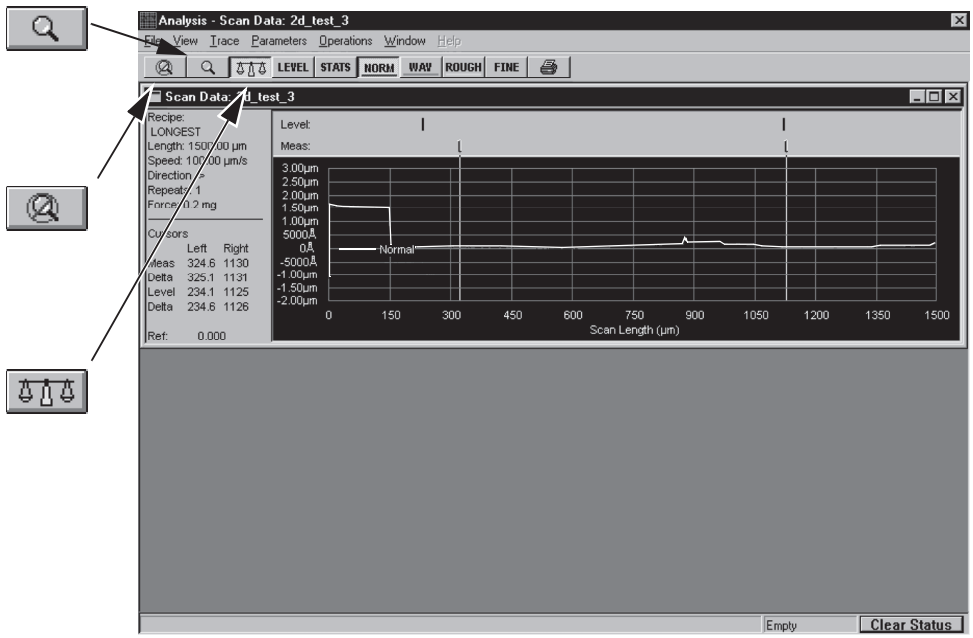
3. Click on the **Zoom-out** icon to return to normal display. (See *Figure 8.29*.)

Figure 8.29 *Analysis Screen with the Zoom and Scale Function Buttons*

Step 2 Click on the **Zoom In** icon for a closer view a portion of the trace.

Step 3 Click on the **Zoom Out** icon to return to the original view.

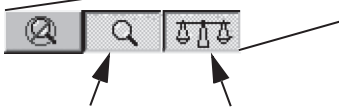
Step 1 Click on the **Scale** icon to activate scaling. If the button is highlighted, the zoom function is a box, if scaling is not on, zoom is between cursors.



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*.)

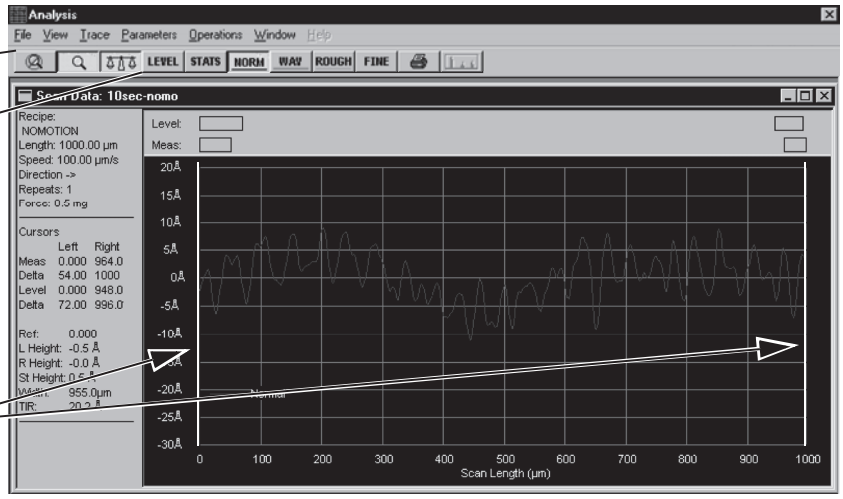
Figure 8.30 *Analysis Screen Using Scaling Zoom*



When the cursors are positioned around the portions to be zoomed, click here.

Click to turn the scale function **on**.

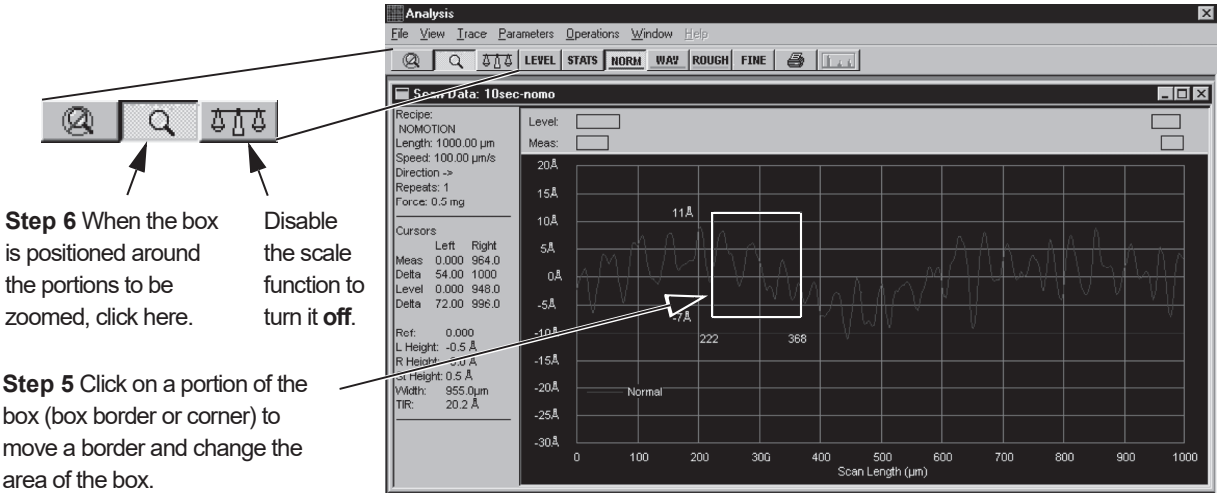
Step 4 Click on each cursor (left and right) and move them to define the zoom area.



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.

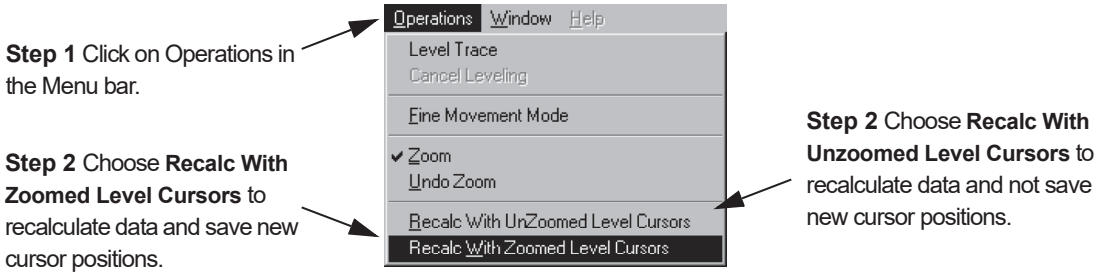
6. Click on the **Zoom In** icon to zoom into the area defined by the cursors or the zoom box. (See *Figure 8.31*.)
7. Perform any measurement or leveling procedure necessary to analyze the zoomed data.
8. Click the **Zoom In** button again to deactivate the zoom cursors and reactivate the measurement 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.

Saving Data From the Zoom Procedure

Saving data and cursor position in **Surface Parameter Summary**

1. To update the data in the **Surface Parameter Summary** window and to store zoomed cursor positions in the recipe, click the **Operations** menu, and select **Recalc with Zoomed Level Cursors.** (See *Figure 8.32*)

Figure 8.32 *Recalculate and Save Zoomed Leveling Cursors*



Saving only data in **Surface Parameter Summary**

2. To update the data in the **Surface Parameter Summary** window without saving the zoomed cursor positions, go to the **Operations** menu and select **Recalc With Unzoomed Cursors**. (See *Figure 8.32*)
3. To return to the original scan view click the **Undo Zoom** icon  , or go to 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.

Table 8.2 *Trace Information Parameter*

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 **Total Indicator Runout**.

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.

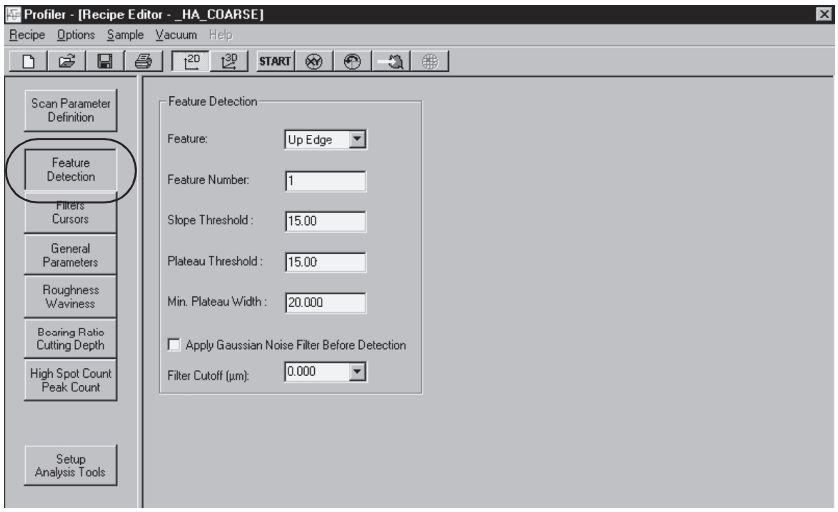
In conjunction with feature detection, both the location of the edge (or the apex of an arc) and the step width, can be calculated and displayed in the Analysis window.

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*

Step 1 To display the **Feature Detection** parameters in the Recipe Editor Information Display window, click on the **Feature Detection** button.



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*

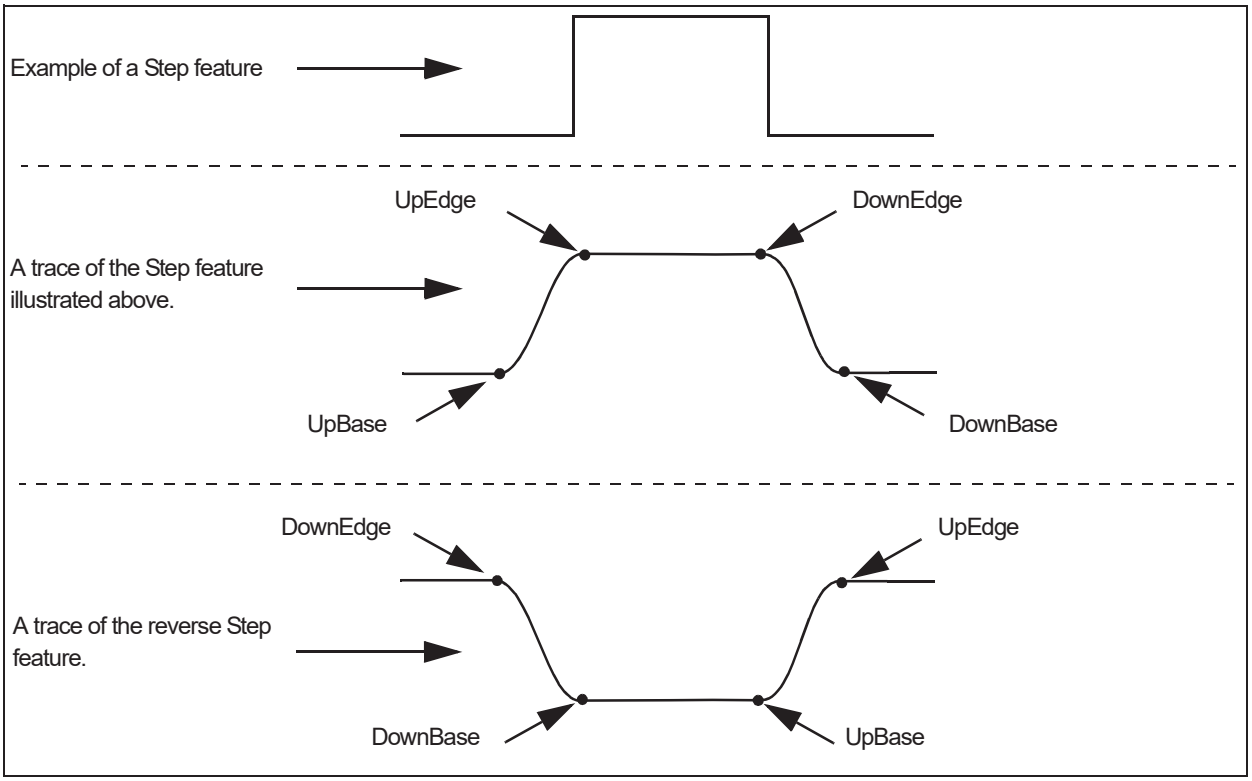


Figure 8.35 *Feature Detection Point Locations for Convex and Concave*

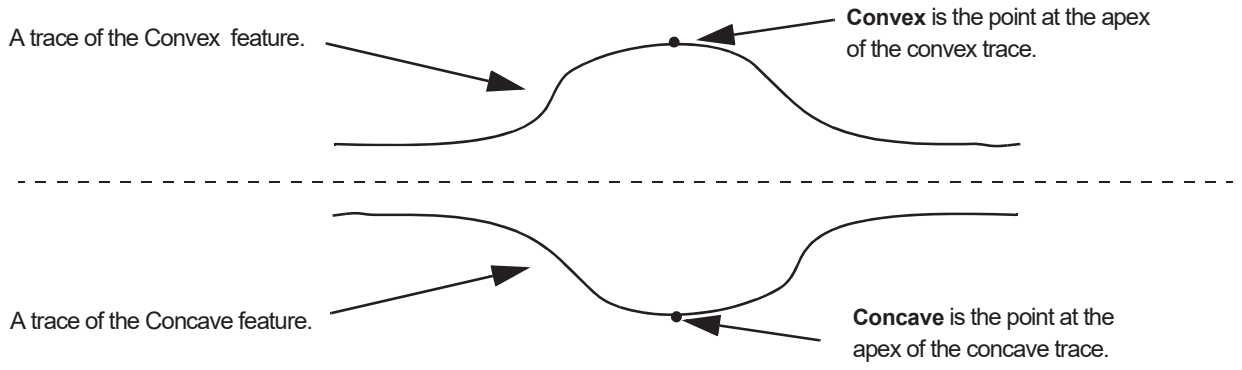


Table 8.3 *Feature Detection Descriptions (See Figure 8.34 and Figure 8.35.)*

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 *Figure 8.34*.) **NOTE**: The point location can be modified using the **Distance to Edge** parameter in the **General Parameters** Window.
UpBase	At the trailing edge of a plateau, it is the point at which the trace begins to turn upward. (See *Figure 8.34*.)
DownEdge	At the trailing edge of a plateau, it is the point at which the trace begins to turn downward. (See *Figure 8.34*.)
DownBase	At the trailing edge of a feature decline, it is the point at which the trace begins the plateau. (See *Figure 8.34*.)
Convex	This is the point at the apex of a convex feature. (See *Figure 8.35*.)
Concave	This is the point at the apex of a concave feature. (See *Figure 8.35*.)

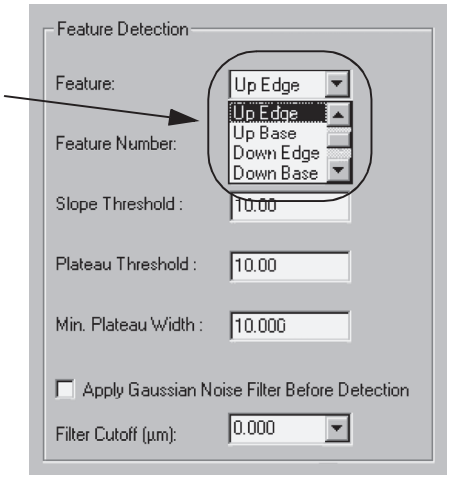
Selecting a feature for detection:

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 Editor*

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.



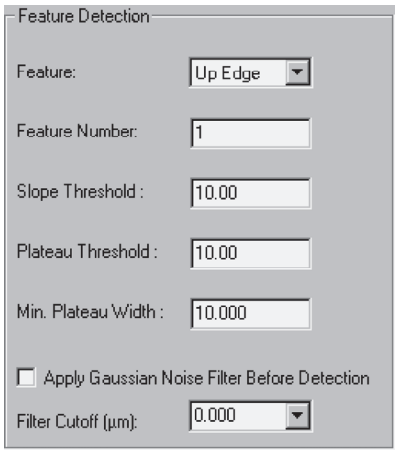
3. **Feature Number:** - If multiple edges are detected in the scan, **Feature Number** provides a way to select a specific edge for detection. (See *Figure 8.37* and also *Quick Reference Table 8.4 on page 8-33*.)

   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 *Detection Variables - Feature Detection - Recipe Editor*

Detection parameters are changed by clicking in the appropriate variable box to highlight the current number. Then type in the new number.



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.

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.

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 0.0002–39.3701 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.

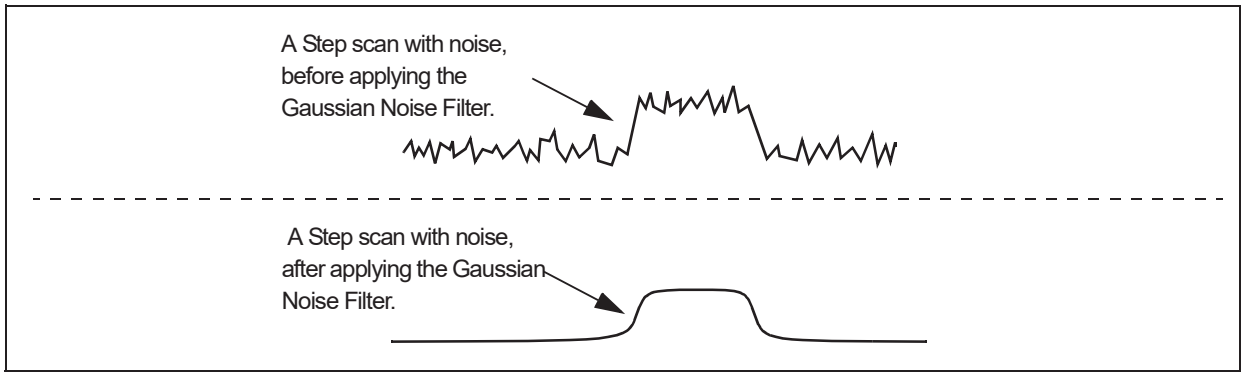
- **For a Convex arc:** The Minimum Plateau Width specifies a minimum width for the feature, and so can be used to reject narrow roughness peaks in the vicinity of the arc.
- **For a Concave arc:** The Minimum Plateau Width is used to specify a minimum size for a level section following a detected arc.

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.

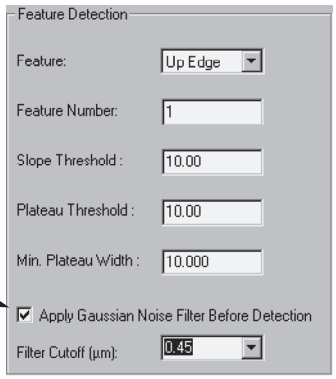
Figure 8.38 *Scan Noise and the Gaussian Noise Filter*



Activating this feature, click in the empty check box to put a ✓ in it. (See *Figure 8.39*.) Then set the **Filter Cutoff (mm)** size.

Figure 8.39 *Activating the Gaussian Noise Filter*

To activate the Gaussian Noise Filter Before Detection feature, click in its check box. A check (✓) indicates that it is chosen.



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*.)

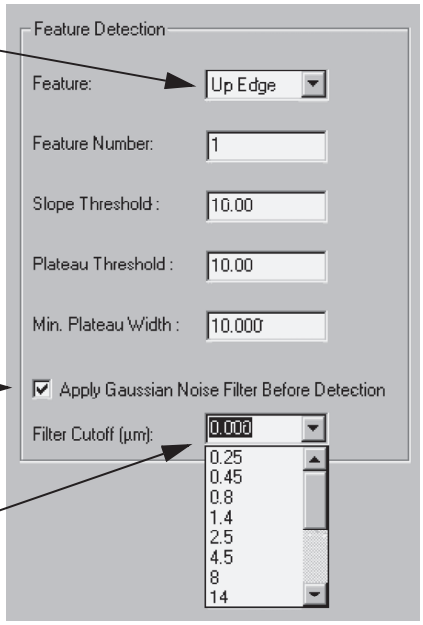
- The Filter Cutoff range is from 0.25 through 800 µm. Only established variables may be chosen.

Figure 8.40 *Filter Cutoff Menu*

Step 8*a*. In order for the Apply Gaussian Noise Filter Before Detection, a Feature must be chosen. The filter is not available unless there is a feature chosen.

Step 8*b*. After a Feature is chosen, put a check (✓) in the check box by clicking in it.

Step 8*c*. Click on the down arrow to display its menu. Click on the desired cutoff filter setting.



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*

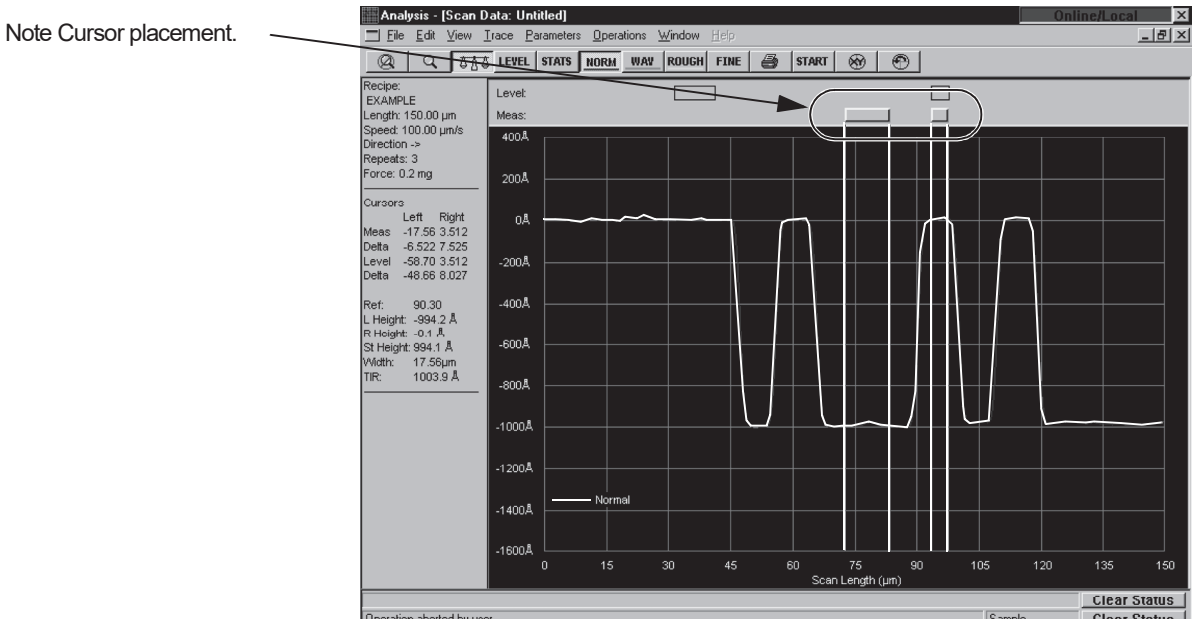


Figure 8.42 *Feature Detection - Run 2 with Automatic Cursor Placement*

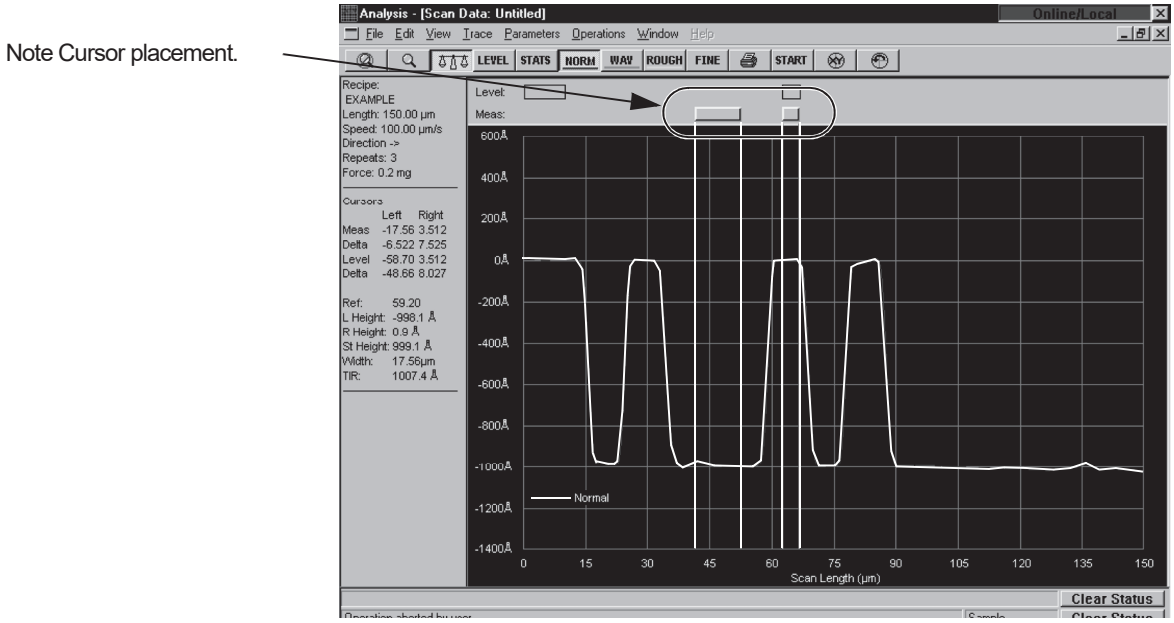
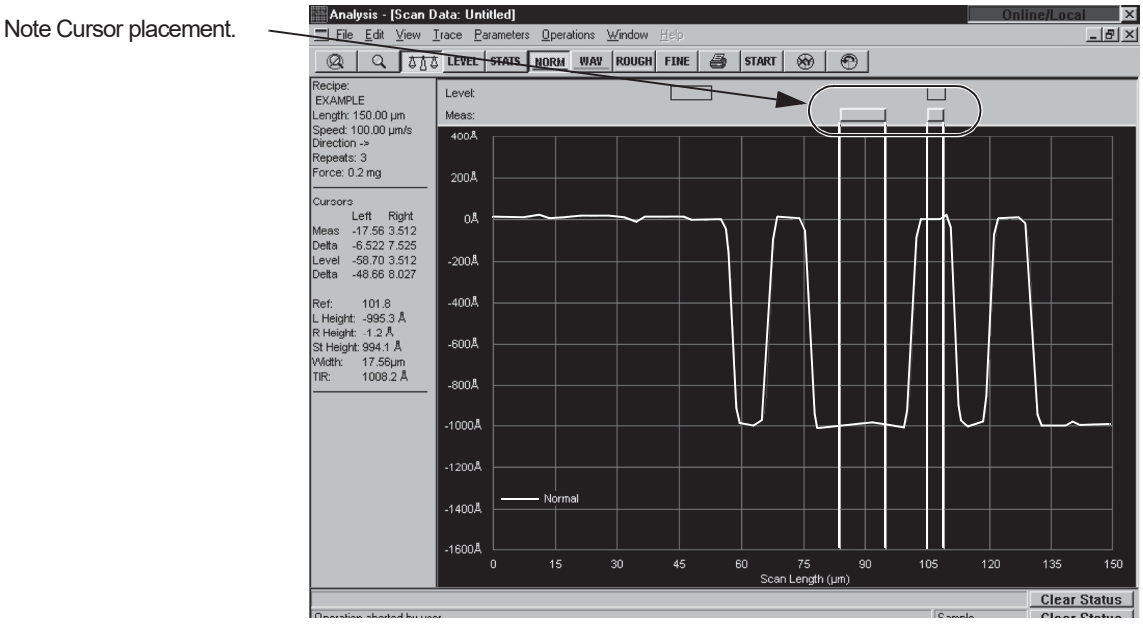


Figure 8.43 *Feature Detection - Run 3 with Automatic Cursor Placement*



Feature Detection Quick Reference Table

Table 8.4 *Feature Detection Variables*

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. **Slope Threshold** 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, **10** 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 **Plateau Threshold** is to set the same value as the **Slope Threshold**.
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:

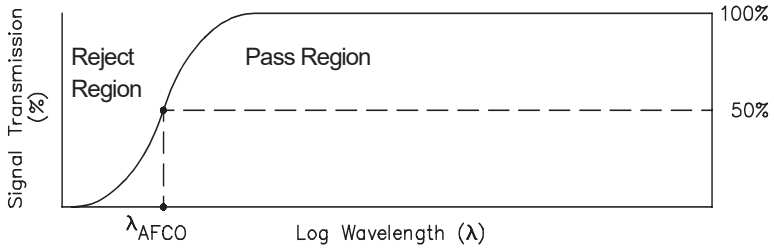
$$Cutoff\ Wavelength = \frac{Scan\ Speed}{Cutoff\ frequency\ of\ combined\ filters}$$

   For example, with a scan speed of 100 µm/s, and a sampling rate of 200 Hz or 100 Hz, the cutoff wavelength is 5.6 µm. With this same scan speed, however, at a sampling rate of 50 Hz, the cutoff wavelength is 7.1 µm.

   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.

Figure 8.44 *Effect of the Analog and Decimation Filters On Signal Transmission*



Setting the Short-Wave Filter Cutoff Values

See also the discussion on Short-Wavelength Cutoff Filters

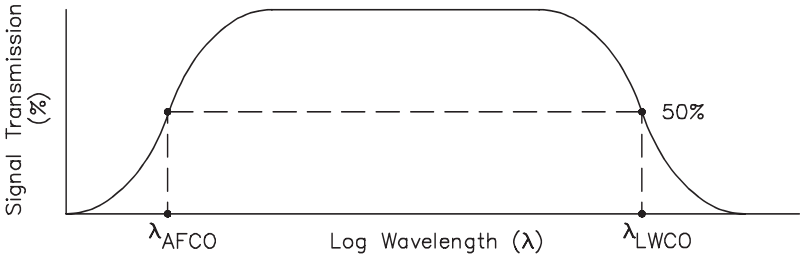
Data can be filtered to provide the following specific results:

- 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*

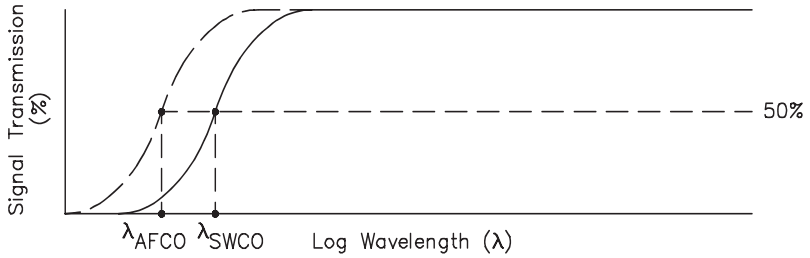


The short wavelength cutoff or noise filter attenuates data with wavelengths below the specified cutoff valve. This has the effect of removing noise from the data. This filter is always active, set either to a specified or a default value.

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*

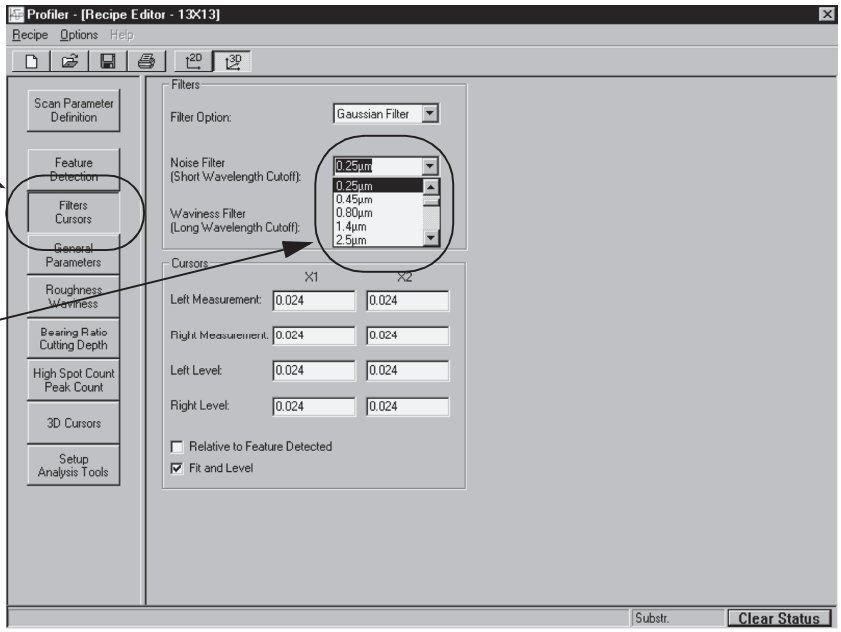


1. Go to the Recipe Editor, click **Filters/Cursors** to open its window. (See *Figure 8.47*.)
2. At the **Noise Filter** (shortwave cutoff) variable field, click the drop-down arrow to select a value from the range of cutoff filters provided. In this menu, the filter can also be turned off by clicking the **Off** option in the menu. The chosen filter appears in the variable field. (See *Figure 8.47*.)

Figure 8.47 *Recipe Editor – Filters and Cursors Options*

Step 1 Click on the **Filter/Cursors** button to display the Filter and Cursor options.

Step 2 To display the Noise Filter menu, click on the down-arrow next tot he variable field. Click to choose the filter or click on **Off** at the top of the menu to turn the filter **Off**.



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 µm/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.

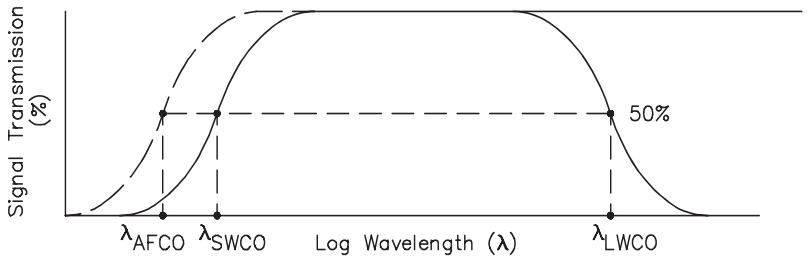
3. From the Filter Option variable menu, select from the following filters:
   - **Gaussian** For Windows-based systems; and
   - **RC** For comparison to scan data obtained with DOS-based systems, such as the KLA-Tencor P-2 Long Scan Profiler.

Setting the Long-Wavelength Filter Cutoff Values

Select the long-wave cutoff (or short-wave pass) filter.

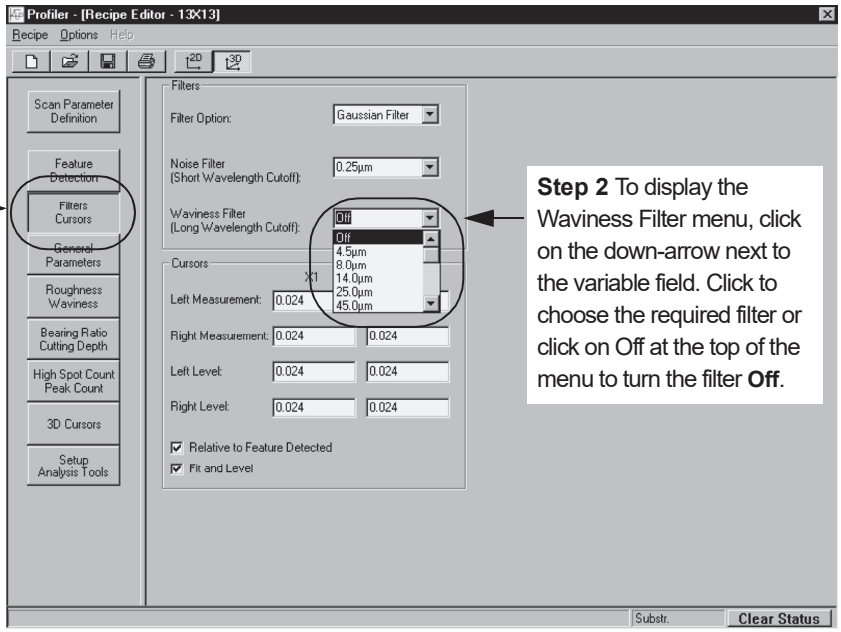
This cuts off the higher wavelengths in the data (those above the filter's cutoff value, see *Figure 8.48*).

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)*



Step 1 Click on the **Filter/Cursors** button to display the Filter and Cursor options.

Step 2 To display the Waviness Filter menu, click on the down-arrow next to the variable field. Click to choose the required filter or click on Off at the top of the menu to turn the filter **Off**.

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*

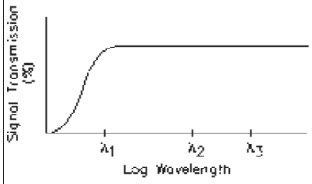
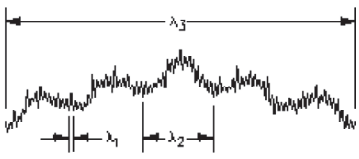
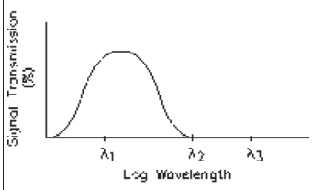
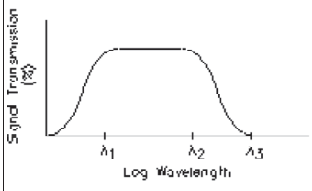
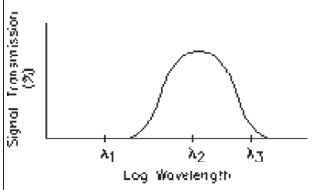
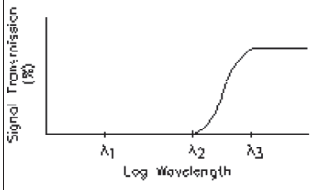
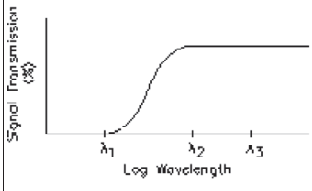
Signal Transmission Curve	Scan Data Effect	Description
		**Normal Data** Only the analog filter acts on the data. Three wavelengths, labeled λ_1, λ_2, and λ_3, are identified.

Figure 8.50 *Signal Transmission Curves And Their Effects On Scan Data*

Signal Transmission Curve	Scan Data Effect	Description
		**Roughness 1** The long-wavelength cutoff filter is applied with a cutoff value just higher than λ_1. The resulting data trace shows only features of the scale of λ_1; higher wavelengths, including λ_2 and λ_3, are suppressed.
		**Roughness 2** A different long-wavelength cutoff value is applied, it value is just higher than λ_2. The resulting data trace shows features of the scale of $\lambda_1$to λ_2; higher wavelengths, including λ_3, are suppressed.
		**Roughness 3** A short-wavelength cutoff filter with a value just higher than λ_1 is applied, in addition to the long-wavelength cutoff, to the Roughness 2 curve. The resulting data trace shows only features of the scale of λ_2; higher wavelengths, including λ_3, and lower wavelengths, including λ_1, are suppressed.
		**Waviness 1** The short-wavelength cutoff filter is applied with a cutoff value just lower than λ_3. The resulting data trace shows only features of the scale of λ_3; lower wavelengths, including λ_1 and λ_2, are suppressed.
		**Waviness 2** The short-wavelength cutoff filter is applied with a cutoff value just lower than λ_2. The resulting data trace shows features of the scale of λ_2 and λ_3; lower wavelengths, including λ_1, are suppressed.

2D GLITCH REMOVAL

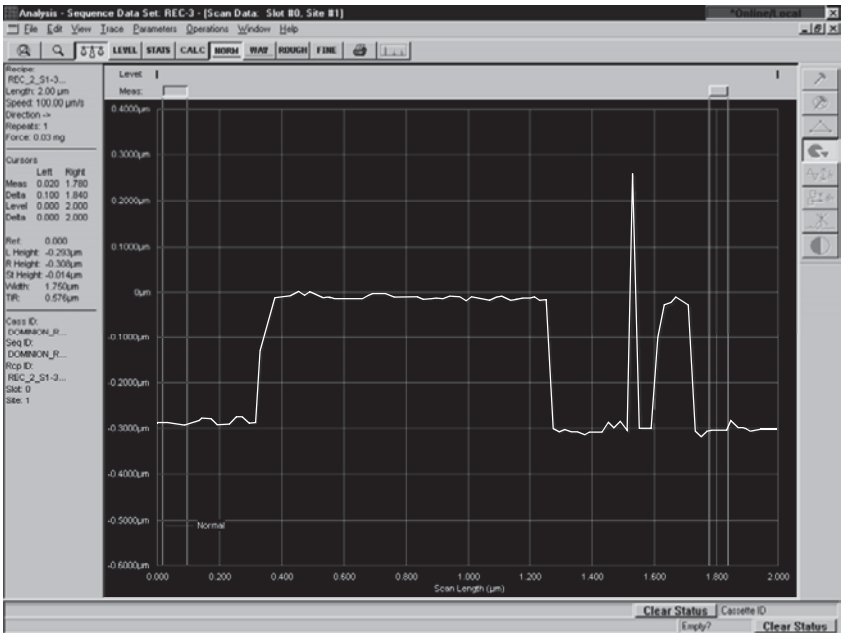
Introduction

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 x 3, 1 x 5, or 1 x 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*

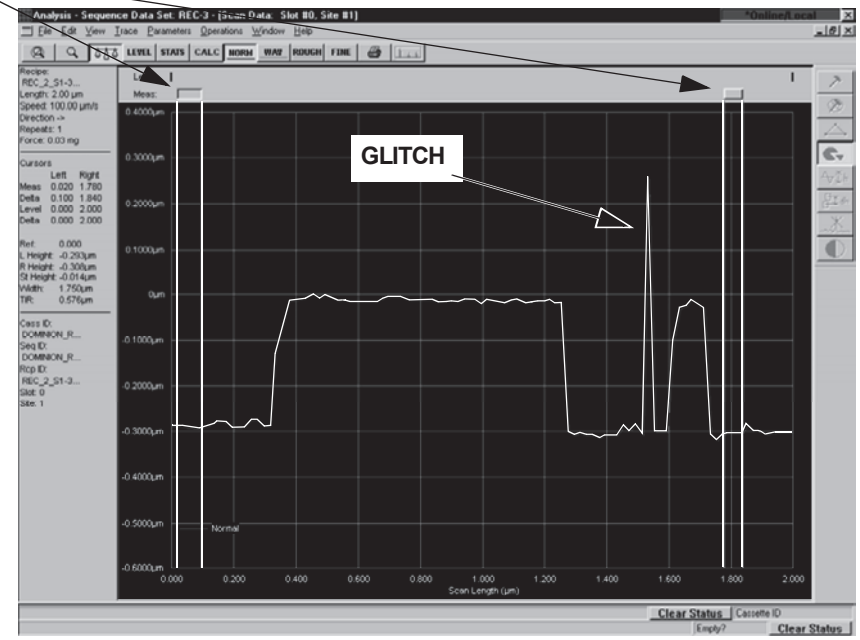


1. Move the left cursor to the next position to the left of the glitch that models the trace where the glitch occurs. Place the cursor's left and right borders to include the data set that is to be used to remove the glitch. (See *Figure 8.52*.)

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*.)

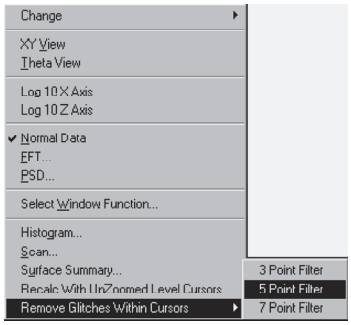
Figure 8.52 *Analysis Screen with Operations Menu*

Set the cursors on data that is a model for the glitch removal. In this case, the bottom of the trace.



3. Right-click to display the Right-Click menu. (See *Figure 8.53*.)

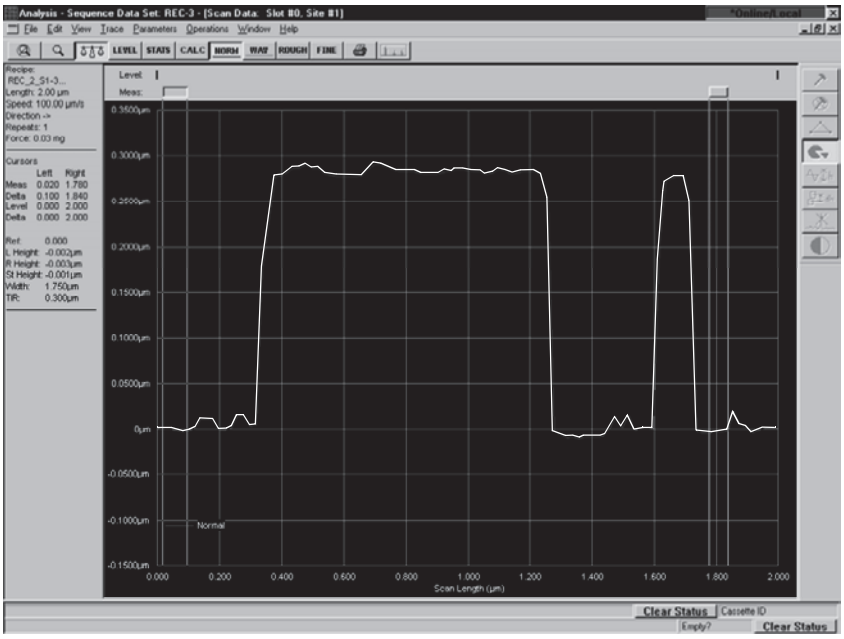
Figure 8.53 *Right-Click Menu - Remove Glitches Menu Options*



4. Move the cursor over **Remove Glitches Within Cursors** to display its menu. (See *Figure 8.53*.)

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 µm (20 µin.) 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.

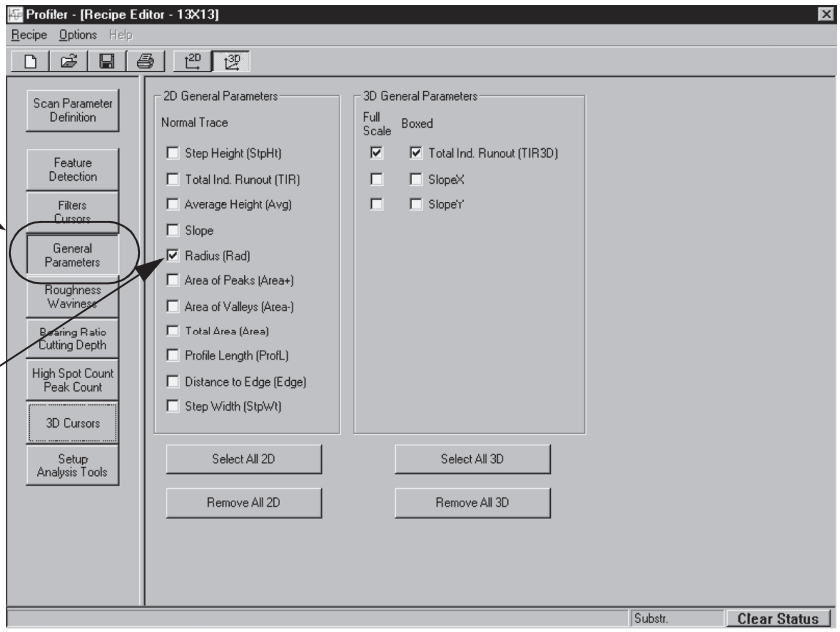
  This can be avoided if the instrument is calibrated with a high precision cylindrical standard whose radius is within a factor of 5 of the sample to be measured. This is the Radius of Curvature calibration. For the highest accuracy, KLA-Tencor recommends that this calibration is performed by a trained technician.

1. Go to the **Scan Recipe Editor** and click on **General Parameters**. **Step 1** (See *Figure 8.55*.)

Figure 8.55 *3D General Parameters - Recipe Editor*

Step 1 In the **Recipe Editor**, click on the **General Parameters** button to display the 2D General Parameters in the Information Display Window.

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 window.



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*.)
3. 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.

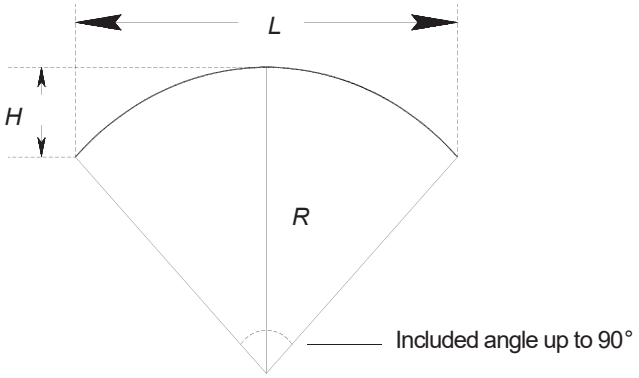
   Measurements *can be made* up to 90% of the vertical range of the measurement head in arc height but precision of the scan cannot be certain. (See *Figure 8.56*).

2. The size of the included angle should be no more than 90°.

   Measurements can be made up to 110° 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-σ 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 8.5 *Scan Recipe Parameters*

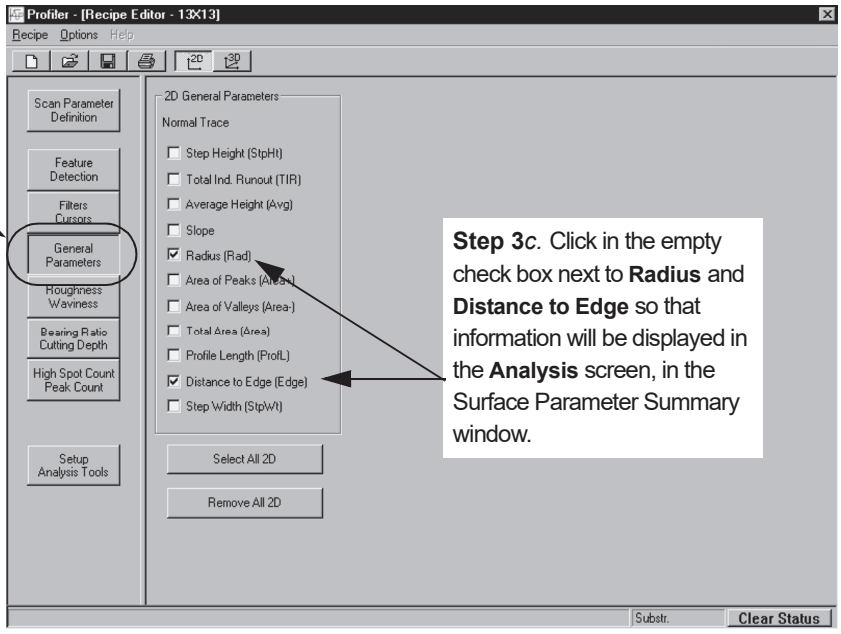
Recipe Field	Setting
Scan Length	See changing **X Scan Size**.
Scan Speed	See changing **Scan Speed**
Sample Rate	200 Hz is optimum. See Sampling Rate.
Surface Parameters	Use the General Parameters window in the Recipe Editor to enable Radius and Distance to Edge.
Stylus Force	See **Applied Force**.
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*.)

Figure 8.57 *General Parameters - Recipe Editor*

Step 3*b.* In the **Recipe Editor**, click on the **General Parameters** button to display the 2D General Parameters in the Information Display Window.

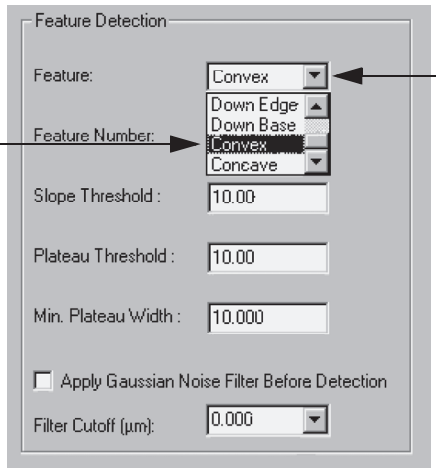


Step 3*c.* Click in the empty check box next to **Radius** and **Distance to Edge** so that information will be displayed in the **Analysis** screen, in the Surface Parameter Summary window.

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*.

Figure 8.58 *Feature Detection - Recipe Editor*

Step 3*f.* Scroll down to the bottom of the menu. Click on **Convex** from the drop-down menu.



Step 3*e.* Click on the down-arrow next to the Feature variable box.

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 µm (20 µin.) for radii larger than 2.5 mm (0.1 in.).

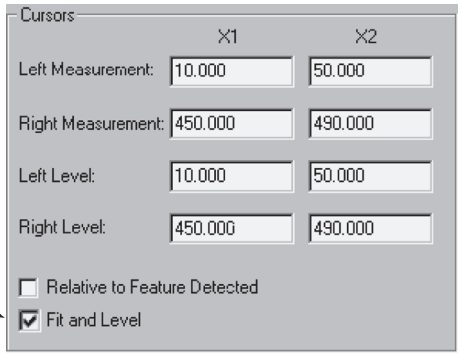
MEASURING STEP HEIGHT ON CURVED SURFACES USING FIT AND LEVEL

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*



Step 2 Click on the empty check box next to **Fit and Level** to enable it.

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

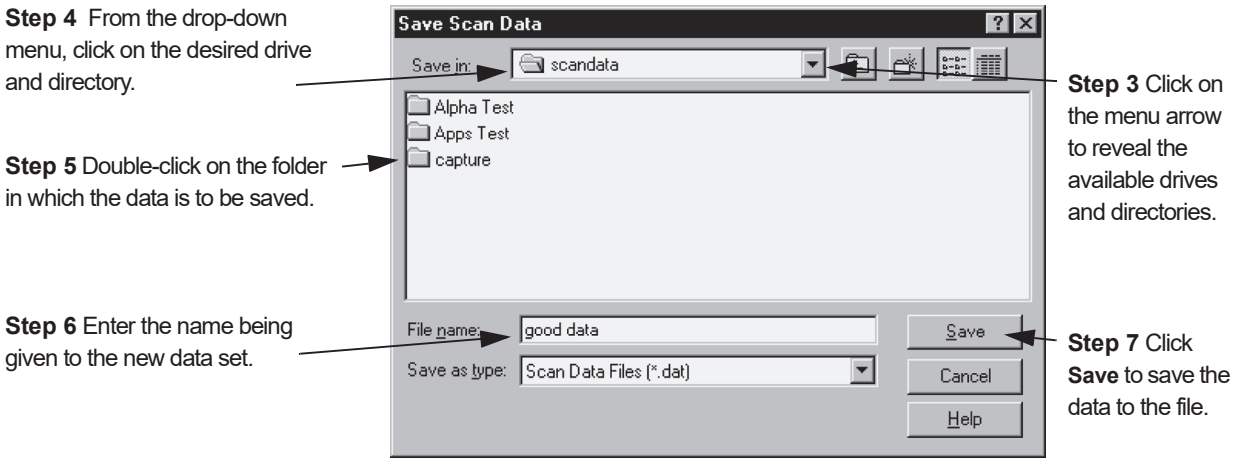
Scan data can be saved for reviewing at a later time. This is especially important because the data that is saved can be reanalyzed at a later date using different scan parameters.

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*



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.

9

ANALYZING 3D SCAN DATA

INTRODUCTION

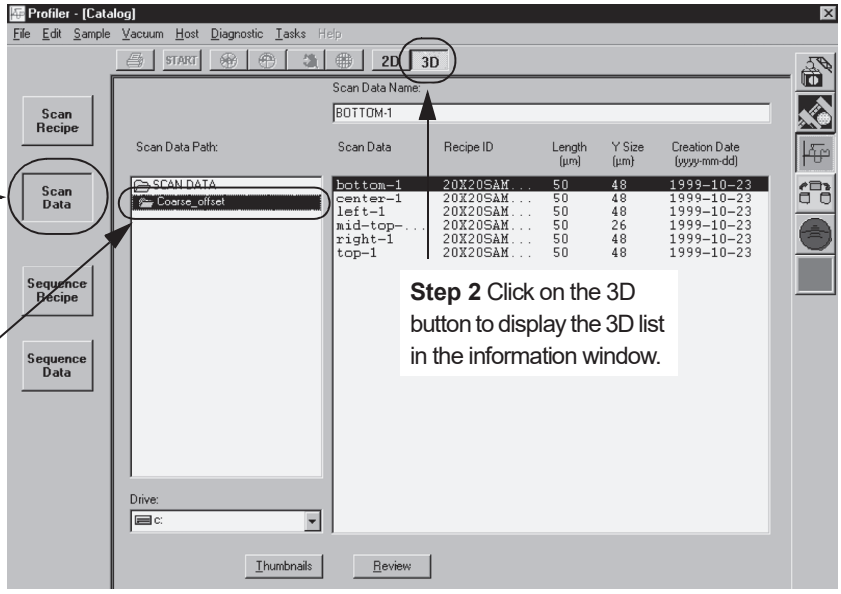
The 3D scan data analysis displays the 3D scan image and trace information after a scan is completed. A 3D scan is an image built by taking a series of 2D scans, arranged in a raster pattern, to form a picture of the sample surface at the scan location. With 3D analysis, complete surface analysis can be performed.

This chapter describes:

STARTING THE 3D ANALYSIS APPLICATION

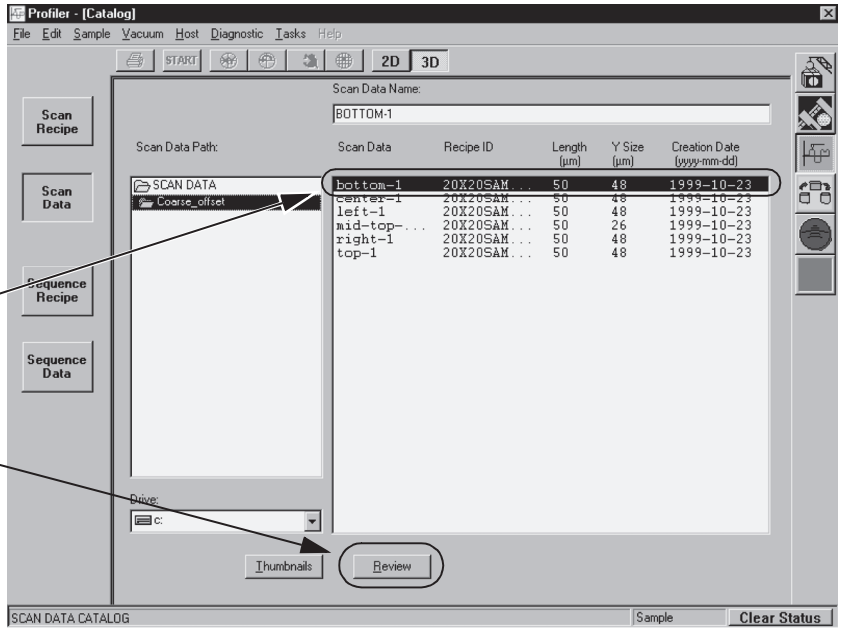
1. Click the **Scan Data** or **Sequence Data** command button to display the data information in the Catalog window. (See *Figure 9.1*.)

Figure 9.1 *Scan Catalog Screen with Scan Data Active.*



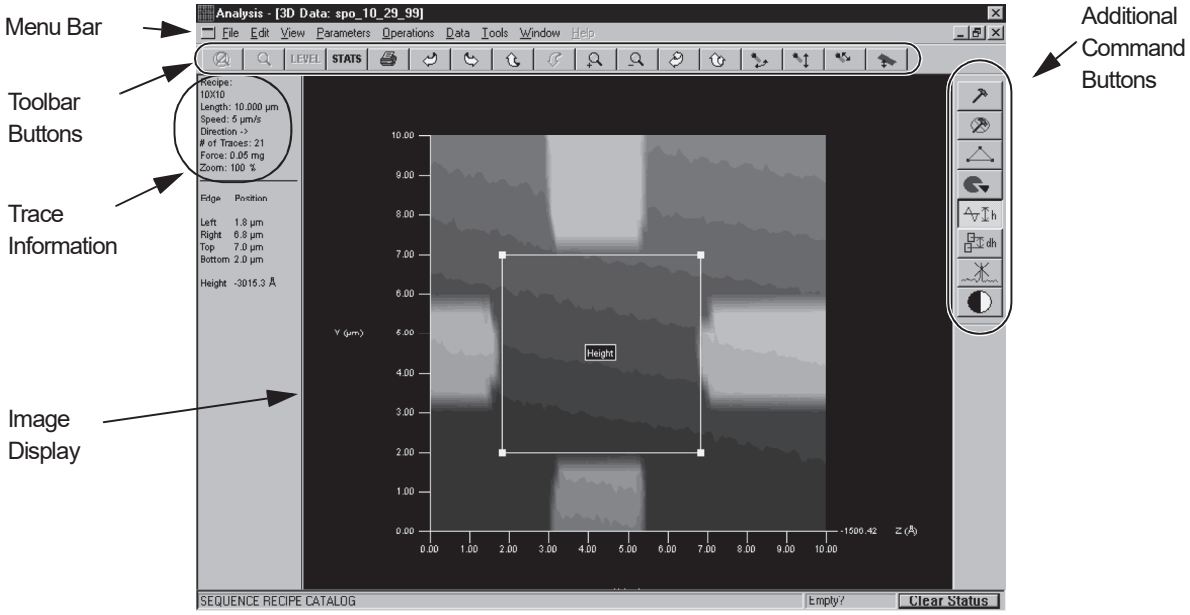
2. Click the **3D** button. (See *Figure 9.1*.)

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*.)

Figure 9.3 *3D Analysis Screen with 3D Object Displayed*



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*.

Figure 9.4 *Analysis Tool Bar Image Rotation Buttons*

Table 9.1 *Automatic Image Rotation Buttons*

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 **left** arrow key.)
	Rotates the image to the right on its horizontal plane. Each click moves the image a small distance. (Identical to the **right** arrow key.)
	Rotates the image in a backward roll. Each click moves the image a small distance. (Identical to the **up** arrow key.)
	Rotates the image in a forward roll. Each click moves the image a small distance. (Identical to the **down** arrow key.)

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
	Rotates the image on its horizontal plane using four handles that are manipulated by click-and-drag method. (See *Figure 9.5.*)
	Rotates the image on its horizontal plane using a single handle that is manipulated by the click-and-drag method. (See *Figure 9.5.*)

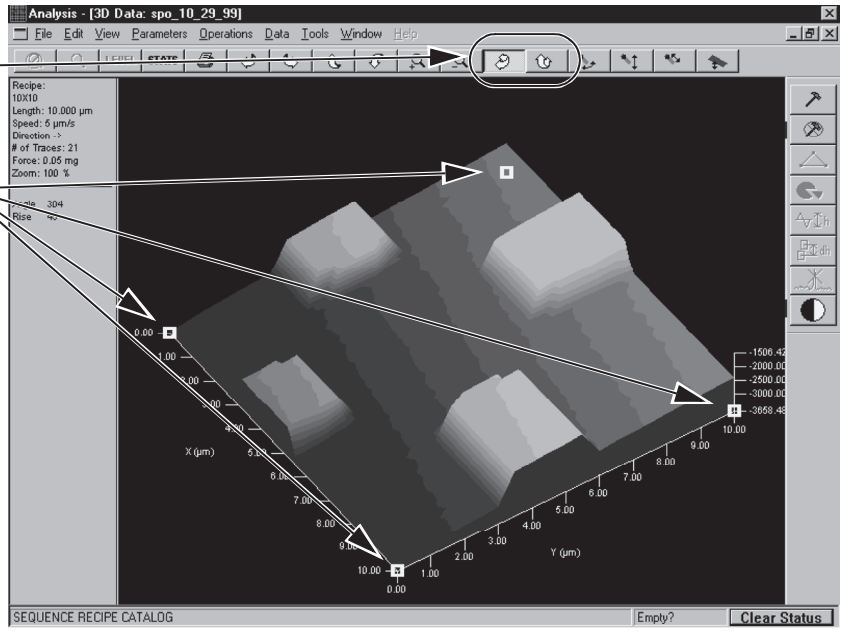
1. Click on the button representing the plane in which the required rotation is to take place. The image appears to have handles attached to it. (See *Figure 9.5*)

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*

Click on the button representing the required plane of rotation.

With the particular angular rotation button clicked, click on one of the four handles and hold the mouse button down while dragging the image in the chosen rotation plane. Release the button to terminate the rotation.



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 *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 **left** rotation button.)
→	Rotates the image to the right on its horizontal plane. Each click moves the image a small distance. (Identical to the **right** rotation button.)
↑	Rotates the image in a backward roll. Each click moves the image a small distance. (Identical to the **up** rotation button.)
↓	Rotates the image in a forward roll. Each click moves the image a small distance. (Identical to the **down** 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*.

Figure 9.6 *Image Rotation Using the Rotate Image Menu*

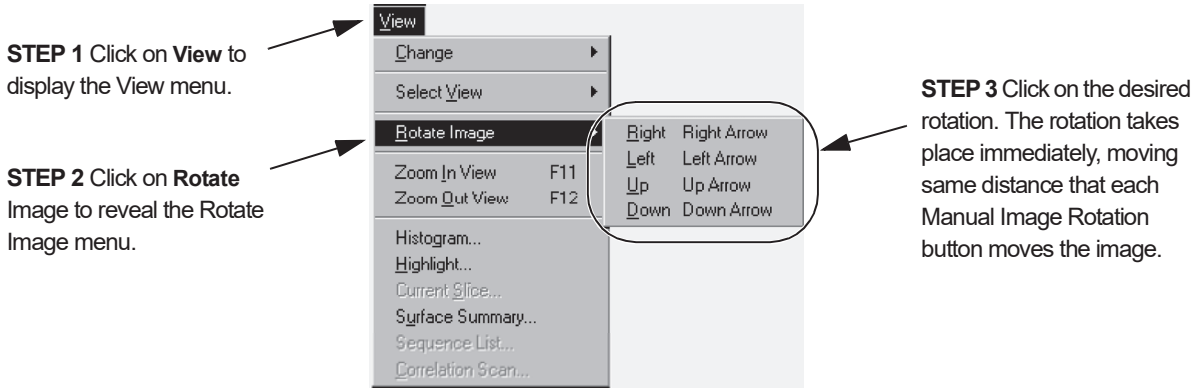


Table 9.4 ***Rotate Image*** *Menu Options (From View Menu)*

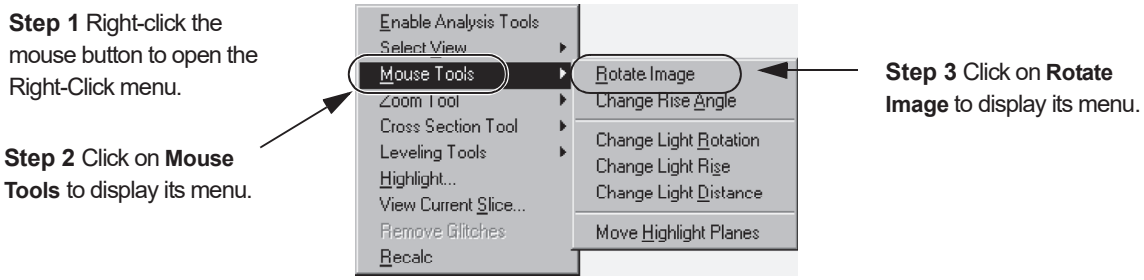
Menu Item	Description of Action
Left Left Arrow	Rotates the image to the left on its horizontal plane. This action only move the image one increment each time. The menu must be opened again for each move.
Right Right Arrow	Rotates the image to the right on its horizontal plane. This action only move 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.

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*

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

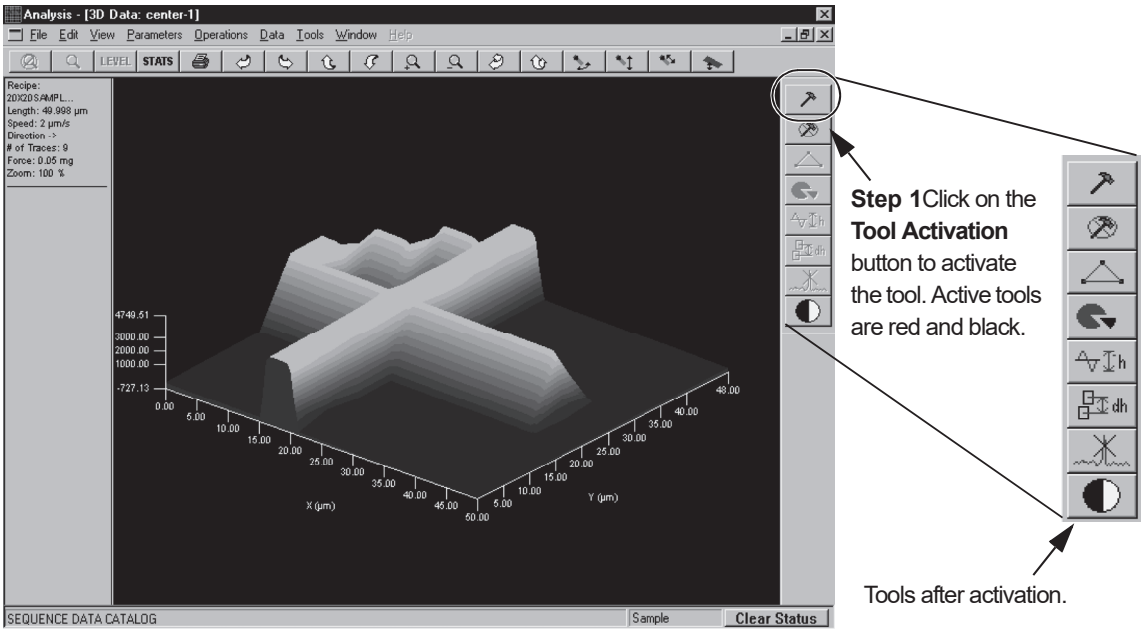
The Zoom features are designed to facilitate zooming in on a portion of the 3D graphic for closer inspection. The zoom can be accomplished through the use of several zoom tools.

- The View menu contains zoom features.
- The tool bar contains zoom features shaped like magnifying glasses.
- The Right-Click menu contains zoom tools.

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.

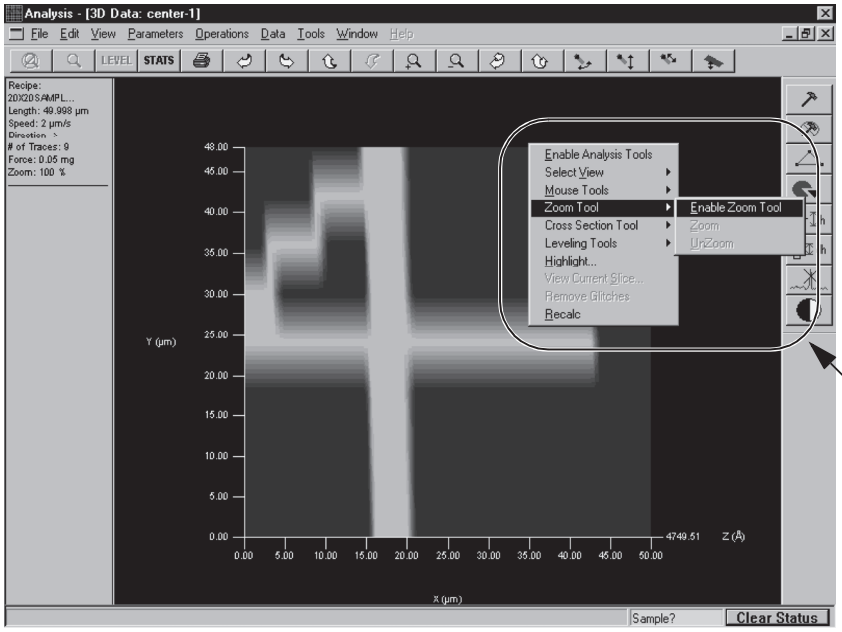
1. In the Analysis screen, click on the **Tool Activation** icon  at the top of the tool bar on the right side of the screen. This activates (enables) the side tool bar tools. (See *Figure 9.9*.) When the side tool bar is activated, the graphic image is changed to **top view**.

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*

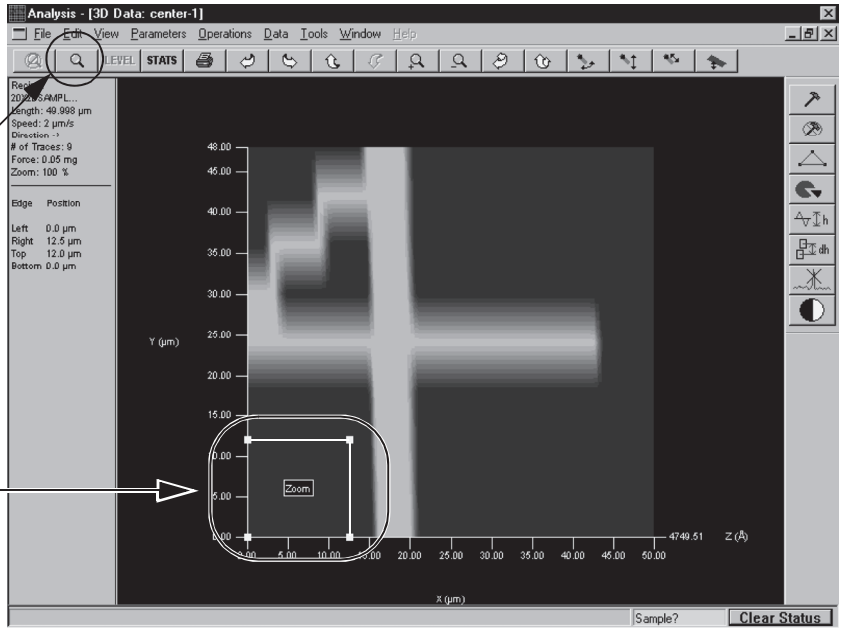


3. In the tool menu, move the cursor over **Zoom Tool** to display its menu. (See *Figure 9.10*.)
4. Click on **Enable Zoom Tool** to activate the zoom process. (See *Figure 9.10*.)

Figure 9.11 *Analysis Screen - Zoom Active*

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.



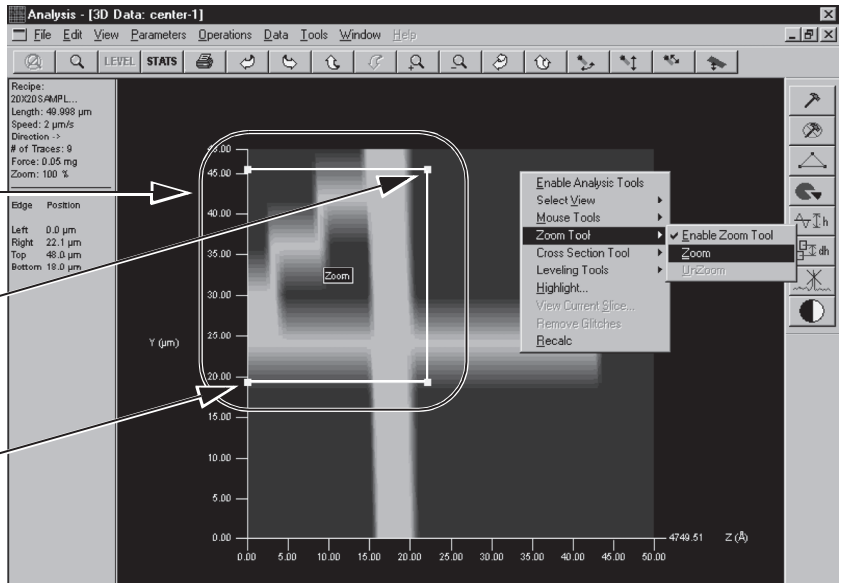
5. When the zoom process is activated, the **Zoom In** magnification glass is activated and the **Zoom** box is deployed at the bottom left of the 3D graphic display. (See *Figure 9.11*.)

Figure 9.12 *Analysis Screen with Zoom Box*

Zoom box relocated to the intended Zoom area.

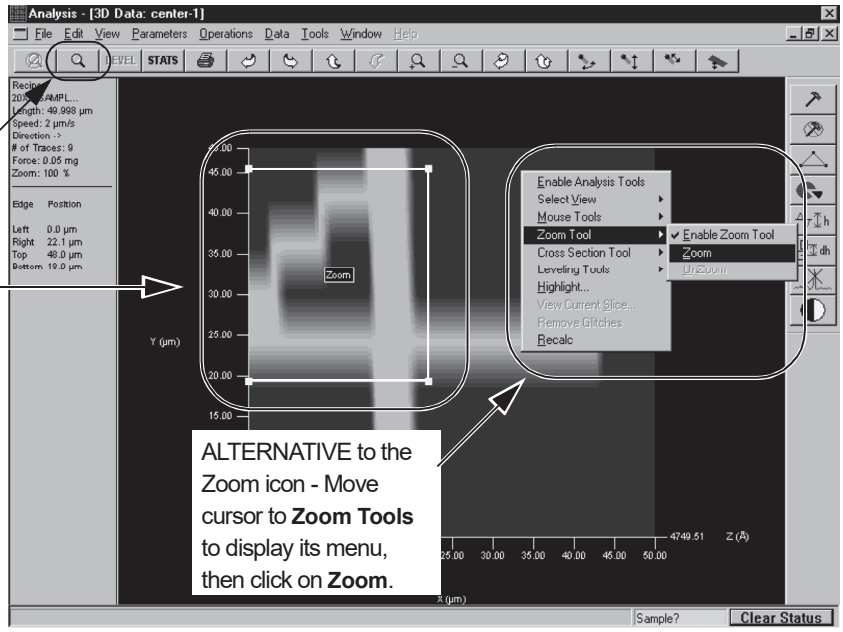
Step 6 Click hold and drag the upper right corner to the top right corner of the **intended zoom area**.

Step 6 Click hold and drag the lower left corner of the **Zoom** box to the lower left corner of the **intended zoom area**.



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*.)

Figure 9.13 *Analysis Screen – Using the Zoom In Icon*



Step 7 Click on the Zoom In icon to zoom into the boxed area.

Zoom box relocated to the intended Zoom area.

ALTERNATIVE to the Zoom icon - Move cursor to **Zoom Tools** to display its menu, then click on **Zoom**.

7. When the **Zoom** box is positioned as the boundary of the intended zoom area, click on the **Zoom In** icon  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*.)

Working with a Zoomed Image

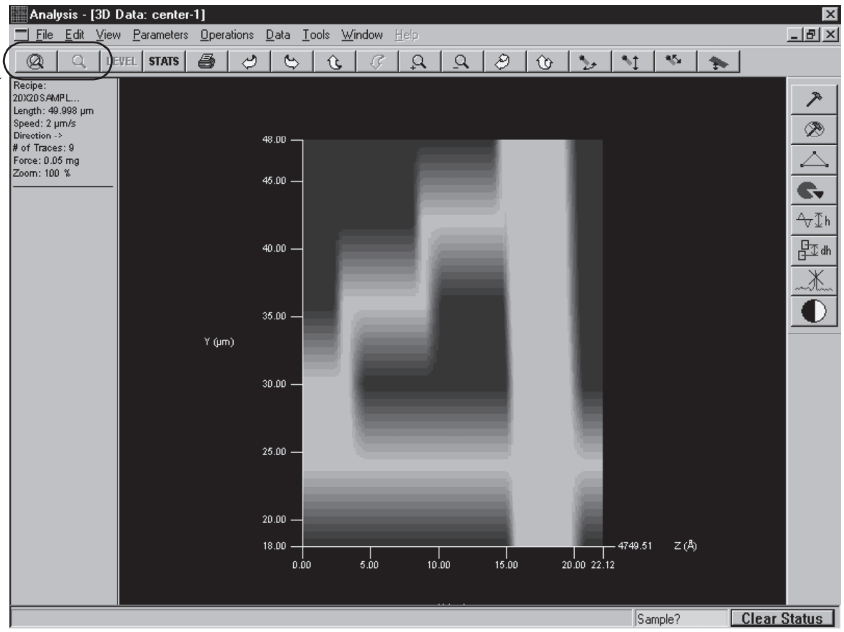
While in the view containing the zoomed image, all the procedures contained in the right side tool bar can be executed on the image. The Level, Slice, Height, Step Height, and Glitch Removal, all function the same way with a zoomed image that they do with a standard top view image.

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*.)

Figure 9.14 *Analysis Screen – Zoomed In Area*

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.

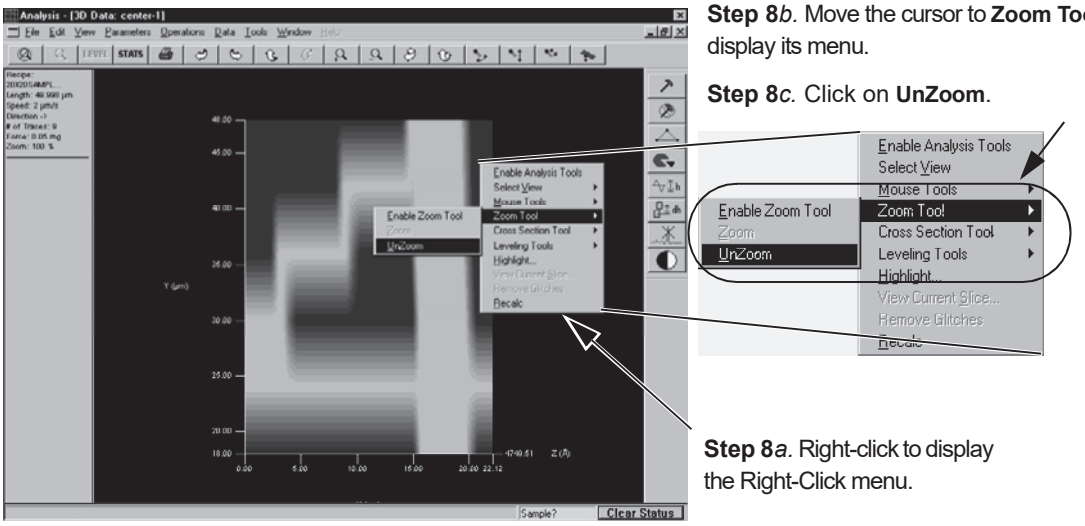


8. To return to the pre-zoom image, click on the **Zoom Out** icon. The image returns to the prior display. (See *Figure 9.14*.)

   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.

Figure 9.15 *Analysis Screen – Unzoom Using Right-Click Menu*



Step 8*b*. Move the cursor to **Zoom Tools** to display its menu.

Step 8*c*. Click on **UnZoom**.

Step 8*a*. Right-click to display the Right-Click menu.

Analysis Screen Toolbar Button Functions

Table 9.5 *Analysis Toolbar Buttons*

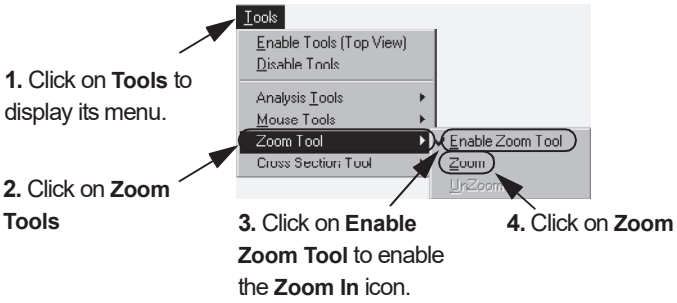
Button	Description of Action
	**Zoom In** on the area bounded using a zoom box to form the boundary. This is for use with the Zoom Box. This icon is used as a trigger to execute zoom of the data according to the parameters set using the Zoom Box. **Procedure**: (See procedure as described beginning with *STEP 1. on page 9-7*.) The following is an abbreviated version of the procedure. 1. Click on the **Hammer**  in the Analysis Tool box to enable the Analysis Tools. 2. Right-click to display its menu. 3. Move the cursor to the **Zoom Tools**. 4. Click on **Zoom** 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 zoomed. 6. Click on the **Zoom In** icon  to zoom to the area bounded by the zoom box (or click on **Zoom** in the **Tools** menu - as illustrated below). 
	**Zoom Out** 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 *STEP 8. on page 9-11*.)
	**LEVEL** 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 **Hammer**  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  is enabled. 3. Use the click-and-drag procedure (click on the center of each vertex) to position them. (For more information on the procedure, see *Activate Leveling Tool on page 9-15*.) 4. Click on the **LEVEL** icon  to complete the leveling procedure.

Table 9.5 *Analysis Toolbar Buttons (Continued)*

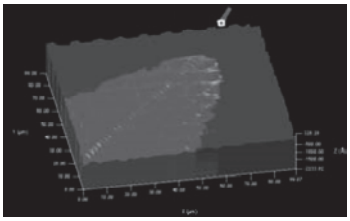
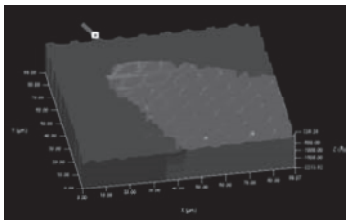
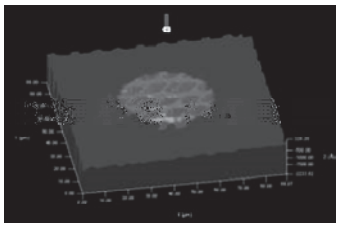
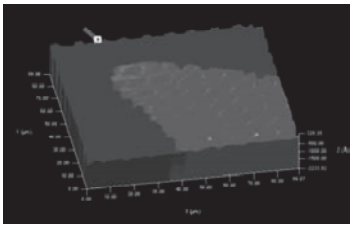
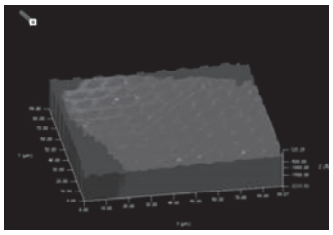
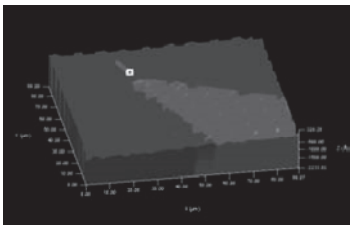
Button	Description of Action
	**Statistics** information box. This displays the statistics information box on the screen, usually beneath the analysis image. The positioning can be manipulated.
	**Print**. This causes the system to print the analysis information.
	**Positive Magnification**. This causes 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.
	**Negative Magnification**. This causes the entire image to be reduced in magnification by one increment each time it is clicked on.
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.
	**Change light rotation**... This shines a light on the image from the beginning location and angle of the light. User can rotate the light source in a horizontal plane, parallel to the image surface.   The light projection swings from left to right in the illustration above.

Table 9.5 *Analysis Toolbar Buttons (Continued)*

Button	Description of Action
	**Change light rise**... 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.
	**Change light distance**... From the starting position and angle of the light, the light moves closer or further from the image at the current angle.   The light moves from high left to a lower position near image center.
	**Move highlight planes**... This moves each highlighted plane for visibility. Up to 10 planes can be identified for viewing.

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*

Button	Description of Action
	**Enable Analysis Tools (Top View)**. This button enables the remaining tools in this tool bar. It moves the image to the **Top View** because all the tools require this view.
	**Disable analysis Tools**. This button disables active tools. This includes the tools in this tool bar as well as those in the top tool bar.

Table 9.6 *Analysis Side Toolbar Buttons (Continued)*

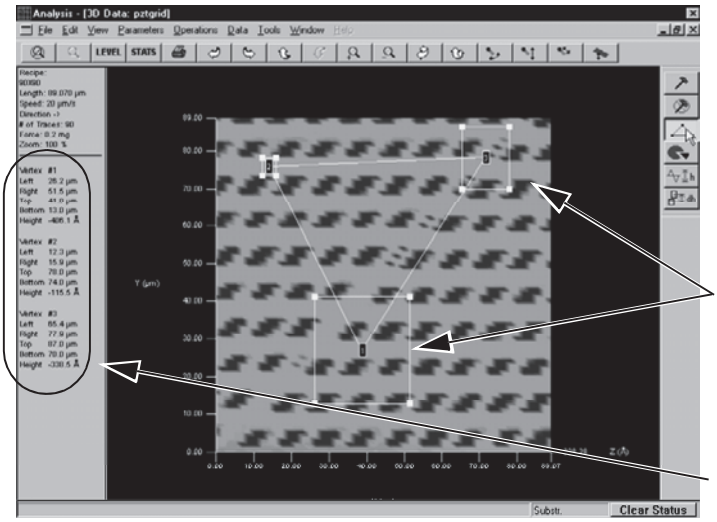
Button	Description of Action
	**Activate Leveling Tool**. This button activates the leveling tool that places three interactive boxes on the image surface for leveling the image. Each box represents a corner of the leveling triangle. Procedure: 1. Click-and-drag the center of the boxes (labeled vertexes 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 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.  **NOTE:** 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 **LEVEL** button  on the top tool bar to level the image.  Each leveling box must be placed in an area containing data that is on one plane. All three boxes must be on the same plane for the leveling to be accurate. Boxes **1** and **2** contain data on more than one plane and will produce inaccurate leveling. Each box has its location statistics displayed in the data column, to the left of the image.
	**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)*

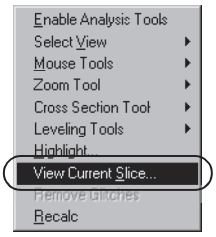
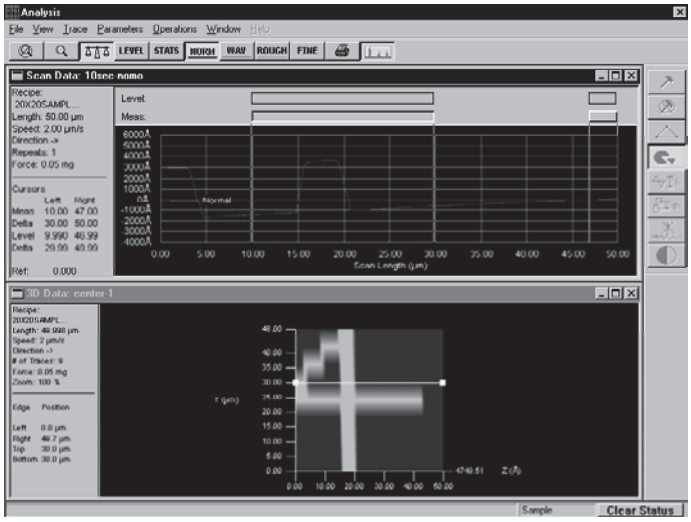
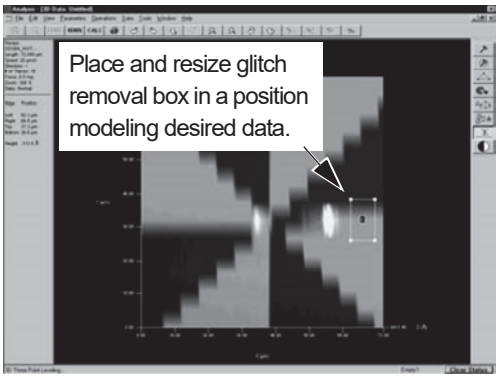
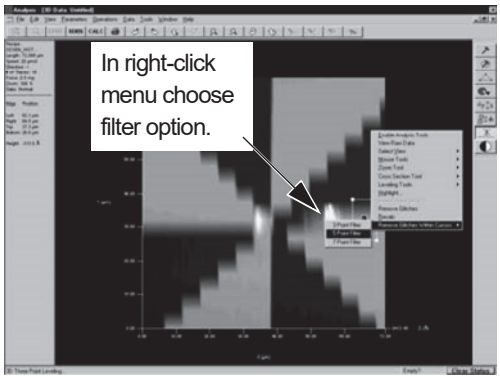
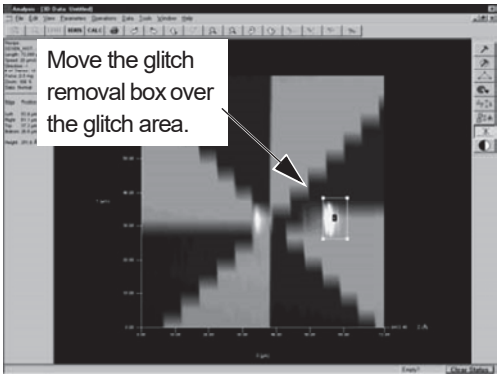
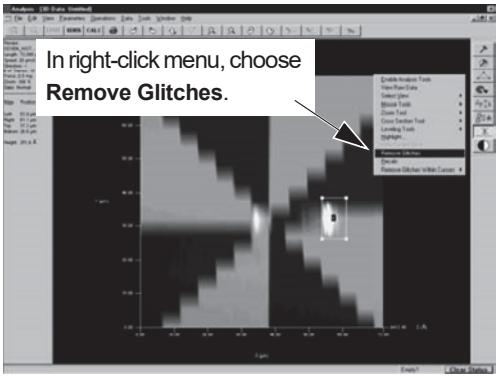
Button	Description of Action
	**Activate Slicing Tool**. This button activates the tool that allows the user to slice the image down from the top surface to the foundation of the image and display a 2D image of the cross section at the slice. This tool provides three options (see also *Table 9.14*) for the slice: horizontal, vertical, and diagonal. (Diagonal can be adjusted to any angle.) All three options can be adjusted to any length. (See *Table 9.9*, in the **Current Slice** 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.) 
	**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)*

Button	Description of Action
	**Activate 3D Glitch Removal Tool**. This button activates the 3D glitch removal option. The tool is used in the following manner: 1. Activate the glitch removal button by clicking on it. A box is displayed at the bottom right of the top view of the 3D image. 2. 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.) 3. Right-click to display the right-click menu.   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 *Median Filter for 2D and 3D Data* on page 3-61.) 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.)   6. Right-click to display the right-click menu. (See right side illustration above.) 7. Move the cursor to **Remove Glitches** and click.(See right side illustration above.) The glitch is removed using the chosen filter and the data gathered in the first box.

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.

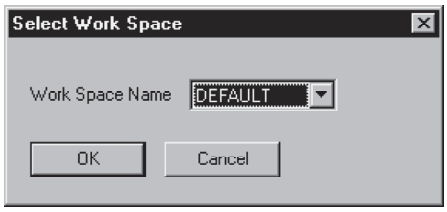
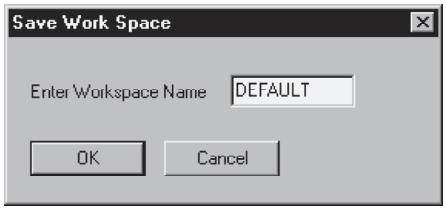
Figure 9.16 *Analysis Screen Menu Bar*

File Menu

Table 9.7 ***File*** *Menu Operations*

Menu Item	Description of Action
Save Data...	Saves the current data to a file. This option displays the Save Dialog box with its associated options.
Export Graph...	Exports the current data. This option displays the Export dialog box with its associated options.
Print... Ctrl+P	Prints the current data. This option displays the Print dialog box with its associated options.
Print Preview	This option displays a thumbnail presentation of the material that is to be printed so it can be reviewed.
Print Setup...	This option displays the Print Setup dialog box with its printer/print setup options.

Table 9.7 ***File*** *Menu Operations (Continued)*

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. 
Save Workspace...	This option presents a dialog box that allows the user to establish a named work space. 
Exit	This option Exits from the Analysis screen.

Edit Menu

Table 9.8 ***Edit*** *Menu Option*

Menu Item	Description of Action
Copy Ctrl+C	This option places the image and data information on the clipboard.

View Menu

Table 9.9 ***View*** *Menu Options*

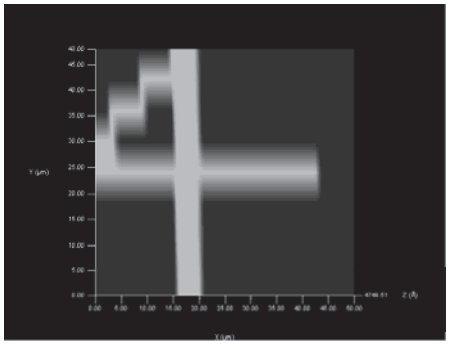
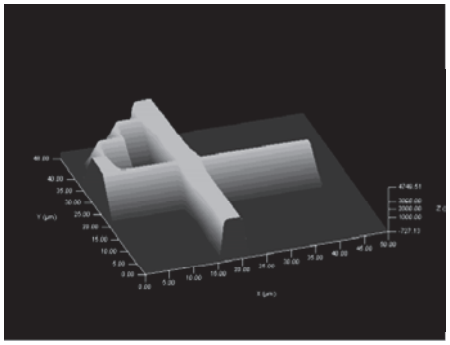
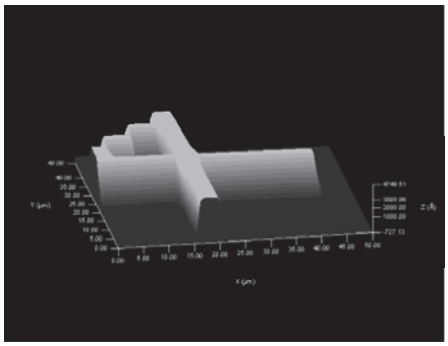
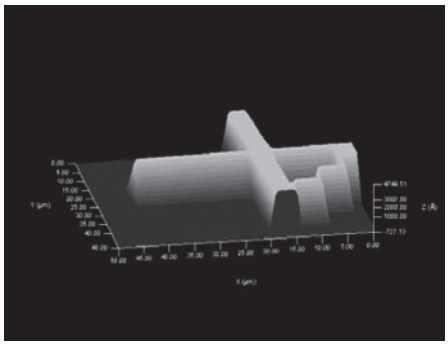
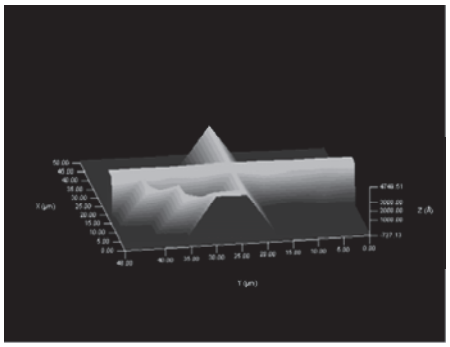
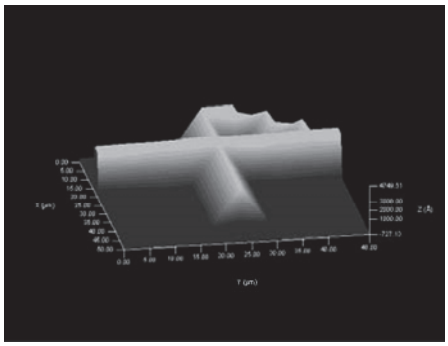
Menu Item	Description of Action
Change ▸	This option displays another menu presenting options effecting the image perspective, view position, lighting and color. View Properties... Light Properties... Display Color...
Select View ▸ Restore Original View Top Oblique Front Back Left Side Right Side	This option displays another menu offering options to view the image from different perspectives. See *Table 9.11* for more detail on each view.  Top View  Oblique View  Front View  Back View  Left View  Right View

Table 9.9 ***View*** *Menu Options (Continued)*

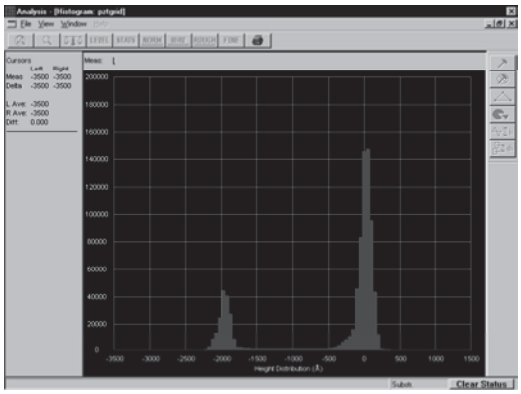
Menu Item	Description of Action
Rotate Image ▸	This option displays another menu presenting options, each of which rotate the image by one increment each time they are chosen. (See *Table 9.4* for a complete explanation of the movement of each option.) **NOTE:** This is the most inefficient way of image 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. Right Right Arrow Left Left Arrow Up Up Arrow Down 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 Out 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)*

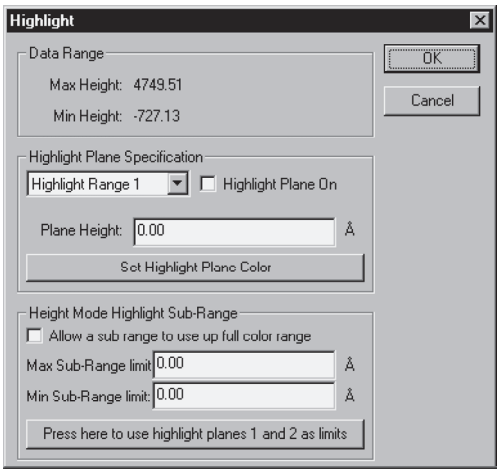
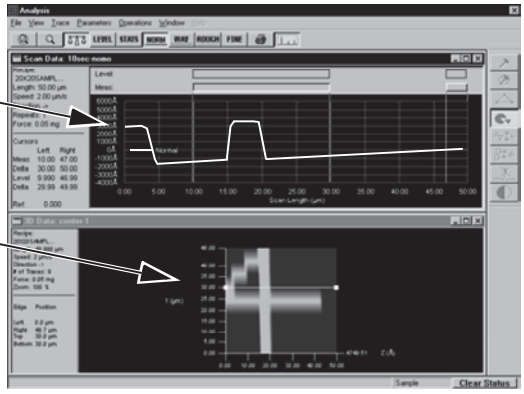
Menu Item	Description of Action
Highlight...	This option displays the Highlight dialog box with its highlight options for chosen planes in the analysis image. 
Current Slice...	This options presents the trace of the **Current Slice** as an Analysis Screen graph. 2D image of the slice. 3D image with a horizontal slice displayed. 
Surface Summary...	This option displays the Surface Summary box in the Analysis Screen. 
Sequence List...	Ignore this button

Table 9.9 ***View*** *Menu Options (Continued)*

Menu Item	Description of Action
Correlation Scan...	Ignore this button

Change Menu From the View Menu

Table 9.10 ***Change*** *Menu Option From the View Menu*

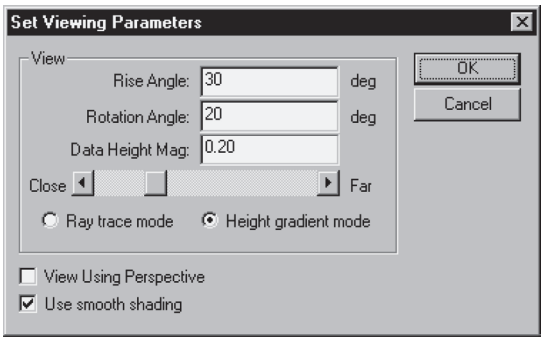
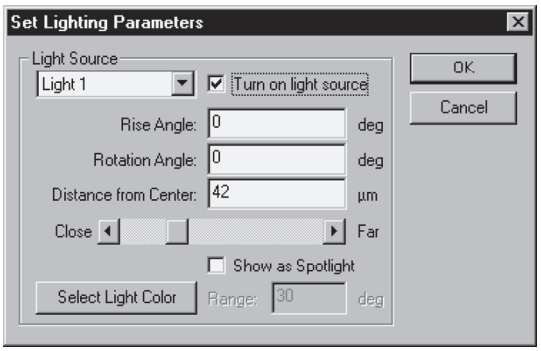
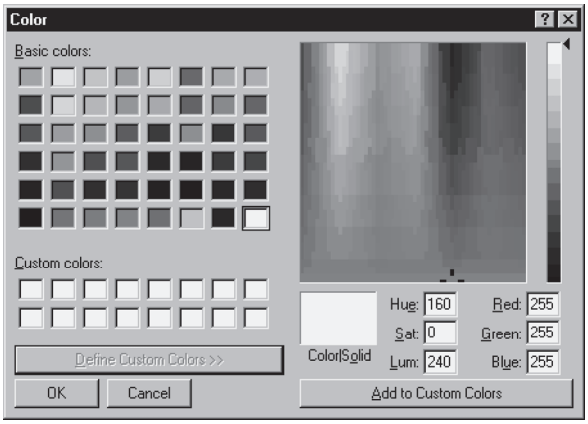
Menu Item	Description of Action
View Properties...	This option displays the **Set Viewing Parameters** dialog box with its options and settings. 
Light Properties...	This option displays the **Light Properties** dialog box with its options and settings. 

*Table 9.10 **Change** Menu Option From the View Menu (Continued)*

Menu Item	Description of Action
Color	This option displays the **Light Properties** dialog box with its options and settings. The color is applied to the primary image on the Analysis screen. 

Select View Menu From the View Menu

*Table 9.11 **Change** Menu Option From the View Menu*

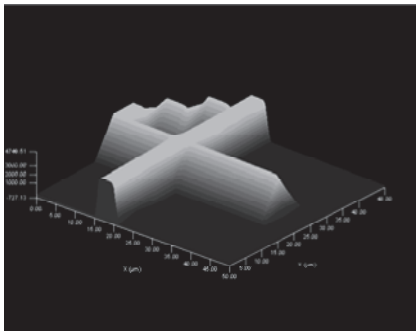
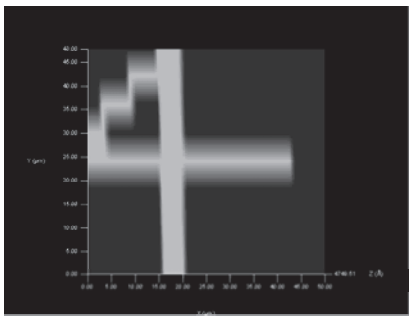
Menu Item	Description of Action
Restore Original View	**Restore Original View** returns the image view to the first view that it is presented in when the **Analysis** screen opens. 
Top	**Top** turns the image surface flat, giving the user a top down view of the image. This is the same view that is presented when the side tool bar is activated. 

***Table 9.11 Change** Menu Option From the View Menu (Continued)*

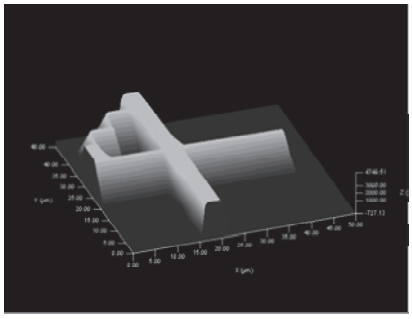
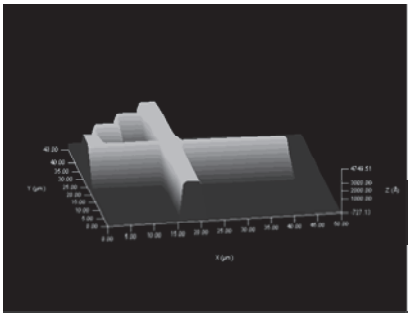
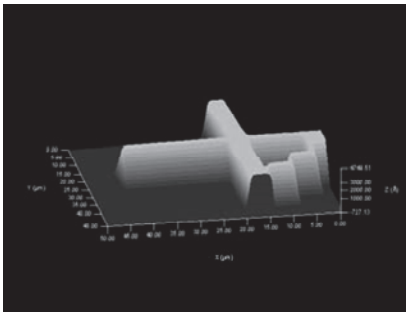
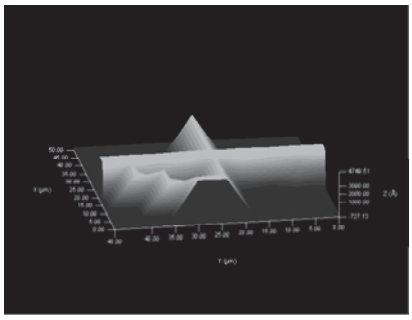
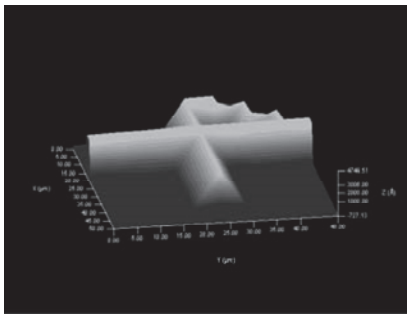
Menu Item	Description of Action
Oblique	**Oblique** turns the image so that it is rotated to the left and down from the Original View, giving more view of the top surface. 
Front	**Front** is rotated a short distance in the counter-clockwise direction from the Original View. 
Back	**Back** rotates the 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. 

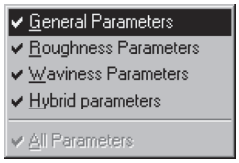
***Table 9.11 Change** Menu Option From the View Menu (Continued)*

Menu Item	Description of Action
Left 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. 
Right 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. 

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*.)

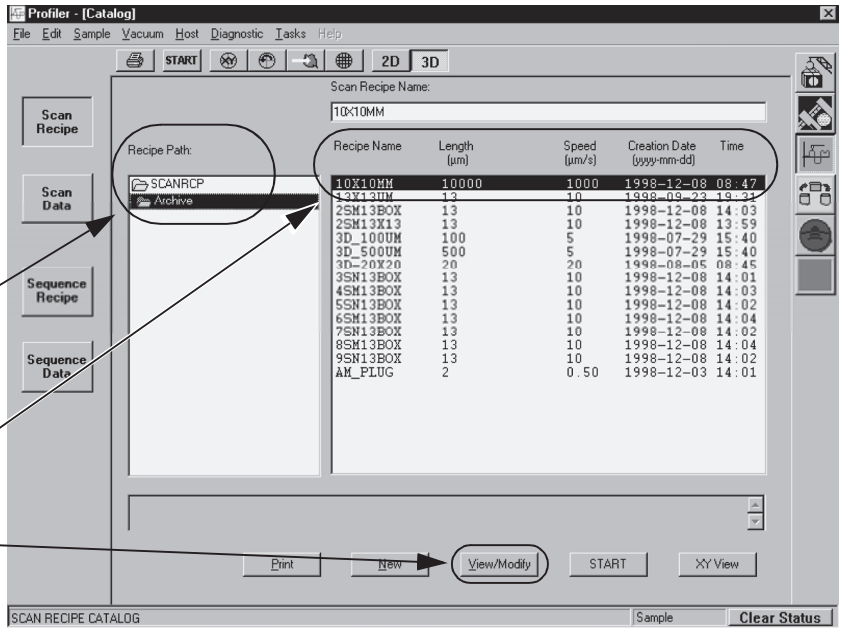
***Figure 9.17 Parameters** Menu from the Analysis Screen Menu Bar*



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.

Figure 9.18 *Catalog Screen – Scan Recipes*



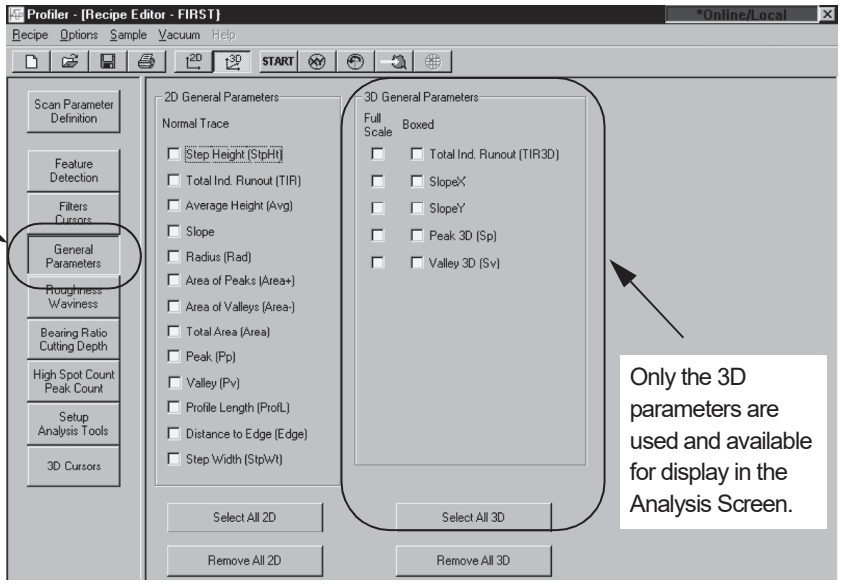
Step 1 Choose the required 3D folder from which the recipe list can be viewed.

Step 2 Double-click on the recipe or click on it and then on **View/Modify**.

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*



Step 3 Click on **General Parameters** to display the parameter set in the Information Display Window.

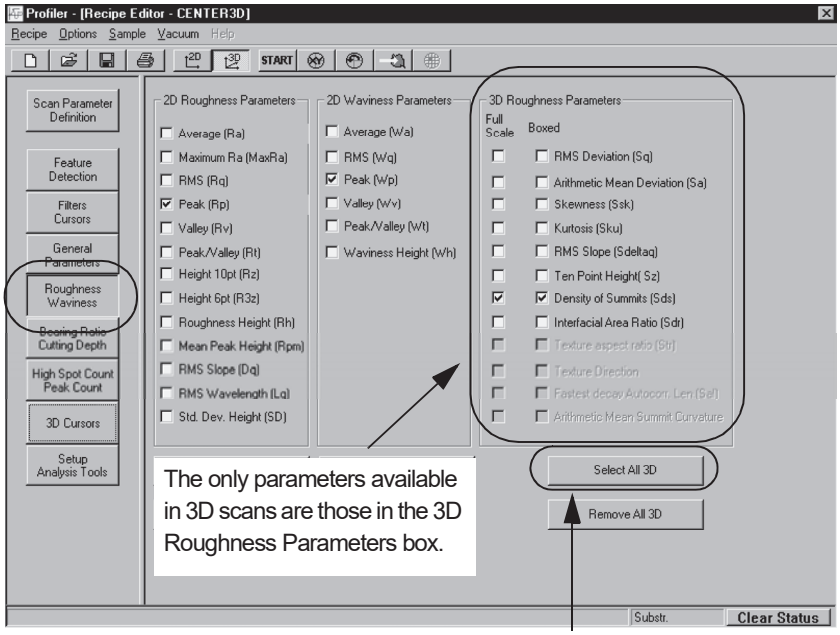
4. Ensure that the required parameters for the scan are chosen. (*Figure 9.19*.)

Roughness/Waviness Parameters

5. Click on **Roughness/Waviness** button to display the **Roughness/Waviness** options in the information display window. (See *Figure 9.20*.)

Figure 9.20 *3D Recipe Editor with Roughness/Waviness Options*

Step 5 Click on the **Roughness/Waviness** button to display the Roughness/Waviness options in the information display window.



Step 6 Click on Select All 3D to choose all the available parameters for inclusion in the Analysis data.

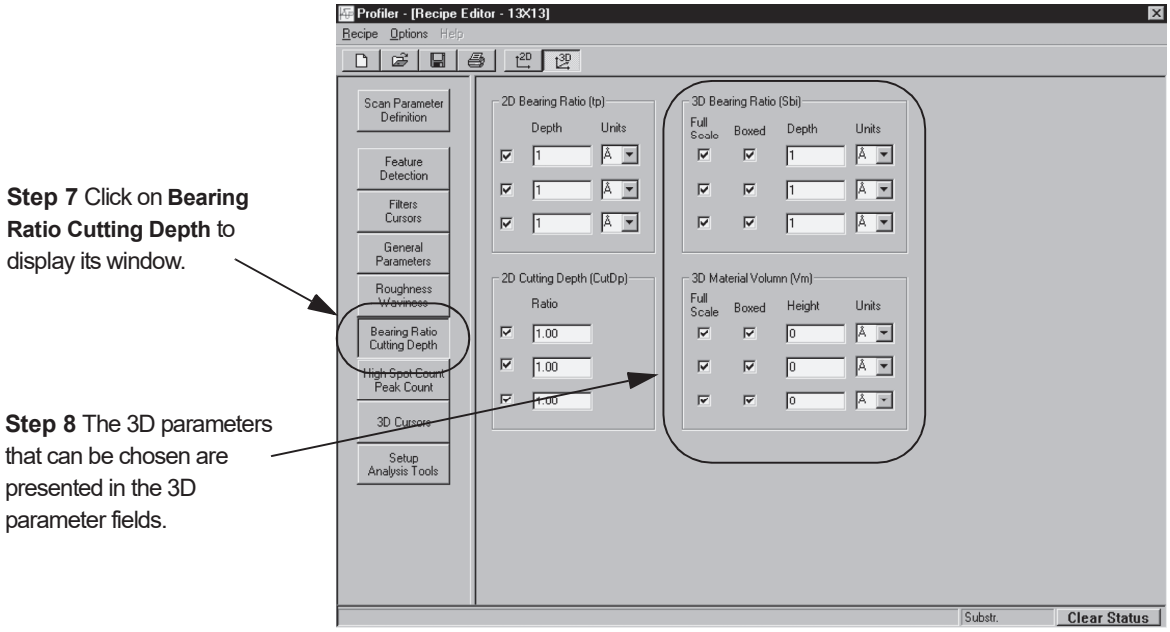
6. Click in each empty check box next to the parameters that are to be displayed in the **Surface Summary** box after the scan. This activates the procedure so that the information is available for data analysis. (See *Figure 9.20*.)

   To choose all of the available parameters, click on the **Select All 3D** button at the bottom of the column.

Hybrid Parameters

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*.)

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 ***Operations*** *Menu Options (From Menu Bar)*

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 **Top View**, and placing the leveling cursors on the image surface. (See *Table 9.5*, **Level tool**.)

***Table 9.12 Operations** Menu Options (From Menu Bar) (Continued)*

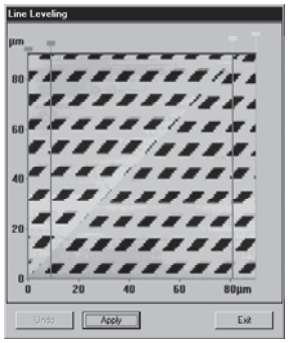
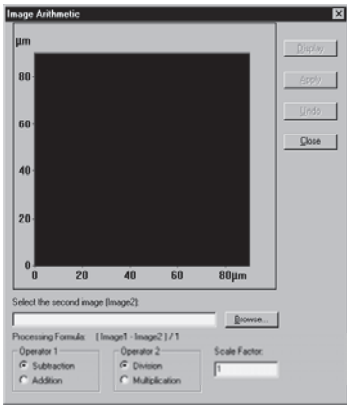
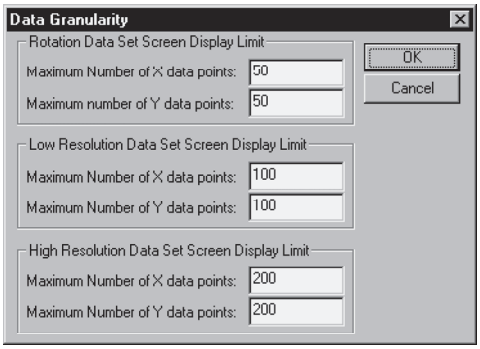
Menu Item	Description of Action
Cancel Leveling	This button is activated when the Leveling procedure is activated. If the Leveling procedure is begun and the user wishes to cancel it prior to completion, this button can be clicked to abort the procedure.
Line Level...	This option displays the Line Leveling 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. 
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. 
Recalc	This option allow the user to **recalculate** the current data using **new** parameters.

***Table 9.12 Operations** Menu Options (From Menu Bar) (Continued)*

Menu Item	Description of Action
Summary Display Options...	

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.
Granularity	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. 
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)*

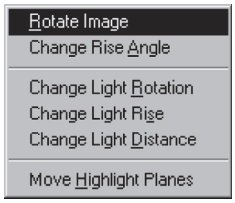
Menu Item	Description of Action
	This options enables the Side Tool Bar Buttons. (See *Table 9.6*.)
	This options disables the Side Tool Bar Buttons.
	This option displays the Analysis Tools menu. 
	This option changes the image to Top View, places the zoom box at the bottom left corner of the image, and activates the Zoom In (magnification) icon  in the top tool bar. (See *Table 9.5*, Zoom In.)
	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.
	This button restores the pre zoom image.
	This option displays the **Mouse Tools** menu. These tools are all duplications of tools on the top tool bar. For **Rotate Image** and **Change Rise Angle**, see *Table 9.2*. For three **Change Light...** options, see *Table 9.5*, look for the same titles. For the **Move Highlight Planes**, see *Table 9.5*, look for the same title. 
	This option is used with the Slicing Tool. (See *Table 9.6*, 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.

***Table 9.14 Tools** Menu Options (From Menu Bar) (Continued)*

Menu Item	Description of Action
✔ Lock to Vertical Cross-Sections	This option is used with the Slicing Tool. (See *Table 9.6*, 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 *Table 9.6*, 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.

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

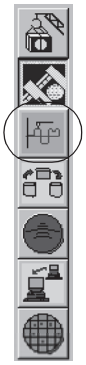
Opening the 3D Cursor Parameters Window

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*

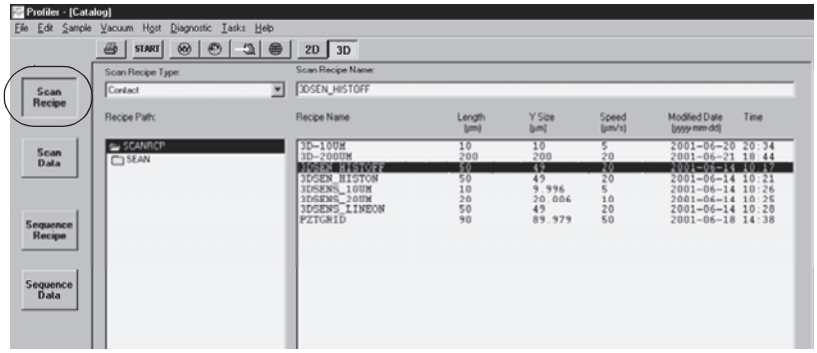
Step 1 From any top level screen click on the Catalog Screen icon.



2. From the Catalog Screen choose the **Scan Recipe** button to display the scan recipe names in the list field portion of the screen.

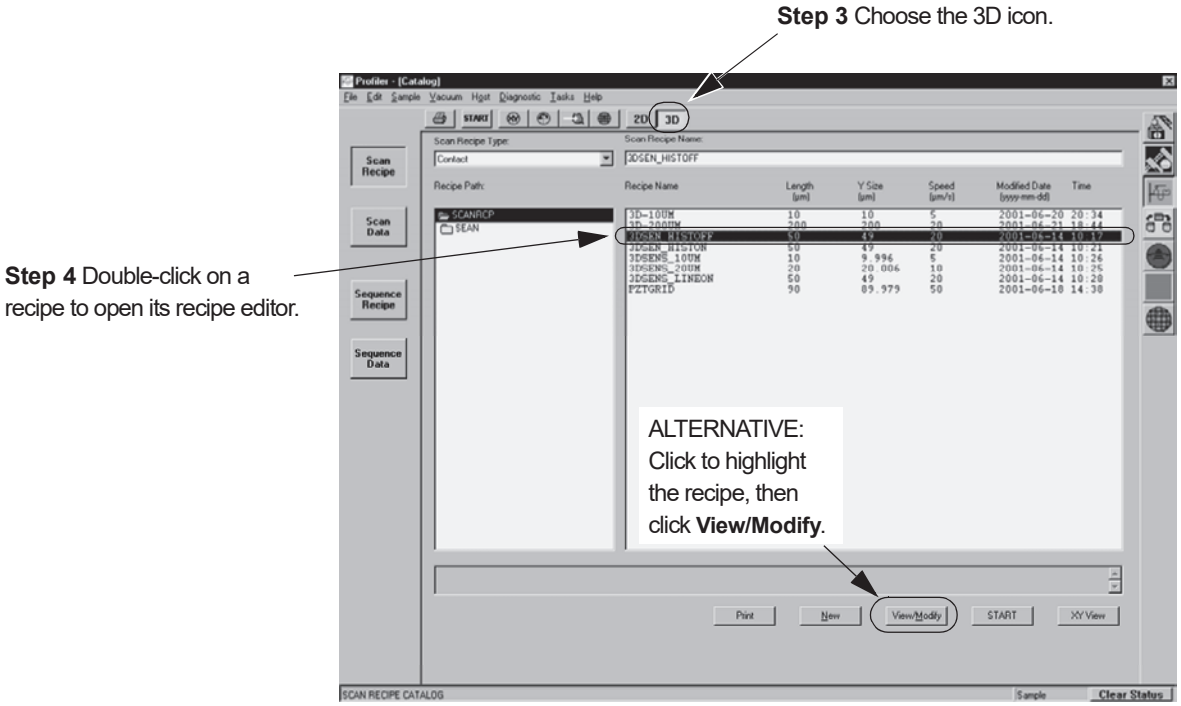
Figure 9.23 *Catalog Screen with Scan Recipe Chosen*

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*.)

Figure 9.24 *3D Scan Catalog Screen*



4. Select the 3D recipe to be edited by double-clicking on the recipe name. This opens the recipe editor. (See *Figure 9.24*.)

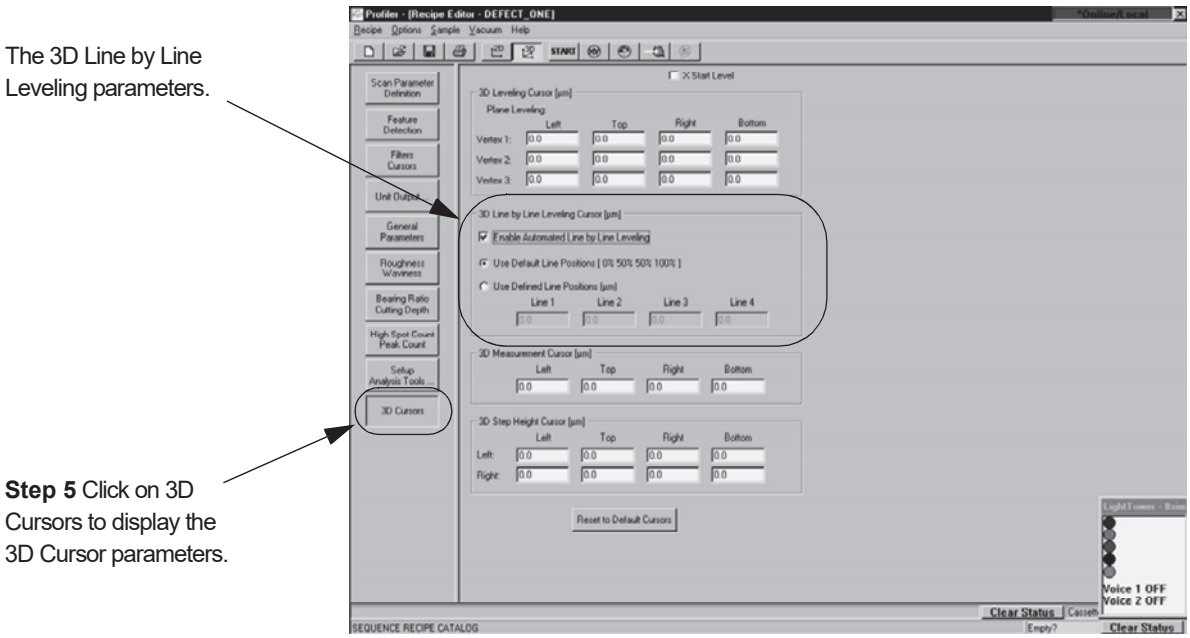
   (ALTERNATIVE: Click to highlight the recipe, then click on **View/Modify** at the bottom of the screen. See *Figure 9.24*.)

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*



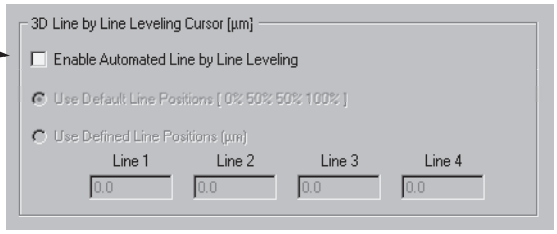
Enabling 3D Line-by-Line Parameters

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*.)

Figure 9.26 *3D Line by Line Leveling Cursor Parameters*

Step 5 Click in the empty checkbox to enable 3D Line-by-Line Leveling.



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:

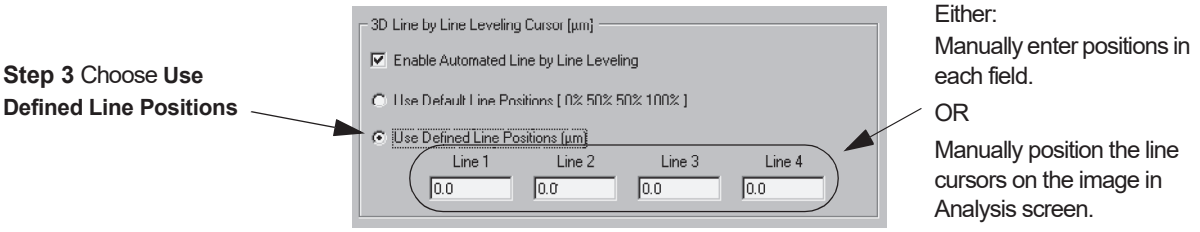
- The operator chooses **Use Defined Line Positions** as the leveling tool. The operator manually enters (sets) the positions of the cursors in microns. These settings are between 0 µm and the number of microns in the scan length, as defined in the recipe.
- The operator can enable line-by-line leveling 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*.)

Figure 9.27 *3D Line by Line Leveling Cursor Field*



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.

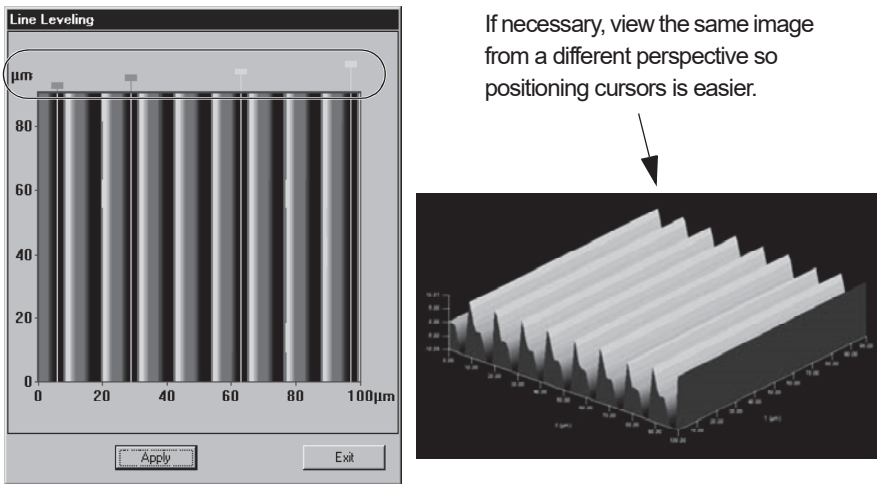
Manually Position Line Cursors on Image to Enter Line Position

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.

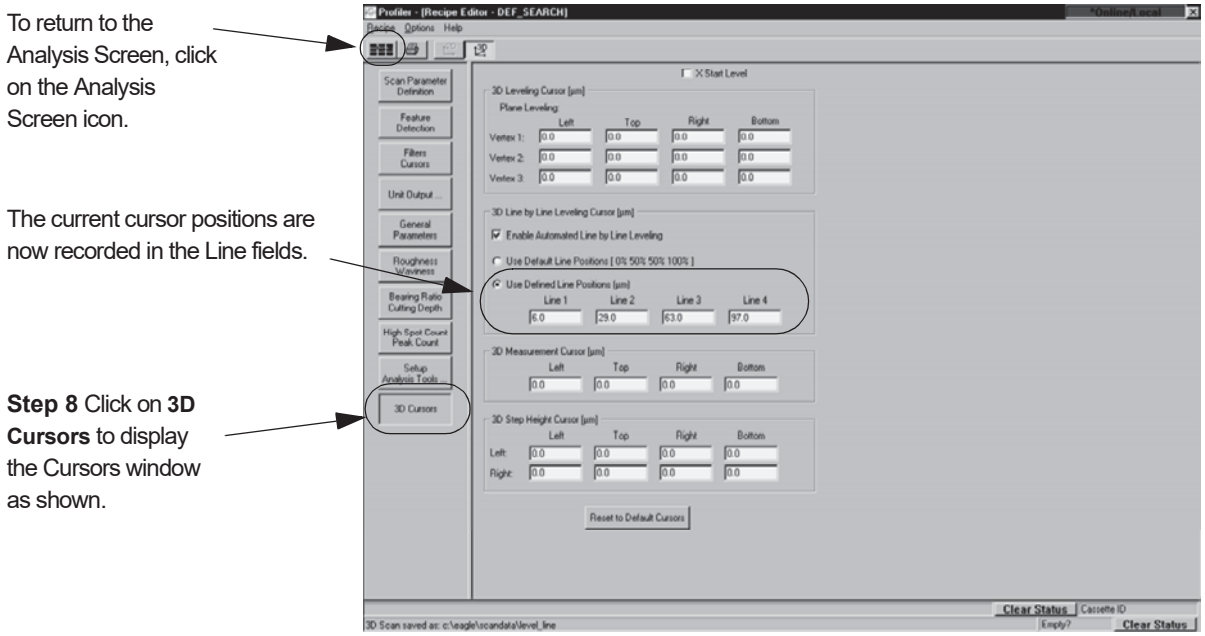
4. Click and drag each line to its required position. All four line cursors must be on the same plane for the data to be properly leveled. (See *Figure 9.28*.)

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 9.29 *Recipe 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.)

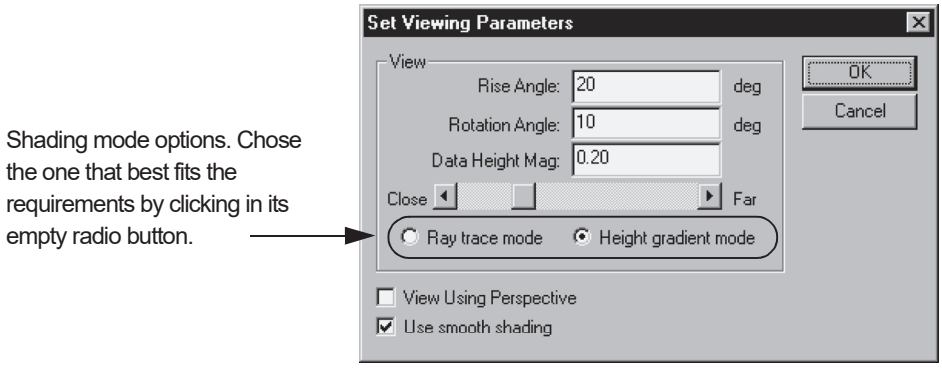
   Since the number depends on the relative heights of the features in the image, select a higher value to obtain a taller image, a smaller value to reduce it. Click **OK**.

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.

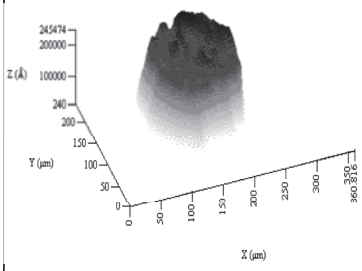
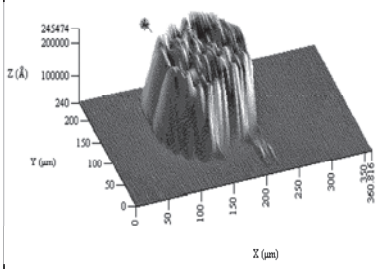
Figure 9.30 *Set Viewing Parameters Dialog Box*



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
	By Height Good for viewing rough features. The higher the feature, the lighter the color.
	By Light Good for viewing smooth features since contours are more obvious. Features appear as if illuminated by a light source.

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	Top
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**.
3. 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.

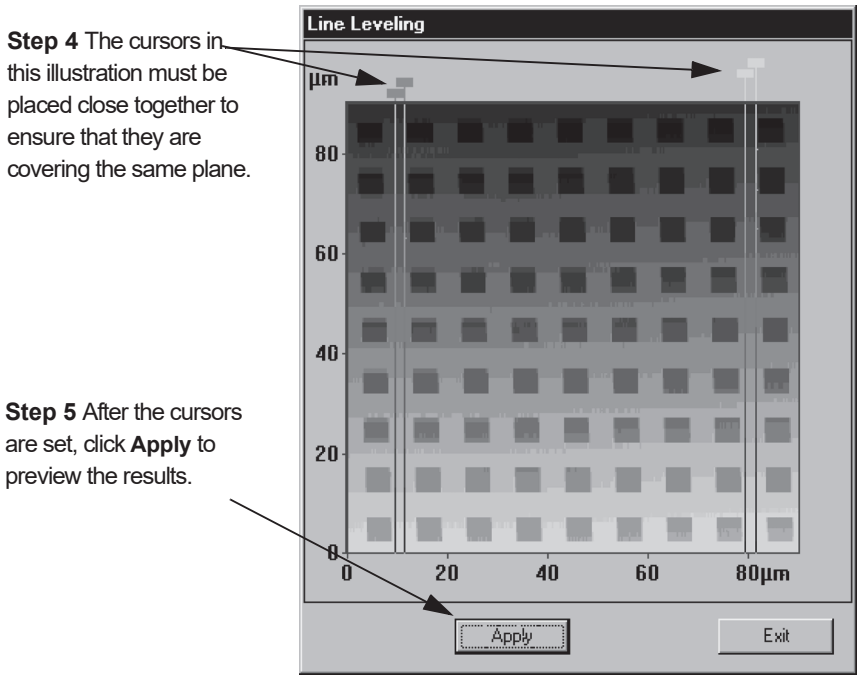
Removing Banding with Line Leveling

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*).

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

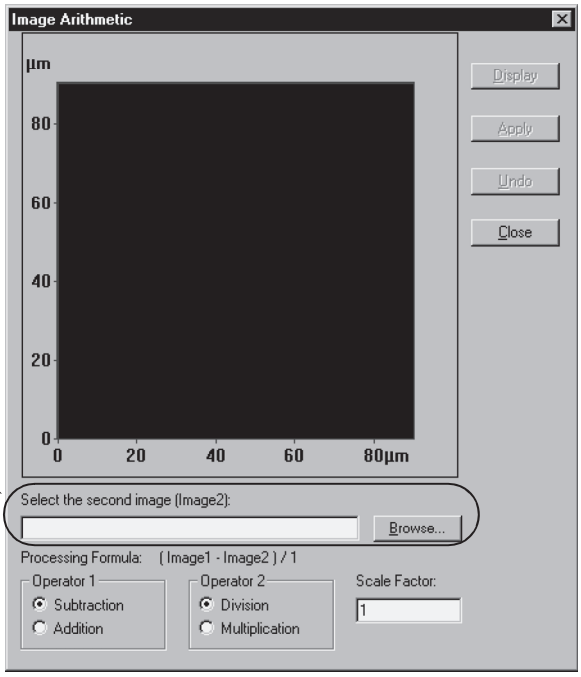
Two 3D scans can be compared with similar surfaces or the same site to evaluate noise and roughness. Both scans must use the same recipe:

- 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*



Step 3 Enter the name of the second image or click the **Browse…** button to search for the image.

3. 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.

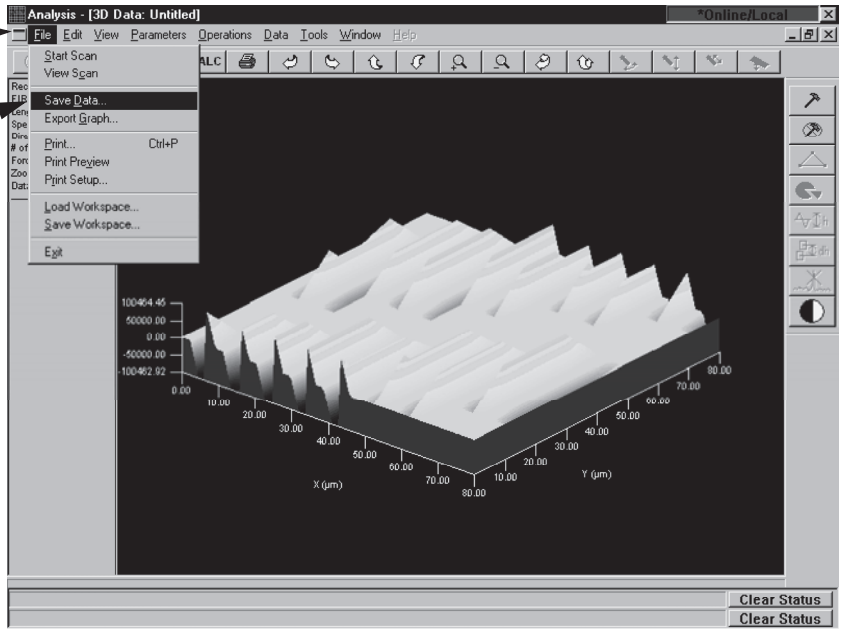
Saving 3D Scan Data

1. Click on **File** in the Menu Bar to display the File menu.

Figure 9.33 *3D analysis Screen with File Menu*

Step 1 Click on **File** to display its menu.

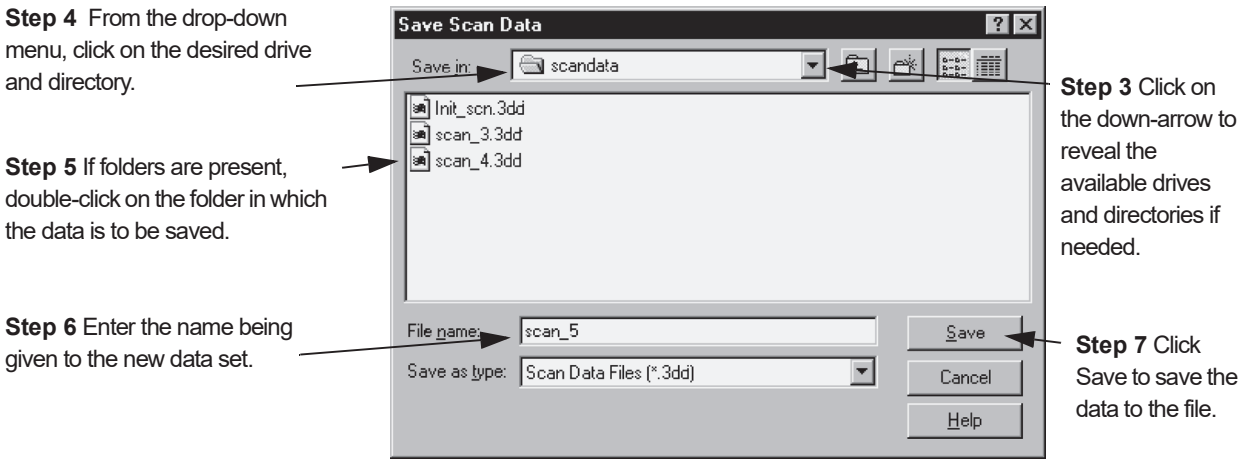
Step 2 Choose **Save Data…** from the menu.



2. Select **Save Data…**

   The Save Scan Data dialog box appears. (See *Figure 9.34*).

Figure 9.34 *Save Scan Data Dialog Box*



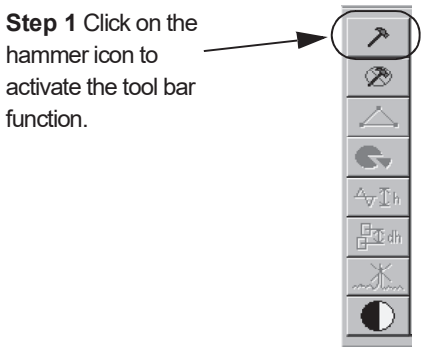
3. Click on the menu arrow next to **Save In** to reveal the available drives and directories. (See *Figure 9.34*)
4. Select the drive and directory from the drop-down menu. (See *Figure 9.34*)
5. Double-click on the folder that the data is to be stored in. A list of all current data files appear. (See *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*

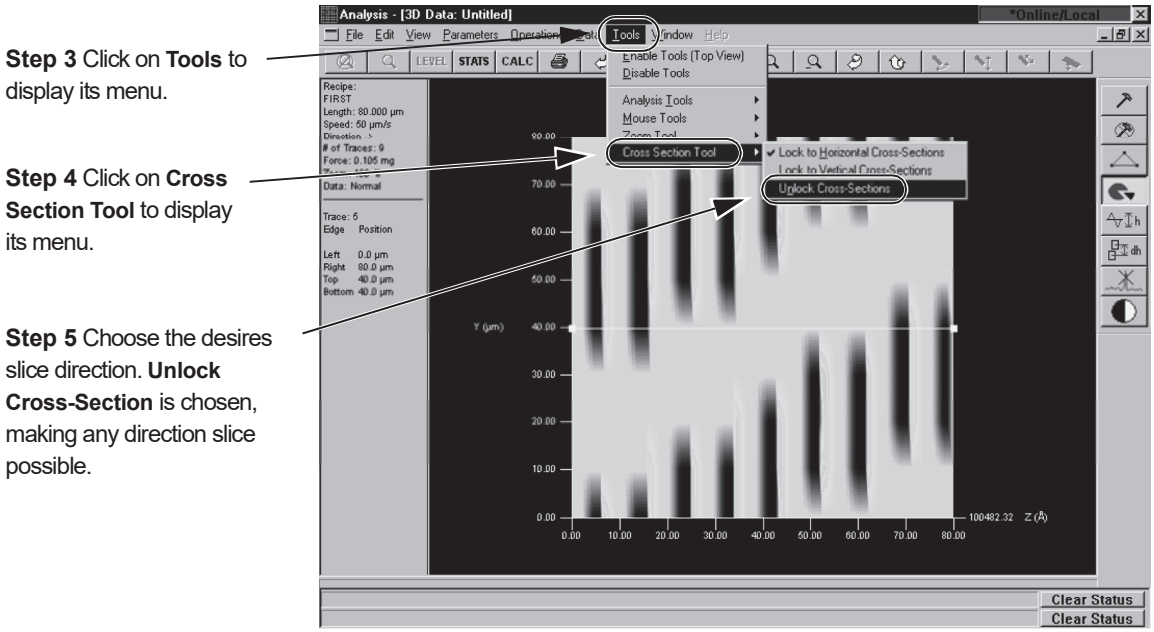


2. In the activated tool bar, click on the slice tool to activate the slice tool.

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*.)

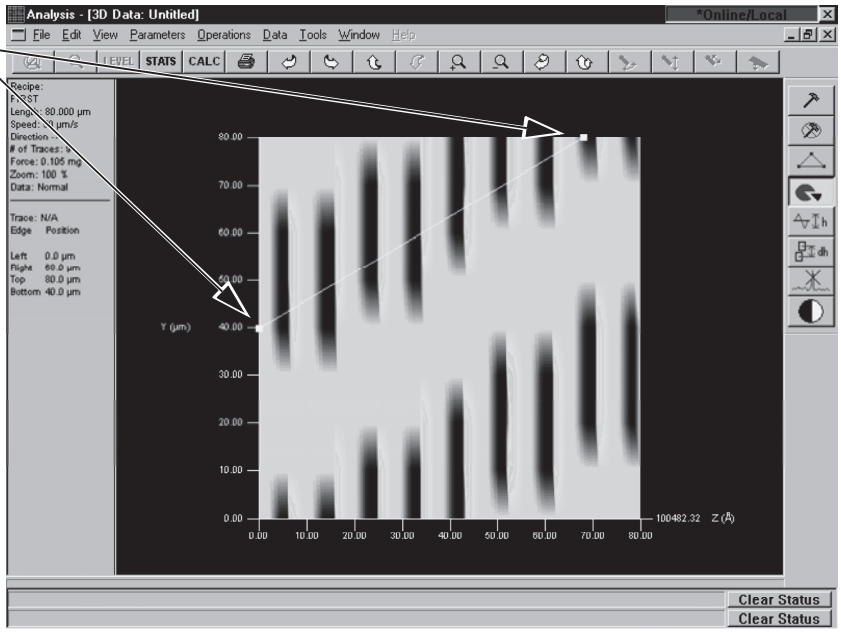
Figure 9.37 *Analysis Screen with View*



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*.

Figure 9.38 *Analysis Screen with Slice Tool Active*

Step 6 Top create the slice, click and drag the endpoints of the unlocked slice tool or the line segment of the vertical or horizontal slice tools.

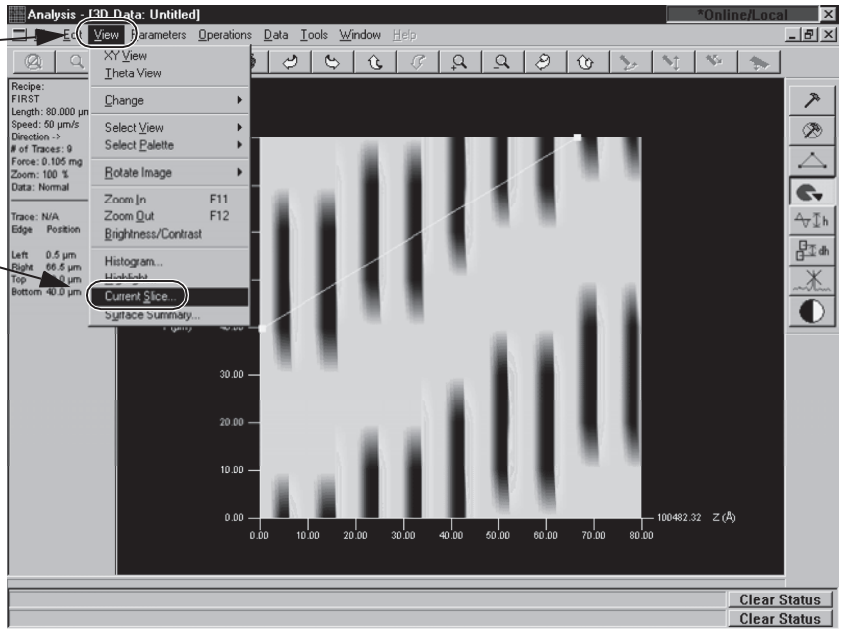


7. When the slice line has been placed, click **View** in the menu bar to display its menu. (See *Figure 9.39*.)
8. Choose **Current Slice…** to display the 2D slice trace. (See *Figure 9.39*.)

Figure 9.39 *Analysis Screen with Both 2D and 3D Images*

Step 7 With the slice tool placed, click on **View** in the menu bar to display its menu.

Step 8 Choose **Current Slice…** from the menu.

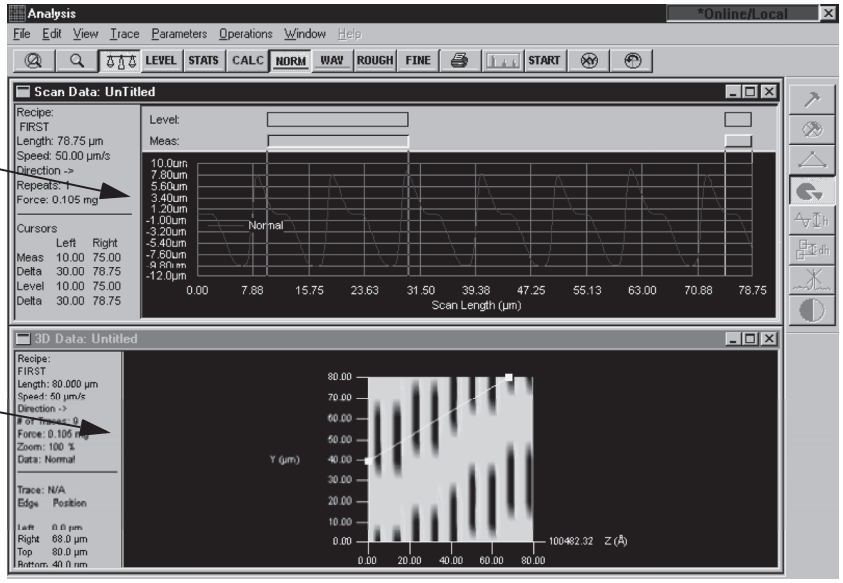


If the Window option is set to Tile Horizontal then the image is displayed as illustrated in *Figure 9.40*. The 2D slice trace is displayed above the 3D image. The 3D image is shown with the slice tool placed across the image at the place where the 2D image is generated.

Figure 9.40 *Analysis Screen with Both 2D and 3D Images*

The current slice is displayed as a 2D image in the Analysis Screen.

The 3D image is displayed in the top down mode, with the slice tool across the image as placed to create the 2D slice.



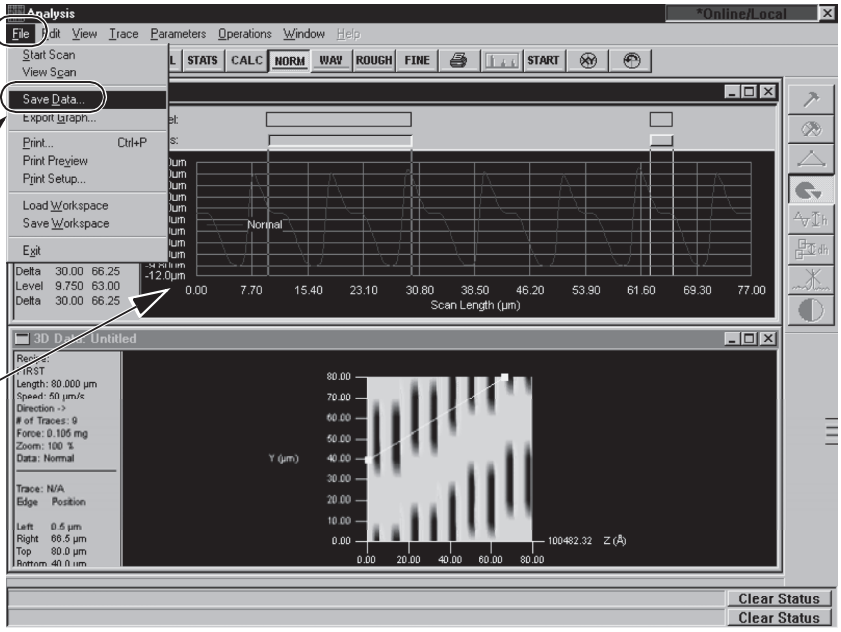
9. To save the 2D trace data from the 3D scan, click in the 2D trace portion of the Analysis screen to activate it.

Figure 9.41 *Analysis Window with File Menu*

Step 10 To save the 2D trace data, click **File** to display its menu.

Step 11 Choose **Save Data…** to open the

Step 9 Click in the 2D trace portion of the Analysis screen to activate it.



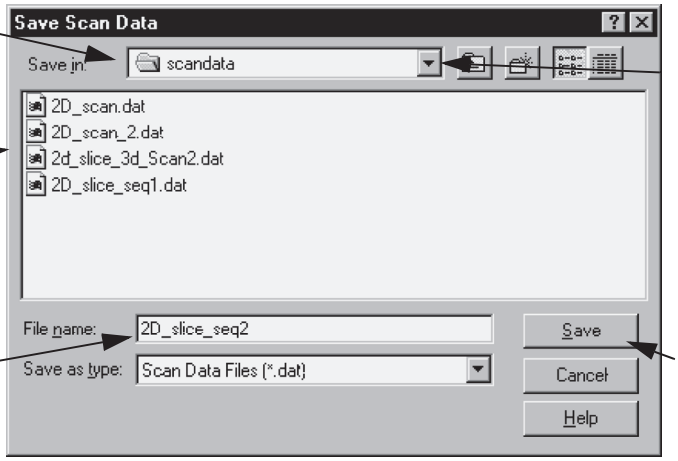
10. To save the 2D slice data click **File** to display is menu. (See *Figure 9.41*.)
11. Choose **Save Data…** to display is dialog box. (See *Figure 9.41*.) This displays the Save Scan Data dialog box. It should be set up to save 2D data as shown by the data type "Scan Data Files (*.dat)" in the **Save as type:** field. (See *Figure 9.42*.)

Figure 9.42 *Save Scan Data Dialog Box*

Step 13 From the **Save in:** drop-down menu, click on the desired drive and directory.

Step 14 If folders are present, double-click on the folder in which the data is to be saved.

Step 15 Enter the name being given to the new data set.



Step 12 Click on the **Save in:** down-arrow to reveal the available drives and directories if needed.

Step 16 Click **Save** to save the data to the file.

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.

10

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

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*.)

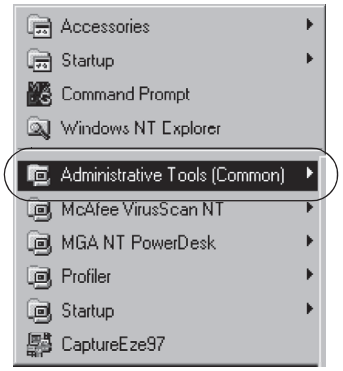
Figure 10.1 *Windows Screen START Menu*

Step 1 Click on **START** at the bottom left corner of the screen to open this menu.

Step 2 Move the cursor over **Programs** to access the Program 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*



Step 3 Move cursor over **Administrative Tools** to display its 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*

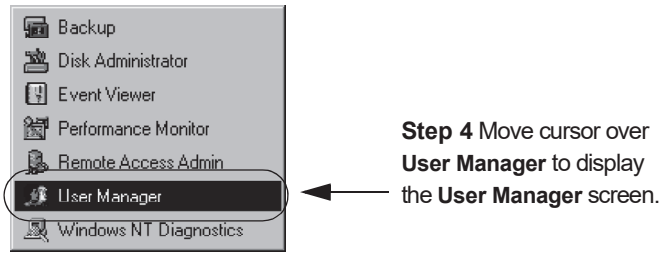
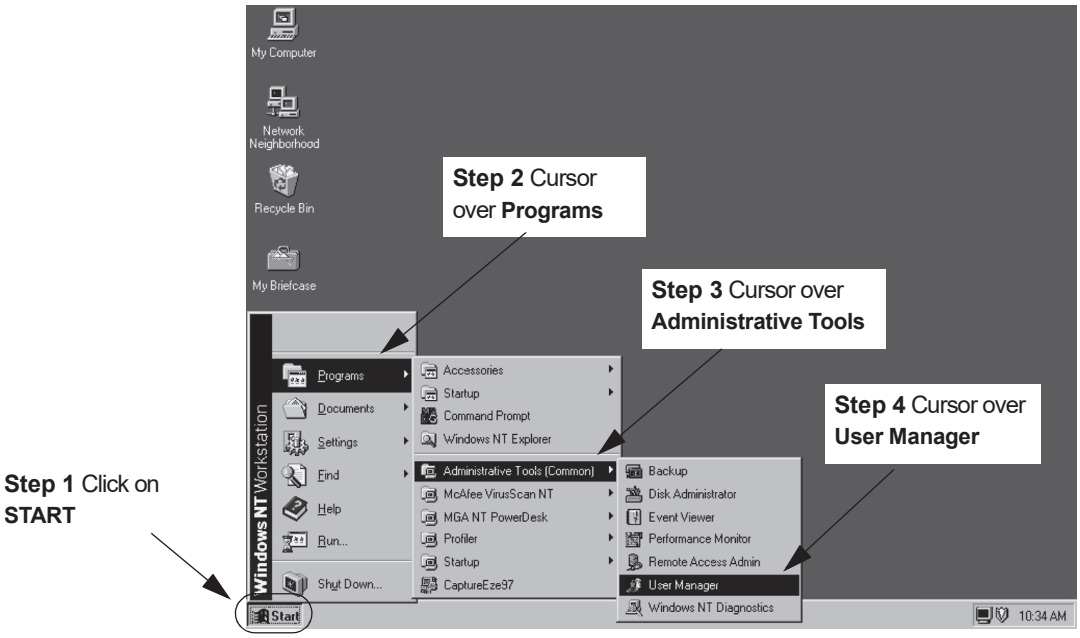


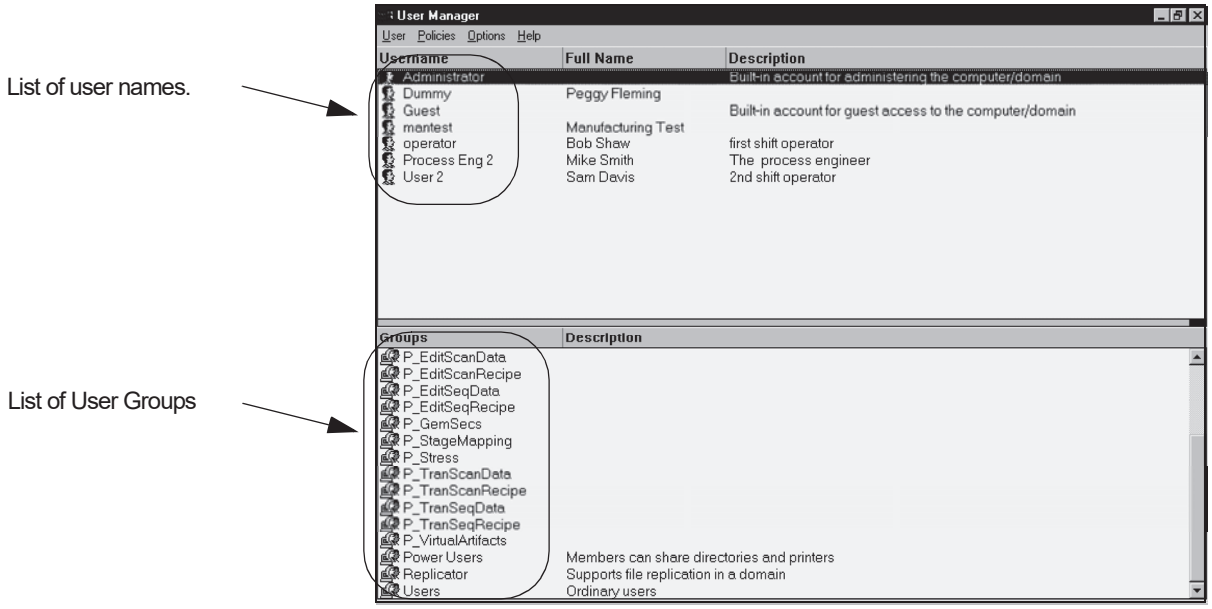
Figure 10.4 *Windows Screen with Path to User Manager Screen*



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.

Figure 10.5 *User Manager*



Creating a New User

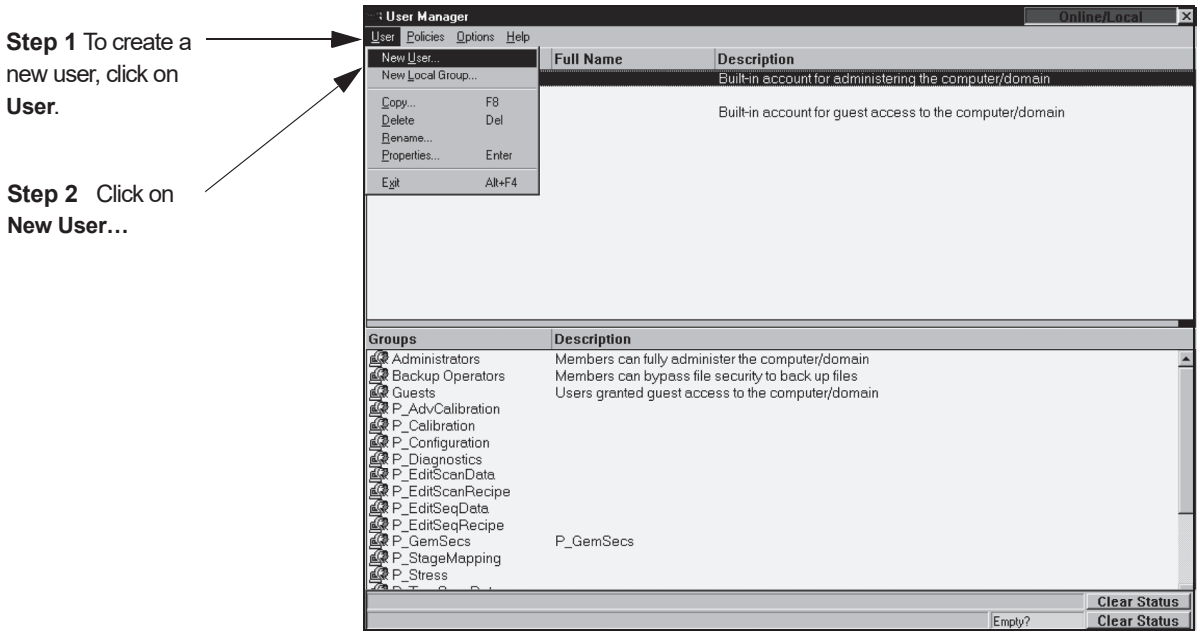
For the P-15 system users, a User Group is a secured access group with specific system privileges.

To create a new user, use the following procedure:

1. Click on **User** to display its menu. (See *Figure 10.6*.)

2. Click on **New User** to open the **New User** dialog box. (See *Figure 10.6*.)

Figure 10.6 *User Manager*



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.

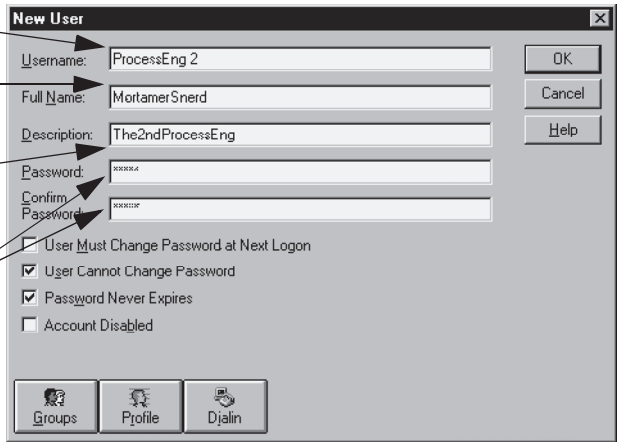
Figure 10.7 *New User Dialog Box - Variables*

Step 3 Enter the user name. This is the logon name.

Step 4 Enter the user name. This is the identity of the person.

Step 5 Enter the user name. This is what the person does in the system.

Step 6 Enter the Password. A confirmation is requested so there is less chance of misspelling since it is not visible.



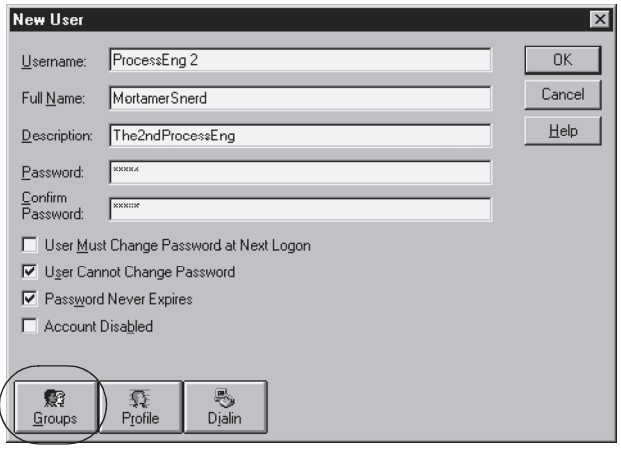
8. There are four logon variables that can be selected from. To enable one of the variables, click in the empty checkbox so that a check (✓) appears in it. The variables are as follows: (See *Figure 10.8*.)
   - **User Must Change Password at next logon.** If checked, the user will be required to enter 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.

END: Setting a Password

Figure 10.8 *New User Dialog Box - Variables*

Click on the empty checkbox of the desired password logon variables.

To change or add access to a group for a user, click on **Group** to display its dialog box.

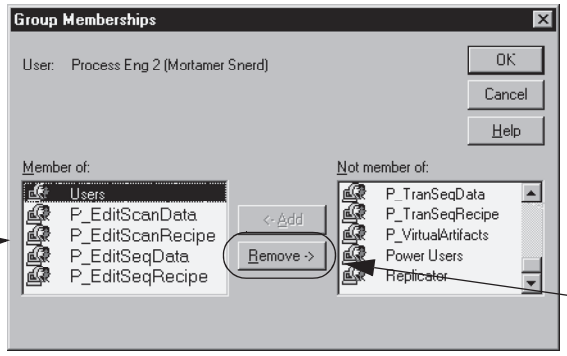


Changing or Adding Access to a User Group

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*

Step 2 Double-click one or more of the current user group. In this case, one of the P_XxxXxxXxx groups.



OR Highlight the current user group, and click on **Remove** to delete the highlighted user group.

Adding a User to a Users Group

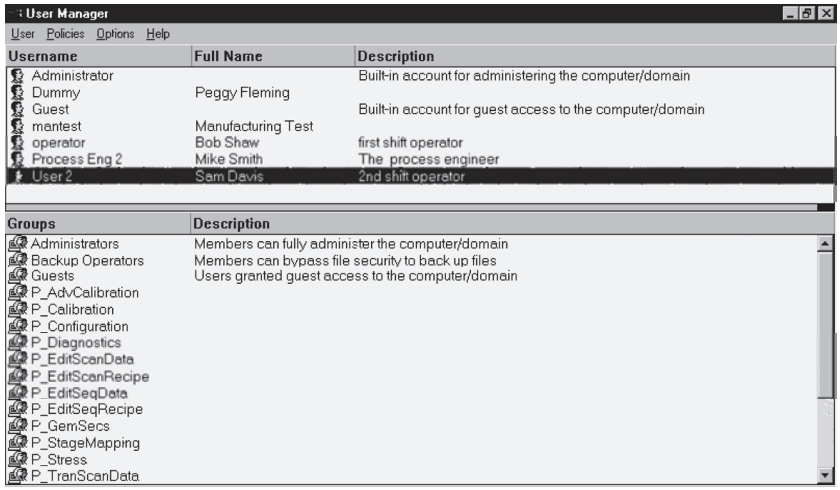
It is possible to add user to a profiler specific users group. This is primarily for those who are in the Windows defined **Users** group, because they have limited access to the profiler groups.

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*

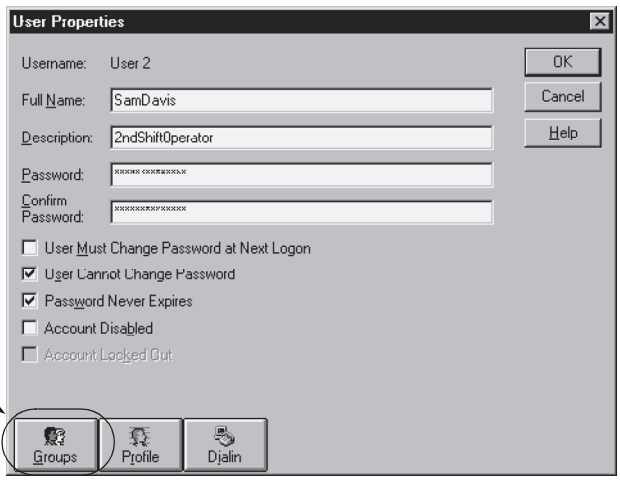
Step 1 Double-click on the name of the user that is to be added to the profiler specific group. (In this case, User2.) This opens the **User Properties** dialog box.



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*

Step 2 Click on the Groups button to open the Group Membership dialog box.

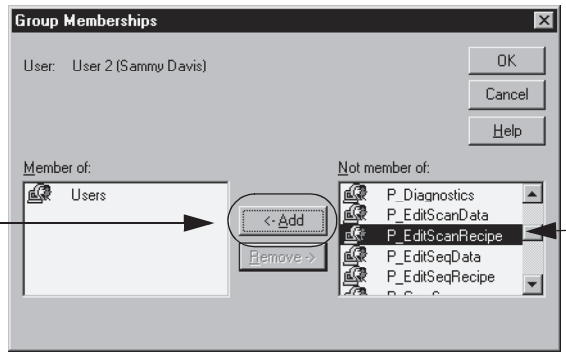


3. Scroll to find the desired user group in the **Not member of** variable box. (See the user groups defined in *Profiler Defined Groups* on page 10-2.) Double-click on the group to move it into the **Member of** field.

   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*.)

Figure 10.12 *Group Membership Dialog Box*

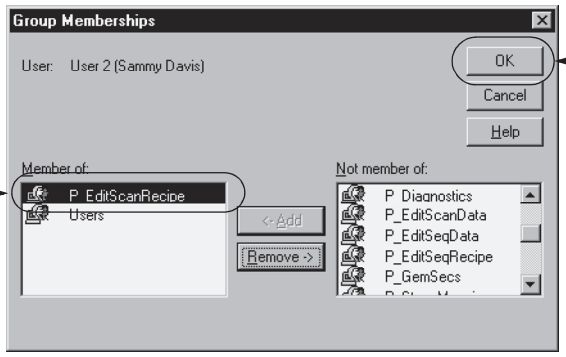
OR, highlight the user group and click on **Add** to place the user group in the **Member of** field.



Step 3 Double-click the new user group. Here **P_EditScanRecipe** is selected.

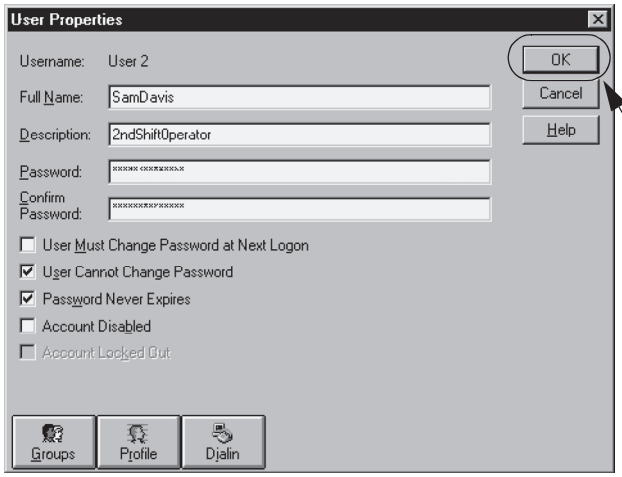
4. After adding all the necessary groups, click on **OK** to finalize the choices. (See *Figure 10.13*.)

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*



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.

Figure 10.15 *Calibrations Screen with Functions Grayed Out*

Notice that in the **Calibration** icon does not have access denied.

However, in the **Calibrations** screen, the operator might only have access to certain calibrations. Inaccessible functions are grayed out.