

# Chapter 6: Analysis Method Menu



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## A. Selection

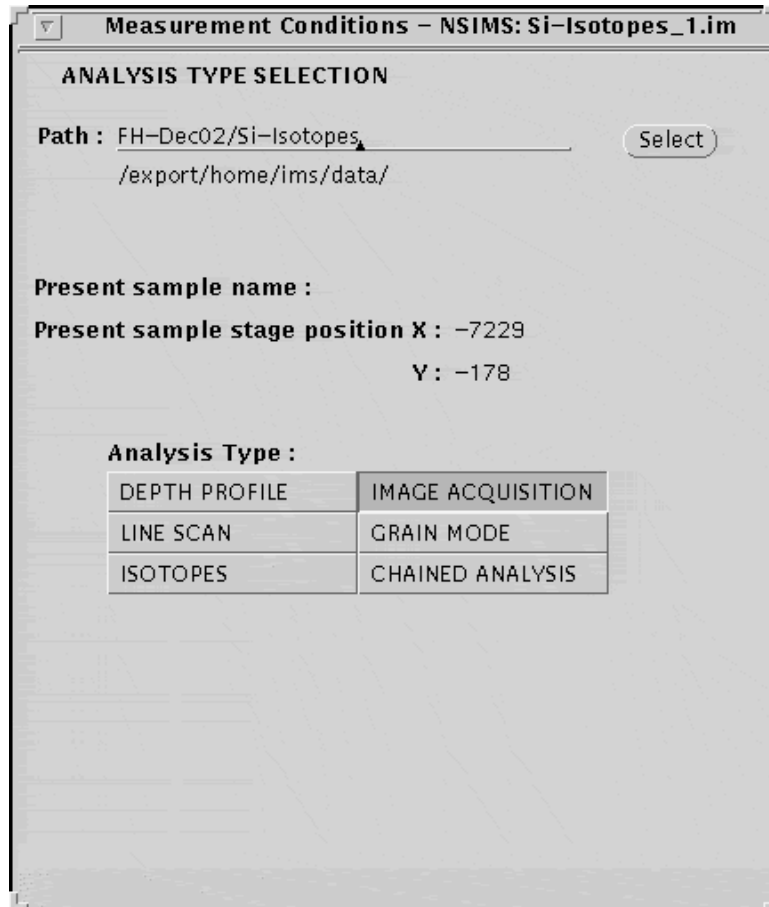


Figure 6-1: Snapshot of Selection Menu.

<b><i>Menu Details: Analysis Method Menu - Selection</i></b>	
<b>Path</b>	This shows the default path. In the directory structure, you can only go two levels below the path that is shown. You can change the default path (thereby using more than two subdirectories) by going to the setup menu; see the section “H. Directories” on page 116.
<b>Select</b>	Brings up File Manager (shown in Figure 6-2)
<b>DEPTH PROFILE</b>	Drills a hole into the sample and records composition at different depths
<b>LINE SCAN</b>	Elemental analysis along a line
<b>ISOTOPES</b>	Get an isotope ratio from a selected point on a sample.
<b>IMAGE ACQUISITION</b>	Imaging mass spectrometry

<b>GRAIN MODE</b>	Batch analysis
<b>CHAINED ANALYSIS</b>	

## B. File Manager

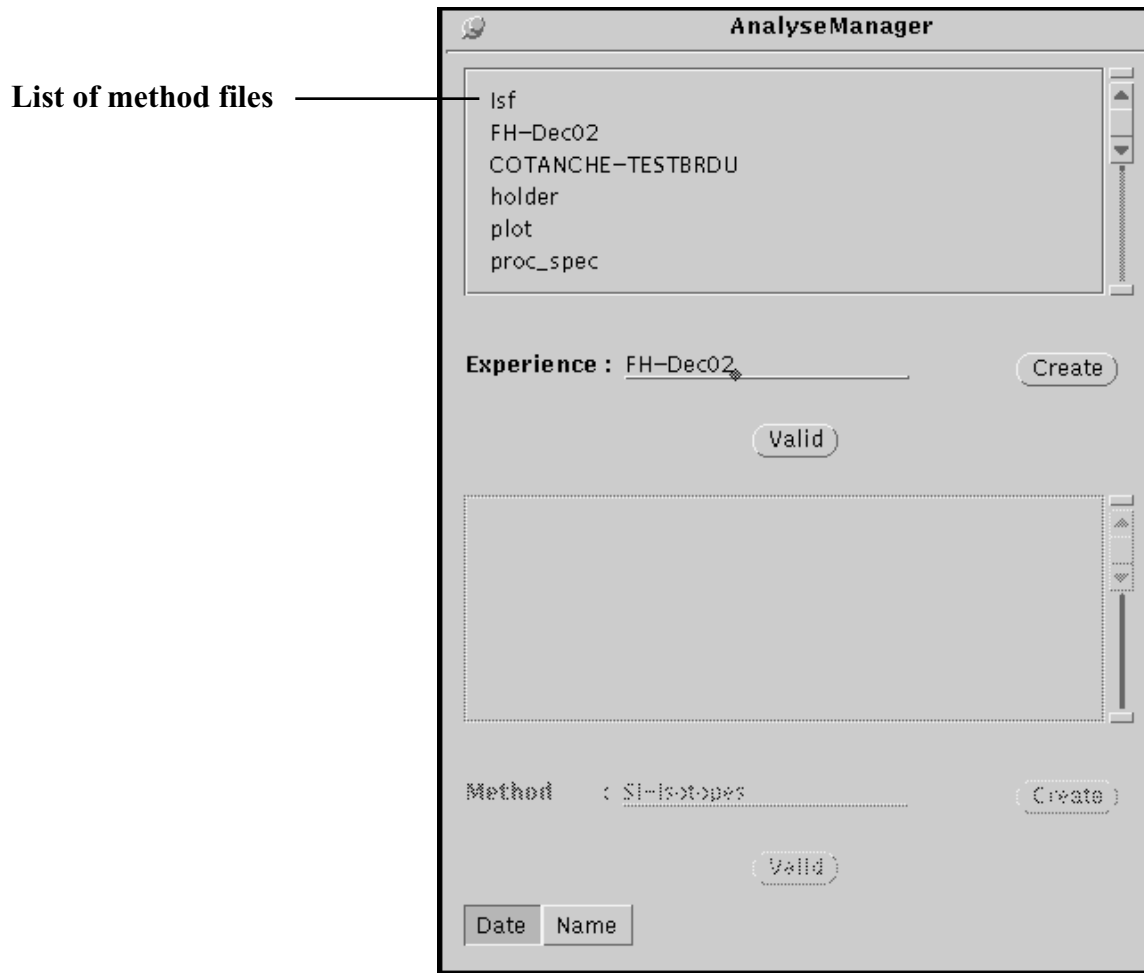


Figure 6-2: File Manager Menu within Analysis Method Menu

<b><i>Menu Details: Analysis Method Menu - File Manager</i></b>	
<b>Experience</b>	Experiment name. This applies to the first sub-level of the current path.
<b>Method</b>	This is where all info for that session will be saved, and is in the second sub-level of the current path.
<b>Valid</b>	Enter
<b>Date / Name</b>	Sorting order for method files

## C. Depth Profile

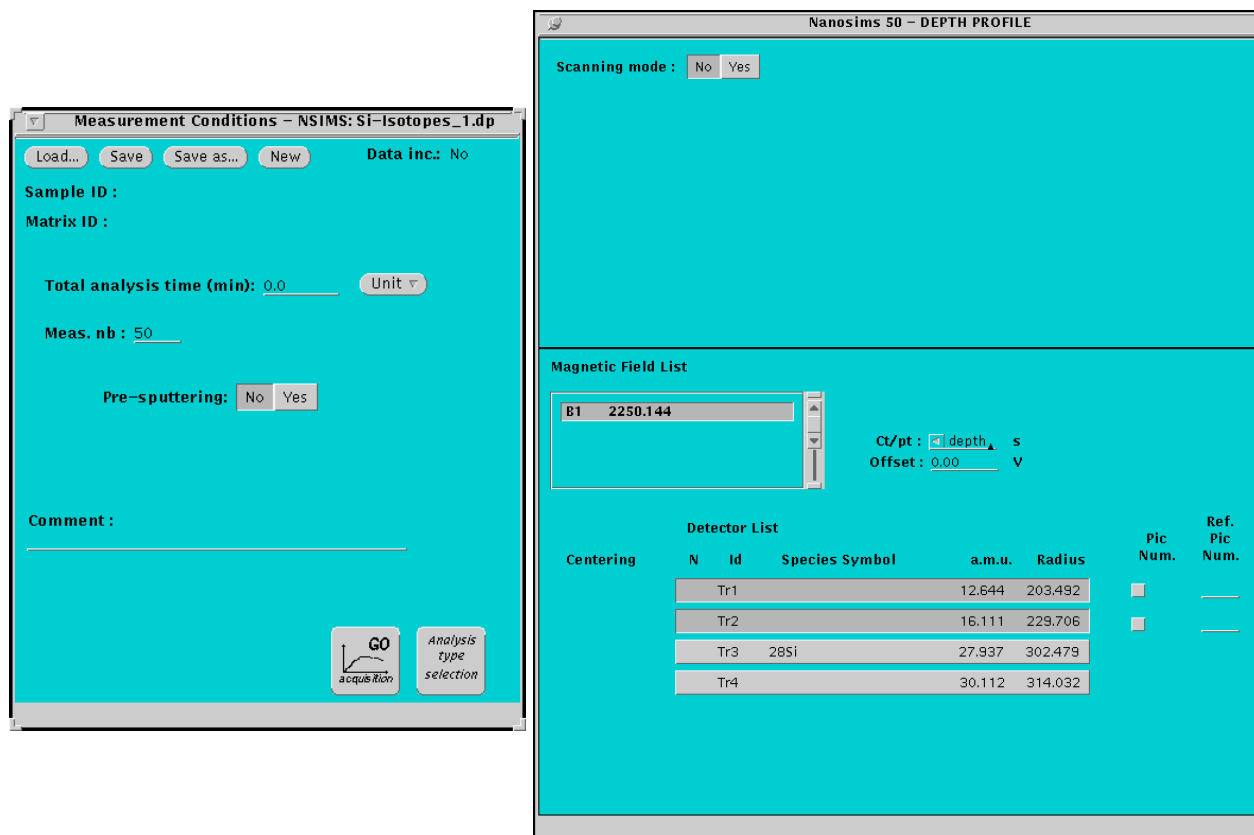


Figure 6-3: Menus for Depth Profile.

<b>Menu Details: Analysis Method Menu - Depth Profile</b>	
Records counts on selected detectors while the primary ion beam erodes material at a single point over time.	
<p><b>Ct/px (us) :</b> <input type="text" value="1000"/></p> <p><b>Offset (V) :</b> <input type="text" value="0.00"/></p>	Ct/px: Acquisition time per point
<p><b>Total analysis time (min):</b> <input type="text" value="0.0"/></p>	Total time for primary beam exposure
<p><b>Meas. nb :</b> <input type="text" value="50"/></p>	Number of data points during the total analysis time.

<p><b>Pre-sputtering:</b> <input type="button" value="No"/> <input type="button" value="Yes"/></p>	<p>Initial exposure to ensure steady-state conditions during data acquisition.</p>
<p><input type="button" value="Load..."/></p>	<p>The Load button on the lefthand menu of Figure 6-3 brings up a list of files taken for a particular type of analysis. The menu brought up by pressing Load is shown below in Figure 6-4.</p>



Figure 6-4: Menu for loading a file.

## D. Line Scan

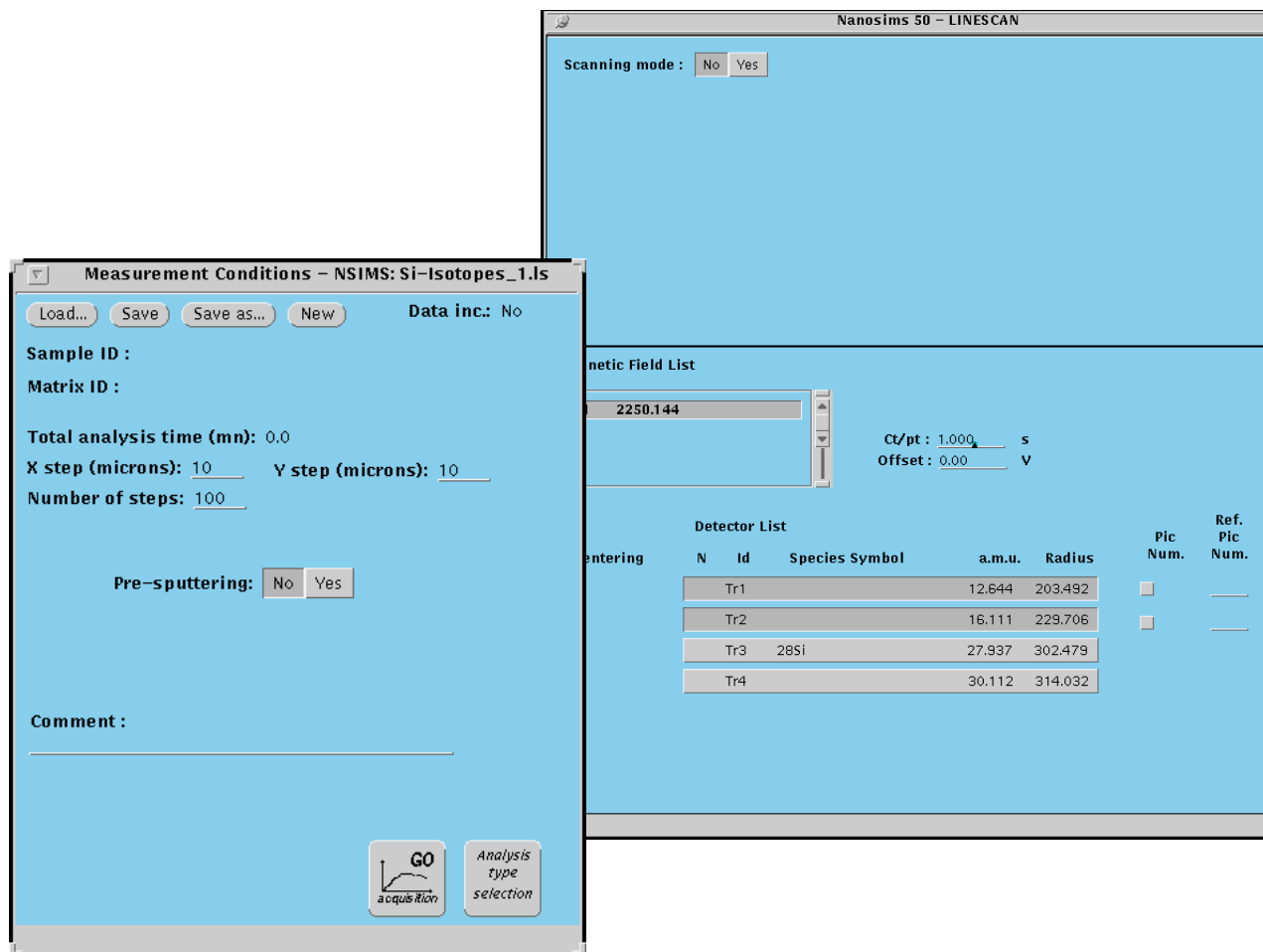


Figure 6-5: Menus for Line Scan.

<b>Menu Details: Analysis Method Menu - Line Scan</b>	
<b>Total analysis time</b>	Total time for analysis - a function of the number of points and the acquisition time.
<b>X step</b>	X increment for each step
<b>Y step</b>	Y increment for each step
<b>Number of steps</b>	
<b>Pre-sputtering</b>	Initial exposure to ensure steady-state conditions during data acquisition.
<b>Ct/pt</b>	Acquisition time per point
<b>Offset</b>	???

## E. Isotopes

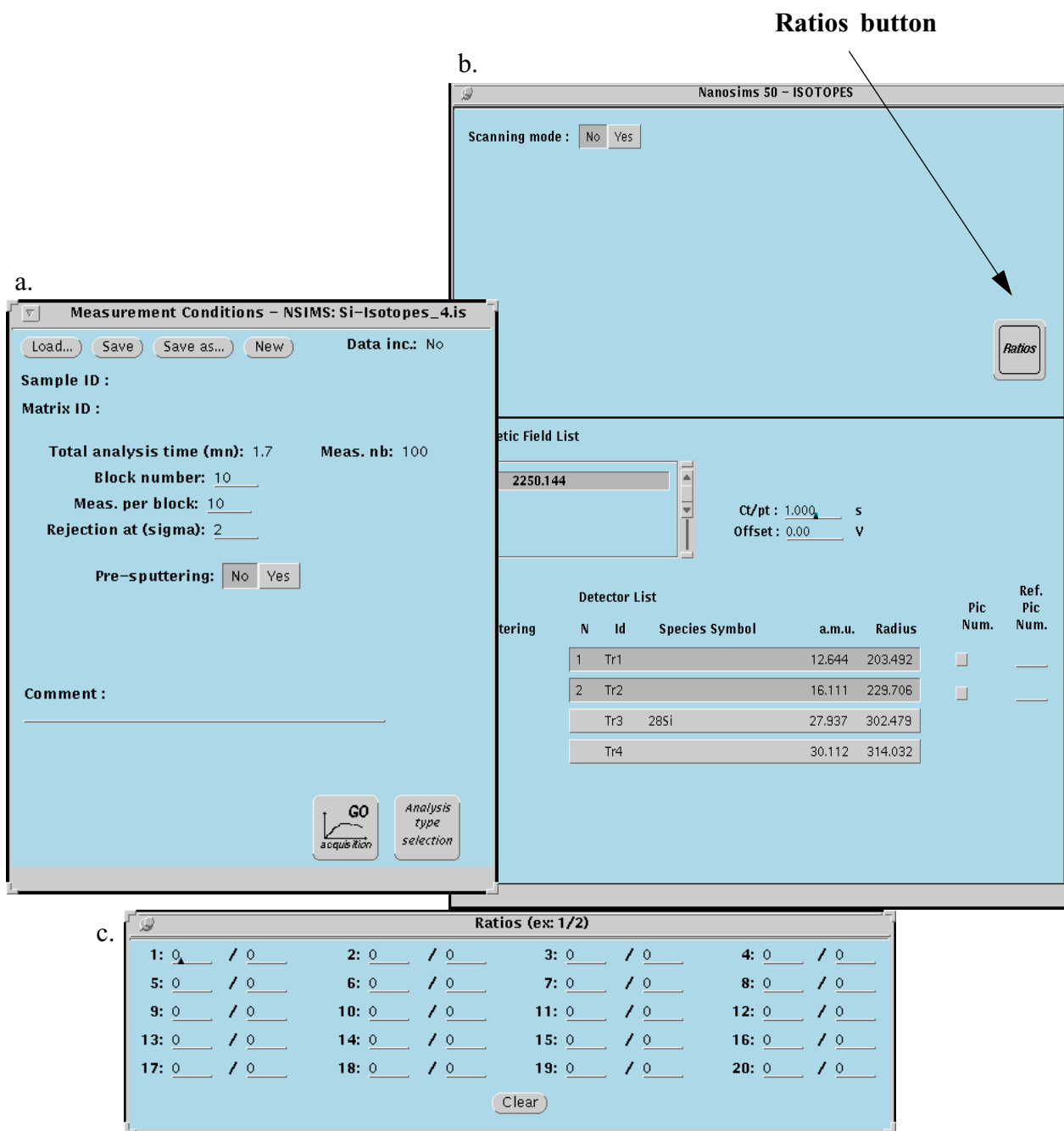


Figure 6-6: Menus for Isotopes Menu within Analysis Method Menu. Clicking on the ‘Ratios’ button in panel ‘b’ brings up panel ‘c’.

<b><i>Menu Details: Analysis Method Menu - Isotopes</i></b>	
<b>Ratios</b>	Clicking on this button brings up the 'Ratios' panel shown in Figure 6-6. You select the trolleys you want in order to specify isotope ratios. For example, if $^{12}\text{C}$ is on trolley 1 and $^{13}\text{C}$ is on trolley 2, to specify the ratio $^{13}\text{C}/^{12}\text{C}$ you would want the ratio 2 / 1. The key sequence to type this is: 2, enter, 1, enter.
<b>Block number</b>	Number of data blocks
<b>Meas. per block</b>	Number of data points per block
<b>Rejection at (sigma)</b>	Data quality criterion per block
<b>Pre-sputtering</b>	Initial exposure to ensure steady-state conditions during data acquisition.
<b>Ct/pt</b>	Acquisition time per point
<b>offset</b>	???

## F. Image Acquisition

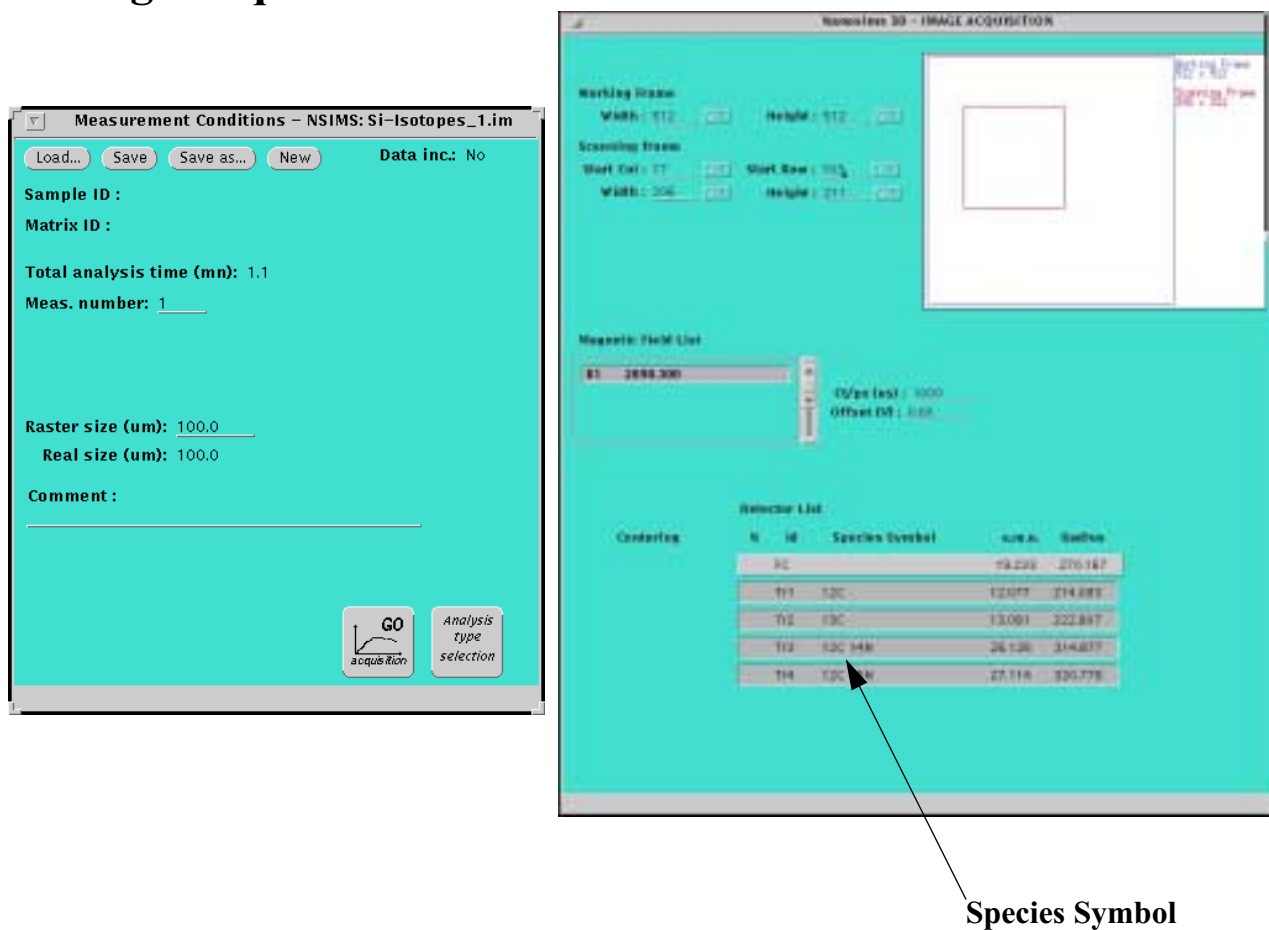
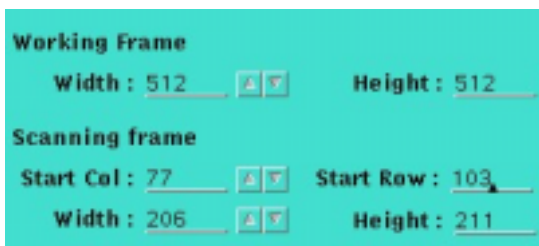
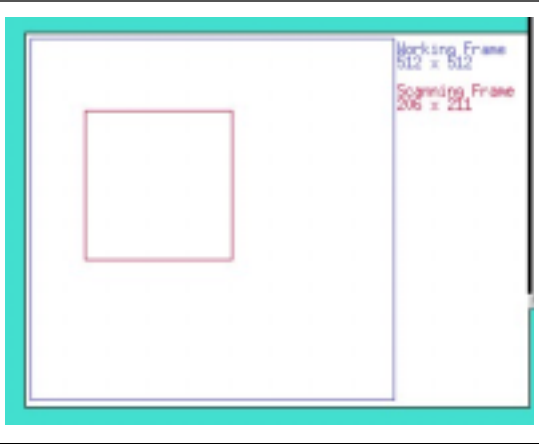
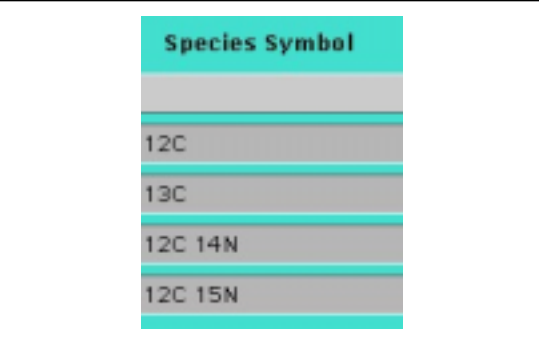


Figure 6-7: Image Acquisition Menus within Analysis Method.

### Menu Details: Analysis Method Menu - Image Acquisition

 <p><b>Working Frame</b> Width : 512    Height : 512</p> <p><b>Scanning frame</b> Start Col : 77    Start Row : 103 Width : 206    Height : 211</p>	<p>The working frame/scanning frame feature allows you to take a quick, lower-resolution image of a larger area (the working frame), and then take a higher-resolution image of a smaller area (the scanning frame) within the working frame.</p> <p>First, take a two-minute image in MIMS. Then go to ISee and use the <code>image_transfer</code> procedure to break the 2-minute image into its four masses and ratios. Select an area of interest in ISee and record the X,Y address of the top left pixel.</p> <p>Then return to the MIMS software and enter this coordinate next to Start Col and Start Row in Figure 6-7. The X coordinate should go in Start Col , and Y in Start Row . You can now launch MIMS acquisition to take an image of the scanning frame.</p> <p><b>IMPORTANT:</b> For a given image size in the scanning frame, the size of the original working frame image must be double (i.e. for a 256 x 256 pixel scanning frame image, the original working frame image would be 512 x 512 pixels).</p>
	<p>This is a graphical illustration of the scanning and working frames described above.</p>
	<p>If the species symbol here doesn't show up, this means that the radius needs adjusting. Check for this by going to the tuning menu and observing if the mass is shown in red (see Figure 2-2 and text on page 7). If it's red, you can do one of two things:</p> <ol style="list-style-type: none"> <li>(1) Change the mass range</li> <li>(2) Adjust the radius. This is the better option. When the radius has been properly adjusted it will show up in blue in the tuning menu.</li> </ol>

<b>Ct/px (us) :</b> <input type="text" value="1000"/> <b>Offset (V) :</b> <input type="text" value="0.00"/>	Ct/px: Acquisition time per point
<b>Meas. number:</b> <input type="text" value="1"/>	Number of repeat images of a field
<b>Raster size (um):</b> <input type="text" value="100.0"/>	Physical size of field of view. Also shown after application of correction factors

## G. Grain Mode

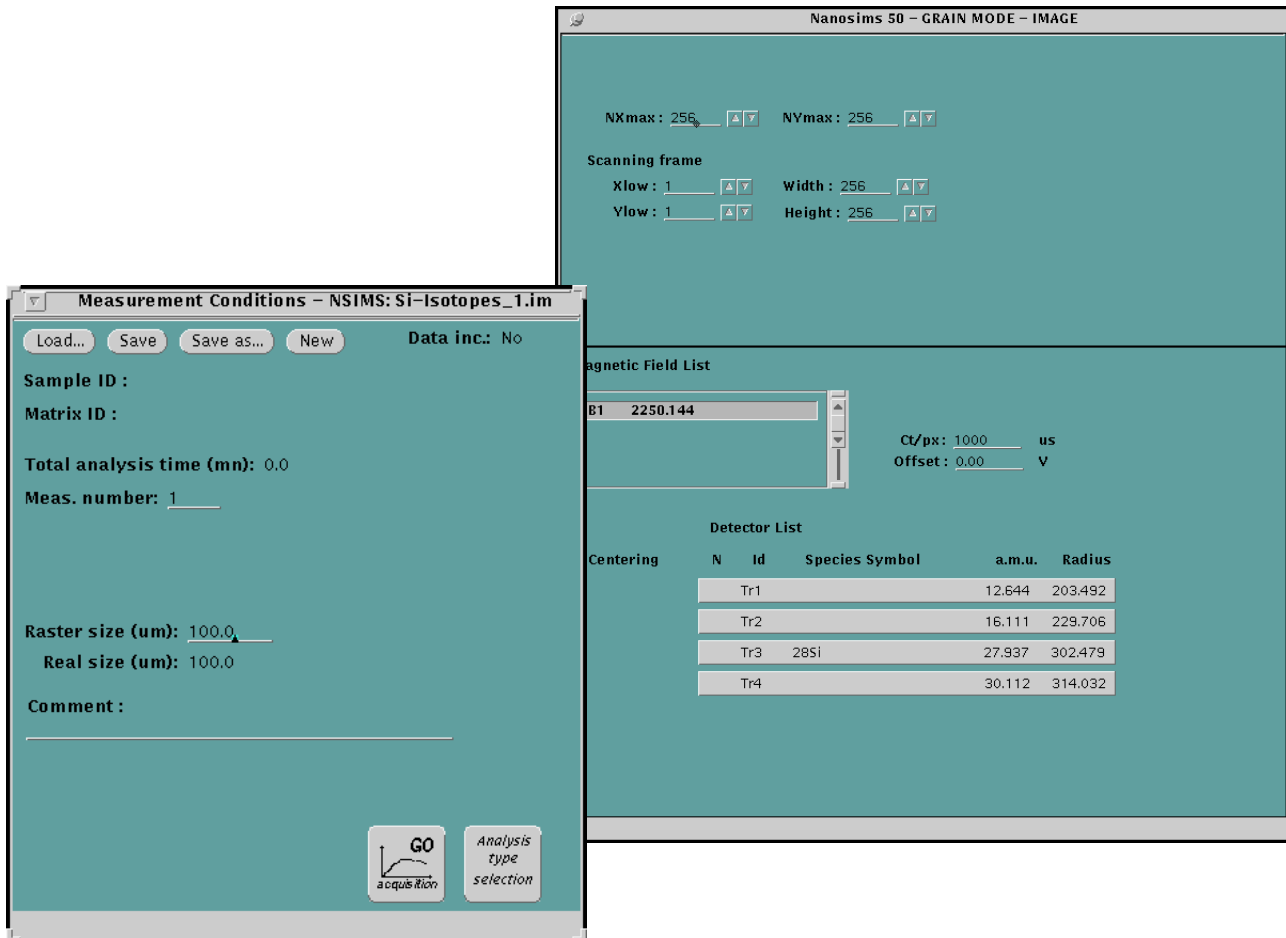


Figure 6-8: Grain Mode Windows.

<b>Menu Details: Analysis Method Menu - Grain Mode</b>	
<b>Meas. number</b>	Number of repeat images of a field
<b>Raster size</b>	Physical size of field of view. Also shown after application of correction factors
<b>NXmax, NYmax</b>	Maximal size of image raster. Limited by instrument
<b>Xlow, Ylow</b>	Starting points for scan based on current field size and position
<b>Width, Height</b>	Dimension of scanned field
<b>Ct/px</b>	Acquisition time per point
<b>Offset</b>	???

# H. Batch Analysis

<b><i>Menu Details: Analysis Method Menu -- Batch Analysis</i></b>	

## I. Chain Analysis

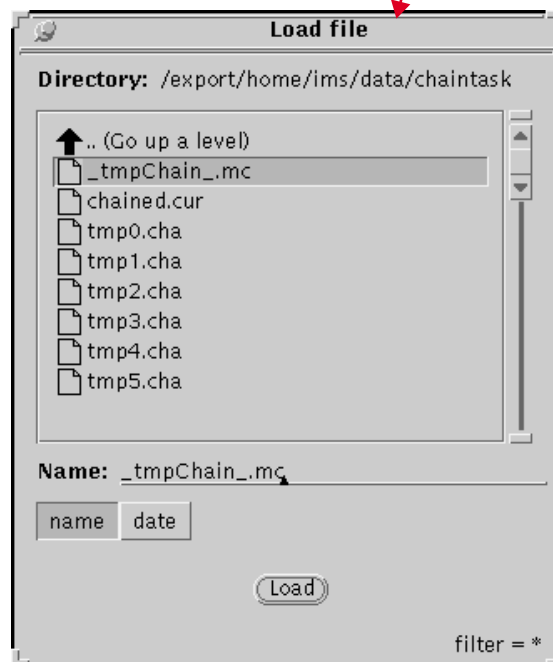
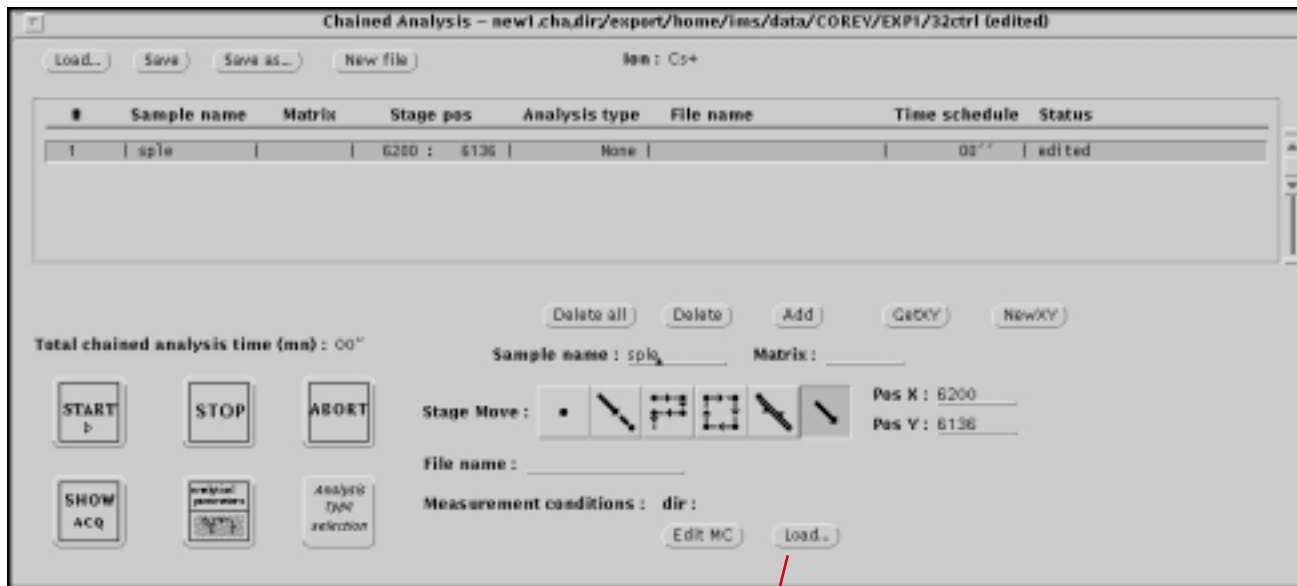





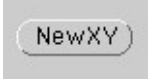
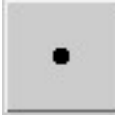


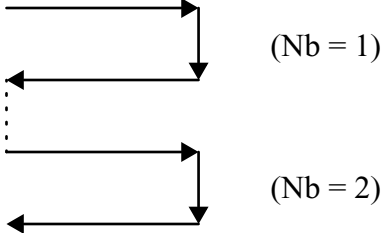





Figure 6-9:Chain Analysis Menu

**Menu Details: Analysis Method Menu -- Chained Analysis**

	<p>Edit MC changes the measuring conditions.</p> <p>Very important: before saving, insert the file name. Then press Save at the top left corner.</p> <p>Load brings up the menu in the lower half of Figure 6-9. Choose the file of interest (which will have the extension .cha). Then hit Load, which will close the Load window and return you to the main chained analysis screen.</p>
	<p>Deletes all sample info in analysis list above.</p>
	<p>Deletes only the highlighted sample in the analysis list.</p>
	<p>Adds an analysis at the location you are at. This button adds the item above the highlighted position.</p>
	<p>Uses the conditions of the loaded file for a run at the current X, Y position.</p>
	<p>Creates a run at a new X, Y position.</p>
<p><b>Types of Chained Analysis</b></p>	
	<p>This is the simplest type of chained analysis. You perform analysis at the position where you are currently at.</p>
	<p>GoTo: This allows you to move a certain dX and dY from the position you are at. You enter values next to dX and dY, and a number next to Nb: . Increasing Nb by X will move the analysis X number of times (each time by the prescribed dX and dY you have entered). Analysis moves in a straight line.</p>

 <p><b>dX :</b> <input type="text" value="1000"/> <b>x</b> <input type="text" value="1"/> <input type="button" value="▲"/> <input type="button" value="▼"/></p> <p><b>dY :</b> <input type="text" value="1000"/> <b>x</b> <input type="text" value="1"/> <input type="button" value="▲"/> <input type="button" value="▼"/></p> <p><b>Nb :</b> <input type="text" value="1"/> <input type="button" value="▲"/> <input type="button" value="▼"/></p>	<p>Snake: The snake option completes an S shaped path. You enter values for dX and dY; Analysis will start at the initial point, move dY, dX, then -dY. If you increase the number, Nb: above one, the path will be repeated. A simple path with Nb=2 would look something like this:</p> 
 <p><b>dX :</b> <input type="text" value="0"/> <b>x</b> <input type="text" value="1"/> <input type="button" value="▲"/> <input type="button" value="▼"/></p> <p><b>dY :</b> <input type="text" value="0"/> <b>x</b> <input type="text" value="1"/> <input type="button" value="▲"/> <input type="button" value="▼"/></p> <p><b>Nb :</b> <input type="text" value="1"/> <input type="button" value="▲"/> <input type="button" value="▼"/></p>	<p>Loop: This option will complete a rectangular loop. You enter values for dX and dY, then the analysis will move dX, -dY, -dX, and dY to return to the original location.</p>
	<p>This option lets you repeat a single path any number of times. You enter values for dX and dY, the beam will move to that location, and then automatically return -dX and -dY to the original position. Enter a value next to Nb to repeat the path as many times as you want.</p>
 <p><b>Pos X :</b> <input type="text" value="6200"/></p> <p><b>Pos Y :</b> <input type="text" value="6136"/></p>	<p>For this analysis, you enter an X coordinate and a Y coordinate, and the beam will move to that one position to perform analysis.</p>