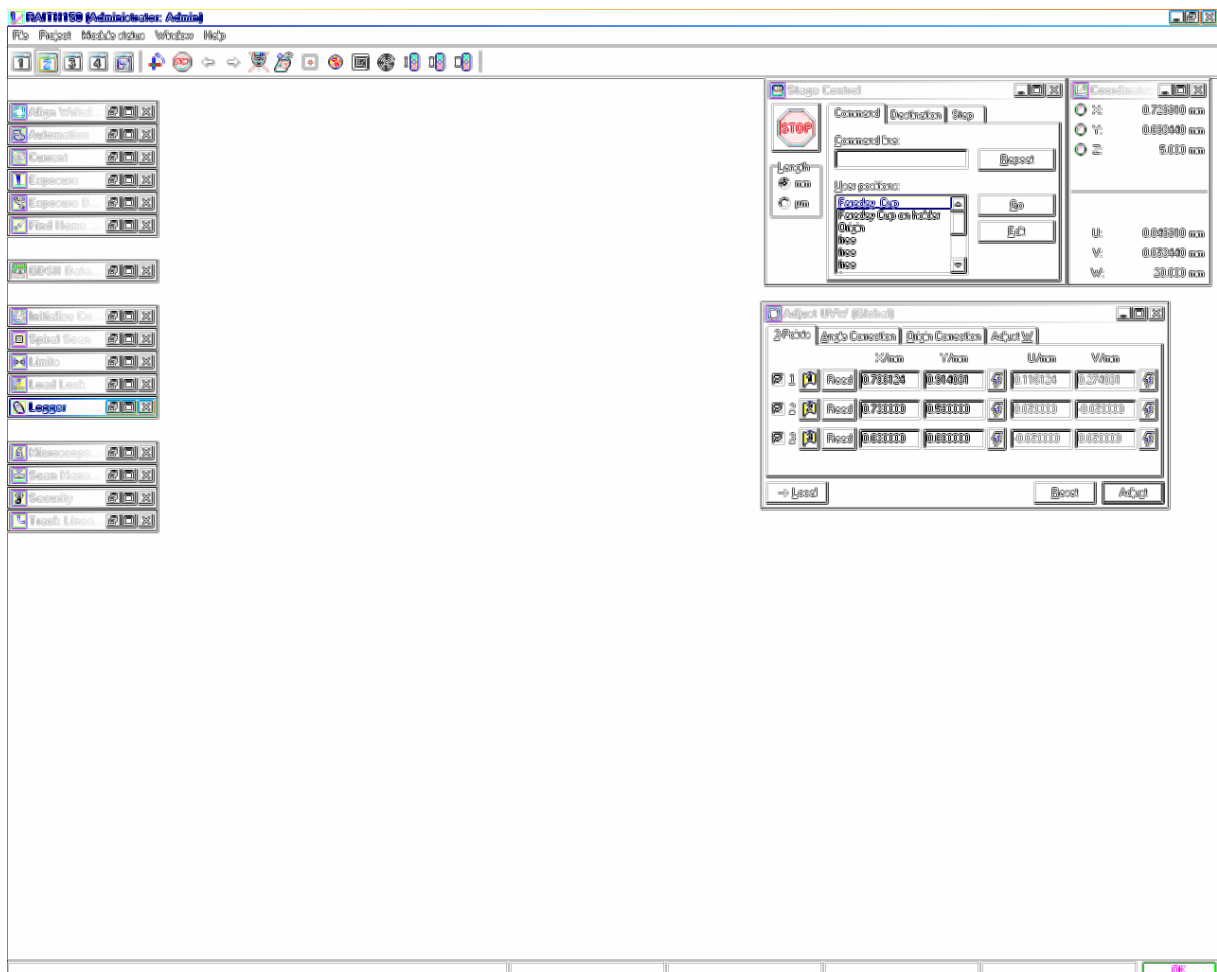


# Raith

Innovation from a world leader in  
e-beam lithography and  
semiconductor navigation solutions



## Software Reference Manual

### Version 4.0

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|                  |                            |
|------------------|----------------------------|
| Product:         | Raith Software             |
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# 1 Using the Manual

This manual is a reference manual; it describes and explains the functionality of the Raith software modules one by one. It is not intended as an operation manual (how to run the instrument.) An operation manual is provided separately.

## 1.1 Conventions

The following conventions are used throughout this manual:

Hints are indicated this way.



Warnings are indicated this way.



Examples are formatted like this.



**STEP 1** ►

Step-by-step explanations are indicated in this way ...

**STEP 2** ►

... as in the operation manual.

**Table 1:** Text attributes used in this manual.

| Style   | used for   |
|---|--|
| <b>Command</b>  | Software elements, e.g. buttons, menu commands, input fields, etc.   |
| <u>A</u>  | Coordinates, e.g. of the stage <u>X</u> and <u>Y</u> .   |
| <b>B</b>  | Key, e.g. <b>Control + B</b> . A standard US-English keyboard layout is assumed.   |
|  | Reference to another section or hyperlink to an external document, e.g. see section  <i>Conventions</i> . |
| <...>   | Variable, e.g. <filename>  |

**Table 2:** Mouse conventions used in this manual.

| <b>Action</b> | <b>Intended meaning</b>  |
|---------------|--|
| Click         | Quickly press and release the left mouse button.                             |
| Double-click  | Click the left mouse button two times in rapid succession.                   |
| Drag          | Hold down the left mouse button while moving the mouse.                      |
| Drop          | Release the left mouse button after dragging.                                |
| Point         | Move the mouse until the mouse pointer (cursor) rests on the item of choice. |

Following the common terminology of Windows, the terms select and choose have different meanings:

- Selecting an item usually means marking it. Very often this is used in connection with check boxes or radio buttons. Selecting alone does not initiate an action.
- Choosing an item usually carries out an action. For example, choosing a command from a menu or choosing a command button in a dialog box.

## 1.2 Described functionality

Please note, this manual describes all software features which are available within the comprehensive Raith software suite. Some Raith products are licensed for only a limited number of software modules so sometimes not all of the features described here are available in all products. Hence, depending on the product ordered, there might be differences between the installed software and functionality described here.

## 1.3 Glossary

The following terms are used throughout this manual:



**Table 3:** Glossary of terms used in this manual.

| <b>Term</b>  | <b>Meaning</b>  |
|--------------|---|
| Chipmap      | Two-dimensional graphical representation of a chip area on a Wafermap, used to navigate as well as to define exposure jobs.   |
| Imagescan    | Two-dimensional plot of detector intensity as a function of the position.   |
| Linescan     | One-dimensional plot of detector intensity as a function of the position.   |
| Positionlist | List which stores various task to be executed one after another.  |
| Wafermap     | Two-dimensional graphical representation of a sample area or work space, used to navigate as well as to define exposure jobs. |



## 2 Starting Raith program

|                              |           |
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To start the Raith software, choose **Start > Programs > Raith** of the Windows operation system and then the name of the product, e.g., **Quantum**. Alternatively, the Raith software can be started by double clicking a related Icon placed on the Windows desktop.

After starting the application the login screen appears.

**Figure 1:** Login Screen of Raith program. Login for RAITH150 shown as an example.

RAITH - RAITH150

Ultra High Resolution Electron Beam Lithography and Metrology Tool

Version 4.0 of 04/04/2004  
by  
Raith GmbH, Hauerl 18, 44227 Dortmund, Germany  
Phone: +49 (0)231 975 000 - 99  
Email: support@raith.de http://www.raith.de

Licensed for:  
Raith Standard Licence

User: Andi  
Password:   
Project: Template1024

Options Cancel Login

If instead the error message “Hardlock API error” appears, please ensure that the hardlock protection key is connected on the LTP1 or USB port of the computer.

### 2.1 Login

Select a **User** name and type the corresponding **Password** to login. Additionally, an available **Project** can be selected. Projects are necessary for storing and recalling specific session settings like screen configuration, related files, etc.

If the entered password is correct, the buttons **Options** and **Login** become enabled. Then the user has the possibilities to change the password or to reset the user configuration.

Choose **Login** to start the Raith application with selected project. Simultaneously, the application loads the same settings, like step size and dose, as used during the previous session. See section [User interface](#) to learn how to utilize a project to load specified files (like GDSII designs, Positionlists, Images, or desktop arrangements, etc.) upon Login.

Choose **Cancel** to interrupt the login procedure.

## 2.2 Changing password

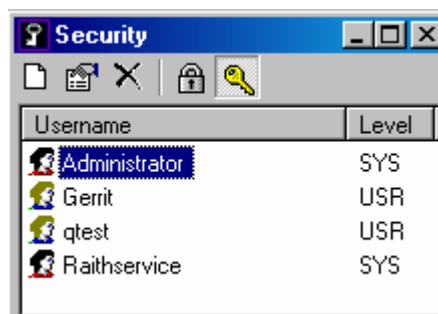
To change the login password, choose **Options > Change password**, enter and retype the new password in the appropriate dialog box.

To restore the “default” user settings, choose **Options > Reset user configuration**. This option deletes any user-specific settings, like step size and dose, of the current user. Other settings which are stored in separate databases, like microscope settings, write field alignment values, and scan type definitions are not deleted.

## 2.3 User management

Through use of the **Security** window each user can be assigned to one of three login (or access) levels: USR (ordinary user), EXP (expert user), and SYS (system level user.) The ability to add a new user is available only for those with system level of access. By default the Administrator possesses this level. For all other login levels the access to this routine is denied.


**Figure 2:** Window **Security** to manage users.




In addition to creating new users, the supervisor may delete users or modify and their passwords, names, and levels.

### 2.3.1 Edit menu

#### User properties

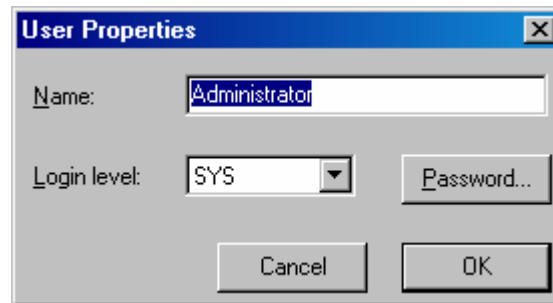
Choose this command or choose  or to change the attributes of a selected user.

**Create new user**

Choose this command or choose  to create a new user.

After choosing **User properties** or **Create new user** the **User Properties** dialog will be opened to enter user-specific attributes.

**Figure 3:** Dialog **User Properties** to create or modify user attributes.



To create/modify a user, enter the user's **Name**, select the **Login level** and define a password by choosing the **Password** button. This will create/rename a user account named after user's name. It is also possible to have no password specified.

**Delete User**

Choose this command or choose  to delete a selected user. After applying, choose if all files and directories should be deleted too.

**2.3.2 Options menu**

The various program settings are stored within a file with the extension VDB, which means variables database. This setup file is simply referred to as the VDB file. There are two types of VDB files. One type retains each individual user's settings and is commonly called the user VDB. The central or main program settings are stored separately, and this file is called the main VDB. To protect the main VDB it is possible to encode the VDB so that it can only be modified by use of the software dialog menus (*i.e.*, encoded so that it is not possible to edit the file with a text editor program.) Normally, the main VDB should be kept encoded. For debugging purposes or if support from Raith is required it might be necessary to decode the VDB file before sending it. To decode the VDB file choose the menu command **Options > Decoded variables database**. To encode the main VDB afterwards again choose the related menu command **Options > Encoded variables database**. At the same time it is possible to use the related buttons.



Please note that modifications of the settings in the main VDB can affect the performance and the ability to use the system. In addition, modifying the main VDB or leaving the main VDB unprotected, might result in hardware malfunction or damage requiring a costly service visit.



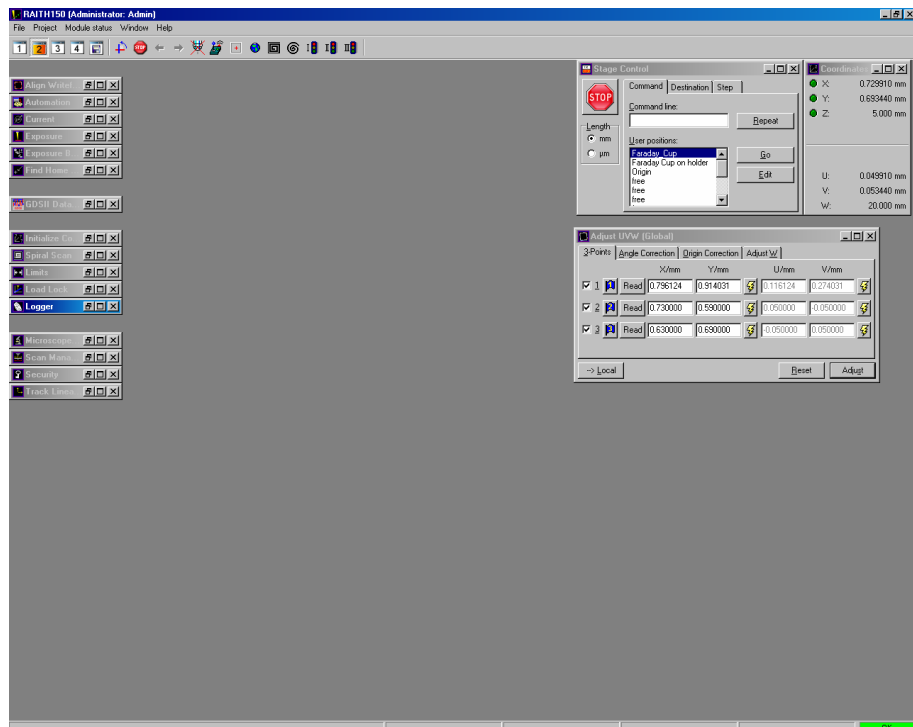
## 3 User interface

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The RAITH program uses standard Window controls with windows, icons and mice. For details of how to operate Windows we refer to the public available documentation. This chapter introduces the extensions used in RAITH program.

### 3.1 Program desktop

**Figure 4:** Main window of RAITH software suite.



|                     |  |
|---------------------|--|
| <b>Title</b>        | The title bar shows the name of the software and in brackets the currently user logged in as well as the currently loaded Project. |
| <b>Menus</b>        | Depending on the active window, more or less menus are available. Standard Windows terminology is used.                            |
| <b>Iconbar</b>      | The toolbar contains icons with some often used menu commands.   |
| <b>Desktop area</b> | Within the Desktop area the various windows of RAITH software are displayed. Various different types of windows exist.             |

- Control windows, e.g. the **Adjust UVW**, the **Exposure**, etc. window.
- Document windows, e.g. Positionlists, Images, etc. Normally, several documents of the same kind can be opened.
- UV-windows or UV-documents, a subset of documents with a sample position for each position within the window.

Windows are displayed as opened or minimized windows. To open a window, double click on the corresponding icon. To close, minimize, increase, etc. the standard Window controls are available. The RAITH software is organized in the following way.

- The various windows of the RAITH software appear within the Desktop area.
- Up to four different Desktop areas build one Project.

In detail, each Project contains for each Desktop the following information about ...

- the position of each window,
- the documents loaded,
- the behavior when opening another document, and
- the overlay displayed in UV-documents.

#### **Status bar**

The status bar summarizes a set of information in different status fields.

- The left status field displays on-line help. Additionally, system messages, e.g. Motors stopped, Emergency Stop, etc., will appear.
- While moving the mouse inside a UV-window, like an image, the stage coordinates XY, the sample coordinates UV, and the window coordinates are displayed in the following status fields.
- On the right side a visual indication of program status is given. Double-click it to open the Module Status (see **Figure 5**) or use the right mouse button to a drop-down menu with additional commands. Following statuses are possible:

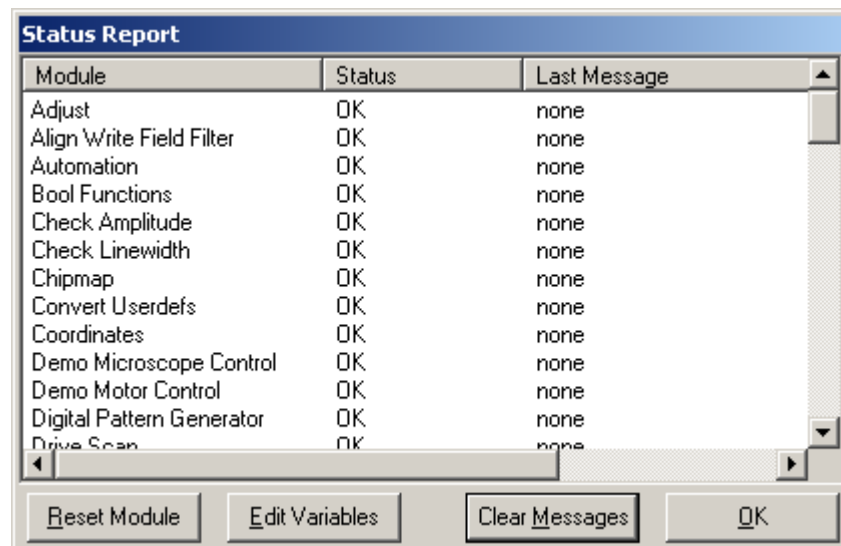


**Table 4:** List of possible Module statuses.

| Status  | Meaning  |
|---------|--|
| OK      | No occurrences of errors, warnings or info.                          |
| INFO    | Information, no influence on program run.                            |
| WARNING | Something is not quite correct.                                      |
| ERROR   | Something went wrong, please check before continuing.                |
| FATAL   | Immediate interaction is required, please check as soon as possible. |

By double-clicking into the status field or selecting menu **Module status** a list of all currently loaded modules, their error status and last messages is displayed.

**Figure 5:** Window Status Report.



This menu comprises two applications: editing of variables and display of status messages. For this there are three functions available.

#### Reset Module

To reset the module, select the module's name first.

#### Edit Variables

To modify or to inspect module variables select the module's name. Select the variable's name and choose the Edit button or double-click on the variable's name. Drop down a list of values, if available, or enter the value manually. To make the changes valid, reset the corresponding value.

#### Clear Messages

To clear all messages without resetting the modules.

### 3.1.1 File menu

#### Close

|                             |  |
|-----------------------------|--|
| <b>Close all</b>            | Choose <b>Close</b> to minimize the active control window to icon size or to close the active document. Choose <b>Close all</b> to close all document windows for the same kind as the active one. |
| <b>New image</b>            |  |
| <b>Open image...</b>        | Generate a new Image respectively opens an existing one. A new Image is named NONAME#.SSC, # indicates consecutive numbering.  |
| <b>Open linescan...</b>     | Opens an existing Linescan.  |
| <b>New positionlist</b>     |  |
| <b>Open positionlist...</b> | Generate a new Postionlist respectively opens an existing one. A new Positionlist is named NONAME#.PLS, # indicates consecutive numbering.   |
| <b>New Wafermap</b>         |  |
| <b>Open Wafermap...</b>     | Generate a new Wafermap respectively opens an existing one. A new Wafermap is named NONAME#.WLO, # indicates consecutive numbering.  |
| <b>New Script</b>           |  |
| <b>Open Script...</b>       | Generate a new Script respectively opens an existing one. A new Script is named NONAME#.JS, # indicates consecutive numbering.   |
| <b>Exit</b>                 | Choose this command to exit the program session.   |

### 3.1.2 Project menu

|                     |  |
|---------------------|--|
| <b>New</b>          | Choose this command to load the Project file NEW.DSK.  |
| <b>Open</b>         | Choose this command to open an existing Project file.  |
| <b>Save</b>         | Choose this command to save changes to a loaded Project. The Project will be saved under the same file name.   |
| <b>Save as ...</b>  | Choose this command to save a loaded Project under a freely selectable file name.  |
| <b>Desktop#</b>     | Choose this command to activate one of the four available desktop configurations. # indicates the number of the desktop.   |
| <b>Save desktop</b> | Choose this command to save a desktop configuration. After choosing, select the number of the related desktop. In addition, enter a suitable name for the desktop configuration. |

### 3.1.3 Window menu

|                      |   |
|----------------------|---|
| <b>Arrange icons</b> | All windows icons are arranged alphabetically. The opened windows are not influenced. |
|----------------------|---|

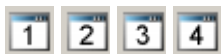
|                              |  |
|------------------------------|--|
| <b>Close all</b>             | All opened windows are closed or minimized to icon size. Additionally, the window icons are arranged               |
| <b>Save settings ...</b>     | Opens dialog to set the behavior of documents when opening a document of the same kind, e.g. an image.             |
| <b>A list of all windows</b> | The listing contains all available windows in alphabetical order. The activated window is indicated by a tick mark |

### 3.1.4 Help menu

|               |   |
|---------------|---|
| <b>Index</b>  | Opens the on-line help at the main topic.   |
| <b>Module</b> | After activating the corresponding window, this command opens a context sensitive on-line help for this module. |
| <b>About</b>  | In addition to the standard version information, it displays the currently logged in user and the used Project. |

### 3.1.5 Icon bar

As menus the displayed icons depends on the active window. General available icons are ...



Recall Project specific desktop configurations. Up to four different configurations are possible.



Save the desktop configuration. After choosing, select the number of the related desktop. In addition, enter a suitable name for the desktop configuration.



Rotates the presentation for active UV-document each time the button is presses by 90° counterclockwise.

## 3.2 Keyboard shortcuts

Generally, all commands are accessible by hitting the **Alt** key together with the key corresponding to the underlined character. See Windows documentation for how to change this behaviour. The following shortcuts are available throughout the software ...

|                     |   |
|---------------------|---|
| <b>F1</b>           | Call up help. Specific help will be called up for the activated module window |
| <b>Crtl + 1...4</b> | Recall desktop configuration 1...4.   |
| <b>Crtl + 5</b>     | Save desktop configuration.   |

**Alt + x** Exit the program session.






## 3.3 Drag and Drop concept

The concept of drag and drop operation is extensively used throughout the Raith software to ensure easy operation of rather complex tasks. It means that some objects, e.g. scan, can be picked up using the mouse in one window and placed or dropped in another window. In those areas where dropping of the object makes no sense, this will be indicated by a no-parking sign type mouse cursor. After reaching a well-defined target window, a realistic representation of the selected object appears. Dropping is just done by releasing the left mouse button and all required set-ups are handled by the system.

## 3.4 Using projects for customizing

### 3.4.1 Window position


To store the position of a window:

- STEP 1 ►** Choose , , , or  to switch to the desktop which should contain the window.
- STEP 2 ►** Place the window on the desktop where it should appear in the future and adapt also its size.
- STEP 3 ►** Choose the  Icon to open the **Save Desktop** dialog.
- STEP 4 ►** Save these setting by clicking the **OK** button. Optionally, the **Name** for this Desktop can be changed before saving.

### 3.4.2 Document opening mode and overlay

To store the mode used when opening a new window or the displayed overlay:

- STEP 1 ►** Activate the corresponding document window.
- STEP 2 ►** Choose from the Menus **Windows > Save Settings ...** to open the **Pane** window.
- STEP 3 ►** Select **Display** and an entry from the list to define what to overlay into this document window.
- STEP 4 ►** Select **Close** so that the opened document will be closed before opening another document of the same kind.

- STEP 5 ▶** Select **Tile** so that all opened documents of the same kind will be tiled within the area of the firstly opened document.
- STEP 6 ▶** Optionally, Choose **Delete** to restore the default values.
- STEP 7 ▶** Accept the selection temporarily by pressing the **OK** button.
- STEP 8 ▶** Choose the  Icon to open the **Save Desktop** dialog.
- STEP 9 ▶** Save these setting by clicking the **OK** Button.

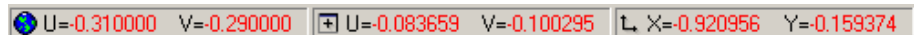


## 4 UV windows

|  |           |
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| <b>4.2 Using the toolbox</b>           | <b>26</b> |
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UV windows are special windows where each point can be identified with a coordinate. Such windows are Images, Wafermaps, Chipmaps, GDSII viewer and GDSII editor. If the cursor is placed within a UV window the status bar indicates the corresponding coordinates.

**Figure 6:**  
Coordinates of a UV window displayed in the program status bar.



The U- and V-coordinates with the globe are the corresponding sample coordinates, The U- and V-coordinates with the window symbol are the corresponding coordinates relative to the window origin, and the X- and Y-coordinates are the corresponding stage coordinates.

### 4.1 Menu commands

#### 4.1.1 Edit Menu

##### Adjustment

Choose this command to place the marks used for 3-point adjustment. To make the markers visible in the current UV window, choose **View > UV display ... > UV window properties > Show adjustment marker** while desired UV window is open.

##### Measure

Choose this command to measure coordinates, distances, angles and areas, defined by two points within the UV window area. After choosing this command, set the points by two subsequent mouse clicks. The results are displayed in a message window.

#### 4.1.2 View menu

##### Redraw

Choose this command to redraw the viewed area. The command can be canceled by pressing the **Esc** key.

##### Zoom

A cascading menu opens with the following commands

Choose command **All** to display the complete area, which is covered by all of the structure elements.

Choose command **In 2x** to magnify the displayed area by factor 2 around the cursor position. Because the size of the magnified area is half as large as of the former area, corresponding width and height are reduced by factor square root of 2.

Choose command **Out 2x** to reduce the displayed area by factor 2 around the cursor position. Because the size of the reduced area is twice as large as of the former area, corresponding width and height are magnified by factor square root of 2.

Choose command **Last** to restore the previous zoom status.

Choose command **Window** to define the area to be viewed digitally. Either select the option **Edges** to enter the lower left and the upper right corner coordinates. Or select the option **Anchor/Size** to enter the anchor coordinates and the size of the area to be viewed. Select the anchor point in advance. Select **Same aspect ratio** to get the same scale un U- and V-direction.

Choose command **Write field** to display the actually defined write field, i.e. the current location of the beam.

Choose command **Zoom in** to magnify any portion of the viewed area. Two possibilities exist. After choosing the command, point to any location and press the left mouse button. This will zoom in to this location. Or point to any corner of the area to be magnified and click the left mouse button. While pressing the mouse button point to the opposite corner of that area and release the mouse button.

Choose command **Zoom out** to increase the viewed area by pointing to any location and pressing the left mouse button.

Choose command **Hand** to move the viewed area.



In addition it is possible to zoom in and out using the wheel of a corresponding mouse.

### Overlays

Choose this option to display the overlay elements like Positionlists, etc.

### Toolbox

Choose this command to display the GDSII Tools add-on window. It will stay on top of all activated windows until it is closed. It provides symbol buttons which allows the user to have permanent and quick access too the most commonly used commands.

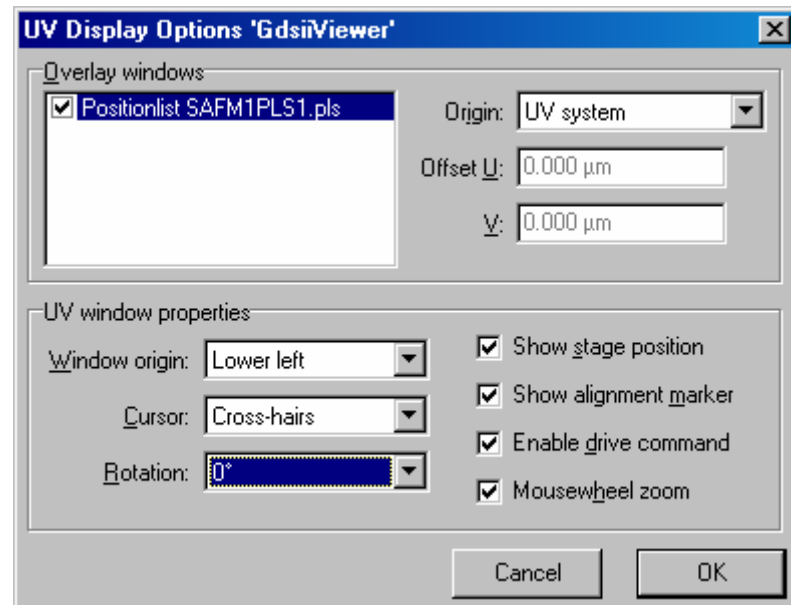


### 4.1.3 Options menu

#### UV display...

Choose this command to select items to be overlaid onto the actually displayed UV window. An additional dialog window opens with the following functionality

**Figure 7** Dialog UV display Options defining overlay windows and several properties.



The list box **Add-On windows** shows all available overlay windows. Select those to be overlaid, by selecting it.

Select the **Origin** or insertion point of the overlay window within on of the following coordinate system.

- **UV system**: Origin of the sample coordinate system.
- **Window**: origin of the window.
- **Window + Offset**: Origin of the window with selectable offset.
- **Chip Center**: Chip center in which stage is located.
- **Chip Lower Left**: Lower left corner of chip in which stage is located.
- **Chip Center + Offset**: Chip center in which stage is located with selectable offset.

If one of the coordinate systems "... + Offset" is selected, enter in fields **Offset U** and **Offset V** the offset values for U and V axes.

**Window origin** selects the origin of the window coordinate system. The window coordinates are displayed within the status bar of the program desktop.

Select the **Cursor** type. If one selects **Default**, the current Windows cursor is used.

Select check box **Show stage position** to show the cross-shaped marker graphically indicating the actual location of the stage.

Select the check box **Show alignment marker** to show the adjustment flags.

Select the check box **Enable drive command** to enable stage movement using the mouse command **Control** + right mouse button.

#### Same aspect ratio

Choose this option to display the viewed area true to scale, e.g. a square is displayed as a square and not as a rectangle. A check mark shows whether this option is in effect or not. To remove the check mark, choose this option once again.

## 4.2 Using the toolbox

For a fast access to the often used commands it is possible to open an add-on window by choosing **View > Toolbox**.

**Figure 8:** Add-on window **Tools** for all UV windows.



The general commands for viewing, measuring, zooming, and placing flags are described in the following.



Selects normal cursor.



Selects a frame selection mode.



Command **View > Zoom > Hand**.



Command **Edit > Measure**.



Command **View > Zoom > Zoom in**.



Command **View > Zoom > Zoom out**.



Command **View > Zoom > In 2x**.



Command **View > Zoom > Out 2x**.



Command **View > Zoom > All**.



Command **View > Zoom > Last**.



Command **Edit > Adjustment > Set mark**.

## 4.3 Mouse and keyboard commands

The following tables give a summary of all available mouse and keyboard commands within all UV windows.

**Table 5:** Mouse commands in all UV windows.

| Action       | Key(s) + Mouse Button | Functionality  |
|--------------|-----------------------|--|
| Single click | none + right          | Opens menu with often used commands.                           |
| Single click | <b>Ctrl</b> + right   | Drive to location.   |
| Single click | <b>Ctrl</b> + left    | Move selected object to new position.                          |
| Single click | <b>Shift</b> + left   | Select elements within an area defined by second mouse clicks. |

**Table 6:** Keyboard shortcuts available in all UV windows.

| Key                        | Functionality                                 |
|----------------------------|---|
| <b>+</b>                   | to zoom in by a factor of 2                   |
| <b>-</b>                   | to zoom out by a factor of 2                  |
| <b>=</b>                   | to view all                                   |
| <b>e</b>                   | to measure dimensions in editor or viewer     |
| <b>h</b>                   | to move viewed area                           |
| <b>t</b>                   | to open toolbox , toggle mode                 |
| <b>z</b>                   | to zoom in and out, toggle mode               |
| <b>Shift</b> + <b>←↑↓→</b> | to scroll the display into direction of arrow |
| <b>Alt</b> + <b>o</b>      | to show overlays, toggle mode                 |
| <b>Alt</b> + <b>r</b>      | to redraw the display                         |



## 5 GDSII data handling

---

|  |           |
|--|-----------|
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---

GDSII data handling is done by means of three components.

|                 |   |
|-----------------|---|
| <b>Database</b> | Layout data are organized in a hierarchical GDSII database. All standard GDSII design files from external CAD stations can be directly used.  |
| <b>Editor</b>   | The editor can be used to design or modify GDSII structures. It operates with absolute coordinates and offers a design resolution of one nanometer. Editor operations are only possible in one active editor. |
| <b>Viewer</b>   | Within the viewer it is possible to represent and inspect all hierarchy levels graphically.   |

### 5.1 GDSII database

To enable handling of even extended GDSII files on a PC based data system, the hierarchical structure of the data is kept as long as possible, e.g. until final exposure. Externally created GDSII files can be handled as well as data files from other design systems. In particular, this module offers the following filters.

- DXF import filter for import of patterns from most common CAD programs, e.g. AutoCAD, DesignCAD, etc,
- ELM import filter for import of data files from RAITH PROXY and PROXY-WRITER,
- ASC import and export filter for reading and saving of ASCII-type data files, and
- CIF import filter for import of data files stored in Caltech Intermediate Format by California Institute of Technology.

After importing, all data will be handled and stored in GDSII formats. Hierarchy information will be automatically scanned and stored in a separate file with extension \*.HIR.

The database within the RAITH software supports all standard GDSII features. However, internally it is extended by a range of new definitions such as text strings or single pixel lines, dose assignments, etc. This means, loading a structure with these definitions into an external GDSII editor, the additional features will not be available. In addition, the field "Data Type" which is available for each element and is defined within the GDSII format is used for assigning a doses factor to each element.

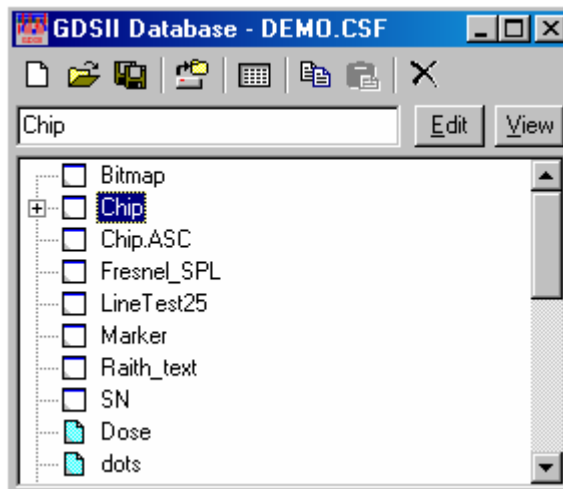
The RAITH software allows only one single database to be open at a time. If one wants to transfer patterns or structures between different databases, use the windows clipboard or use the commands ASCII import and export.

Normally not the whole GDSII structure is of interest for example to inspect it or to expose it. To expose only a fraction of the whole GDSII structure it is possible to define several areas of interest so called working areas. These working areas are defined for each structure individually and are stored together with the GDSII database.

### 5.1.1 GDSII database window

The GDSII Database window shows the name of the opened database file in the title bar and a list of all included structures in a tree view.

**Figure 9:** Database window for GDSII handling.



Within the tree window the following elements appear ...



Main structure which is not referenced within any other structure



Single structure which is referenced within another structure



Single structure referenced in main structure tree



Area structure referenced in main structure tree



Structure hold in computer memory



Structure opened in viewer or editor

In addition the following two buttons are available ...

**Edit**

Choose to open the selected structure for editing.

**View**

Choose to open the selected structure for viewing.

For further operations, e.g. viewing, editing, deleting, any structure may be selected by the mouse. The selected structure will be highlighted and given in the input field. This input field works also as a search box assisting selection of structures. Type in the first characters of the structure name and the matching structure will be selected automatically.

If the GDSII Database window is activated, additional menus and menu items are available within the menu bar, which will be explained in detail in the following sections. Clicking the right mouse button anywhere within the list area of the GDSII Database window, a shortcut menu will pop up.

### 5.1.2 File menu

**New...**

Choose this command to create an empty GDSII database file. Standard extensions are \*.CSF for Calma Stream Format and \*.GDS.

**Open...**

Choose this command to open an existing GDSII database file. A file selector box shows all existing GDSII database files of the actual path. Choose the GDSII database to be worked on. Within the window GDSII database the complete hierarchy and set of structures will be displayed. To display the GDSII in such a way, a build of the hierarchy file will be performed automatically, if the database is opened for the first time.

RAITH supports the GDS-II™ Calma Stream Format. However, there are occasions when we cannot import a GDS-II file. This is due to third party applications not conforming to the standard or storing the file in an internal binary format. Documentation for the third party program should be checked first, if one is having problems importing a GDSII file. The definition of the GDS-II format can be found at numerous WWW sites.

**Save as...**

Choose this command to store the currently opened database file under a freely selectable name.

**Build Hierarchy**

Choose this command to scan the hierarchical structure of the opened database and to create a corresponding hierarchy file (\*.HIR).

**Properties...** Choose to display a window with some statistical information and general information about the structure.

### 5.1.3 Edit menu

**View** Choose to open the viewer window which is used for inspection purposes, especially to resolve hierarchical structures. To modify a structure, use the editor window.

**Edit** Choose to open the internal GDSII editor. The editor window is used to design new structures and to modify existing structures. It includes the functionality of the viewer window.

**Delete...** Choose this command to delete the selected structure. Only structures that are not referenced within any other structure can be deleted.

**Duplicate...** Choose this command to make a copy of the selected structure within the same database. The copy will be named `Copy_of_<name>` automatically, where `<name>` is the name of the original structure.

**Rename** Choose this command to change the name of a structure.

**Properties...** Choose this command to display information of the currently selected structure. The information includes the size, the number of referenced structures, rectangles, boundaries, SREF = structure references, AREF = area references and paths. In addition, the used layers are indicated.

**New...** Choose this command to create a new structure. After assigning a structure name, the editor will be opened automatically.

**Copy** Choose this command to copy the selected structure to the clipboard. Afterwards it can be pasted within another database by choosing the command **Edit > Paste**.

**Paste** Choose this command to paste the copied structure within a database.

**Clear clipboard** Choose this command to clear the clipboard. and to free the memory after storing large structures in the clipboard.

**Load \*.ELM** See  section *Loading files in ASCII format* for details.

**Load \*.ASC** See  section *Loading files in ASCII format* for details.

**Save \*.ASC** See  section *Saving files in ASCII format* for details.

**Load \*.DXF** See  section *Loading files in DXF format* for details.

**Load \*.CIF** See  section *Loading files in CIF format* for details.

### Loading files in ASCII format

It is possible to import elements into a GDSII database using a file in ASCII format as a source. Thus these filters are ideal to import self-



created structures, e.g. by means of calculation programs. The commands are **Load \*.ELM** and **Load \*.ASC**. The main difference between the two commands **Load \*.ELM** and **Load \*.ASC** is the handling of negative signs. While the ELM import filter erases all negative signs, the ASC import filter leaves them as they are. The reason for this is the internal handling of negative signs by PROXY-WRITER software within the ELM format. A negative sign characterizes within this software hidden lines. So, if structure elements are located in any but the first quadrant of the GDSII design coordinate system, the ASC import filter has to be used instead of the ELM import filter.

Any standard editor or program, which is able to save data as ASCII text, may be used. Within current GDSII database there is a structure named <filename>.asc or <filename>.elm respectively after loading.

The file format for the two import filter is defined as follows. Each element starts with a character defining the type of GDSII element followed by several parameters separated by space. The following table lists available GDSII elements and the corresponding character.

**Table 7:** List of available elements.

| <b>GDSII element</b> | <b>Character</b> | <b>name in GDSII programs from other vendors</b> |
|----------------------|------------------|--|
| box or polygon       | 1                | BOUNDARY   |
| arc                  | A                | not available                                    |
| circle               | C                | not available                                    |
| ellipse              | E                | not available                                    |
| path                 | L                | PATH   |
| point                | P                | PATH, start point = end point                    |
| text                 | T                | not available                                    |

The syntax for the different elements and their parameters is as follows using the general rules that  $\mu\text{m}$  is the base unit for all length, width, etc., degree the base unit for all angles, and the dose is given in percentage.

**Table 8:** Syntax of GDSII elements in

| <b>GDSII element</b>  | <b>Syntax</b>                | <b>Comment</b>           |
|-----------------------|------------------------------|--------------------------|
| polygon               | 1 <dose> <layer>             |                          |
|                       | <u1> <v1>                    | coordinates 1st point    |
|                       | <u2> <v2>                    | coordinates 2nd point    |
|                       | ...                          |                          |
|                       | <u1> <v1>                    | must be repeated         |
|                       | #                            | end of element           |
| arc                   | A <dose> <layer> [<width>]   | not filled, width usage  |
|                       | <u-center> <v-center>        | center coordinates       |
|                       | <radius> [<radius2>]         | 2nd radius for ellipse   |
|                       | <vertices>                   |                          |
|                       | <rotation> <angle1> <angle2> | angles defining arc      |
|                       | #                            |                          |
| circle                | C <dose> <layer> [<width>]   | not filled, width usage  |
|                       | <u-center> <v-center>        | center coordinates       |
|                       | <radius>                     |                          |
|                       | <vertices>                   |                          |
|                       | <rotation>                   |                          |
|                       | #                            |                          |
| ellipse               | E <dose> <layer> [<width>]   | not filled, width usage  |
|                       | <u-center> <v-center>        | center coordinates       |
|                       | <radius> <radius2>           |                          |
|                       | <vertices>                   |                          |
|                       | <rotation>                   |                          |
|                       | #                            |                          |
| path                  | L <dose> <layer> <width>     |                          |
|                       | <u-center> <v-center>        | coordinates 1st point    |
|                       | <u-center> <v-center>        | coordinates 2nd point    |
|                       | ...                          |                          |
|                       | #                            |                          |
|                       | point                        | P <dose> <layer> <width> |
| <u-center> <v-center> |                              | coordinates point        |
| #                     |                              |                          |
| text                  | T <dose> <layer> <width>     |                          |
|                       | <u-center> <v-center>        | coordinates start point  |
|                       | <height> <angle>             |                          |
|                       | <u-align> <v-align>          | alignment values 0 to 2  |
|                       | <text>                       | text itself              |

The following example contains four elements. All elements are assigned with 100% dose in four different layers.

```

1 100.0 0
-5.000 5.000
-5.000 -5.000
5.000 -5.000
5.000 5.000
-5.000 5.000
#
L 100.0 1 1
0.000 -7.000
3.000 -10.000
7.000 -10.000
10.000 -7.000
#
C 100.0 2 0.200
10.000 10.000
5.000
100
90.000
#
T 100.0 3 0.000
3.000 3.000
1.000 0.000
2 2
Example
#

```

### **Saving files in ASCII format**

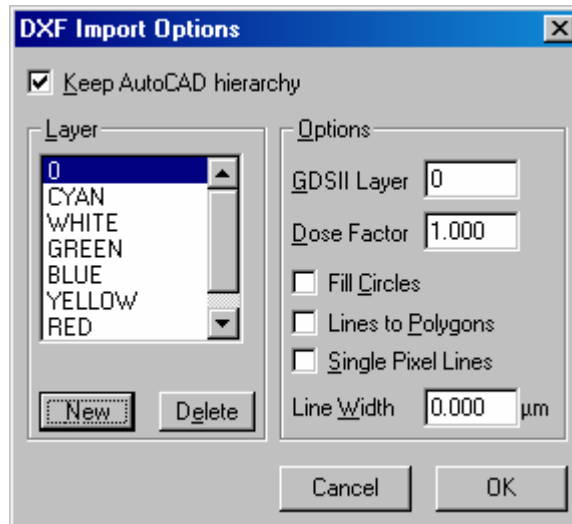
This export filter enables the exporting of a selected structure into an ASCII file format. Hierarchy will be made flat. Structure modification has to be done by means of the GDSII editor before exporting. Import and export of ASCII files offer the capability to copy flat designs within one database or to transfer them into other databases.

### **Loading files in DXF format**

Import filter for CAD files in DXF file format, e.g. made by means of AutoCAD, DesignCAD, etc. The imported data are stored within structure filename\_DXF in the current GDSII database.

When choosing this import filter a dialog is opened where several parameters can be set to control the import process. For example, if the CAD file contains several layer definitions, these may be assigned to different GDSII layers. In addition the settings under **Options**, e.g. dose factor etc., can vary for each DXF layer.

**Figure 10:** Dialog DXF import options used during import of AutoCAD files.



**Keep AutoCAD hierarchy** Hierarchy is kept, if this check box option is selected. Otherwise the imported structure is made flat.

**Layer** This list box contains the names of those CAD layers, import **Options** have been defined for. For each layer one can set different pattern conversion **Options** individually. To add a CAD layer name to the list box, choose the **New** button. To remove a CAD layer name from the list box, select it, and then choose the **Delete** button.

**GDSII Layer** Enter the GDSII destination layer for all elements of the selected CAD layer.

**Dose Factor** Enter the common dose for all elements of the selected CAD layer with 1.000 = 100% of clearing dose.

**Fill Circles** Circles are imported as filled polygons, if this check box option is selected. Otherwise they are imported as lines, i.e. borders only.

**Lines to Polygons** Polylines within the DXF format are converted into filled polygons, if this check box option is selected. Otherwise they are handled as lines, e.g. borders only.

**Single Pixel Lines** The width of all imported lines is set to 0, if this check box option is selected. Otherwise the width is set to the line width defined in the **Line width** text box.

**Line Width** Enter the line width, valid for all lines, which have no line width definition in the DXF format. If line width is included in the CAD definition, this parameter is not applied. If **Single Pixel Lines** are selected, this text box is disabled and all imported lines are set to 0.


If the size of the imported structure does not meet the original CAD-structure size, one has to change the value of the variable **Module status > Import DXF Files > Scale factor**. For example:

Original size = 200  $\mu\text{m}$   
 Imported size = 200 nm  
 Set scale factor = 1000



The DXF file definition is a comprehensive standard for 2D and 3D graphical drawings. Each new release adds additional features to the definition. The current release DXFTM 2004 has over 1000 tag ID's. Because the RAITH software supports only the relevant sub set of the DXF standard, one may occasionally come across features, which are not supported. Therefore it is highly recommend to keep too the standard elements listed in the following.

**Table 9:** Available DXF sections.

| <b>DXF section</b> |  |
|--------------------|--|
| HEADER             | Will be ignored.   |
| TABLES             | Will be ignored.   |
| BLOCKS             | See section  section <i>DXF Import features</i> . |
| ENTITIES           | Will be ignored.   |

**Table 10:** Available hierarchical DXF elements.

| <b>Hierarchical DXF element</b> | <b>is converted to GDSII element</b>  |
|---------------------------------|---|
| LINE                            | PATH with 2 points  |
| CIRCLE                          | BOUNDARY with 50 points<br>- Filled circle, if check box option <b>Fill circles</b> is selected<br>- Circle ring, if check box <b>Fill circles</b> is cleared |
| ARC                             | BOUNDARY with 50 points as circle arch  |
| SOLID                           | BOUNDARY with 4 points  |
| INSERT                          | SREF leaving hierarchy<br>AREF leaving hierarchy and multi insert   |

**Table 11:** Available flat DXF elements.

| Flat DXF element | is converted to GDSII element  |
|------------------|--|
| POLYLINE         | BOUNDARY<br>polygon, if check box option <b>Lines to Polygons</b> is selected, open paths will be closed automatically<br>PATH<br>if check box <b>Lines to Polygons</b> is cleared |
| VERTEX           | belongs to POLYLINE  |
| SEQUEND          | belongs to POLYLINE  |
| LAYER            | DATATYPE via dose class file LAYER.DOS   |

### DXF Import Features

During conversions, additional structures maybe added into the GDSII database.

\*model\_space, \*paper\_space, \*paper\_space0: These are internal definitions in a DXF BLOCKS section. They can be safely ignored and deleted. They will however cause a warning message of an illegal character for the structure name. The DXF name is \*model\_space, however the GDSII standard allows only:

“A” through “Z”, “a” through “z”, and 0 through 9 and the special characters Underscore “\_”, Question mark “?”, Dollar sign “\$”

Therefore, the “\*” is an illegal character. The Raith software simply replaces the “\*” with a “\_” and issues a warning renaming the structures as:

\_model\_space, \_paper\_space, \_paper\_space0.

The DXF reference manual can be obtained from Autodesk Inc.

### Loading files in CIF format

Import filter for data files stored in Caltech Intermediate Format by California Institute of Technology. The hierarchy of CIF files is equal to the GDSII hierarchy and will be kept during import. Supported data types for CIF import are listed in the following.

**Table 12:** Available elements in Caltech Intermediate Format.

| CIF element | converted to GDSII element |
|-------------|----------------------------|
| B           | BOX                        |
| P           | BOUNDARY                   |
| 9           | STRUCTURENAME              |
| C           | SREF                       |
| R0          | STRANS with angle 90°      |
| L           | LAYER                      |
| (* ... *)   | comment                    |

Dose values are related via dose classes (file LAYER.DOS) - the same procedure as for import of DXF files. A (symbolic) layer name is assigned via the file CIF.INI (see example below).

```
[LAYER]
TLEN=1
META=2
BND=31
```

## 5.1.4 Tools menu

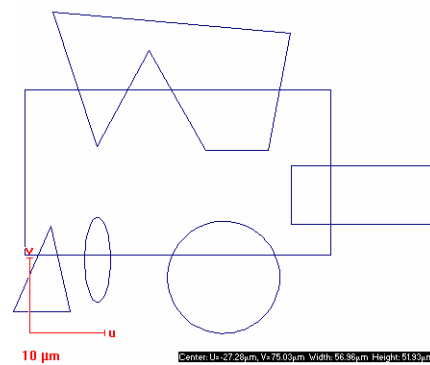
### Overlap removal

Choose this command to cut all overlapping elements within the selected structure. The overlap removal command checks, if there are overlapping elements. If so, then one of the two elements will be cut to size so that it just contacts the other one. This command is not removing overlaps within different structure references.

Field of Application: To avoid an over exposure of overlapping elements.

### Removing overlaps

**Figure 11:** Before overlap removal.



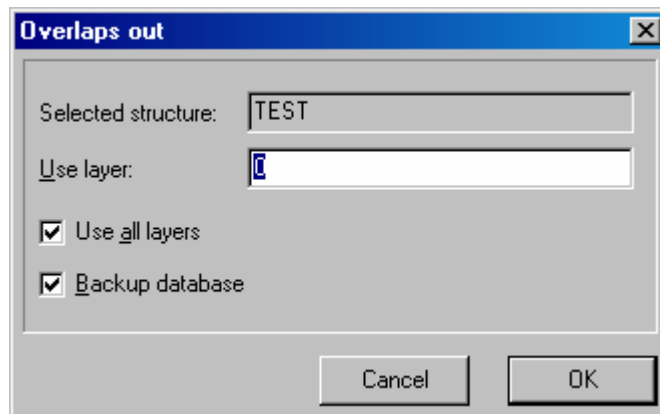


The command **Overlaps removal** overwrites the original structure. Therefore, we recommend working on a copy.

**STEP 1 ►**

Select a structure from GDSII database and choose then **Tools > Overlap removal**. A dialog provides then additional parameters to control this tool. Within the dialog the selected structure is indicated at the top.

**Figure 12:** Dialog Overlap Removal.

**STEP 2 ►**

Select layers separated by comma to which the function should be applied by editing **Use layer**. The Overlap removal tool will remove overlapping areas of all elements of the same layer. Therefore it is not possible to remove overlaps between two different layers.

**STEP 3 ►**

By selecting the check box **Use all layers**, the overlap removal will be applied all layers, not depending on a given layer.

**STEP 4 ►**

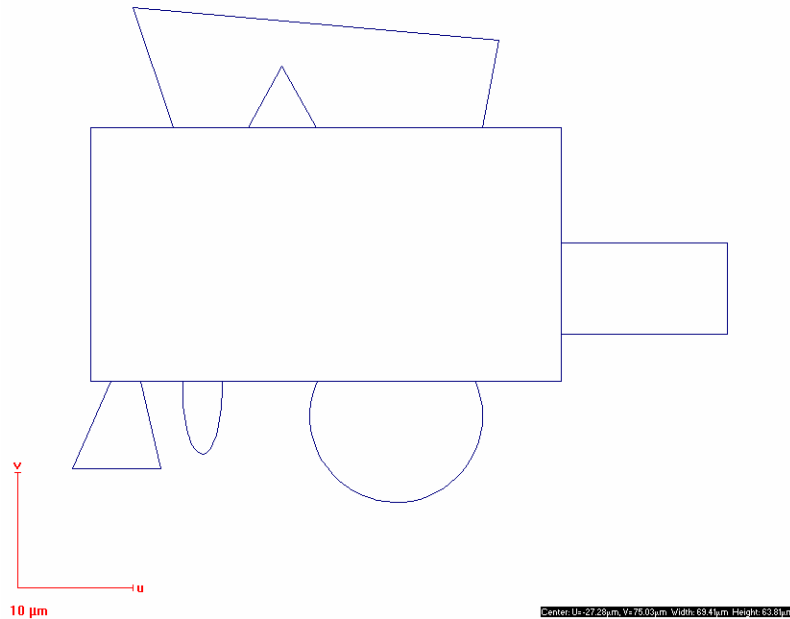
By selecting the **Backup GDSII file** check box, the overlap removal creates a backup.

**STEP 5 ►**

Choose **OK** to execute the tool.



**Figure 13:** After overlaps removal.



### Layer removal



Choose this command to delete complete layers.

**Layer removal** overwrites the original structure. Therefore, we recommend working on a copy.

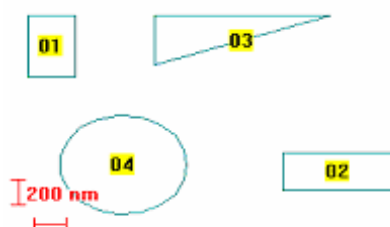
### Sort elements

Choose this command to change the order of all elements within the selected structure. This command is not sorting within different structure references.

Field of Application: To optimize a design for the exposure step.

### Sorting elements

**Figure 14:** Before sorting elements by location.

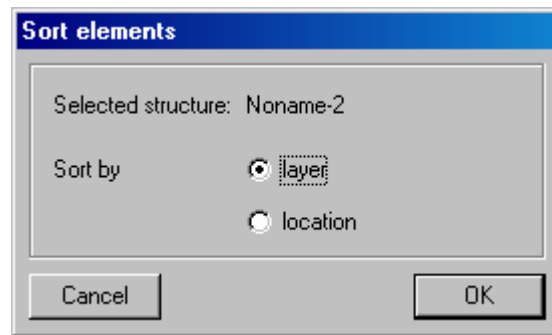


The command **Sort elements** overwrites the original structure. Therefore, we recommend working on a copy.

**STEP 1 ►**

Select a structure from GDSII database and choose then **Tools > Sort elements**. A dialog provides then additional parameters to control this tool. Within the dialog the selected structure is indicated at the top.

**Figure 15:** Dialog Sort elements.

**STEP 2 ►**

Select **Sort by layer** to sort elements layer by layer successively. This makes it easier to sort elements within a certain layer manually by using the editor command "Modify / Order". The result can be, for example,

|   |
|---|
| Layer 0: elements #1 - #4<br>Layer 1: elements #5 - #15<br>Layer 2: elements #16 - #158 |
|---|

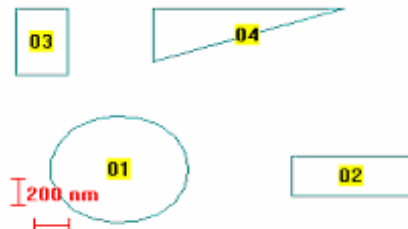
**STEP 3 ►**

Select **Sort by location** to sort all elements independently of the layer so that the jump distance from element to element during exposure is minimized automatically.

**STEP 4 ►**

Choose **OK** to apply tool.

**Figure 16:** After sorting elements by locations.

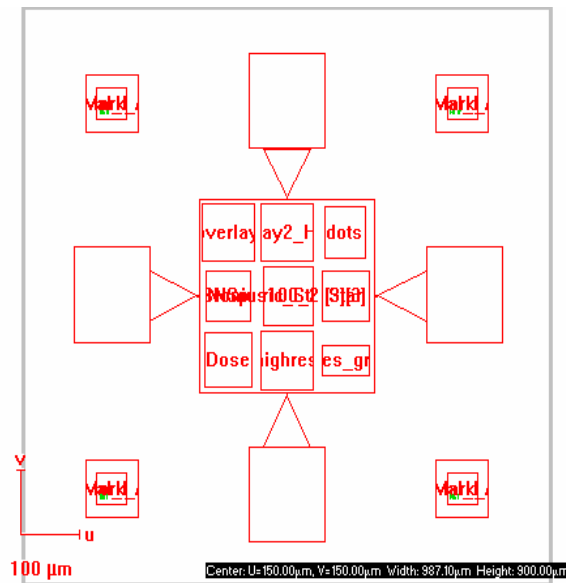
**Unify structures**

Choose this command to resolve all references within the selected structure i.e. to get one large flat structure. The result is stored in a new GDSII database.

Field of Application: Not all GDSII programs from another vendors support hierarchical files. Use this command to import GDSII files edited on RAITH program into those programs.

## Removing GDSII hierarchy

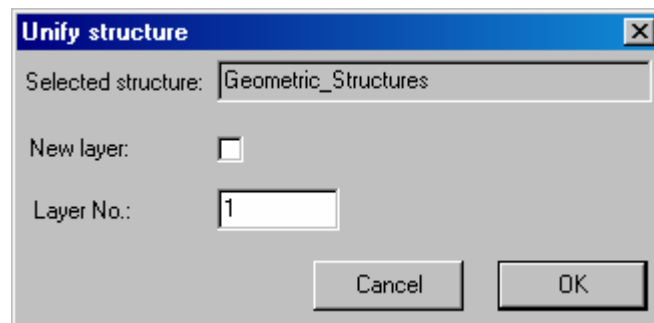
**Figure 17:** Before unifying shown with hierarchy level 0.



### STEP 1 ►

Select a hierarchical structure from GDSII database and choose then Tools > Unify structures. A dialog provides then additional parameters to control this tool. Within the dialog the selected structure is indicated at the top.

**Figure 18:** Dialog Unify structure.



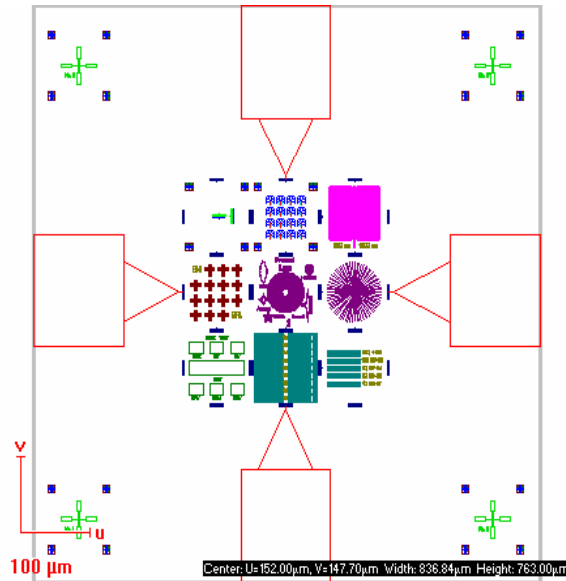
### STEP 2 ►

Select **New layer** to store the result in another layer and specify the layer in **Layer No.**

### STEP 3 ►

Choose **OK** to apply tool.

**Figure 19:** After unifying shown with hierarchy level 0.



### Convert userdefs

Choose this command to convert RAITH specific user defined elements to common CAD elements. Most of the CAD systems use different definitions to store special elements like "Text", "Curves", "Circles", etc. In addition, the dose information, e.g. as dose factor to scale the exposure time, may be stored in different ways. To become compatible with common CAD systems, it is necessary to create a general GDSII format. The **Convert userdefs** tool converts all RAITH specific elements, e.g. text, circles, into polygons or open paths. In addition, the dose information can be removed. All changes are done in the same GDSII file.

### Converting to standard GDSII

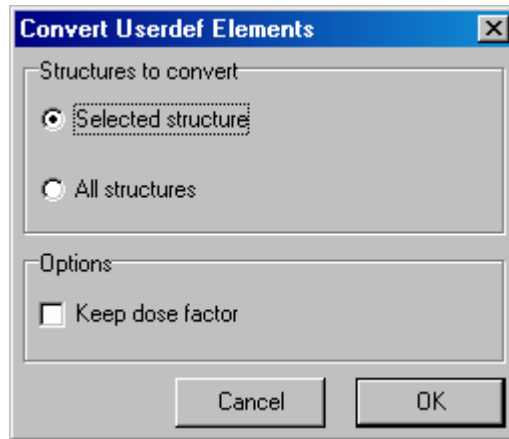


The command **Convert userdefs** overwrites the original structure. Therefore, we recommend working on a copy.

#### STEP 1 ►

Select a structure from GDSII database and choose then **Tools > Convert userdefs**. A dialog provides then additional parameters to control this tool. Choose **All structures** to convert the complete GDSII database.

**Figure 20:** Dialog Convert Userdef Elements.



**STEP 2 ►**

Select keep dose factor to preserve the dose factor. Otherwise the dose factor will be set to 0.001 so that the number 1 is stored in the GDSII file, which will be ignored by other CAD systems.

**STEP 3 ►**

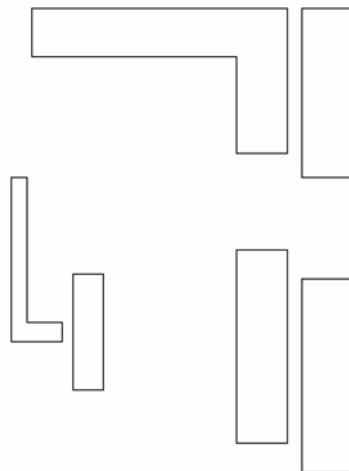
Choose OK to apply tool.

**Merge elements**

Choose this command to remove gaps between elements. This command is not merging elements within different structure references.

**Merging GDSII elements**

**Figure 21:** Before using merge functionality.

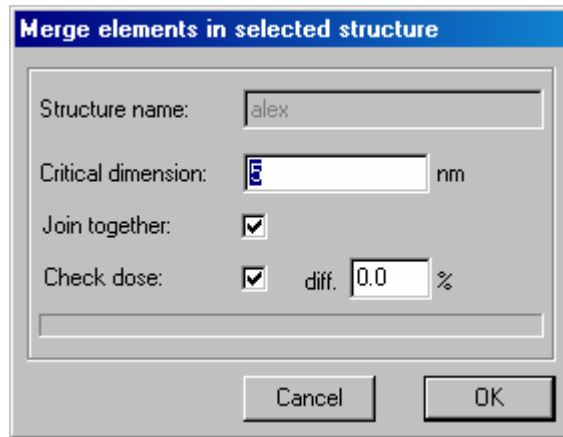


**Merge elements** overwrites the original structure. Therefore, we recommend working on a copy. This tool is applied to elements of the same layer. Gaps between elements of different layers would not be removed.

**STEP 1 ►**

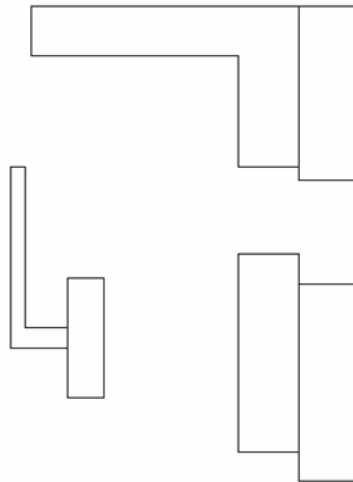
Select a structure from GDSII database and choose **Tools > Merge elements**. A dialog provides then additional parameters to control this tool. Within the dialog the selected structure is indicated at the top.

**Figure 22:** Dialog Merge elements.



- STEP 2 ►** Type in a Critical dimension to merge elements, if the distance between them is the same or less than the entered value.
- STEP 3 ►** Select Join together to merge elements, i.e. the elements will not only be combined visually but they will also become one single GDSII element.
- STEP 4 ►** Select the Check dose to merge only elements which have a dose difference of less than the entered value.
- STEP 5 ►** Choose **OK** to apply tool.

**Figure 23:** After using merge functionality without joining them together.



**Join sorted elements** Choose this command to join in the minimum two GDSII elements to one larger GDSII element. For this the elements have to be sorted by location.

### Joining GDSII elements together

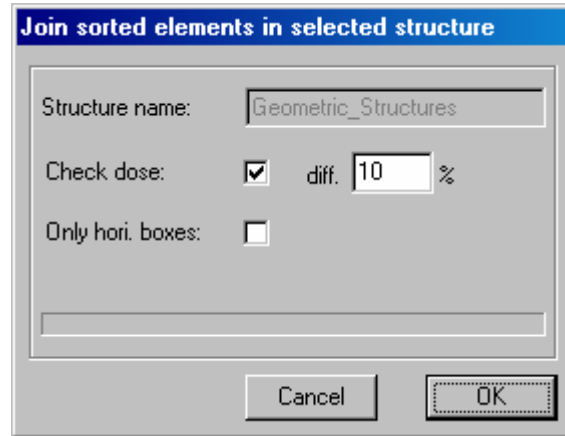


**Join sorted elements** overwrites the original structure. Therefore, we recommend working on a copy. This tool is applied to elements of the same layer. Gaps between elements of different layers would not be removed.

**STEP 1 ►**

Selected a structure from the GDSII database after sorting the elements (see [section \*Sorting Elements\*](#)). Then choose **Tools > Join sorted elements**. A dialog provides then additional parameters to control this tool. Within the dialog the selected structure is indicated at the top.

**Figure 24** Dialog Merge elements.

**STEP 2 ►**

Select the **Check dose** to join only elements which have a dose difference of less than the entered value.

**STEP 3 ►**

Select **Only hori. boxes** to join boxes along u-direction only.

**STEP 4 ►**

Choose **OK** to apply tool.

### 5.1.5 Right mouse menu commands

The commands of the right mouse menu are mainly listed under menu **Edit**. There is only one additional command.

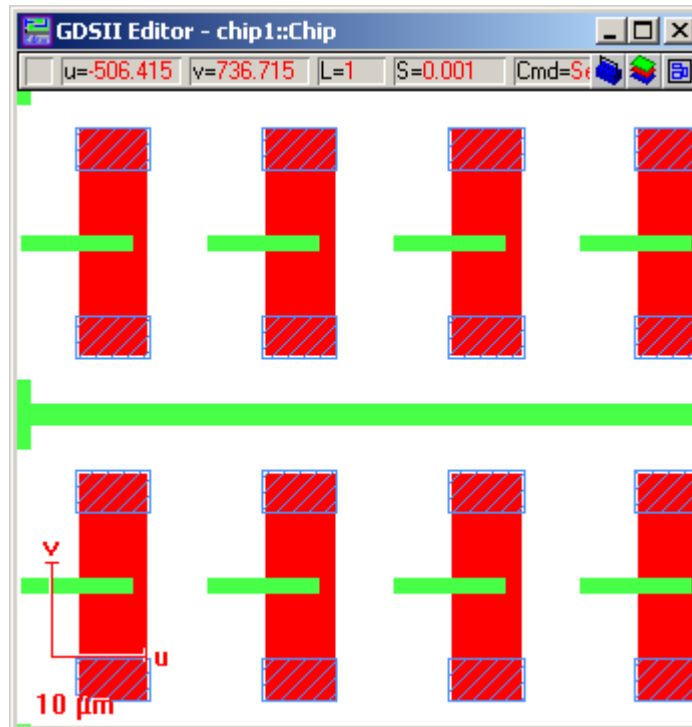
#### Sort structures

An additional drop-down menu appears. Choose here to define the order of the display in the tree view. Three options are available **by type and name, by name and by file order**.




## 5.2 GDSII editor and viewer

GDSII editor and viewer cannot be opened at the same time, i.e. when opening the editor the viewer is closed automatically and vice versa. But it is possible to open more than one viewer window at the same time.

**Figure 25:** Editor window showing elements building transistors.



Both editor and viewer windows are headed by an information and icon bar.

- The actual U and V positions of the design cursor within the design field. Values are given in micrometer with a resolution of 1 nm.
- The number of the layer currently activated for editing (editor only). To change the layer for editing, click the layer indicator to open corresponding dialog.
- The currently used design grid. Within the editor the design grid defines a grid, which is used to place elements. To change its step size, click the step size indicator to open corresponding dialog. Minimum step size is 0.001  $\mu\text{m}$ , i.e. 1 nm, maximum step size is 100  $\mu\text{m}$ .
- The currently active command.
- Additional information, e.g. rotation angle, are displayed when using specific commands.
- To open the toolbox click toolbox icon .
- To choose the displayed layers click the layer icon .
- To edit the working areas for this GDSII click the working area icon .



### 5.2.1 File menu

Please note, in the following an (E) or a (V) indicates that this command is available only in the editor or in the viewer respectively.

- Save (E)** Choose this command to save the current structure without leaving the editor.
- Save and Close (E)** Choose this command to leave the editor with automatically saving the current structure. If changes have been made in referenced structures the hierarchy information of the database will be automatically scanned and updated.
- Print...** Choose this command to print out the actually viewed area of the viewer or the editor.
- Save viewer Image as... (V)** Choose this command to store the actually viewed area in Tagged Image File Format, i.e. as a TIFF file, or in Bitmap format, i.e. as a BMP file.

### 5.2.2 Edit menu

Please note, that the following commands are available within the editor window only.

- Undo, Redo** Choose these commands to undo or redo the last action. Internally a list of all changes is managed meaning that the number of actions stored is limited only by memory.
- Cut** Choose this command to cut out the selected elements and copy them into the Microsoft Windows clipboard for further usage, especially to paste them into another structure or database.
- Copy** Choose this command to copy the selected elements into the Microsoft Windows clipboard for further usage, especially to paste them into another structure or database.
- Paste** Choose this command to paste the elements actually located in the Microsoft Windows clipboard into the actually opened structure.
- Delete** Choose this command to delete the selected elements without further query.
- Select** The selection of at least one element within a structure is necessary for most of the "Edit" commands. All currently selected elements are characterized by having yellow points at the corners. The number of selected elements will be displayed in the status bar on bottom of the Program Desktop. After choosing the "Select" command, a cascading menu appears offering additional functionality.
- Choose command **All** to select all elements of the structure irrespective of their layer assignments.

Choose command **Dose factor...** to select elements within the specified range of dose factors.

Choose command **In** to select all elements within the active layer located inside a box to be dragged. After choosing the command, point to any corner of the area covering all elements to be selected and click the left mouse button. Then point to the opposite corner of that area and click the left mouse button again. Pressing the **Shift** key while doing so, the first point defines the center and not the first corner of the rectangle. Pressing the **Control** key while doing so, the field of selection will become quadratic.



As a shortcut, do not choose this command, but point directly to any corner of the area covering all elements to be selected, press and hold the Shift key and click the left mouse button. Then proceed as described.

Choose command **Layer** to select all elements within the active layer.

Choose command **New** to select all elements within the active layer, which have been added after saving respectively after opening the editor window.

Choose command **Next** to select the next element within the active layer of the structure. The sequence for selecting next elements is the sequence of these elements in the design. Operation is cyclic. Starting element is the last element that has been selected before choosing this command.

Choose command **Previous** to select the previous element within the active layer of the structure. The sequence for selecting previous elements is the inverse sequence of these elements in the design. Operation is cyclic. Starting element is the last element that has been selected before choosing this command.

A **Structure reference** can be selected by one of the following three selection modes. **All** structures are selected. **At** selects all structures, which cover the point defined by a subsequent mouse click. **In** selects all structures, which are located inside a box to be dragged.

**Structure reference by name** Choose this command to select structure references specified by the name of a referenced structure. After choosing one of the cascading commands **All**, **At** or **In**, a structure can be specified by means of a dialog box, showing all existing structures. If command **All** has been chosen, all structure references containing the specified structure are selected. If command **At** has been chosen, a structure reference containing the specified structure is selected by a subsequent mouse click. If command **In** has been chosen, all structure references containing the specified structure are selected by a box to be dragged.

|                   |  |
|-------------------|--|
| <b>Unselect</b>   | Consists of the same set of commands as the <b>Select</b> command. The target is remove element's selection for desired elements or substructures. |
| <b>Adjustment</b> | Command common to all UV windows, described in section <a href="#">UV Windows</a> .  |
| <b>Measure</b>    | Command common to all UV windows, described in section <a href="#">UV Windows</a> .  |

### 5.2.3 View menu

|                    |  |
|--------------------|--|
| <b>Hierarchy</b>   | <p>Choose this command to resolve hierarchy levels of the opened GDSII structure. After choosing this command, a drop-down menu appears offering additional commands. A check mark indicates the resolved hierarchy level.</p> <p>Choose command <b>Increase</b> to increase the hierarchy by one level.</p> <p>Choose command <b>Decrease</b> to decrease the hierarchy by one level.</p> <p>Choose one of the commands <b>0 – 8</b> to resolve the hierarchy to the specified level, where <b>0</b> is the highest level.</p> <p>Choose command <b>Auto</b> to resolve the hierarchy as a function of the current viewed area.</p> <p>Choose command <b>Max</b> to always resolve to the highest hierarchy level.</p> <p>Sometimes, maximum hierarchy level may contain so many elements that it would take minutes to build up the entire structure. In this case one may cancel this operation by cancel the redraw which can easily be achieved by pressing the <b>Esc</b> key.</p> |
| <b>Redraw</b>      | Command common to all UV windows, described in section <a href="#">UV Windows</a> .  |
| <b>Zoom</b>        | <p>A cascading menu opens with additional commands, described in section <a href="#">UV Windows</a>.</p> <p>Choose command <b>Active Working area</b> to display the currently defined working area.</p>   |
| <b>Design grid</b> | Choose this option to display the design grid as small light gray dots, which are related to the actually chosen cursor step size. Creation of new elements or modification of elements is possible only within this design grid, irrespectively whether it is displayed or not. Depending on the relation between displayed area and chosen step size, it may happen that not all of the grid dots will be displayed.   |

|                            |  |
|----------------------------|--|
| <b>Exposure grid</b>       | Choose this option to display the exposure grid, i.e. the division of the active working area into stitch fields. Note this option is only available when having corresponding license.            |
| <b>Working area</b>        | Choose this option to display the active working area, i.e. the rectangle used for exposure.   |
| <b>Layer selection</b>     | Choose this command to display the layer selection add-on window. It will stay on top of all activated windows until it is closed. It allows the selection of layers to be displayed.              |
| <b>Overlays</b>            | Command common to all UV windows, described in section <a href="#">🌐 UV Windows</a> .  |
| <b>Toolbox</b>             | Command common to all UV windows, described in section <a href="#">🌐 UV Windows</a> .  |
| <b>Working area editor</b> | Choose this command to display the GDSII Working area add-on window. It will stay on top of all activated windows until it is closed and manages a series of defined working areas for the design. |

### 5.2.4 Options menu

Please note, in the following an (E) or a (V) indicates that this command is available only in the editor or in the viewer respectively.

|                             |  |
|-----------------------------|--|
| <b>Background</b>           | Choose this command to set the background gray level. A check mark indicates the currently selected gray level.  |
| <b>Backside view (V)</b>    | Choose this option to mirror the layout horizontally and to display the layers in reverse order. This becomes necessary, if the sample is viewed from the bottom side.   |
| <b>Fill</b>                 | <p>Choose this option to indicate filled structure elements, i.e. boxes, polygons, etc. A check mark shows whether this option is in effect or not. To remove the check mark, choose this option once again. If this option is not in effect, elements are indicated by frame, only. The fill color can be defined for each layer individually.</p> <p>If an element is covered completely by another element, it is no longer visible after choosing the option. To overcome this effect, set the variable <b>Module status &gt; GDSII Database &gt; Solid Fill</b> to "OFF". After closing and opening the editor or viewer window once again, choose <b>Fill</b>. Hatching will now indicate the filled structure elements.</p> |
| <b>Physical layer order</b> | Choose this command to display the different layers in their physical order meaning layers which are deeper are displayed first. The layer order is defined in the <b>Layer editor</b> .   |
| <b>Same aspect ratio</b>    | Command is common to all UV windows, described in section <a href="#">🌐 UV Windows</a> .   |

|                        |   |
|------------------------|---|
| <b>Layer editor...</b> | Choose this command to open an additional dialog to assign name, fill color, border color and pattern to each layer individually.   |
| <b>Show dose</b>       | Choose this option to fill the elements with a color indicating the dose factor. The layer assignment is indicated by the corresponding frame colors.   |
| <b>Dose colors</b>     | Choose this command to define the color assignment of the dose scale. This command is only available, if the dose distribution is displayed. The relation between colors and dose scale can be defined by editing the related text boxes. Use the pipette icon to insert dose values from the design into the dose range. |
| <b>Show video</b>      | Choose this option to show the currently opened images simultaneously with the GDSII structure. In order to show the entire background image, the viewer / editor area coordinates (command: "View / Window") have to be fit to the image coordinates.  |
| <b>UV display...</b>   | Command is common to all UV windows, described in section <a href="#">UV Windows</a> .  |

### 5.2.5 Annotate menu

The complete menu is available only in the viewer but not in the editor. The items within this menu serve to add and handle comments and markers. They are stored within a separate file and do not influence the related GDSII database file.

|                         |  |
|-------------------------|--|
| <b>Show annotations</b> | Choose this option to activate the annotation functionality. After choosing the annotation location is indicated by a red triangle.  |
| <b>Text</b>             | Choose this command to create an annotation text. After choosing the command, move the mouse to the point of interest and click the left mouse button or press the space bar opening a dialog box with additional options. Use text boxes <b>Position U/V</b> to define the coordinates of the annotation location. Use <b>Creation angle</b> to enter the angle for rotating the annotation location around the coordinate origin ( $U/V = 0/0$ ). To modify a text annotation, click on this red triangle, and a dialog will be opened. To delete an annotation, select it by clicking on the red triangle and press <b>Del</b> key.                           |
| <b>Rectangle</b>        | Choose this command to create an annotation box. After choosing the command, point to any corner of the area to be annotated and click the left mouse button or press the space bar. Then point to the opposite corner of that area, a rectangular frame will be drawn, and click the left mouse button again or press the space bar. Pressing the <b>Shift</b> key while dragging, the first point defines the center and not the first corner of the rectangle. Pressing the <b>Control</b> key the rectangle will become quadratic. To modify an annotation rectangle double click it and a dialog box appears offering additional options. The functionality |

of **Position U/V** and **Creation angle** are the same as for **Text** command.

- Ellipse** Choose this command to create an annotation ellipse. Handling is similar to **Annotation > Box**.
- Move** Choose this command to move the selected annotations. The movement vector has to be defined by two subsequent mouse clicks: first mouse click defines the start point of movement vector; second click defines the end point of movement vector. For digital control, the resulting shift values in both axes are displayed within the information line. To perform a combined move and copy operation, press and hold the **Control** key while defining the movement vector.
- Delete** Choose this command to delete a selected annotation.

## 5.2.6 Modify menu

The complete menu is available only, if an editor window is open, but not in the viewer window.

- Attributes** Select a structure element and choose this command to open a dialog box for modifying the selected element digitally. The dialog box contains all parameters that are specific for the selected element, i.e. the type of dialog box is automatically related to the currently selected element. If more than one element is selected, modification is possible only for the element with the lowest serial number. Please note this command is also available by double-clicking with the left mouse button on an element.
- Cut** Choose this command to cut the selected structure element(s). This command is not available for dots or structure references. Two different possibilities exist.
- Choose command **Horizontal** to cut the selected elements along a horizontal line. After choosing the command, select the start point of the cutter line. Then move the mouse pointer, while a horizontal line will be drawn, and select the end point of the cutter line. All selected elements will be cut along that line, if they are touched.
- Choose command **Vertical** to cut the selected elements along a vertical line. Handling is analog to horizontal cutting. Text elements will be converted to paths and circles will be converted to polygons after cutting.
- Dose factor** Choose this command to assign another dose to the selected elements. Two different possibilities exist.
- Within related dialog box **Set**, enter the dose factor to be assigned to all selected elements.

- Within related dialog box **Scale**, enter the scale factor to be multiplied to the dose factor of all selected elements.
- Duplicate** Choose this command to duplicate the selected elements. Two different possibilities exist.
- Choose command **Single** to make a copy of the selected elements. This command copies the selected elements and activates the **Move** command.
- Choose command **Matrix** to copy the selected elements in multiple columns and rows with dose scaling. Within the related dialog box, enter the **Matrix size** in U and V, i.e. the number of columns and rows. Enter the **Base vectors** in U and V with the possibility to keep them orthogonal or to define them in a non-orthogonal way, i.e. free. In addition the dose can be varied by entering **Dose scaling** values for each direction.
- Layer** Choose this command to assign another layer to the selected elements. Within the related dialog box, select the layer to be assigned. All layers in use within the opened structure are listed.
- Line width** Choose this command to assign another line width to the selected paths. Within the related dialog box, enter the line width to be assigned in micrometer.
- Mirror** Choose this command to perform a mirror operation for all selected structure elements. To perform a combined mirror and copy operation, press and hold the **Control** key while defining the mirror axis. Three different possibilities exist. Three different possibilities exist.
- Choose command **Horizontal** to perform a horizontal mirror operation of the selected structure elements with respect to a vertical mirror axis, i.e. V direction, which is automatically placed in the centre of the enclosure of the selected structure elements.
- Choose command **Vertical** to perform a vertical mirror operation of the selected structure elements with respect to a horizontal mirror axis, i.e. U direction which is automatically placed in the centre of the enclosure of the selected structure elements.
- Choose command **Line** to perform a mirror operation of the selected structure elements with respect to a mirror axis, which has to be defined by two subsequent mouse clicks.
- Move** Choose this command to move the selected elements. The movement vector has to be defined by two subsequent mouse clicks: first mouse click defines the start point of movement vector; second click defines the end point of movement vector. For digital control, the resulting shift values in both axes are displayed within the information line. To perform a combined move and copy operation, press and hold the **Control** key while defining the movement vector.

**Rotate**

Choose this command to rotate the selected structure elements. This command is not available for structure references and text elements. Two different possibilities exist.

Choose command **Centre** to rotate the selected structure elements digitally. The rotation centre is defined by the centre point of the enclosure of the selected elements. The related dialog provides a range of most used rotation angles on buttons and in addition, a text box for digital input of the rotation angle. To perform a combined rotation and copy operation, select the corresponding check box.

Choose command **Free** to rotate the selected elements by mouse control. The rotation procedure has to be defined by two subsequent mouse clicks. The first mouse click defines the rotation centre. The second click defines the rotation angle. In detail, select the rotation centre by the first mouse click. Then move the mouse circularly around until the enclosure of the selected elements has reached the requested target position. Fix this target position with the second mouse click. For digital control, the resulting shift values in both axes and the rotation angle are displayed within the information line. To perform a combined rotation and copy operation, press and hold the **Control** key while defining the target position.

**Scale**

Choose this command to scale the selected structure elements. This command is not available for structure references and text elements. Two different possibilities exist.

Choose command **Factors** to scale the selected structure elements digitally. The scaling centre is defined by the centre point of the enclosure of the selected elements. The related dialog box provides a range of most used scaling factors and in addition, text boxes for digital input of scaling factors for both directions, separately. Negative scaling factors include an additional mirror operation. To perform a combined scale and copy operation, select the corresponding check box.

Choose command **Free** to scale the selected element(s) by mouse control. The scaling procedure has to be defined by two subsequent mouse clicks: first mouse click defines the new position of the lower left corner, second click defines the new position of the upper right corner of the enclosure of the selected elements. In detail, the enclosure of the selected elements, i.e. old area, is transferred into a new area, which is defined in size and orientation by two subsequent mouse clicks. Consequently, this operation may involve moving, zooming and mirroring actions, simultaneously. Select the target position of the lower left corner of the old area by the first mouse click. Then move the mouse to the target position of the upper right corner of the old area. Fix this target position with the second mouse click. For digital control, the width and height, i.e.  $du$  and  $dv$ , of the new area are displayed within the information line. To perform a combined scale and copy operation, press and hold the **Control** key while defining the target position.



|                        |  |
|------------------------|--|
| <b>Grow...</b>         | Choose this command to grow all selected elements by the amount, entered within the related dialog box.  |
| <b>Order</b>           | Choose this command to enable modification of the element sequence. The sequence may be essential for exposure routines. After choosing this command, the serial numbers of all elements are displayed. To change this order, select the first element of the new order, then the second one etc. Press <b>ESC</b> to interrupt this command.  |
| <b>Overlaps out</b>    | Choose this command to remove overlaps of at least two selected elements to avoid an over-exposure.  |
| <b>Remove Layer...</b> | Choose this command to delete the elements of all specified layers within the selected structure. The related dialog box indicates the used layers, and enables the user to enter the layers to be removed. Selecting the check box <b>With references</b> , the specified layers within the main structure and within all referenced substructures will be removed.   |
| <b>Shrink...</b>       | Choose this command to shrink all selected elements by the amount, entered within the related dialog box.  |
| <b>Snap to grid...</b> | Choose this command to enlarge too small elements respectively too small gaps between elements. Before choosing this command, select the elements to be modified. After choosing this command, modify the base point of the grid. The related dialog box is preset by the selected base point of the selected elements. Enter the used grid size. The grid size is the smallest allowed distance between two structures respectively the smallest dimension of an element. |

### 5.2.7 Add menu

The complete menu is available only in the editor window but not in the viewer window. All added elements can be modified afterwards by means of the command **Modify > Attributes**.

|               |   |
|---------------|---|
| <b>Preset</b> | Choose this command to assign layer, dose and line width as a standard value for subsequent "Add" operations. After choosing this command, a cascading menu appears offering to set the <b>Dose factor</b> , <b>layer</b> , <b>line width</b> . |
|---------------|---|

The standard **Dose factor ...** is valid for all subsequently added basic elements. Within the related dialog box, enter the dose to be pre-set as a factor (1 = 100% of clearing dose).

The standard **Layer** is valid for all subsequently added basic elements. Within the related dialog box, select the layer to be pre-set. All layers in use within the opened structure are listed. To select a new layer, create this new layer by choosing the command **View > Layer selection > Edit...** The pre-set layer is indicated within the information line of the window.


The standard **Line width ...** is valid only for subsequently added paths. Within the related dialog box, enter the line width to be pre-set in micrometer. Zero values lead to single pixel lines. These are no standard GDSII elements but useful for special ultra-high resolution applications.

## Circle

Choose this command to add a circle or an ellipse, filled or border only, to the active layer.

After choosing the command, move the cursor to any corner of the rectangle surrounding the ellipse and click the left mouse button. Then move the cursor to the opposite corner of the rectangle and click the left mouse button again. Simultaneously, an ellipse will be drawn. Each mouse click can be replaced by pressing **Enter** or by pressing the **Space** bar. By pressing **Shift** after the first mouse click the first point is interpreted as the center of the ellipse. By pressing **Control** the ellipse will be made a perfect circle. Both keys can be pressed simultaneously.

An ellipse can also be added digitally. After choosing the command, press any digit key (0 through 9) to call up the dialog box for digital input. The input fields are pre-set with the coordinates of the current cursor position. Enter the coordinates of the first corner of the rectangle surrounding the ellipse. Choose **Next** to type in the coordinates of second corner. Choose **OK** to complete the ellipse.

This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.


To access all properties of a circle double click it using the left mouse button. A window opens providing the following options. Use **Centre** to enter the U and V centre coordinates of the circle or the ellipse in micrometer. Use **Ellipse** to change the element shape. Use **Radius** to enter the radius of the circle respectively the U and V radii of the ellipse in micrometer. Use **Arc** to change the element style. If the check box is selected, two text boxes appear to enter an **Angle Start** value and an **Angle End** value for the circular or elliptical arc to be created in the range of  $-360^\circ$  through  $+360^\circ$ . If the check box is cleared, a full size circle or ellipse is added. Use **Fill** to change the element kind. If the check box option is selected, a circle or ellipse will be filled and an arc will be closed to become a filled segment not a sector. If the check box is cleared, a text box appears to enter a **Width** value for the circular or elliptical ring respectively for the arc in micrometer. Use **Vertices** to enter the number of vertices for the element to be designed. This number must be in the range of 8 through 1024. The start point is equal to the end point and this is counted twice. Enter **Rotation** to rotate the circle or ellipse counterclockwise. Use **Dose** factor to set factor which is multiplied to the dwell time. Select **Layer** to define the layer.

## Dot

Choose this command to add a dot to the active layer. Dots are single points with zero extension.

After choosing the command, click the left mouse button or press **Enter** or press **Space** bar at the location of the dot.

A dot can also be added digitally. After choosing the command, press any digit key (0 through 9) to call up the dialog box for digital input. The input fields are pre-set with the coordinates of the current cursor position. Enter the coordinates of the dot. Choose **OK** to complete the input.

This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.


## Open path

Choose this command to add a closed or open path to the active layer. There is a difference between a closed path and a polygon; a polygon has an area whereas a path consists of a border only. This difference can be made visible by choosing the menu command **Options > Fill**.

After choosing the command, click the left mouse button at each corner of the path sequentially. Each mouse click can be replaced by pressing the **Space** bar. Simultaneously, an open path will be drawn. Click the right mouse button at the last corner to complete the path. This mouse click can be replaced by pressing **Enter**.

It is possible to assign each open path a line width and zero value leads to **single pixel lines**. These single pixel lines are not standard GDSII elements but useful for ultra-high resolution applications.

An open path can also be added digitally. After choosing the command, press any digit key (0 through 9) to call up the dialog box for digital input. The input fields are pre-set with the coordinates of the current cursor position. Enter the coordinates of the first corner. Choose **Next** to type in the coordinates of the following corners. After entering the coordinates of the last corner, choose **Last** to complete the path. Choose **OK** at any time to position the next corner with the mouse again.

This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.


## Polygon

Choose this command to add a polygon to the active layer.

After choosing the command, click the left mouse button at each corner of the polygon sequentially. Each mouse click can be replaced by pressing the **Space** bar. Simultaneously, a polygon will be drawn. Click the right mouse button at the last corner to complete the path. This mouse click can be replaced by pressing **Enter**.

A polygon can also be added digitally. After choosing the command, press any digit key (0 through 9) to call up the dialog box for digital input. The input fields are pre-set with the coordinates of the current cursor position. Enter the coordinates of the first corner. Choose **Next** to type in the coordinates of the following corners. After entering the coordinates of the last corner, choose **Last** to complete the polygon.

Choose **OK** at any time to position the next corner with the mouse again.


This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.

## Rectangle

Choose this command to add a rectangular box to the active layer.

After choosing the command, move the cursor to any corner of the rectangle to be added and click the left mouse button. Then move the cursor to the opposite corner of the rectangle and click the left mouse button again. Simultaneously, a rectangular box will be drawn. Each mouse click can be replaced by pressing **Enter** or by pressing the **Space** bar. By pressing **Shift** after the first mouse click the first point is interpreted as the center of the rectangle. By pressing **Control** the rectangle will be made a perfect square. Both keys can be pressed simultaneously.

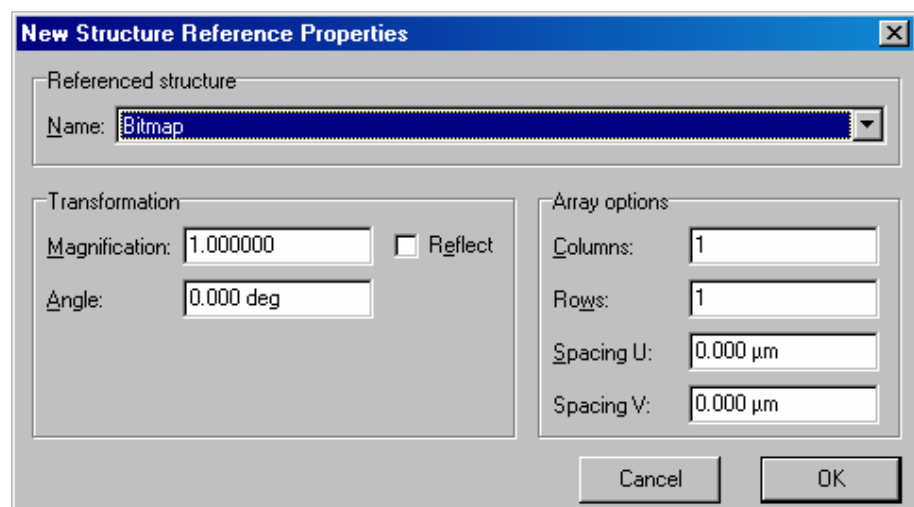
A rectangle can also be added digitally. After choosing the command, press any digit key (0 through 9) to call up the dialog box for digital input. The input fields are pre-set with the coordinates of the current cursor position. Enter the coordinates of the first corner of the rectangle. Choose **Next** to type in the coordinates of second corner. Choose **OK** to complete the box.

This command will be repeated automatically until pressing **Esc** or until choosing the button  within the icon bar.

## Structure reference

Choose this command to add a structure reference, i.e. to design hierarchical GDSII files. Any structure of the loaded database with the exception of structures containing the opened structure as a reference can be referenced. These referenced structures itself of course may contain also references to other structures. In addition, the referenced structures can be arbitrarily placed, repeated in a matrix form, rotated and scaled within the opened structure.

**Figure 26:** Dialog New Structure Reference.



Select one of the structures offered within the list box **Referenced structure**.

Enter the scaling factor for the referenced structure within the field **Magnification**. A factor 1 includes the referenced structure in its original dimensions and for example a factor 0.1 includes it with 1/10 of the original size.

If **Reflect** is set, the element is reflected about the u-axis before angular rotation. For an array reference, the entire array is reflected, with the individual array members rigidly attached.

**Magnification** operation is applied to the selected structure only, but it is not applied to **Spacing U** and **Spacing V**. Therefore the values for the spacing have to be calculated from the magnified structure.

Enter the rotation angle for the entire structure matrix within the field **Angle**. The rotational center is the lower left corner of the first referenced structure, i.e. the lower structure, within the matrix. Please note, the entire matrix is rotated, not the single matrix elements.


Enter the number of repetitions of the referenced structure along the rotated horizontal structure axis within the field **Columns** and along the rotated vertical structure axis within the field **Rows**.

Enter the distance in micrometer between equivalent points of adjacent, magnified structures along the rotated horizontal structure axis within the field **Spacing U** and along the rotated vertical structure axis within the field **Spacing V**.

Choose **OK** to confirm the entries. The resulting structure reference is indicated as a rectangle, attached to the mouse cursor, which has to be finally placed within the currently opened structure. For this, move the mouse to the target position and confirm by pressing the left mouse or by pressing **Enter**. In any case, the design cursor indicates the rotational center of the structure matrix. Hence, this is not equal to the lower left corner of the enclosure, if a rotation angle is applied.

The placement can also be done digitally. After confirming the the entries in the dialog, press any digit key (0 through 9) to call up the dialog box for digital input. The input fields are pre-set with the coordinates of the current cursor position. Enter the target coordinates of the rotational center of the structure matrix. Choose **OK** to complete placement.

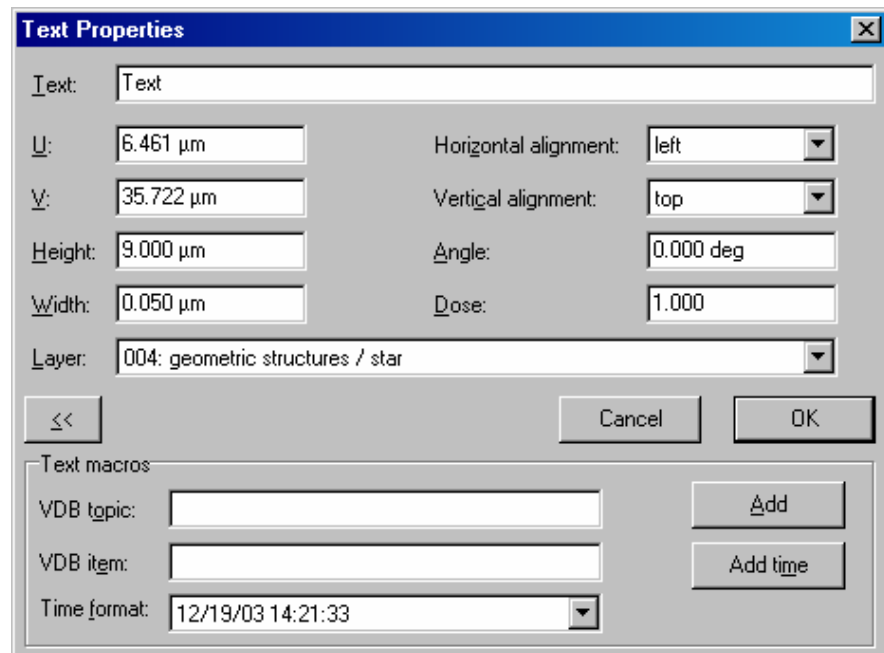
By default each structure reference is represented as a rectangular red-framed rectangle indicating the location and size of the field enclosing all referenced structures. The name of the referenced structure and its matrix repetition, i.e. the numbers of rows and columns, is displayed in the center of this rectangle. For detailed inspection through the hierarchical levels, choose the menu command **View > Hierarchy**.

This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.

## Text

Choose this command to add a text element to the active layer.

**Figure 27:** Dialog Text Properties to add a text element to GDSII.



Enter the text itself into the **Text** field.

Enter the position a reference point for the text in micrometer within the field **U** and **V**. Select the alignment of the text with respect to this reference point by selecting the **Horizontal alignment** and **Vertical alignment**.

Enter the **Height** of the letters in micrometer.

Enter the **Width** of letters in micrometer. A value of zero will lead to letter consisting of single pixel lines. The preset line width **Add > Preset > Line width** is ignored.

Enter the rotation **Angle** of the text in degrees.

Enter the **Dose** to be assigned as a factor with 1 = 100% of clearing dose.

Select the **Layer** to be assigned to the text element. The preset layer **Add > Preset > Layer** is ignored.

Additional input fields are available by pressing <<. for date and time strings as well as contents of VDB variables.

Enter the **VDB topic** and **VDB variable** and press **Add** to copy corresponding string into the **Text** field. The syntax is  $\$(vdb:<topic>.<variable>)$  and can be edited afterwards. The parameters  $\langle topic \rangle$  and  $\langle variable \rangle$  define the name of the topic and

the name of the variable listed under that topic within the variables data base file (VDB).

Example: The dwell time used for an exposure is stored in the variable "Dwelltime" under the topic "Variables". One may want to expose this used dwell time together with the pattern for test purposes. For this, use the string

Dwell time = \$(vdb:variables.dwelltime) ms

If the dwell time is set to 0.01, this leads to an exposure of


Dwell time = 0.01 ms.

Select from the list **Time format** and press **Add time** to copy time string into the **Text** field. The syntax for this kind of text entry is \$(time:<topic>.<variable>:<format>). The parameters <topic> and <variable> have the same meaning as described above. If these parameters are left free, the actual date and time is used. If parameters are used then the VDB is interpreted as the number of seconds since 1/1/1970 1:00:00. The parameter <format> defines the output format of the time string and can be edited afterwards. Following formats are available.

**Table 13:** Format of time string.

| <b>&lt;format&gt;</b> | <b>Result</b>             | <b>Description</b>            |
|-----------------------|---------------------------|-------------------------------|
| %a                    | Sun, Mon, ...             | short name of weekday         |
| %A                    | Sunday, Monday, ...       | full name of weekday          |
| %b                    | Jan, Feb, Mar, ...        | short name of month           |
| %B                    | January, February, ...    | full name of month            |
| %c                    | e.g. 04/21/01<br>10:21:33 | date and time                 |
| %d                    | 01 – 31                   | day number of month           |
| %D                    | e.g. 04/21/01             | date                          |
| %H                    | 00 – 23                   | hour (24 hour format)         |
| %I                    | 01 – 12                   | hour (12 hour format)         |
| %j                    | 001 – 366                 | day number within year        |
| %m                    | 01 – 12                   | month number within year      |
| %M                    | 00 – 59                   | minute                        |
| %p                    | am – pm                   | Used together with %I         |
| %S                    | 00 – 59                   | seconds                       |
| %U                    | 00 – 52                   | week number (first day = Sun) |
| %w                    | 0 – 6                     | weekday number (0 = Sun)      |
| %W                    | 00 – 52                   | week number (first day = Mon) |
| %x                    | e.g. 04/21/01             | date                          |
| %X                    | e.g. 10:21:33             | time                          |
| %y                    | 00 – 99                   | year without century          |
| %Y                    | e.g. 2004                 | year with century             |

If the parameter <format> is left free %c is used as a default value.

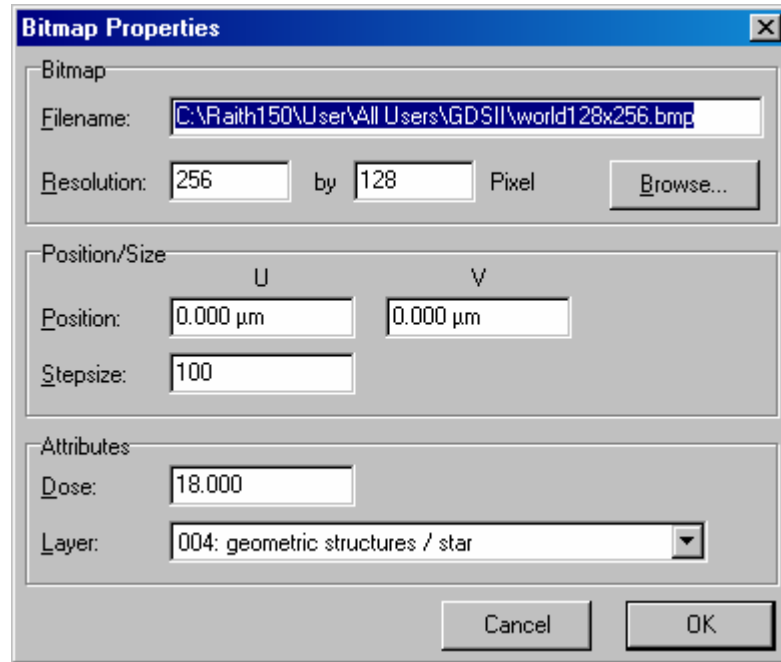
This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.



**Bitmap**

Choose this command to add a black and white bitmap to the active layer.

**Figure 28:** Dialog Bitmap Properties to add an image of bitmap format.




Enter the **Filename** and the **Resolution** in pixels or use **Browse** to search for the bitmap file.

Enter the **Position** of the lower left corner of the bitmap in micrometer.

Enter the **Step size** in DAC steps used between pixels within the bitmap. Take care that the product 'Stepsize' · 'bitmap pixel' does not exceed the total number of DAC steps, otherwise the size of the bitmap will exceed the writefield size.

Enter the **Dose** to be assigned as a factor with 1 = 100% of clearing dose).

Select the **Layer** to be assigned. The preset layer **Add > Preset > Layer** is ignored.

This command will be repeated automatically until pressing **Esc** or until choosing the stop button  within the icon bar.

**Group of curves**

Choose this command to add a group of curves to the active layer. This command gives access to a generator for groups of curves, which can be specified by flexible mathematical formulas.

The available mathematical functions and fundamental arithmetic operations are listed below. If one enters functions or variables, which are not defined, an error message will be displayed below the corresponding input field.

**Figure 29:** Dialog **Curve generator** to add mathematically defined curves.

**Curve Generator**

Title: Astroid

$U(X) = A * (\cos(X))^3$   
Ok

$V(X) = A * (\sin(X))^3$   
Ok

$X = 0$  to  $2 * \pi$  Number of steps: 200  
= 0.000000 = 6.283185

Terms: [Empty text box] Edit New Delete

Curves: 5 Width: 0.000  $\mu\text{m}$

| Parameter: | Name | Start value | End value |
|------------|------|-------------|-----------|
|            | A    | 2           | 3         |
|            | B    | 2           | 3         |

Limits:  U: [ ] to [ ] Invalid expression  
Ok

V: [ ] to [ ]  
Ok

Save Load Cancel OK

Enter a suitable **Title** or comment for a newly generated group of curves.

In general, each curve is described by a set of points and the positions of these points are calculated by the two equations  $U(X)$  and  $V(X)$ . The curve itself is described in a parameter form with the running variable  $X$ . This variable  $X$  is incremented in a range defined by a start value and an end value with the specified **Number of steps**. This **Number of steps** is limited to 2048, i.e. if one enters a number greater than 2048, it will be reduced to 2048, automatically. Each curve is defined as an open path, i.e. the connections between adjacent steps are straight lines.

#### Example 1

A single circle with radius 10 and center coordinates 3/5 can be generated by

$$U(X) = 10 * \cos(X) + 3$$

$$V(X) = 10 * \sin(X) + 5$$

$$X = -\pi \text{ to } \pi.$$

#### Example 2

A single standard parabola can be generated by

$$U(X) = X$$

$$V(X) = X^2$$

$$X = -4 \text{ to } 4$$

Basic function **Terms** may be defined to simplify entry of complex or interlaced equations. Choose **New** to create a term or select an existing term and choose **Edit** to modify this term. In both cases the user will

be assisted by a dialog box to enter the term characteristics. Within this dialog, enter a suitable name for the term to be used within all other equations. But do not use any of the signs for fundamental arithmetic operations, i.e. + - \* / ^. The length of the name is limited to the size of the text box. Within the same dialog, enter the term itself, which may contain any combination of numbers and pre-defined mathematical functions as listed below. The length of the term is not limited.

Enter the number of **Curves** to be generated. If this number is greater than 1, it is a good idea to include **Parameters** within the equations for **U(X)**, **V(X)**, or the **Terms**. Otherwise all curves will be located one upon the other, which may lead to accidentally over-exposure.

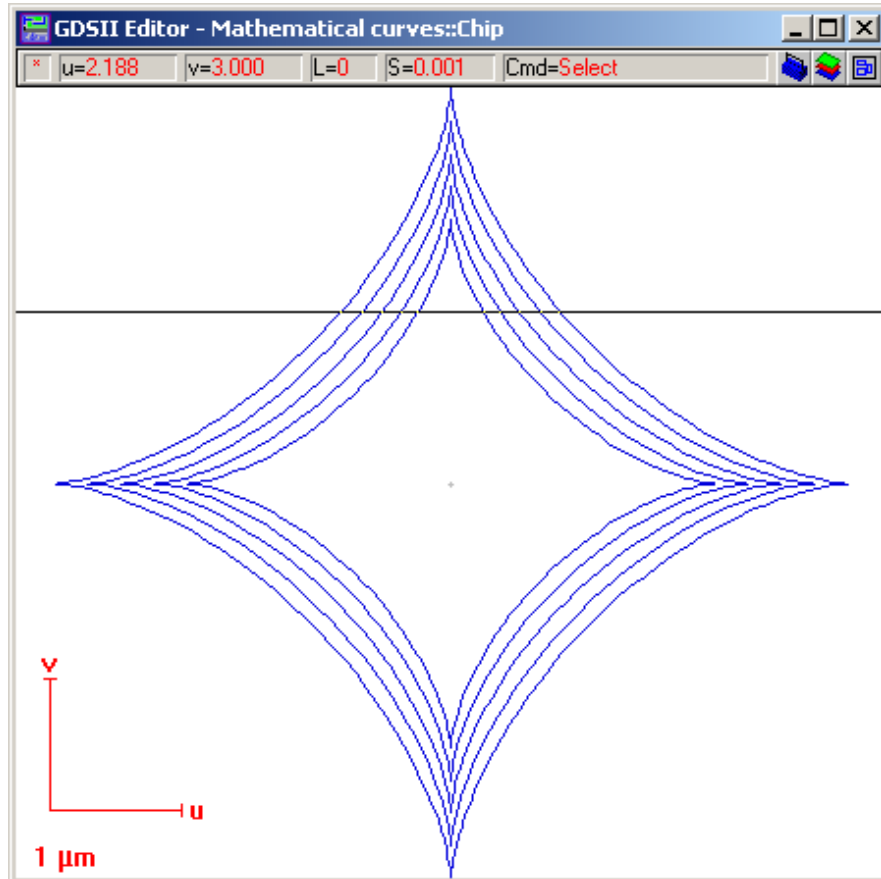
The curves are generated and stored as GDSII-elements of the type Open path. The individual paths are created with the specified **Width** and a width of zero means, that the curves are created as single pixel lines.

In order to generate a group of curves and not only a single curve, a set of **Parameters** can be defined each with a **Start value** and an **End value**. Within the resulting range each parameter is varied as often as specified. For the variation from curve to curve these parameters must be included within **U(X)**, **V(X)**, or the **Terms**. Choose **New** to create a parameter or select an existing parameter and choose **Edit** to modify this parameter. In both cases the user will be assisted by a dialog box to enter the parameter characteristics. Within this dialog, enter a suitable name for the parameter but do not use any of the signs for fundamental arithmetic operations, i.e. + - \* / ^. Within the same dialog, enter a **Start value** and an **End value** for the parameter. When generating a group of curves, all specified parameters are varied in a linear mode from applying the start values to the first curve and applying the end values to the last curve. Hence, the step size of the parameters from curve to curve is defined as  $(\text{End value} - \text{Start value}) / (\text{Curves} - 1)$ . Both **Start value** and **End value** may contain not only numbers, but also any combination of numbers and pre-defined mathematical functions as listed below.

The resulting curves may be limited in their U and V range. Activate the check box **Limits** and enter the lower and the upper limits for U and V into the input fields. If the check box **Limits** is cleared, the limits settings will be ignored.

Choose **Save** and **Load** to store and reload all specified settings to dedicated files with the extensions \*.MAT.

**Figure 30:** Group of curves generated with setting given above.



### Conventions for mathematical formulas

For the mathematical curve generation the normal INFIX notation is applied. In order to achieve a good readability, one may add spaces anywhere within the formulas. Arguments for mathematical functions must be enclosed in round brackets, e.g. SIN(X). The circular constant  $PI=3.14159\dots$  is predefined.

**Table 14:**  
Fundamental  
arithmetic functions.

| Key | Function                     |
|-----|------------------------------|
| +   | Addition or positive sign    |
| -   | Subtraction or negative sign |
| *   | Multiplication               |
| /   | Division                     |
| ^   | Power                        |

### Pre-defined Mathematical Functions

The following mathematical functions are available to define almost any type of 2-dimensional curves.

**Table 15:** Pre-defined mathematical functions.

| Function | Meaning                                    | Return values  |
|----------|--|--|
| S        | Step or Heaviside function                 | $S(X) = 0$ for $X < 0$<br>$S(X) = 1$ for $X \geq 0$                                |
| R        | Ramp                                       | $R(X) = 0$ for $X < 0$<br>$R(X) = X$ for $X \geq 0$                                |
| SGN      | Signum                                     | $SGN(X) = -1$ for $X < 0$<br>$SGN(X) = 0$ for $X = 0$<br>$SGN(X) = +1$ for $X > 0$ |
| ABS      | Absolute                                   | $ABS(X) = -X$ for $X < 0$<br>$ABS(X) = X$ for $X \geq 0$                           |
| SQRT     | Square Root                                | $SQRT(X) = X^{1/2}$  |
| CBRT     | Cube Root                                  | $CBRT(X) = X^{1/3}$  |
| EXP      | Exponential to base $e = 2.71828\dots$     | $EXP(X) = e^X$   |
| LN       | Natural Logarithm, base $e = 2.71828\dots$ |  |
| LOG      | Decimal Logarithm, base 10                 |  |
| FAK      | Factorial                                  | $FAK(X) = X! = 1 * 2 * 3 * \dots * (X-1) * X$                                      |
| RND      | Random                                     | $X \leq RND(X) \leq 0$ for $X < 0$<br>$0 \leq RND(X) \leq X$ for $X \geq 0$        |
| SIN      | Sine                                       | Argument in radiant  |
| COS      | Cosine                                     | Argument in radiant  |
| TAN      | Tangent                                    | Argument in radiant  |
| COT      | Cotangent                                  | Argument in radiant  |
| ARCSIN   | Inverse Sine                               | Result in radiant  |
| ARCCOS   | Inverse Cosine                             | Result in radiant  |
| ARCTAN   | Inverse Tangent                            | Result in radiant  |
| ARCCOT   | Inverse Cotangent                          | Result in radiant  |
| SINH     | Hyperbolic Sine                            |  |
| COSH     | Hyperbolic Cosine                          |  |
| TANH     | Hyperbolic Tangent                         |  |
| COTH     | Hyperbolic Cotangent                       |  |
| ARSINH   | Inverse Hyperbolic Sine                    |  |

**Manual mark scan** Choose this command to add a 2-dimensional mark scan, i.e. an Imagescan, which can be used for aligning the write field during an exposure in a semi-automatic fashion. After positioning the mark by using the mouse or digitally the command opens an additional dialog which aids the definition of the mark scan. **Center** defines the position of the mark in U- and V-direction. Enter **Size** to modify the area which will be scanned around the center position. . The number of points used for the scan mark can be defined using **Scan points**. A point-by-point averaging is defined by modifying **Average**.

The functionality is described in section [Beam to sample alignment](#) in more detail.

**Auto mark scan** Choose this command to add a 1-dimensional mark scan, i.e. a Linescan, which can be used for aligning the write field during an exposure in an automatic fashion. After positioning the mark by using the mouse or digitally the command opens an additional dialog which aids the definition of the mark scan. **Center** defines the position of the mark in U- and V-direction. Select the **Scan direction** to define the direction of the Linescan. Enter **Size** to modify the length of the scan whereas the **Average size** modifies the width used for averaging. The number of points used along the length of the scan can be defined as well as how often scans were recorded for averaging using **Scan points** and **Average points**. A point-by-point averaging is defined by modifying **Average**.

The functionality is described in section [Beam to sample alignment](#) in more detail.

## 5.2.8 Proximity menu

The **Proximity** menu gives access to two commands related to proximity effect correction (PEC) of GDSII patterns. As the **Proximity** command modifies the pattern the menu is available only in the editor.

Before describing the command and its various parameters controlling the algorithm, a general introduction is given.

- The first step is to subdivide all large elements which cannot be described by one dose factor automatically into smaller elements.
- The subdivision of all selected elements into non-interacting parts (partitioning by design) is the second step.
- If such a partition cannot be treated within the resources of the computer, each partition is subdivided further (partitioning by memory).  
Around each "memory partition" a region is defined which takes into account that elements from outside the partition may affect

the elements with the partition. But elements from inside the partition do not affect elements outside its boundaries.

- For all partitions the following loop is executed: All elements of one partition are mapped to a calculation grid, the grid is transferred into a system of linear equations and this system is solved resulting in a dose factor assignment for each element.

**Recommended Parameters** This command helps to select initial values for the proximity parameters for different resists and substrates. The values are stored in a database which can be modified and extended by the user. It is recommended to perform careful tests to determine these parameters because they depend on a broad range of variables like resist thicknesses, development parameters, etc. which may vary from lab to lab. Recipes to determine the parameter are available on request.

Enter the diameter of the primary beam **Alpha0**, the voltage and the resist thickness **H0**. Select the kind of resist and the kind of substrate from the drop-down lists. The related values for  $\alpha$ ,  $\beta$  and  $\eta$  will be calculated.

To store new database values perform careful determinations of  $\alpha$ ,  $\beta$  and  $\eta$  for several different beam energies. For  $\alpha$  and  $\beta$  fit the following function to the measurements

$$\alpha = \sqrt{\alpha_0^2 + C \frac{H_0^3}{E^2}} \quad \text{and} \quad \beta = C_1 E^{C_2}$$

with  $E$  the beam energy in keV and  $\alpha$ ,  $\alpha_0$ ,  $\beta$  and  $H_0$  in  $\mu\text{m}$ . To modify, store or delete values from the database choose **Resists...** or **Substrates...**. Enter  $C$  given in  $\text{kV}^2/\mu\text{m}$  as **Const** for the resist. For the substrate enter  $C_1$  given in  $\mu\text{m}$  and  $C_2$  which is unitless as **Const1** and **Const2**, respectively.

### Correction

Choose this command to control and to start the algorithm which is used to correct the pattern. Before the command can be used, select all elements to be corrected. All unselected elements will not be considered. Using this command opens a window which gives access to all parameters which are required for the correction

**Figure 31:** Window giving access to all parameters for proximity correction.

**Proximity Correction**

**Parameters**

Proximity | Partitioning/Fracturing | Info

Alpha:   Use exponential function

Beta:  Gamma:

Eta:  Nu:

Equalization factor:

Proximity function:

$$f = \frac{1}{\pi(1 + \eta + \nu)} \left( \frac{1}{\alpha^2} e^{-\frac{x^2}{\alpha^2}} + \frac{\eta}{\beta^2} e^{-\frac{x^2}{\beta^2}} + \frac{\nu}{2\gamma^2} e^{-\frac{x}{\gamma}} \right)$$

**Output**

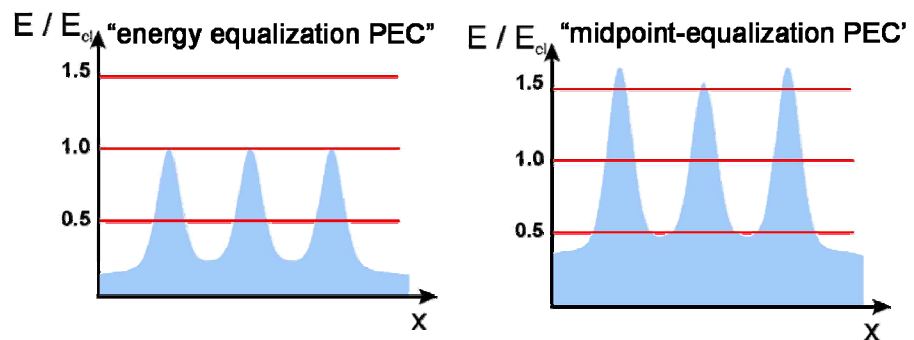
Log | Process

Cancel OK

Use the **Proximity** tab to set all parameters defining the proximity function. In the most simple representation these parameters are  $\alpha$ ,  $\beta$  and  $\eta$ . By checking the corresponding box, it is possible to use an additional exponential function with its parameters  $\gamma$  and  $\nu$ .

The **Equalization factor** determines to which energy originating from forward scattering the deposited energy is equalized (For details see G.P. Watson et al., J. Vac. Sci. Technol. B 15(6), 2309–2312 (1997) and R. Wüest et al., Optical Engineering 44(4), 043401 (April 2005)). The scheme is illustrated in **Figure 32**. For example, using a factor of 1.0 the algorithm calculates all dose factors in such a way that the deposited energy for all elements is at  $1.0 \times$  "energy originating from forward scattering", i.e. at the top of the forward scattering cone ("energy equalization PEC"). Thus a factor of 1.0 corresponds to the commonly used proximity effect correction. A factor of 0.5 results in an equalization at half of the forward scattering energy ("midpoint equalization PEC"). In summary, the **Equalization factor** incorporates the effect of beam broadening due to forward scattering.

**Figure 32:** Graphs showing the effect of two equalization factors.







For the first tests it is recommended to start with an **Equalization factor** of 0.5 to achieve best results. Use 1.0 to imitate other proximity effect correction software.

Use the tab **Partitioning / Fracturing** to enter the parameters controlling partitioning and fracturing.

The parameter **Atomic size** given in nm determines, if an element is fractured. For each shape, the algorithm looks at the width and height of the shape, i.e. its bounding box. If both width and the height are less than the atomic size, the shapes will not be fractured. A good value for the atomic size is 4 times the raster size.

The parameter **Maximum interaction distance** given in nm affects the partitioning on two levels. First, during partitioning by design, the distance between a shape's bounding box and the bounding boxes of all shapes within a particular partition is computed. If the distance is greater than the maximum interaction distance, it is considered to be outside of this partition. Second, when partitioning by memory, it determines the overlap region generated. A good value for the **Maximum interaction distance** is 3 times  $\beta$ .

The **Raster size** given in nm is the computational grid. In the proximity-effect correction it is assumed that each shape being corrected is located at the center of a lattice point on a periodic square lattice. This grid is called the raster. The process of mapping a shape onto its raster element is called rasterization. The rasterization will generate an inaccuracy due to the fact that in general the center of an element lies not exactly on one point of this raster. Thus, the **Raster size** must be sufficiently small so that for the smallest shape being corrected, the approximation of locating its center on a lattice point is still valid. On the other side, considering the calculation time the parameter should be chosen as large as possible without introducing rasterization errors. The **Raster size** should be in the range of  $0.1 \beta$ . It affects in several ways the algorithm. First, the algorithm fractures the outer edge of a shape into child shapes which are smaller than or equal to the raster size plus the factor **Fracturing error allowed**. Secondly, in connection with the Maximum matrix size it affects the partitioning by memory.

The unitless parameter **Fracturing error allowed** controls the fracturing. The fracturing routine works recursively, on a particular shape and divides it into horizontal and vertical slices. It then seeks to divide these slices into close to square shapes. This parameter determines how much leeway the fracturing routine has in terms of making the subdivisions. A too low value can result in overly small remainder shapes, which may lead to numeric errors when the shape is centered too far from a lattice point. Excessively large values may result in overly rectangular shapes (not square enough), which can

result in rasterization errors. A value of about 0.5 leads to good results.

The unitless parameter **Maximum matrix size** affects the "partition by memory" routine. When partitioning by memory, the quantity

$$N_{\max} = \frac{\sum \text{"area"}}{\text{"Raster size"}}$$
 is calculated which creates a very pessimistic

estimate of the number of non-zero elements which will be inserted into the proximity effects matrix. If this number is greater than the maximum matrix size, partition by memory will attempt to divide the partition again. It is possible to have a combination of the parameters **Raster size**, **Maximum matrix size** and **Maximum interaction distance** such that for a particular design, i.e. sufficiently dense design, partitioning by memory fails.

### Settings for administrators

The following tabs and parameters are available on as user with system privileges.

On the **Solver** tab it is possible to determine the behavior of the function executing the matrix inversion. For the **Solver** itself, it is possible to choose between the two algorithms BiCG (Bi-Conjugate Gradient) and BiCGSTAB (Bi-Conjugate Gradient STABILized). BiCGSTAB gives superior performance for our problem sets. After every iteration of the solver routine an estimate of the error is generated. As the solver progresses the error converges to, but never quite reaches zero. Thus, it is necessary to tell the computer at what point it is close enough to zero. This value is **Solver tolerance** with typical values around  $1 \cdot 10^{-5}$ . Higher values will result in faster computation, lower ones in more accuracy. There may be configurations for which the solver routine does not converge. For example, this may occur if an invalid dose is sent to the solver, e.g. zero area or negative doses, but it makes sense to cap the solver to eliminate the potential for an infinite loop. The maximum number of loops is determined by **Maximum solver iterations**. The typical number of necessary iterations is about 5 to 10. Thus a value of 100 being significantly higher guarantees convergence.

The commands on the **Debug** tab were created to aid in debugging the algorithm. **Create boxes for partitions**: When debugging the partitioning procedure, or finding spurious shapes, it may be useful to see the dimensions of the partitions by design and by memory. Set this flag, and boxes with the dimensions of the partitions will be created on layer 9 and higher. Default should be off. **Correct doses**: Useful when debugging aspects of algorithm that do not depend on the correction of the doses, say partition by memory or fracturing. Unset this flag and the dose factors are not changed. Default should be on. **Output PEM**: Set this flag, and the program will display the values of

the proximity effect matrix in Process window. In practice the output is too large to be of practical value outside of simple test cases and it is time consuming. Default should be off. **Fussy partition by design:** Crude partition by design checks the bounding box of a shape against the bounding box of a partition and includes it, if their boxes are within the maximum interaction distance. **Fussy partition by design** chooses a shape and checks it against each shape in a partition until an interaction is found and the shape is added to this partition. Or if no interaction is found, the shape is returned to the queue and added to another partition. Using this flag, it is more time consuming but results in smaller partitions. The flag could be set to off to save time on a design consisting of many small shapes which are known apriori to be within the interaction distance. The default should be on.

On the **Process** tab it is possible to set the PEC application, its working directory and the output given by the application.

## 5.3 Correcting for proximity effect

As proximity effect correction is quite a complex, only a general overview over the steps is given. For further details, especially when fine-trimming the results we refer to the literature and further documentation provided by Raith.

- STEP 1 ►** Remove overlaps and hierarchy from the relevant elements.
- STEP 2 ►** Within the GDSII editor select all elements to be corrected.
- STEP 3 ►** Choose command **Proximity > Correction** to open the corresponding add-on window. Enter all relevant parameters, such as  $\alpha$ ,  $\beta$  and  $\eta$ , etc, which are described in section [Proximity menu](#).
- STEP 4 ►** Press **Start** to execute the algorithm. The progress can be observed within the **Log** output and while running the process it can be interrupted using **Stop**.
- STEP 5 ►** After completion, the result is automatically taken over into the GDSII editor. By choosing Undo the previous status is reconstructed.
- STEP 6 ►** After closing the add-on window choose **Options > Show dose** and **Options > Dose colors** to inspect the result.

## 5.4 Working with layers

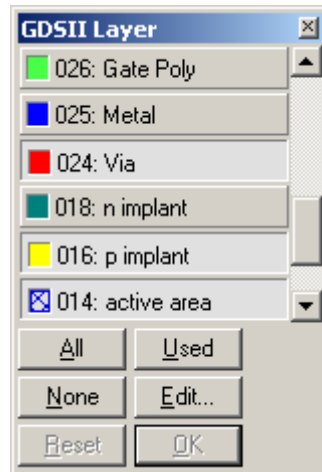
Normally a device is build during several process steps and the idea is to assign all the elements used in one process step to one layer. To display only the layer of interest the add-on **GDSII Layers** can be opened while using the editor or the viewer at the same time. To distinguish between the various layers it is very convenient to assign

each layer different properties like colors. This is done via dialog window **Layer Properties**. The layer properties are stored in separate file with extension LAY, path and file name are the same as of the corresponding GDSII database file.

### 5.4.1 Displaying layers

Choose command **View > Layer selection** to display the GDSII Layer add-on window used for selection of layers to be displayed.

**Figure 33:** Add-on window **GDSII Layer** used for selection of layers to be displayed.

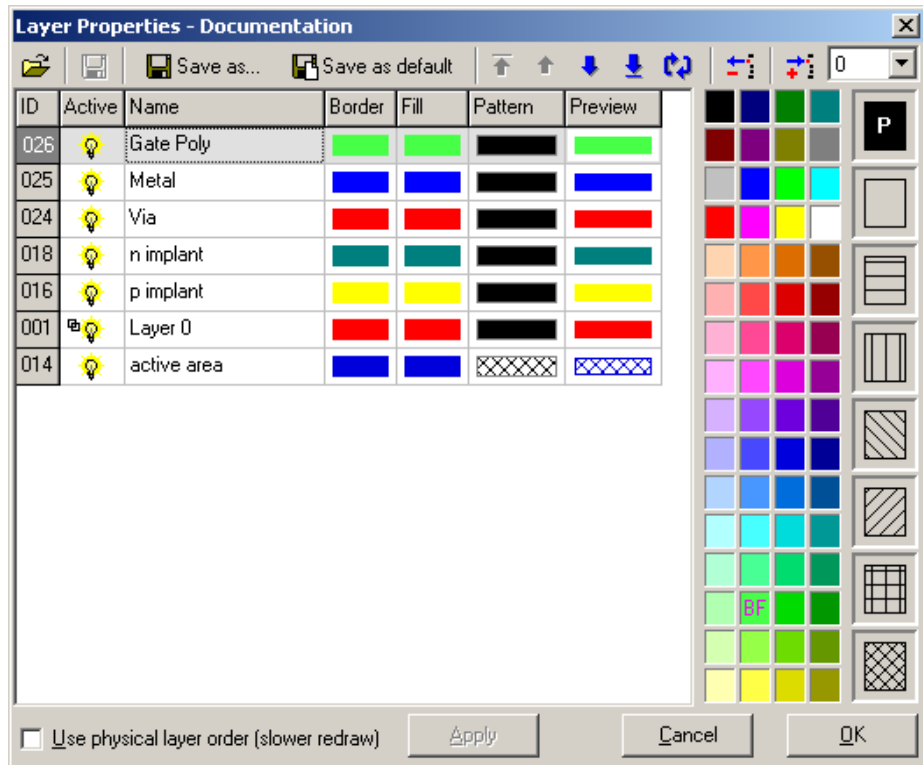


There are 256 layers available. To display a layer select corresponding layer. Selected layers are indicated by a pressed button. Choose **OK** to display selection, choose **Reset** to cancel changes made to the selection. In addition the following commands are available. **All** selects all available layers, **Used** selects only layers with content, and **None** cancels selection. **Edit** opens dialog Layer Properties.

### 5.4.2 Defining layer properties

Choose command **Options > Layer Editor ...** to assign name, fill color, border color and pattern to each layer individually.

**Figure 34:** Dialog Layer Properties to modify the various properties of all layers.



To aid the management of these LAY files the following commands are available. Choose the open icon to open a LAY file from another GDSII database for example to take over these properties. Choose save icon to store the current properties to LAY file. Choose **Save as ...** to store current properties to another LAY file, for example to attach current properties to another GDSII database. Choose **Save as default ...** and current properties are used for all new created GDSII databases.

Choose the arrow icons to change the order of the different layers within the list. It is now interesting to interpret the order in the list also a physical order. Physical order means that a layer at the end of the list is processed first while a layer at the top of the list is processed later. Hence the order is interpreted as a sequence of process steps. To display also the layers in this physical order, i.e. later processed layers overlay previous processed layers, select **Use Physical layer order**.

Choose to remove the selected layer and choose to add the layer with the number from the list box.

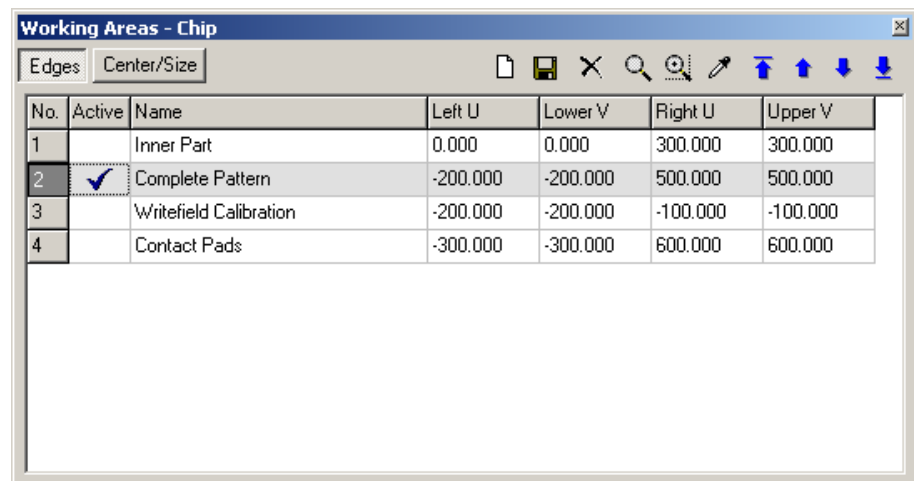
To modify the layer properties select first the corresponding layer in the list. Place the mouse cursor in the input field **Name** to modify the name. The name is limited to 13 characters. Assign a border color by clicking in the color table with the right mouse button. Assign a fill color by clicking in the color table with the left mouse button. Assign a pattern by clicking in the pattern table. The last column presents then a preview against the current background color.


Click on the bulb in the **Active** column of the list to activate or deactivate corresponding layer from the **GDSII Layer** add-on window. Two small boxes in the **Active** column indicate if corresponding layer contains GDSII elements.







## 5.5 Using working areas

Normally not the whole GDSII structure is of interest for example to inspect it or to expose it. To expose only a fraction of the whole GDSII structure it is possible to define several areas of interest so called working areas. These working areas can be defined for each structure individually. The working areas for all structures are stored in separate file with extension WOR, path and file name are the same as of the corresponding GDSII database file.

**Figure 35:** Add-on window **Working Areas** used for selecting and modifying of working areas.



Use the new  icon to add a new working area. To change the properties like the **Name** of a working area place cursor in corresponding field to modify values. To define the working areas over their edges select button **Edges**, to define working area over its center and size select **Center/Size**. Note when selecting a new working area the corresponding area flashes several times within viewer or editor.

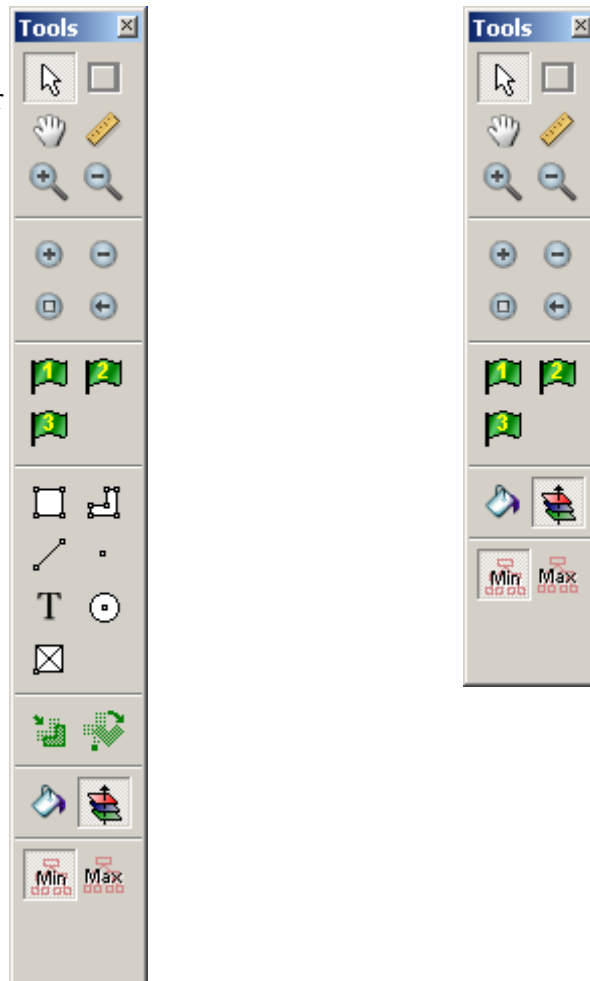
Save changes with the save icon . The current active working area can be deleted using delete icon . The selected area can be viewed using the  icon. To move only the center of the viewpoint choose . Choose the pipette icon  to take over the editor or viewer window coordinates into the currently selected working area. Use the arrow icons  to change the order of the defined areas.

To define an area as the active one click into the **Active** field and a tick is placed in this field.

## 5.6 Using the toolbox

For a fast access to the often used commands it is possible to open an add-on window by choosing **View > Toolbox**.

**Figure 36:** Add-on window **Tools** for editor (left) and viewer (right) to access some often used commands.



The general commands for viewing, measuring, zooming, and placing flags are described in section [UV Windows](#).



Editor command **Add > Rectangle**.



Editor command **Add > Polygon**.



Editor command **Add > Open path**.



Editor command **Add > Dot**.



Editor command **Add > Text**.



Editor command **Add > Circle**.



Editor command **Add > Structure reference**.



Editor command **Modify > Move**.



Editor command **Modify > Rotate**.



Viewer and editor command **Options > Fill**.



Viewer and editor command **Options > Physical layer order**.



Viewer and editor command **View > Hierarchy > 0**.



Viewer and editor command **View > Hierarchy > Max**.

## 5.7 Mouse and keyboard commands

Within the editor selecting and deselecting of single elements is also possible by using the mouse. For selection, click anywhere within the element area. Selection of another element by mouse click will unselect the already selected elements. To unselect all elements, click within a free area. If a single element is selected, information about type, layer and dose is shown within the status bar.

Selecting and deselecting of multiple elements by using the mouse is possible in two ways. Point directly to any corner of the area covering all elements to be selected, press and hold the **Shift** key and click the left mouse button. Releasing the **Shift** key lets the user define now the second corner of an area, holding it down the first point defines the center of an area. Or select one element after another while pressing and holding the **Control** key. In addition, one may use any combination of mouse click selection and **Select** respectively **Unselect** commands. If multiple elements are selected, the status bar shows the number of selected elements.

Within the editor and the viewer, zooming can be done using the wheel of a corresponding mouse.

If the crosshair is used as mouse pointer its movement is also done on the meshes defined by the design grid. If the default mouse pointer is used, the mouse can be placed also in between. The placement of the GDSII elements is not effected.

The following tables give a summary of all available mouse and keyboard commands within the GDSII database, the viewer as well as the editor window.



### 5.7.1 GDSII database

**Table 16:** Mouse commands in GDSII database window.

| Action       | Key(s) + Mouse Button | Functionality              |
|--------------|-----------------------|----------------------------|
| Single click | none + left           | Select a structure.        |
| Single click | none + right          | Open the right mouse menu. |
| Double click | none + left           | Open the viewer window.    |
| Double click | <b>Control</b> + left | Open the editor window.    |

**Table 17:** Available GDSII database keyboard shortcuts.

| Key                        | Functionality                                     |
|----------------------------|---|
| <b>F2</b>                  | to rename a structure                             |
| <b>Control + C</b>         | to copy a structure                               |
| <b>Control + N</b>         | to create a new structure within a GDSII database |
| <b>Control + O</b>         | to open a new GDSII file                          |
| <b>Control + V</b>         | to paste a structure into GDSII database          |
| <b>Control + Shift + N</b> | to create a new GDSII database                    |
| <b>Control + Shift + S</b> | to save GDSII database into a new file            |

### 5.7.2 GDSII viewer

**Table 18:** Mouse commands in viewer window.

| Action       | Key(s) + Mouse Button  | Functionality            |
|--------------|------------------------|--------------------------|
| Single click | none + right           | Repeat the last command. |
| Single click | <b>Control</b> + right | Drive to location.       |

**Table 19:** Available GDSII viewer keyboard shortcuts.

| <b>Key</b>          | <b>Functionality</b>                          |
|---------------------|---|
| <b>+</b>            | to zoom in by a factor of 2                   |
| <b>-</b>            | to zoom out by a factor of 2                  |
| <b>=</b>            | to view all                                   |
| <b>*</b>            | to increase the design grid by factor 2       |
| <b>/</b>            | to decrease the design grid by factor 2       |
| <b>a</b>            | to display GDSII element properties           |
| <b>e</b>            | to measure dimensions in editor or viewer     |
| <b>f</b>            | to fill out the elements, toggle mode         |
| <b>g</b>            | to show / hide the design grid, toggle mode   |
| <b>h</b>            | to move viewed area                           |
| <b>l</b>            | to open layer selection box, toggle mode      |
| <b>t</b>            | to open toolbox , toggle mode                 |
| <b>w</b>            | to open working area editor, toggle mode      |
| <b>z</b>            | to zoom in and out, toggle mode               |
| <b>Shift + ←↑↓→</b> | to scroll the display into direction of arrow |
| <b>Alt + i</b>      | to increase hierarchy by one step             |
| <b>Alt + d</b>      | to decrease hierarchy by one step             |
| <b>Alt + o</b>      | to show overlays, toggle mode                 |
| <b>Alt + r</b>      | to redraw the display                         |
| <b>Del</b>          | to delete an annotation                       |

### 5.7.3 GDSII editor

**Table 20:** Mouse commands in editor window.

| Action       | Key(s) + Mouse Button  | Functionality   |
|--------------|------------------------|---|
| Single click | none + left            | On an unselected structure element: select that element and unselect all other elements<br>Anywhere else:<br>Unselect all elements<br>Related menu command:<br><b>Edit &gt; Unselect &gt; All</b>                     |
| Single click | <b>Control</b> + left  | On an unselected structure element: Select that element additionally (without unselecting all other elements)<br>On a selected structure element: Unselect that element only (without unselecting all other elements) |
| Single click | <b>Shift</b> + left    | Select all elements additionally within a frame to be dragged (without unselecting all other elements - but only for active layer)<br>Related menu command:<br><b>Edit &gt; Select &gt; In</b>                        |
| Single click | none + right           | Repeat the last command   |
| Single click | <b>Control</b> + right | Drive to location   |
| Double click | none + left            | On a structure element: select that element, unselect all other elements and open a dialog box to modify the attributes of that element<br>Related menu command:<br>Modify > Attributes                               |

**Table 21:** Available GDSII editor keyboard shortcuts.

| <b>Key</b>          | <b>Functionality</b>                          |
|---------------------|---|
| <b>+</b>            | to zoom in by a factor of 2                   |
| <b>-</b>            | to zoom out by a factor of 2                  |
| <b>=</b>            | to view all                                   |
| <b>c</b>            | to add a circle                               |
| <b>d</b>            | to duplicate the selected elements            |
| <b>e</b>            | to measure dimensions in editor or viewer     |
| <b>f</b>            | to fill out the elements, toggle mode         |
| <b>g</b>            | to show / hide the design grid, toggle mode   |
| <b>h</b>            | to move viewed area                           |
| <b>l</b>            | to open the layer selection box, toggle mode  |
| <b>m</b>            | to move the selected elements                 |
| <b>o</b>            | to modify the order of elements               |
| <b>p</b>            | to add a polygon                              |
| <b>r</b>            | to add a rectangle                            |
| <b>t</b>            | to open the toolbox, toggle mode              |
| <b>w</b>            | to open working area editor, toggle mode      |
| <b>z</b>            | to zoom in and out, toggle mode               |
| <b>Del</b>          | to delete the selected elements               |
| <b>Tab</b>          | to select the next element                    |
| <b>Shift + Tab</b>  | to select the previous element                |
| <b>Shift + ←↑↓→</b> | to scroll the display into direction of arrow |
| <b>Control + a</b>  | to select all elements                        |
| <b>Control + c</b>  | to copy the selected elements                 |
| <b>Control + s</b>  | to save the structure                         |
| <b>Control + v</b>  | to paste the previously copied elements       |
| <b>Control + x</b>  | to cut the selected elements                  |
| <b>Control + z</b>  | to undo last editing command                  |
| <b>Control + y</b>  | to redo last undo command                     |
| <b>Alt + i</b>      | to increase hierarchy by one step             |
| <b>Alt + d</b>      | to decrease hierarchy by one step             |
| <b>Alt + o</b>      | to show overlays, toggle mode                 |
| <b>Alt + r</b>      | to redraw the display                         |

## 5.8 Drag and drop

A summary of drag and drop operations involving GDSII structures are listed below.

**Table 22:** GDSII drag and drop functionality.

| Source         | Object    | Target          | Action   |
|----------------|-----------|-----------------|--|
| GDSII Database | Structure | Image           | Place structure in Image and generate complete data line in related Positionlist                                     |
| GDSII Database | Structure | Positionlist    | Generate data line in Positionlist; read and use actual sample coordinates as object location (origin).              |
| GDSII Database | Structure | Wafermap        | Place structure in Wafermap and generate complete data line in related Positionlist for automated exposure routines. |
| GDSII Database | Structure | Program desktop | Delete structure.  |
| GDSII Database | Structure | GDSII Database  | Copy selected structure to current database. The original structure will not be overwritten.                         |



## 6 Stage Control

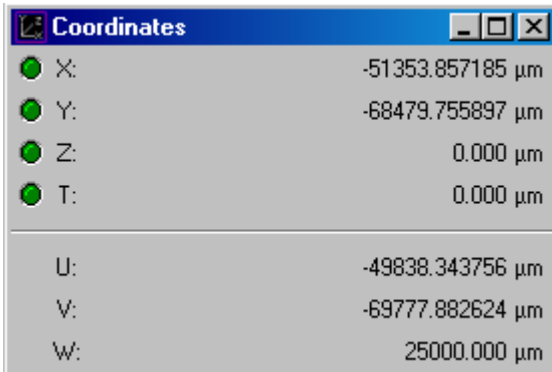
|                                       |           |
|---------------------------------------|-----------|
| <b>6.1 Coordinate display</b>         | <b>87</b> |
| <b>6.2 Stage control</b>              | <b>88</b> |
| <b>6.3 Find home position window</b>  | <b>93</b> |
| <b>6.4 LASER stage control window</b> | <b>94</b> |

Normally the lithography system is equipped with a stage to position the sample. If this stage is motorized then it is possible to control the stage movement by means of the software. In addition it depends on the stage what axes are available. In the following all supported axis are listed.

|          |   |
|----------|---|
| <u>X</u> | One of the physical axis of the stage. The axis is normally oriented perpendicular to the beam.   |
| <u>Y</u> | One of the physical axis of the stage. The axis is normally oriented perpendicular to the beam and perpendicular to <u>X</u> .  |
| <u>Z</u> | One of the physical axis of the stage. Normally parallel to beam.   |
| <u>R</u> | If available, the rotation axis of the system.  |
| <u>T</u> | If available, the tilt axis of the system.  |
| <u>U</u> | One of the axis of the sample coordinate system. The axis is in the plane of the sample surface.  |
| <u>V</u> | One of the axis of the sample coordinate system. The axis is in the plane of the sample surface and perpendicular to <u>U</u> .   |
| <u>W</u> | One of the axis of the sample coordinate system. The axis is perpendicular to sample surface and, if corrected for the sample height, equal to column working distance. |

### 6.1 Coordinate display

**Figure 37:** Window displaying current stage and sample coordinates.



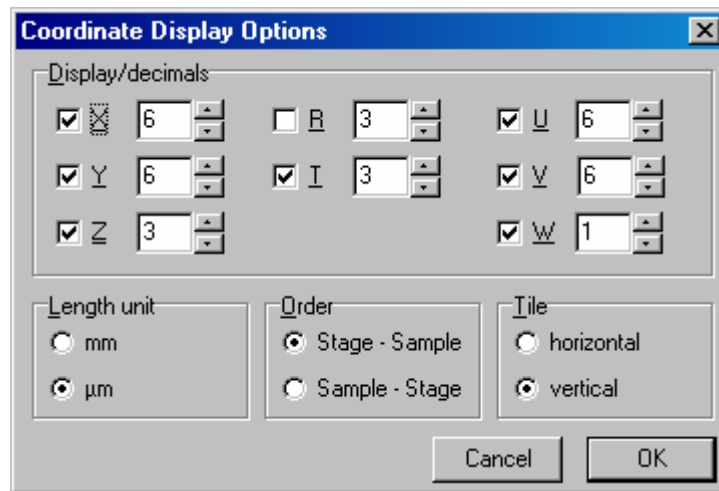
| Coordinates |                  |
|-------------|------------------|
| X:          | -51353.857185 μm |
| Y:          | -68479.755897 μm |
| Z:          | 0.000 μm         |
| T:          | 0.000 μm         |
| <hr/>       |                  |
| U:          | -49838.343756 μm |
| V:          | -69777.882624 μm |
| W:          | 25000.000 μm     |

The number of displayed coordinates depends on the number of motorized axes of the system. It may vary between 2 axes, i.e. X and Y, and up to 5 axes, i.e. X, Y, Z, R, and T. Any combination is possible. In most cases however, there are only the X Y or the X, Y, Z axes motorized. All displayed values are refreshed periodically. The difference between stage X, Y, Z coordinates and sample U, V, W coordinates is defined by a complete two-dimensional transformation.

### 6.1.1 Display options

Basic display option settings can be done by choosing the command **Edit > Options** or by right mouse click anywhere in the Coordinates window. These settings are assisted by the Coordinate Display Options dialog.

**Figure 38:** Dialog to set options for the Coordinates window.



#### Display/decimals

Select the check box for each axis to be displayed., i.e. if one of the axes should not be displayed, the related check box has to be cleared. The display resolution, i.e. number of decimals, can be entered for all axes individually within the related text boxes.

#### Length unit

The metric unit setting is valid only for metric axes XYZUVW but not for R and T. It can be set to mm or  $\mu\text{m}$ . Due to this setting, the number of digits will change, but the position data remain to be the same. Please change the number of decimals accordingly.

#### Order

Select with this option which coordinates are displayed first.

#### Tile

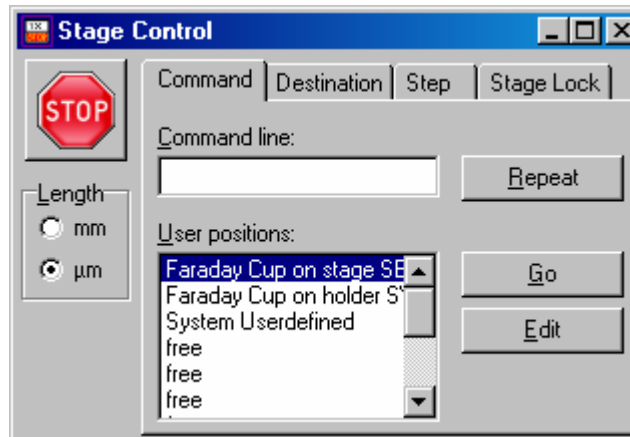
Select the option **horizontal** to display stage coordinates and sample coordinates side by side. In case of selecting the option **vertical**, they will be displayed one beneath the other.

## 6.2 Stage control

The stage control window allows controlling stage movement by sending single commands to the motor controller.



**Figure 39:** Central window controlling stage movements, **Command** tab.



On the left hand side it contains the following items.

### Stop

Choose this button to stop all motors immediately. The command is used as an Emergency Stop to cancel any stage movement or to avoid damage in a dangerous situation. This button is only available for Raith motor control or for demo motor control.

### Length

Select here the basis unit for all drive command except drive commands in the **Command line**.

## 6.2.1 Command tab

### Command line

Digital command input is done via this text box. To repeat the last command, choose the **Repeat** button besides the text box.

The following digital commands can be given via the command line.

**Table 23:** Available drive commands.

| Syntax                              | Function                  |
|-------------------------------------|---------------------------|
| <coordinate><lowercase-axis-letter> | absolute addressing       |
| <distance><uppercase-axis-letter>   | relative addressing       |
| <axis#> <b>b</b>                    | backlash compensation     |
| <b>Space</b>                        | backlash on all axis      |
| <line#> <b>g</b>                    | absolute Positionlist No. |
| <line#> <b>G</b>                    | relative Positionlist No. |
| i<id#> <b>g</b>                     | absolute Positionlist ID  |
| i<id#> <b>G</b>                     | relative Positionlist ID  |

The functionality of these commands is as follows:

**Absolute Addressing** To move one axis to a requested position in stage or sample coordinates.

The syntax is <coordinate><lowercase-axis-letter>.

Where the positive or negative <coordinate> value has to be entered in mm. Available <lowercase-axis-letter> values are **x, y, z, r, t, u, v, w**. To move to 0.0, just type the axis' letter.

Example:

The command "-5.5x" moves the stage to the X coordinate -5.5 mm.

**Relative Addressing** To move one axis relative to its current position over a requested distance in stage or sample coordinates.

The syntax is <distance><uppercase-axis-letter>.

Where the positive or negative <distance> value has to be entered in mm. Available <uppercase-axis-letter> values are **X, Y, Z, R, T, U, V, W**.

Example:

The command "2.5X" moves the stage over 2.5 mm into positive X direction.

**Backlash Compensation** Backlash compensation is essential for exact positioning with not-LASER stages. It is done by moving the stage away from the final position and returning always from the same direction, normally against the spring force.

The syntax is <axis#>**b**.

Where <axis#> is 1 for X axis, 2 for Y axis, 3 for Z axis, 4 for R axis, 5 for T axis. Use **Space** to perform a backlash on all axis.

Example:

The command "2b" moves the Y motor for backlash compensation.

**Positionlist Addressing** Within the latest opened Positionlist, any position can be addressed by data line number (No.) or by data line identification number (ID). Each of these commands can be specified to be absolute or relative to the currently selected data line.

The syntax for absolute Positionlist No. addressing is <line No.>g.

Where <line No.> is No. of corresponding line.

Example:

The command "15g" selects data line with No. 15 and moves the stage to the position specified in that data line.

The syntax for relative Positionlist No. addressing is <line No.>G

Where <line No.> value has to be entered as the difference between the number of the currently selected line and the number of the line to be selected.

**Example:**

If data line with No. 10 is currently selected, the command "15G" selects data line with No. 25 (=10+15) and moves the stage to the position specified in that data line.

The syntax for absolute Positionlist ID addressing is  $i<\text{line ID}>g$ .

Where  $<\text{line ID}>$  is ID of corresponding line.

**Example:**

The command "i15g" selects data line with ID 15 and moves the stage to the position specified in that data line.

The syntax of relative Positionlist ID addressing is  $i<\text{line ID}>G$

Where the  $<\text{line ID}>$  value has to be entered as the difference between the ID of the currently selected data line and the ID of the data line to be selected.

**Example:**

If data line with ID 10 is currently selected, the command "i15G" selects data line with ID 25 (=10+15) and moves the stage to the position specified in that data line.

**User position**

A set of 10 positions can be defined by the user and recalled on request.

**Go**

Choose this button to drive the stage to the position, selected from the drop-down list.

**Edit**


Choose this button to edit the position, selected from the drop-down list. A dialog opens.

**Figure 40:** Dialog to define and store a position.

To edit a position, proceed as follows:

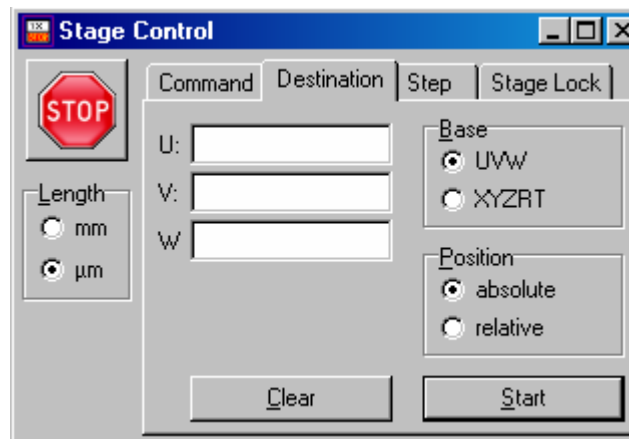
**STEP 1 ►**

Select the position to be edited from the drop-down list box.

- STEP 2 ►** Choose the **Edit** button. The "Edit User Defined Position" dialog box appears.
- STEP 3 ►** Enter a suitable name for this position.
- STEP 4 ►** Enter the position coordinates into the text boxes X, Y, Z, R, T or choose the **Read** button to take over the coordinates of the current stage position.
- STEP 5 ►** Enter the sequence of axis movement into the text box, e.g. zXY for movement first in Z- and then in XY-direction. Only those axes will be driven which are listed within this text box. After entering capital letters the stage moves in these axes simultaneously. With small letters the stages moves one axis after the other.
-  This may be important, if a tilted wafer is moved to a position near the pole piece. In this case it is recommended first to drive the tilt axis to zero and the Z axis to a low position before moving X and Y axes.
- STEP 6 ►** For information purposes, enter a comment within the respective text box.
- STEP 7 ►** Choose **OK** to use settings.

## 6.2.2 Destination tab

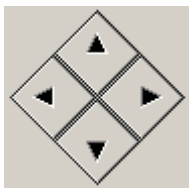
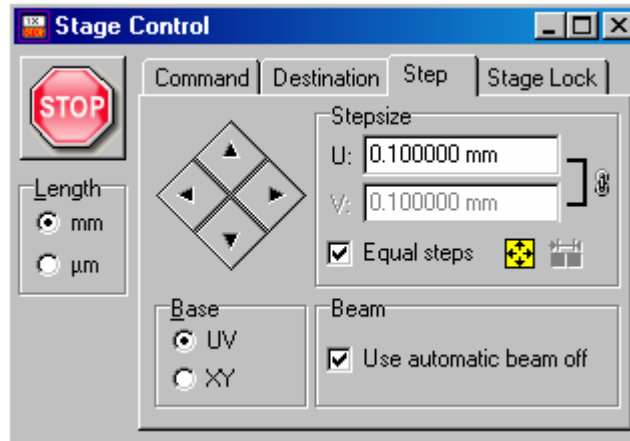
**Figure 41:** Central window controlling stage movements, **Destination** tab.



- Axis input fields** Enter the destination values for UVW or for XYZRT depending on the **Base** selection.
- Base** Choose the coordinate system to be used for addressing, i.e. sample coordinates or stage coordinates.
- Position** Choose the addressing mode, i.e absolute movement or relative movement.
- Start** Choose this button to start movement.
- Clear** Choose this button to clear all text boxes.

### 6.2.3 Step tab

**Figure 42:** Central window controlling stage movements, Step tab.





Choose one of the arrow buttons to move stage into corresponding direction using the distance given in the input fields **Step size**.

#### Base

Select the base for following drive commands.

#### Step size

Type in the distance for following drive commands. Select **Equal steps** to link the movement in the two orthogonal directions. Choose one of the two buttons   to read current write field or current distance between chips.

#### Beam

If the check box **Use automatic beam off** is selected, the beam will be blanked during stage movements. To observe the sample, leave this option unchecked.



To control the general functionality to switch off the beam at each drive command, use the setting **Module Status > Virtual beam Control > Auto Beam Off**.

### 6.2.4 Stage lock tab

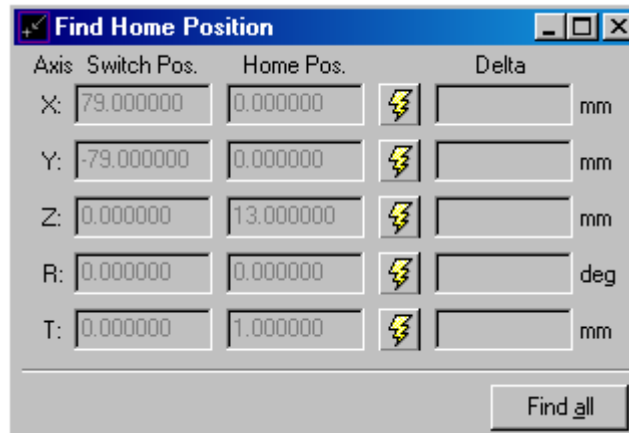
This functionality is only available, if user possesses user level SYS and for Raith motor control or for demo motor control. Here it is possible to lock single axis to prevent them from moving.

## 6.3 Find home position window

If one accidentally loose the coordinate system, the Find Home Position routine recovers and resets the setup.

It requires the definition of limit switches and home positions for the relevant axes within the initialization routine. Hence the Find Home Position routine can be performed only for motorized axes which are equipped with limit switches.

**Figure 43:** Dialog to initiate each stage axis.



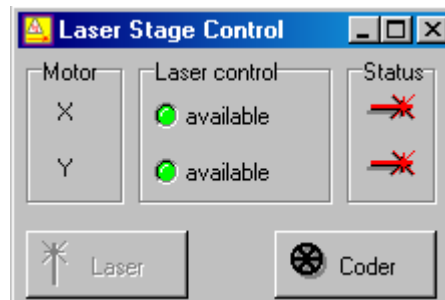
Either choose a single axis by pressing on of the lightning buttons or choose the **Find All** button.

After this, the stage moves towards the limit switches and the system sets the corresponding Switch position. Then the stage moves to the corresponding home position.

## 6.4 LASER stage control window

Note this module is only available when having a stage which can move under LASER or encoder control.

**Figure 44:** Window to check stage mode and change mode.



**LASER control**

A green LED indicates that the LASER signal is available for the corresponding axis.

**Status**

Indicates what mode is currently used.

**LASER**

Switch to LASER mode.

**Coder**

Switch to encoder mode.

## 7 Positionlists

---

|  |            |
|--|------------|
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A Positionlist is a spread sheet orientated tool within the Raith software which serves the execution, generation, administration, and documentation of various tasks.

- Adjustments and alignment tasks, i.e. performing a complex sequence of mark scans and their evaluations.
- Stage controls tasks, i.e. driving the stage sequentially to multiple positions in stage or sample coordinates.
- Exposure tasks, performing exposures of one or more selected structures at different sites on the sample with optionally different parameters.
- Performing scans of images or of waveforms and automation tasks.

The various tasks defined in a Positionlist can be configured by the customer in any selected sequence and combination. Positionlists required for standard adjustment and alignment procedures are generated automatically.

A Positionlist is defined and internally stored as an ASCII data file, which normally is indicated by extension PLS. The Positionlist concept of the Raith software allows very flexible configurations, handling of different list formats, and thus can be adapted to almost any application. Although for normal operation a single Positionlist is used and fully sufficient, it is possible to load and operate multiple lists simultaneously.

### 7.1 Positionlist window

Open an existing Positionlist with extension \*.PLS, by choosing the command **File > Open positionlist** or define a new one by choosing **File > New positionlist**.

**Figure 45:** Typical Positionlist window with its several elements.

| ID | U/mm      | V/mm     | Attribute | Template | Comment           | Options | Type     | Pos1/μm | Pos2/μm | Pos3/μm | Link | File                     | Layer | DoseFactor | Time |
|----|-----------|----------|-----------|----------|-------------------|---------|----------|---------|---------|---------|------|--------------------------|-------|------------|------|
| 0  | 0.000000  | 0.000000 | XS        | UV       | Fresnel           |         | EXPOSURE | 26.458  | 26.458  |         |      | %UserRoot%GDSII\DEMO.CSF | 4     | 1.00       |      |
| 1  | -0.000458 | 0.000670 | A         | UV       | UV cursorposition |         |          |         |         |         |      |                          |       |            |      |

### Task list

The task list displays each task as a separate line. Each task is defined by various data which are stored in separate fields. Thus the task list can be seen as a spread sheet.

### Icon bar

The most often used commands are directly available from the icon bar. Using the lists boxes it is possible to include or exclude some tasks according to their attributes.

### Information line

Here some information associated with this Positionlist are displayed.

## 7.1.1 Task list

Each line contains the data set of a task. Tasks can be alignment procedures, Imagescans, Linescans, structures to be exposed, line width measurements, or simply stage positions which can be addressed.

The task list is represented in a common table format, so that the standard editing functionality is available also for a Raith Positionlist. This mean it is possible to adapt the column width using the mouse and edit the contents of each cell by placing the cursor into it.

Each Positionlist consists of some fixed columns as a serial number **No.**, an identification number **ID**, coordinates **XYZRTUVW**, characterization **Attribute**, addressing information (Template), individual remark **Comment**. In addition each Positionlist can have some application specific columns. The columns have their own properties like name, optional units, display width, data size, default value, etc. Settings these properties is described in section [Configuration](#).

### No.

Serial numbers are set automatically by the Raith software, they cannot be changed by operator. They are used for addressing commands and to select a data line for scanning or editing purposes.

The layout of serial numbers can be changed by setting the variable **Module status > Positionlist > Line Number Format**. The syntax is: **Line Number Format** = "%<0><digits>d" where <0> is optional to display leading zeros, and <digits> is the maximum number of digits for each serial number.

#### Examples:

Line Number Format = %3d displays 1, 2, 3, ...

Line Number Format = %03d displays 001, 002, 003, ...

Line Number Format = %04d displays 0001, 0002, 0003, ...



The serial number is dynamically generated and may change due to another sorting of the lines, e.g. after a filter command, etc.

**ID**


**ID** numbers may be freely defined and changed by operator. They are used for addressing commands and to select a data line for scanning or editing purposes.

In contrast to the serial number, the ID number of a data line will not change due to display or filter restrictions.

**XYZRTUVW**

Any Positionlist must have at least one or more coordinates out of the range X, Y, Z, R, T, U, V, and W.

**Attribute**

Attributes are very important features of the Positionlist concept, since they may contain key codes for controlling purposes or other important information. In addition, attributes are used for display restrictions as described in section  *Including and excluding*. So, attributes should be used to qualify or classify individual objects or positions.

Allowed inputs for attributes are all small letters a-z, all capital letters A-Z, single digit numbers 0- 9, and all combinations of the above.



The standard value for attributes can be changed by setting the variable **Module status > Positionlist > New Attributes**. This variable is used to set a standard entry when creating a new data line, e.g. by using the command **Edit > New**.

**Template**

Templates are used to define, how the addressing of the stage is done, i.e. which of the values given under X, Y, Z, R, T, U, V, and W are used and in which order. Within the Raith software, template generation and handling is fully automated and requires no interaction by the user.

For special purposes the user can use and modify the templates in order to define which coordinate combinations are to be used for driving the stage. Data lines without a template are ignored for stage addressing.

The standard value for templates can be changed by setting the variable **Module status > Positionlist > New Template**. This variable is used to set a standard entry when creating a new data line, e.g. by using the command **Edit > New**.



Generally, it makes no sense to have templates X and U at the same time. This is also true for Y and V, as well as for Z and W.

**Comment**

Can be used to store additional information for each position.



For predefined tasks like an exposure or a mark scan, the **Comment** field is used internally, e.g. to define which structure to expose or which scan to execute. Do not alter its content.

### 7.1.2 Icon bar

This bar contains some the often used commands as icons. These commands are **File > Open**, **File > Save**, **Edit > List properties**, **File > Open assigned Wafermap**, **Edit > New > Insert before**, **Edit > New > Insert after**, **Edit > Delete**, **Scan > Previous**, **Scan > Selection**, and **Scan > Next**. Then two fields are available to include and exclude lines with some specific attributes.

#### Including and excluding

To display or to select only a fraction of the tasks, it is possible to include or exclude lines, which contain a certain character in their **Attribute** field. By typing a character into the **Include** field, only the lines containing this character in their **Attribute** field are included in the display. Whereas typing a character into the **Exclude** field prevents the lines containing this character in their **Attribute** field from being displayed. One may enter several attributes without separation. Attributes are case sensitive, so entry of lower case characters or upper case characters will achieve different results. In addition, including and excluding can be used at the same time and only lines fulfilling both conditions are shown. Default values are all for **Include** and none for **Exclude**. The attribute entry is stored within the related drop-down list as a history, but this history is available only until the Positionlist is closed.



The search restrictions do not change the content of the Positionlist. This means that those data lines, which are not displayed, keep although staying in the Positionlist data file and can be made accessible by changing the search restrictions.

### 7.1.3 Information Line

This line contains the following information from left to right:

- Which line is currently selected and how many lines exist.
- A star indicates that this Positionlist was modified and contains some data which has not been stored so far.
- If the Positionlist is used in connection with defect finder Lot ID, Wafer ID, and Slot can be used to identify a specific wafer. The information itself can be changed by using the command **Edit > Sample information**.

## 7.2 Menu commands

It is possible to handle more than one Positionlist on the desktop. In the case that more than one Positionlist has been opened all commands are applied to the active one, only.




The behavior on opening a new Positionlist can be defined using the command **Window > Save Settings**. This command is described in section [Using projects for customizing](#).

### 7.2.1 File menu

- Open** Choose this command to load a Positionlist into the current Positionlist window. A dialog box offers the capability to keep the format, i.e. all list properties, of the already opened list. Answering no uses the format for the newly opened list.
- This command is different from **File > Open positionlist ...**, which adds another Positionlist window to the desktop.
- Save** Choose this command to save the activated Positionlist under its current name.
- Save as ...** Choose this command to save the activated Positionlist under a freely selectable name.
- New positionlist ...** Choose this command to open an empty Positionlist window.
- Open positionlist ...** Choose this command to open a previously saved Positionlist.

### 7.2.2 Edit menu

- Cut** Choose this command to cut out the currently selected lines and copy them to the clipboard.
- Copy** Choose this command to copy the currently selected lines to the clipboard.
- Paste** Choose this command to paste lines from the clipboard to the Positionlist before the currently selected line.
- Delete** Choose the command to delete the currently selected lines.
-  If no data line is selected, this command will not work. A deleted data line cannot be restored.
- Select all** Choose this command to select all lines of a Positionlist.

- New > Insert before** Choose this command to insert a new line before the currently selected line. The new line contains only the current stage position, the default template as well as the default attributes.
- New > Insert after** Choose this command to insert a new line after the currently selected line. The new line contains only the current stage position, the default template as well as the default attributes.
- New > Stage Position** Choose this command to open the dialog **Store new position ...** which contains already the current stage position, the default template as well as the default attributes. After editing the position properties and applying **OK**, a new line is appended at the end of the Positionlist. Press **Cancel** to quit dialog without adding a new position.
- Current ...** Choose this command to open a window for editing of the selected line.

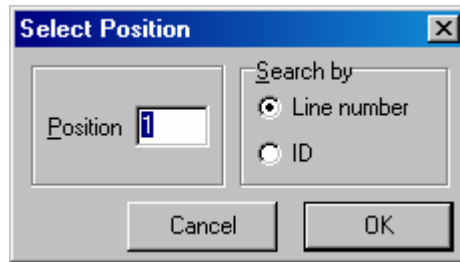
**Figure 46:** Window to edit the various data fields of a line within a Positionlist.

| Field    | Value    | Units |
|----------|----------|-------|
| Options  |          |       |
| Type     | EXPOSURE |       |
| Size-U   | 52.920   | μm    |
| Size-V   | 52.920   | μm    |
| Points-U |          |       |
| Points-V |          |       |
| Dir      |          |       |
| Avg      |          |       |
| Pos1     | 26.458   | μm    |
| Pos2     | 26.458   | μm    |
| Pos3     |          | μm    |
| Link     |          |       |

The meaning of the fields **ID** to **Comment** is described in section [Universal Columns](#). Whereas the meaning of the **User defined fields** depend on the application and is therefore described in various section of this manual.

- Line number/ID ...** Choose this command to select a line by using the line number or its ID. Hence this command is useful to avoid scrolling through extremely long Positionlists.

**Figure 47:** Window to select a line within a Positionlist either by its number or ID.

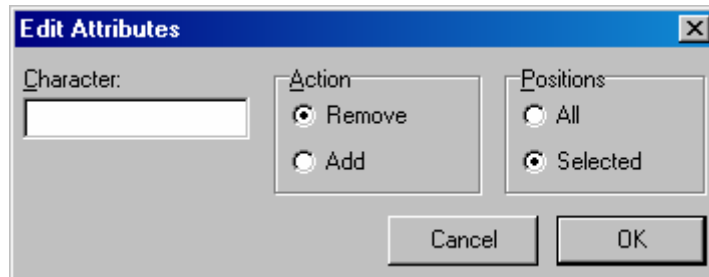


Within the following dialog, choose the select mode and enter the **Line number** or the **ID** within the **Position** field.

**Attributes ...**

Choose this command to add attributes to or remove attributes from all lines or only selected ones.

**Figure 48:** Dialog to edit Attributes of lines within a Positionlist.

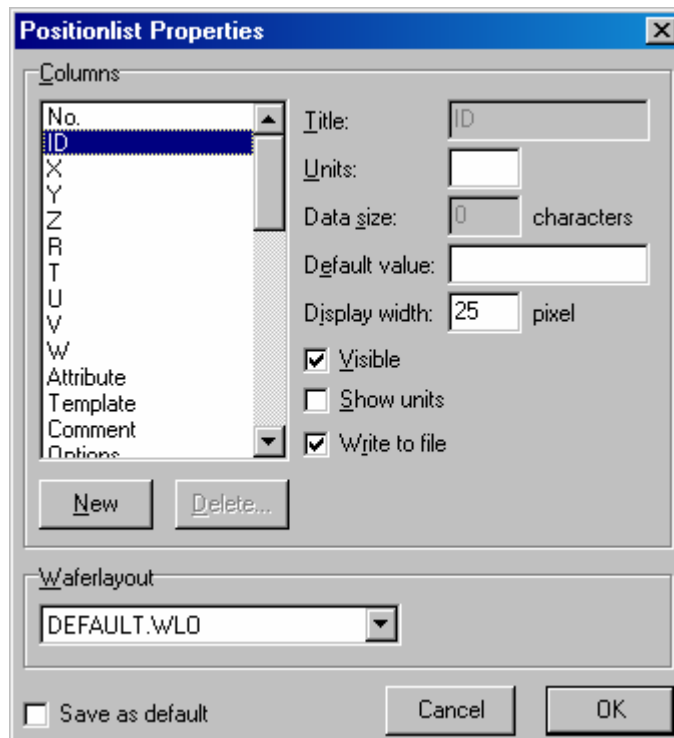


Within the related dialog box, enter the **Character**, select the editing mode **Remove** or **Add**, and specify to which **Positions** the modification should applied to. Please note that the evaluation of the **Attributes** is case sensitive and matches only whole words.

**List properties ...**

Choose this command to open a dialog to modify the properties of the columns and to select the assigned Wafermap.

**Figure 49:** Dialog to modify the column properties as well as the assigned Wafermap.





The list box on the left hand side contains names of the **Columns**. The list starts with the fixed columns serial number (**No.**), identification number (**ID**), coordinates (**X**, **Y**, **Z**, **R**, **T**, **U**, **V**, **W**), **Attribute**, addressing information (**Template**), **Comment**. Then additional application specific columns follow.

To add a new application specific column, click on **New**. To delete a application specific column, select the column first and then click on **Delete**. Only application specific column can be deleted.

To set or to change the layout properties of a column, the column name has to be selected within this list box. A selected column name appears to be highlighted.

On the right hand side, the layout properties for each selected column name are displayed. The meaning of the layout properties is as follows:

|   |  |
|---|--|
| <b>Title</b>  | The title can be changed only for user defined columns but not for fixed columns.  |
| <b>Units</b>  | The entered dimension is displayed directly behind the column title, if <b>Show units</b> is selected. They serve for information purposes only, but have no influence on calculation routines.                            |
| <b>Data Size</b>  | This setting reserves space for storing the data within the Positionlist file. It can be changed only for application specific columns.  |
|  | A fixed memory of 1024 Bytes is reserved for each line. Therefore, the user has to make sure that enough space for the data is available. Not enough space to store the data is the main reason for losing information.    |
| <b>Default value</b>  | The default value can be set or changed only for application specific columns but not for fixed columns. It is used to set a standard entry when creating a new line.  |
| <b>Visible</b>  | If the check box is selected, the column will be displayed within the Positionlist.  |
| <b>Write to file</b>  | If the check box is selected, the column data will be stored within the Positionlist file. The serial number <b>No.</b> will never be written to file. The application specific columns will always be written to file.    |
| <b>Display width</b>  | The graphical representation of the columns can be accommodated by assigning a display width for each of them.   |
|  | This can also be set directly within the Positionlist window by using the mouse. For this, select the separating line between two column names and move it. To set the optimum column width, double click the column name. |

- Waferlayout** Select the Wafermap which should be assigned to the current Positionlist. The drop-down list contains all Wafermaps stored in the user directory "Wafer".
- Save as default** Select this option to use the applied settings for all newly generated Positionlists.
- Sample information** Choose this command to open the dialog for editing the sample information.

### 7.2.3 Filter menu

- Matrix Copy** The Matrix Copy filter serves to easily generate a position matrix consisting of a rectangular array positions.



The command is not available, if the activated Positionlist is empty.

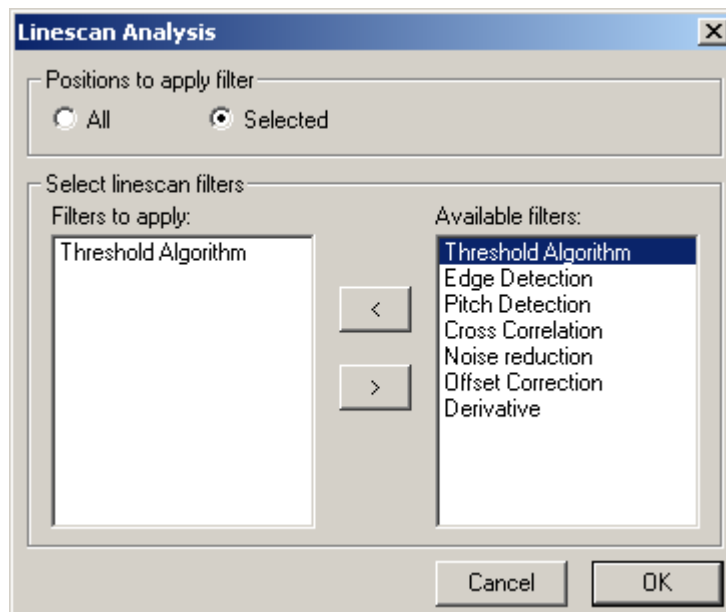
The result of the matrix copy operation is a list of newly generated lines, which are added automatically. The related dialog has the following functionality:

**Figure 50:** Dialog to set parameters for Matrix Copy filter.

- Positions to copy** Choose whether all data lines are to be used as the base data lines or only the selected ones.
- Matrix size** Enter the numbers of matrix elements in U and in V direction.

- Step** Enter the distances between adjacent matrix positions in U and in V direction. The numbers may also be negative. In this case the copying action is performed into the negative U or V direction.
- Element order** Choose whether element order is row by row, i.e. **U (rows) first**, or column by column, i.e. **V (columns) first**. If Meander option is active the positions are ordered, the sequence of positions alternates from row to row or column to column. This optimizes the spatial order and therefore decreases the exposure time.
- Dose factor** Choose here by which amount the exposure dose factor is increased from matrix element to element. The factor can be set for **U**- and **V**-direction independently. The amount can be added or multiplied to the previous matrix element. By selecting **Calculate automatically** it is possible to use one amount for the complete matrix.
- Linescan analysis** This command is used to apply one or more Linescan filters to previously scanned Linescans in a Positionlist. So, its main use is retrospective data processing and analysis. Those filters which obtain a result will store this result as Pos1 through Pos3 in the Positionlist. The old data are overwritten!

**Figure 51** Dialog to define which Linescan filters to apply to Linescans in a Positionlist.

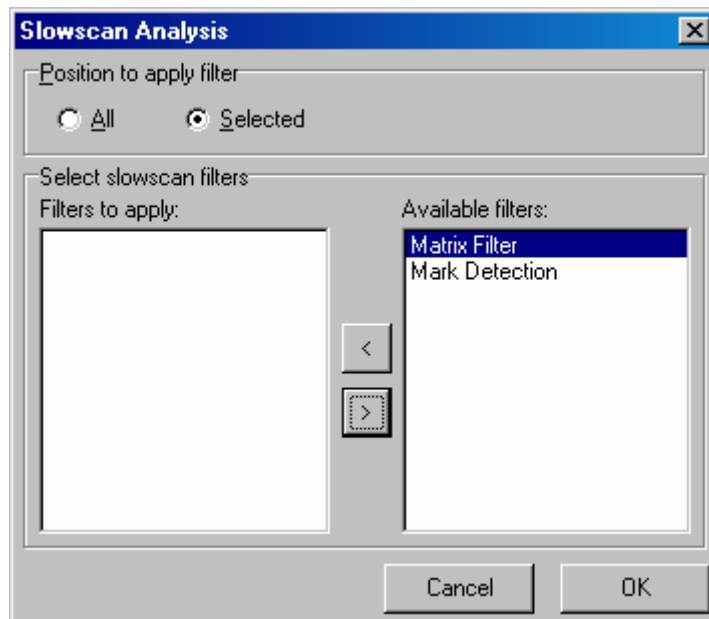


Within the dialog choose first, if the filters should be applied to **All** or only to the **Selected** Linescans. By using < and > buttons, it is possible to copy the filters from the list **Available filters** to the list **Filters to apply**. The functionality of the filters is the same as described in section [Evaluation algorithms](#).

- Slowscan analysis** This command is used to apply one or more Image filters to previously scanned Images in a Positionlist. So, its main use is retrospective data processing and analysis. Those filters which obtain a result will store this result as Pos1 through Pos3 in the Positionlist. The old data are overwritten!



**Figure 52:** Dialog to define which Image filters to apply to Imagescans in a Positionlist.

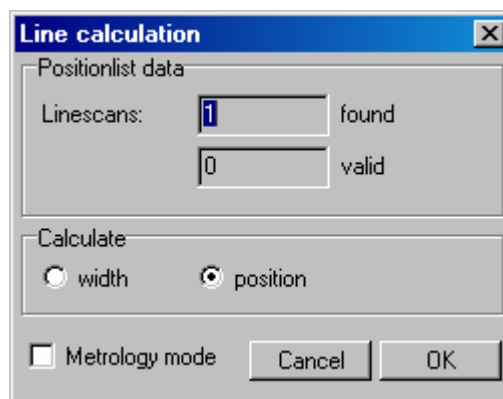


Within the dialog choose first, if the filters should be applied to **All** or only to the **Selected** positions. By using < and > buttons, it is possible to copy the filters from the list **Available filters** to the list **Filters to apply**. The functionality of the filters is the same as described in section [Evaluation algorithms](#).

### Line calculation

This command calculates the distance between Pos1 and Pos2, or the mean value of Pos1 and Pos2 of all valid Linescans in a Positionlist. In the case of the difference, the result can be interpreted as a **width**. In the case of the mean value, the result can be interpreted as a **position**. After applying the result will be shown in the Positionlist column "Pos3".

**Figure 53:** Dialog to calculate the width or the position of all valid Linescans.

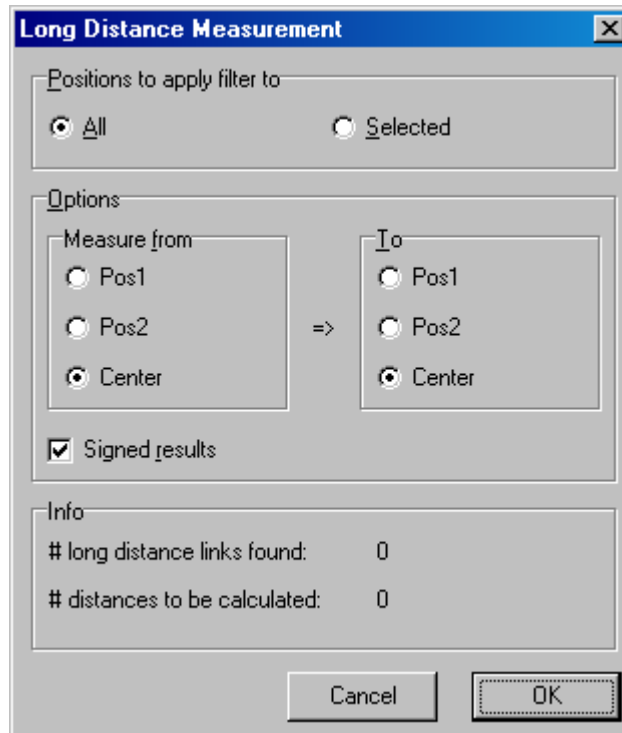


Select **Metrology mode**, to use the scaling previously defined in an Adjust UV procedure. Hence, the measurement is given in units of the stage.

### Long distance

This command calculates the difference between Pos1, Pos2, or Pos3 of one line and Pos1, Pos2, or Pos3 of another line within a Positionlist. If Pos1, Pos2, Pos3 are the results of position measurements the result is the distance between them.

Figure 54 Dialog to calculate the distance between two



Within the dialog chose first, if the filter should be applied to **All** or only to **Selected** positions. For distance calculation, the two lines must have a link assigned between them. To establish this link, type into the column **Link** of one of the two lines the ID of the other line. After applying the command, this line contains now the result.

Unselect **result with sign**, to calculate only the absolute values.

## Statistics

This command calculates and displays the mean, the minimum, the maximum and the standard deviation values for all data within the columns Pos1, Pos2 and Pos3 of a Positionlist.

Figure 55: Window displaying some statistical values of Pos1, Pos2 and Pos3.

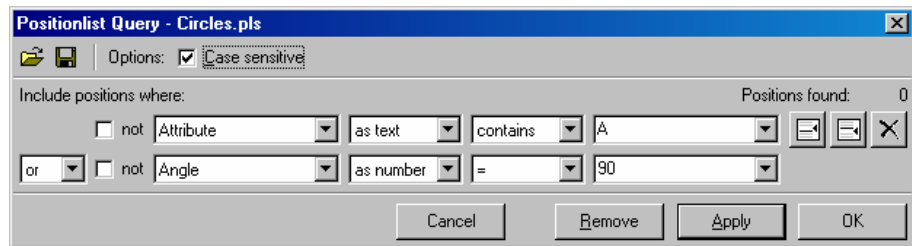
| field   | # values | mean   | minimum | maximum | std. dev. |
|---------|----------|--------|---------|---------|-----------|
| Pos1/μm | 1        | 26.458 | 26.458  | 26.458  | 0.000     |
| Pos2/μm | 1        | 26.458 | 26.458  | 26.458  | 0.000     |
| Pos3/μm | 0        | 0.000  | 0.000   | 0.000   | 0.000     |

By using **Filter**, it is possible to exclude positions from being displayed and used during calculation. To display and to use all, press **All**.

## Query

This command selects all positions which fulfill the criteria specified by means of the appearing dialog.

**Figure 56:** Dialog to select some positions fulfilling certain criteria.



The text comparison can be made **Case sensitive**.

Select first the name of the column, then if the comparison is made **as text** or **as number**. Select in the following the comparison condition. In case of a text comparison, the conditions **<** and **>** assume an alphabetical order. Then type in the data. The comparison can be negated by selecting the **not** option. To build a more complex comparison, press the **insert before** or **insert after** icons and connect the sub-conditions by using **or**, **and** and **xor**. Each sub-condition can be deleted using the **Delete** icon.

Press **Apply** to see the result of the selection. Press **Remove** to neutralize the filtering.

The whole comparison can be saved and recalled for later usage, using the **Open** and **Save** icons.

## Export

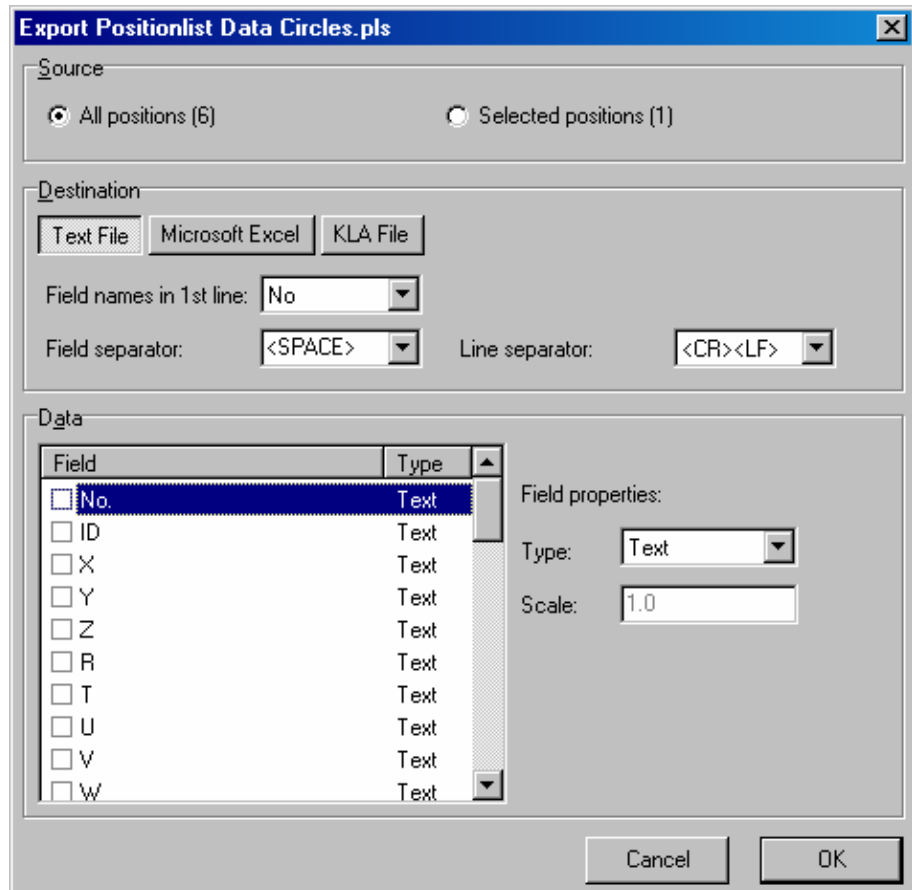
This command provides an universal export for all Positionlists.

There are three kinds of data export available:

- configurable **Text file** export,
- configurable export to **Microsoft Excel**,
- configurable export to **KLA File**.

The related dialog box (see figure) has the following functionality:

**Figure 57:** Dialog to export positions into a Text file.



Select **Source** whether all data lines are to be exported or only the selected ones. The entire number of data lines within the activated Positionlist is indicated in brackets.

Choose for **Destination** one of the options **Text File**, **Microsoft Excel** or **KLA File**.

- **Text File:** A text file needs the selection of a field separator. Common field separators are ";", ",", <SPACE> or <TAB>. If **Field name in 1st line** is selected, the column headers will be added to the target file.
- **Microsoft Excel:** This export option requires that the Microsoft Excel program is installed on the computer and it is running. Enter the name of the Microsoft Excel file to be used for export.
- **KLA File:** Export to a file which then can be imported into KLA system or many yield management programs.



To adapt the output to your regional settings, set the variable **Module status > Export Filter > Decimal Separator** to the used character.

To select one column for exporting, place a tick in front of its name. Choose then the **Type** depending on the columns contents. In case of selecting the option **Float**, one may enter a scaling factor. If for

example the external program handles the coordinates as  $\mu\text{m}$  instead of mm, the scale factor is 1000.

If export to a **KLA File** has been chosen, select from list **KLA field** the column which is used within KLA software and which corresponds to the active Positionlist column.

#### Statistic results

Choose this command to display a distribution of the content of column **Pos3**.

### 7.2.4 Scan menu

These commands assist the user to execute a list of task in a Positionlist.

Before scanning, make sure that the required or wanted scan options **Drive to position**, **Scan Manager**, **Exposure**, **Execute Macro** are in effect which is indicated by check marks. The Positionlist automatically differentiates what needs to be done to execute a selected line. This differentiation is performed by interpreting the Positionlist column **Type**.

#### Cancel Scan

This command stops the execution of a Positionlist.



While executing a Positionlist, it can be difficult to reach this menu command. Press the **ESC** key instead.

#### Selection

Choose this command to scan the selected positions. If no data line is selected, this command has no effect. If a group of lines is selected, only these lines are executed.

#### Next

Choose this command to scan the next position after the currently selected one. If no data line is selected, this command has no effect.

#### Previous

Choose this command to scan the previous position before the currently selected one. If no data line is selected, this command has no effect.

#### Line number/ID

Choose this command to select a specific data line for scanning. Within the additional dialog choose the **Line number** or **ID** and enter the number.

#### All

Choose this command to scan once through all positions within the Positionlist starting from the first data line and ending with the last data line.

#### From current

Choose this command to scan once through the positions within the Positionlist starting from the currently selected position and ending with the last data line.

|                          |   |
|--------------------------|---|
| <b>Endless</b>           | Choose this command to scan endless through all positions within the Positionlist starting from the currently selected position. Choose the command <b>Scan &gt; Cancel Scan</b> or the <b>ESC</b> key to cancel scan.  |
| <b>Drive to position</b> | Choose this option to drive the stage to each selected position. If this option is not in effect, the stage will not drive to the positions. Thus normally this option should be switched on.   |
| <b>Scan manager</b>      | Choose this option to execute adjustment and alignment procedures as well as Imagescans and Linescans. Thus normally this option should be switched on.   |
| <b>Exposure</b>          | <p>Choose this option to execute exposure steps of GDSII structures.</p> <p>The name of the GDSII structure is listed in the column <b>Comment</b>, the GDSII file is listed in the column <b>File</b>, and their destinations are defined as sample coordinates <b>U</b>, <b>V</b> within the Positionlist. In addition, the position can store information about a dose factor, step sizes, dwell times, the working area and layers. These parameters are described in more detail in section <a href="#">Exposures</a>.</p> |
| <b>Execute macro</b>     | <p>Choose this option to execute macros and scripts.</p> <p>The name of the macro to be executed is listed in the column <b>File</b> within the Positionlist.</p>   |

## 7.3 Mouse and keyboard commands

The usage is very similar to other spread sheet programs. A task can be selected by mouse click. The so selected task is marked by highlighting. A selection of groups or multiple lines is possible by applying the standard Microsoft Windows operations using the **Shift** respectively **Control** key. Whereas all tasks can be selected using **Control + A**.

Double-click within task opens an object with is linked to this position. This can be a GDSII design within the GDSII viewer, an image which was taken at this position, or in the case of an alignment or adjustment task another Positionlist.



To open the corresponding object, the software stores in the data field **File** a link to this object, e.g. filename and path of a GDSII. If the software can find this object, it opens a simple dialog to edit the data fields. This can be used to test, if the link to the object is broken.

Using the right mouse button opens a menu where addition commands are available.

Whenever a data line is selected and if a corresponding UV window has been opened in parallel, a related marker will be highlighted by

flashing it three times. This enables a quick orientation on where an object of interest is located.

The table below gives a summary of all available mouse commands within a Positionlist window.

**Table 24:** Mouse commands available within a Positionlist.

| Action       | Key(s) + Mouse Button | Functionality   |
|--------------|-----------------------|---|
| Single click | none + left           | Select line and unselect all other lines.   |
| Single click | <b>Control</b> + left | Select or unselect line without unselecting all other lines.  |
| Single click | <b>Shift</b> + left   | Select all lines from the first selected one to the latest selected one and unselect all other lines. |
| Single click | none + right          | Open a menu with the commands: <b>Open, Edit, Properties, Scan, New, Delete and Select all.</b>       |
| Double click | none + left           | Open a window related to the type of the line, e.g. an Imagescan, a Linescan, a GDSII viewer.         |

## 7.4 Drag and drop

A line can be copied or deleted by drag and drop technique:

- To copy a line to another Positionlist, select it, move it to the other Positionlist and release the mouse button.
- To copy a line within the same Positionlist, select it, move it to its new location by pressing the **Control** key.
- To move a line within the same Positionlist, select it, move it to its new location.
- To delete a line, drop it anywhere else within the program desktop.

A task can be relocated using drag and drop technique as well by picking it up in the list and dropping it within any UV window.

A summary of drag and drop operations is listed below:

**Table 25:** Positionlist drag and drop functionality.

| Source         | Object            | Target          | Action   |
|----------------|-------------------|-----------------|--|
| Positionlist   | line              | Positionlist    | Copy lines   |
| Positionlist   | line              | Image           | Redefine location of line using Image coordinates of mouse cursor as new location.                                     |
| Positionlist   | line              | Wafermap        | Redefine location of line using Wafermap coordinates of mouse cursor as new location.                                  |
| Positionlist   | line              | Program desktop | Delete line.   |
| Scan Manager   | Procedure or Scan | Positionlist    | Generate position with adjustment or alignment procedure or scan using current <u>UV</u> location.                     |
| GDSII database | Structure         | Positionlist    | Generate position with exposure line using current <u>UV</u> location.   |
| Automation     | File              | Positionlist    | Generate position with automation line with no stage movement, i.e. <b>Options=STAY</b> and <b>U=V=0, Template=dUV</b> |

## 7.5 Configuration

Using the command **Edit > List properties**, the Positionlist format can be configured for different applications. The default configurations within the Raith software are prepared to allow all standard tasks such as adjustment and alignment procedures, exposure runs and automation jobs. If the drag and drop technique is used, the all relevant parameters are transferred automatically into the Positionlist. A reconfiguration is not necessary. But to customize the functionality of a Positionlist or for debugging purposes, it is essential to know the functionality of each column and of the stored data.

For a general overview, the relevant Positionlist columns are sorted by the task they are reserved for.



## 7.5.1 Universal columns

**Table 26:**  
Functionality of  
universal columns.

| Column                         | Functionality  |
|--------------------------------|--|
| No.                            | Serial numbers are set automatically by the software. They are used for addressing commands and to select a position.  |
| ID                             | Identification number can be set by the operator. They are used for addressing commands and to select a position.  |
| <u>X</u> , <u>Y</u> , <u>Z</u> | Cartesian stage coordinates, generally <u>X</u> , <u>Y</u> , in horizontal direction and <u>Z</u> in vertical direction. Values are given in mm.   |
| <u>U</u> , <u>V</u> , <u>W</u> | Cartesian sample coordinates, generally <u>U</u> , <u>V</u> , in horizontal direction and <u>W</u> in vertical direction. Values are given in mm.  |
| <u>R</u> , <u>T</u>            | Rotation and tilt sample coordinates. Values are given in degree.  |
| Attribute                      | A combination of letters is used to assign and identify task and status of the position.<br>"X" identifies an exposure,<br>"W" identifies an adjustment or alignment procedure,<br>"I" identifies an Imagescan,<br>"L" identifies a Linescan,<br>"N" identifies a newly created position,<br>"S" identifies a successfully scanned position, and<br>"E" identifies an error.<br><br>The attributes controlling the status ("N", "S", "E") are used for a color coded line indicator: a blue dot for "N", a green dot for "S", a red dot for "E". |
| Template                       | The template defines how the addressing of the stage is done. Use the letter of a coordinate to use the corresponding axis. Use a "d" in front to perform a relative drive command. For example for lithography tasks almost exclusively "UV" are used.  |
| Comment                        | This column is automatically filled with additional information which is specific for one task. For example, in the case of an exposure task, it identifies the GDSII structure.   |
| Options                        | "STAY" or "DRIVE" to prevent or enforce a stage movement.  |
| Type                           | The type is internally used to identify and differentiate between the various tasks. The type is automatically generated. The Raith software uses the following types: EBEAMSCAN, IMAGESCAN, SLOWSCAN, MACRO, EXPOSURE, ALWF_MANUAL, ALWF_AUTO, ALWF_AUTOLINE, ADUV_MANUAL, ADUV_AUTO, ADUV_AUTOLINE, MARKSCAN, AUTOSCAN, AUTOMARKSCAN, RMARKSCAN, RAUTOSCAN, RAUTOMARKSCAN, CALIBSCAN, VIDEOSCAN, REFMARKSCAN, GDSII_MAN, GDSII_AUTO)   |

## 7.5.2 Linescans and Imagescans

The following types are used in connection with Linescans and Imagescans: EBEAMSCAN, IMAGESCAN, SLOWSCAN, MARKSCAN, AUTOSCAN, AUTOMARKSCAN, RAUTOSCAN, RMARKSCAN, RAUTOMARKSCAN.

**Table 27**  
Functionality of  
columns used by Scan  
Manager for  
Imagescans and  
Linescans.

| <b>Column</b>         | <b>Functionality</b>  |
|-----------------------|---|
| U, V                  | Sample coordinates of the center of the scan.   |
| Attribute             | Has to be "L" in the case of a Linescan and "I" in the case of a Imagescan.   |
| Comment               | Name of the scan which is executed; has to be defined in the Scan Manager.  |
| Options               | "STAY" or "DRIVE" to prevent or enforce a stage movement.   |
| Size-U,<br>Size-V     | Defines the scan length and width, e.g. of a mark, in sample coordinates. Data are given in micrometer.   |
| Points-U,<br>Points-V | Number of points, which can be defined freely up to 4096 points.  |
| Dir                   | Scanning direction of a Linescan in sample coordinates, i.e. U or V.  |
| Avg                   | Number of point-by-point averaging.   |
| Pos1, Pos2,<br>Pos3   | This column is used to store the result of a detection process, e.g. of the threshold algorithm.<br>Pos3 may contain the line width, the center or, in the case this scan is linked to another one, the distance.   |
| Link                  | By means of this column two scan can be connected to each to calculate the distance between them.<br>A link is used to configure long distance measurements between different entry points in the Positionlist. Based on a link between scanned and evaluated entries in the Positionlist, the distance may be either calculated between Pos1, Pos2, or Pos3 or combinations of it. It makes only sense to link Linescans of the same type and orientation. Links can be generated by text editing, graphically on any UV window. |
| File                  | Name of the file, which contains the scan.  |
| Time                  | Seconds since 1/1/1970, i.e. UNIX timestamp.  |
| Timestamp             | Human-readable time when a scan was recorded.   |
| Angle                 | Angle relative to the scanning direction under which scan is acquired.  |
| Mark-<br>Sequence     |   |

### 7.5.3 Adjustment and alignment procedures

The following types are used in connection with adjustment and alignment procedures: ALWF\_MANUAL, ALWF\_AUTO, ALWF\_AUTOLINE, ADUV\_MANUAL, ADUV\_MANUAL, ADUV\_AUTOLINE.

**Table 28:**  
Functionality of columns used by Scan Manager for adjustment and alignment procedures.

| Column         | Functionality   |
|----------------|---|
| U, V           | Sample coordinates where the adjustment and alignment procedure starts.                                 |
| Attribute      | Has to be "W".  |
| Comment        | Name of the scan which is executed; has to be defined in the Scan Manager.                              |
| Options        | "STAY" or "DRIVE" to prevent or enforce a stage movement.   |
| Size-U, Size-V | Defines the scan length and width, e.g. of a mark, in sample coordinates. Data are given in micrometer. |
| Dir            | Automatically set to U.   |
| File           | Link to the Positionlist containing the sub-tasks for the procedure.                                    |
| Mark-Sequence  |   |

### 7.5.4 Exposure runs

The type EXPOSURE is used in connection with an exposure run.

**Table 29:**  
Functionality of  
columns used for an  
exposure.

| Column            | Functionality  |
|-------------------|--|
| U, V              | Sample coordinates of the center of the first write field.   |
| Attribute         | Has to be "X".   |
| Comment           | Name of the structure which is exposed; has to be defined in the GDSII file.   |
| Options           | "STAY" or "DRIVE" to prevent or enforce a stage movement.  |
| Size-U,<br>Size-V | Gives the length and width of the exposed area only for information purposes.  |
| Pos1, Pos2        | Half of the write field size.  |
| File              | Link to the GDSII file.  |
| Layer             | Layer which will be exposed; the layers are separated by "/", ", " or ";". A range of layers is indicated by "-".                          |
| Area              | The working area which will be exposed; the GDSII coordinates are separated by ";".  |
| DoseFactor        | A factor which is multiplied to the dose, i.e. the dwell times, prior to an exposure.  |
| Dwelltime         | Exposure dwell time in ms to be used for the exposure. If this column is empty, the dwell time is taken from the Exposure window.          |
| Stepsize          | Exposure step size in $\mu\text{m}$ to be used for the exposure. If this column is empty, the step size is taken from the Exposure window. |
| SplDwell          | Dwell time in ms for exposing single pixel lines. If this column is empty, the SPL dwell time is taken from the Exposure window.           |
| SplStep           | Step size in $\mu\text{m}$ for exposing single pixel lines. If this column is empty, the SPL step size is taken from the Exposure window.  |
| DotDwell          | Dwell time in ms for exposing single pixel dots. If this column is empty, the dot dwell time is taken from the Exposure window.            |
| SplDot            | Flag controlling, if single pixel lines and a single pixel dots are exposed, if corresponding setting from the Exposure window is used.    |

### 7.5.5 Automation task

The type MACRO is used in connection with an automation task.

**Table 30:**  
Functionality of  
columns used for an  
automation task.

| <b>Column</b> | <b>Functionality</b>  |
|---------------|---|
| U, V          | By default set to U=V=0.0 in combination with Template="dUV" to prevent stage from moving |
| Attribute     | Has to be "M".  |
| Template      | By default set to "dUV" in combination with U=V=0.0 to prevent stage from moving.         |
| Options       | "STAY" or "DRIVE" to prevent or enforce a stage movement.                                 |
| File          | Link to the macro or script file to be executed.  |





## 8 Linescans and Imagescans

|                                  |            |
|----------------------------------|------------|
| <b>8.1 Linescan window</b>       | <b>121</b> |
| <b>8.2 Imagescan window</b>      | <b>125</b> |
| <b>8.3 Evaluation algorithms</b> | <b>129</b> |

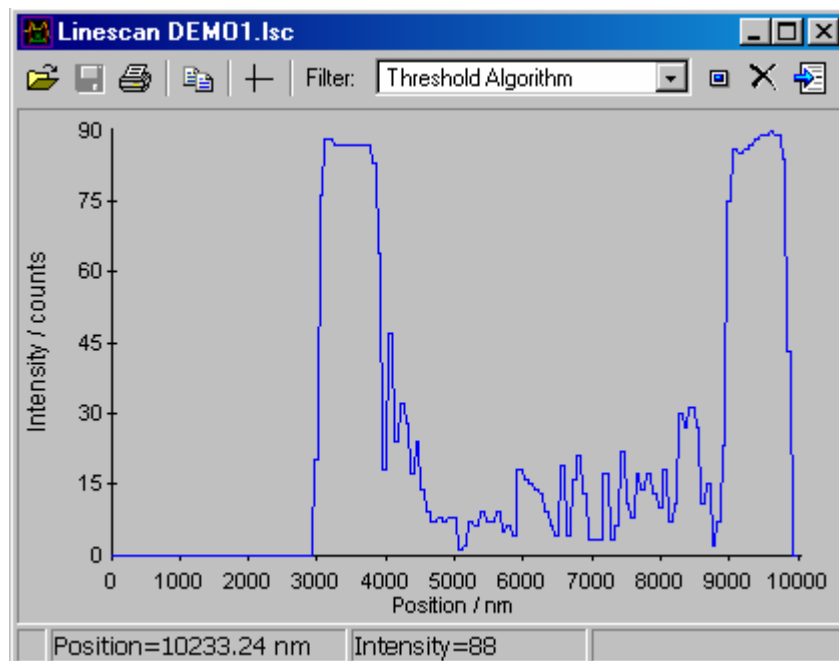
The intensity, e.g. of the secondary electron, can be recorded and displayed within the Raith software as a function of the position. One has to distinguish between two different types.

- Linescans: The intensity is recorded one-dimensionally. Even if several different cycles covering a certain area are recorded, in the end the results of each scan are summed up to an intensity curve as a function of the position along a straight line.
- Imagescan: The intensity is recorded two-dimensionally. The intensity is given as function of a position on the sample within an area. A normal image is acquired.

The main use of both types is detecting the position of marks, the performing CD, pitch, placement measurements, and for archiving the result after each process steps.

### 8.1 Linescan window

**Figure 58:** Linescan window displaying the intensity as a function of the position.



The Linescan window is opened automatically whenever a Linescan has been started, when using the command **File > Open Linescan**, or when double-clicking on a scan with a Positionlist.

The title bar shows the file name. In the vertical axis, the measured intensity is displayed within the range from 0 to the maximum intensity. The horizontal axis shows the scan range in nm. Within the icon bar the following commands are available **Edit > Open**, **Edit > Save**, **Edit > Print**, **Edit > Copy**, **Edit > Cross cursor**, **Filter > Select active filter**, **Filter > Apply active filter**, **Filter > Delete filter results**, and **Filter > Store filter results**.



### 8.1.1 File Menu


- Print** Choose this command to print a Linescan. This command opens the default print dialog. This command is also available over the Linescan window itself.
- Open ...** Choose this command to load an existing Linescan. This command replaces the actually loaded Linescan by the newly selected one. This command is also available over the Linescan window itself.
- Save** Choose this command to save the Linescan under its current name. This command is also available over the Linescan window itself.
- Save as ...** Choose this command to save the Linescan under a freely selectable name.

### 8.1.2 Edit Menu

- Cross Cursor** Choose this command to toggle between a mouse cursor and a cross hair.
- Copy** Choose this command to copy the Linescan into the Window's clipboard. From here it can be pasted into another application, for example for documentation purposes.

### 8.1.3 Filter Menu

- Apply active filter** Choose this command to apply the selected filter and to display automatically the result. This command is also available over the Linescan window itself by pressing .
- Select active filter** An additional drop-down menu appears. Choose here to define the active filter. An Overview over the available filters is given in section [Linescan filters](#). This command is also available over the Linescan window itself by selecting a filter from the drop-down list.
- Delete filter results** Choose this command to delete the result of the selected filter. This command is also available over the Linescan window itself by pressing .

**Store filter results** Choose this command to store the result of the selected filter to the Positionlist. This command can only be used, if the Linescan was opened from a Positionlist. When using one of the threshold algorithms the left edge is stored in column **Pos1**, the right edge is stored in column **Pos2**, and the width or position is stored in column **Pos3**. This command is also available over the Linescan window itself by pressing .

### 8.1.4 Linescan filters

In the following it is described, how a Linescans can be processed, for example to reduce the noise, and how a specific structure can be found, for example a maximum in the intensity.

#### Post-processing filters

Very often not only a recording but also a processing is required. The setup of these parameters is described in the following. It is important to know that these filters modify the data itself. Thus it is not possible to switch back to the unmodified data after applying one of these filters.

**Noise reduction** Choose this filter to perform a numerical averaging after recording the data. Two parameters define the averaging. **Number of average points** is used to define over how many points along the scan direction the average is calculated. Whereas **Number of iterations** defines how often the averaging is done.


**Offset correction** Choose this filter to subtract a background. The calculation is done in such a way that the minimum of the intensity is set to zero.

**Derivate** Choose this filter to calculate the derivation of the intensity signal.

#### Finding structures


After recording and optionally processing, Linescans can be evaluated also for line width, position, and distance measurements. It is important to know that these filters do not modify the data itself. These filters store only the result of the evaluation.

**Check Amplitude** Choose this filter to verify that the intensity is larger than a certain level. A typical application would be search for a structure and to identify those locations on the sample where the structure is missing.


**Peak detection** Choose this filter to identify a peak structure within the recorded data for an example to determine its width. Select first the Edit button  to set the parameters for the peak detection algorithm. A detailed description of the parameters is given in section [Threshold](#)

*algorithm*. After selecting these parameters activate the option and define if the position or the width should be stored.


**Edge detection**

Choose this filter to search for an edge within the recorded data for an example to determine its position. Select first the Edit button  to set the parameters for the edge detection algorithm. A detailed description of the parameters is given in section [Threshold algorithm](#). After selecting these parameters activate the option and define if the position or the width should be stored.

**Pitch detection**

Choose this filter to search for an edge within the recorded data for an example to determine the distance between two edges. Select first the Edit button  to set the parameters for the pitch detection algorithm. A detailed description of the parameters is given in section [Threshold algorithm](#). After selecting these parameters activate the option and define if the position or the width should be stored.

**Cross correlation**

Choose this filter to compare the measured intensity with a previous recorded intensity. Therefore this option is very helpful when a irregular shape of a structure prevents the operator from using another algorithm. Select first the Edit button  to set the parameters for the cross correlation algorithm. A detailed description of the parameters is given in section [2-dimensional mark detection](#). After selecting these parameters activate the option. The result of the algorithm can only be a position. Therefore, the **Check detected width** option is disabled, when selecting this option.

**Check detected width** If a structure with a certain width was scanned, this filter can be used to verify that the width is of a certain size. Therefore this option is helpful to identify such structures which are too small or too large.

### 8.1.5 Mouse and keyboard commands

Use **Control** + **C** to copy an image of the Linescan into Window's clipboard to paste it then into any other application.

Use **Control** + **O** to load an existing Linescan into current window.

Use **Control** + **S** to save current Linescan.

Use the right mouse button to sequentially set two marks within the Linescan. These marks can be for example edges or significant features. The positions of these two marks are indicated by two red lines and are stored together with the Linescan.

Use the left mouse button and move the mouse to zoom into the Linescan data. Thus it is possible to have a closer look onto a specific substructure. Use the left mouse button again to zoom out.

**Table 31:** Mouse commands available within a Linescan.

| Action       | Key(s) + Mouse Button | Functionality   |
|--------------|-----------------------|---|
| Single click | none + right          | Sets sequentially two marks to define manually edges, etc.          |
| Drag         | none + left           | Zoom into Linescan data. To zoom out press left mouse button again. |

## 8.2 Imagescan window

Digital images can be acquired and displayed conveniently within the Raith system by making use of the high resolution scan generator. The main use of the image acquisition for lithography applications is related to mark recognition which is an essential part of every lithography task.

The image acquisition commands within this mode make use of the high resolution scan generator. The images are acquired with the current scan calibration, i.e. write field zoom, shift, and rotation. In addition, the images are displayed in UV-coordinates.

The link to the absolute sample coordinate system is detected from the position sensing system of the sample stage. The operator has access to this transformation in the status bar when moving the cursor over the image window. The status bar displays the sample coordinates UV, the stage coordinates XY, and the window coordinates. Scaling is indicated by scale bars in the lower left corner of the Image window.

The images are handled as UV windows allowing addressing, drag and drop, overlay options.

### 8.2.1 File Menu Commands

|                         |  |
|-------------------------|--|
| <b>Close</b>            | Choose this command to close the activated image.  |
| <b>Close all images</b> | Choose this command to close all opened images.  |
| <b>Save image</b>       | Choose this command to store the activated image under its current name. File format is BMP or TIFF due to the "Picture file format" settings within the <b>Imagescan Options</b> dialog (see command <b>Options &gt; Imagescan</b> ).         |
| <b>Save image as</b>    | Choose this command to store the activated image under a freely selectable name. File format is BMP or TIFF due to the "Picture file format" settings within the <b>Imagescan Options</b> dialog (see command <b>Options &gt; Imagescan</b> ). |
| <b>Print</b>            | Choose this command to print out the actually viewed area of the Image.  |

**New image** Choose this command to open a new image window. The image size is automatically set to the write field size from the Microscope control. The image location in sample coordinates is taken from the stage control unit.

**Open image** Choose this command to open an existing image.

### 8.2.2 Edit menu

**Copy** Choose this command to copy the active image into the Microsoft Windows clipboard. This allows pasting the image directly into a different application.

**Image information** Choose this command to show position, size and scan resolution of the activated image. Values for image position and size can be edited.

**Adjustment** Command common to all UV windows, described in section [UV Windows](#).

**Measure** Command common to all UV windows, described in section [UV Windows](#).

### 8.2.3 View menu

**Redraw** Command common to all UV windows, described in section [UV Windows](#).

**Zoom** A cascading menu opens with additional commands, described in section [UV Windows](#).

**Overlays** Command common to all UV windows, described in section [UV Windows](#).

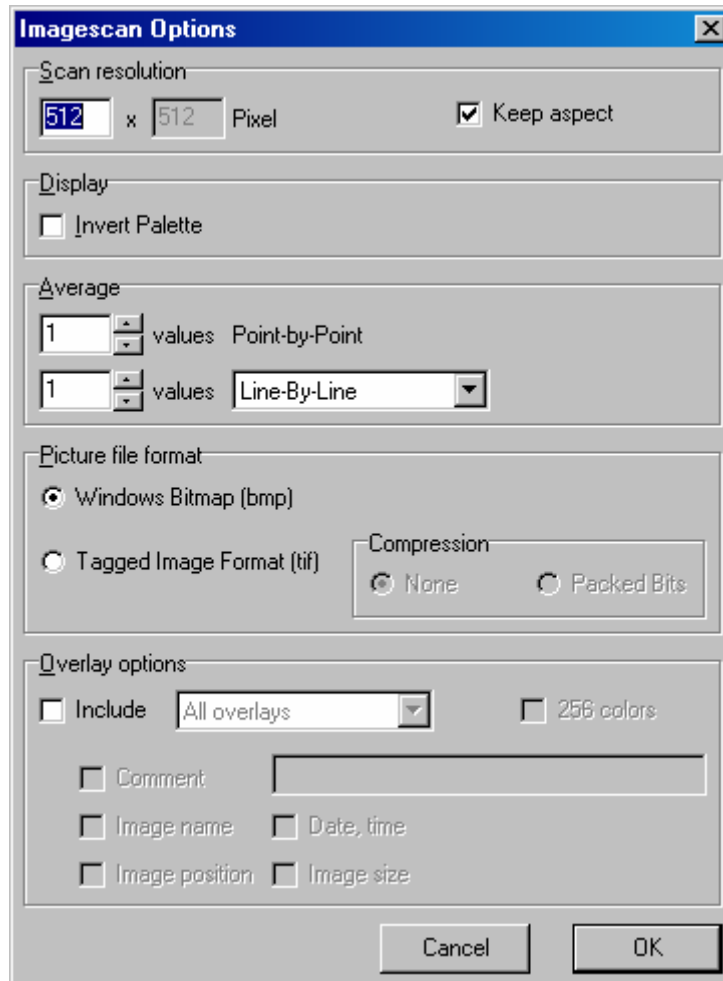
**Toolbox** Command common to all UV windows, described in section [UV Windows](#).

### 8.2.4 Options menu

**Histogram** Choose this command to show the distribution of gray levels.

**Imagescan** Choose this command to set image scan parameters.

**Figure 59:** Dialog to set Imagescan parameters.



The related dialog box allows to set and to change the Imagescan parameters. These Imagescans are scanned with the scan generator unit and are based on the alignment of the write field. The scan size is the selected write field size.

The dialog box has the following functionality:

- |                        |   |
|------------------------|---|
| <b>Scan resolution</b> | Enter the number of pixels along the U and V axes. The number of pixels must be from 64 up to 4096. Select <b>Keep aspect</b> to record a quadratic image.  |
| <b>Display</b>         | If <b>Invert Palette</b> is selected, the inverted gray level palette is displayed on the screen. Otherwise the original gray level palette is displayed. This setting will be saved within the image file.   |
| <b>Average</b>         | Enter the number of <b>Point-By-Point</b> averaging cycles, which results in a multiple intensity sampling at each individual point to enhance the signal-to-noise ratio.<br><br>Enter the number cycles and choose either <b>Line-By-Line</b> or <b>Frame-By-Frame</b> for signal averaging by multiple scans. If <b>Frame-By-Frame</b> is chosen, the entire image is scanned as often as defined by the number of averaging cycles. The screen will be refreshed |

continuously. If **Line-By-Line** is chosen, each line is scanned as often as defined by the number of averaging cycles.

**Picture file format** Choose one of the file format option buttons for storing of the scanned image. Choose **TIFF compression** to compress the data in the case that the **Tagged Image Format (TIF)** is used.

### Overlay options

Select **Include** to store overlays together with the image. In this case, choose between **Scaling bars only** and **All overlays**, i.e. overlays of Positionlists, GDSII elements, etc. In addition, it is possible to include a comment: the image name, the image position, the date and time, or the image size. Select 256 to store a colored image. If overlays are included, the overlay information is stored within the image itself. Hence, a post-processing of this image, e.g., image filter, can not applied etc.

### Scale Image

Choose this option to display the Imagescan in such a way on the screen that one image pixels correspond to one screen pixel. This option has to be set for each opened Image window individually.

### Cursor grid

Select the step size the cursor can be moved in an image.

### UV display...

Command common to all UV windows, described in section [UV Windows](#).

## 8.2.5 Imagescan menu

### Continuous

Choose this command to start a continuous image scan at the actual sample coordinate.

### Single

Choose this command to start a single image scan at the current sample coordinate.

### Stop

Choose this command to stop an image scan immediately.

## 8.2.6 Filter menu

### Matrix Filter

This command can be used for post-processing images. After choosing a dialog opens to type in a matrix or to select a predefined matrix from a list. The filter works in such a way that the given matrix is folder with the image which is also interpreted as a matrix. The result is then stored back to the image. For example folding the matrix

$$\begin{pmatrix} 0 & 0 & 0 & 0 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix}$$

with an image is equivalent to an averaging over

all neighbors of each pixel.



## Mark Detection

This command can be used for detecting a structure and its deviation from a reference position by comparing the image with a reference image. Its functionality is described in section [2-dimensional mark detection](#).

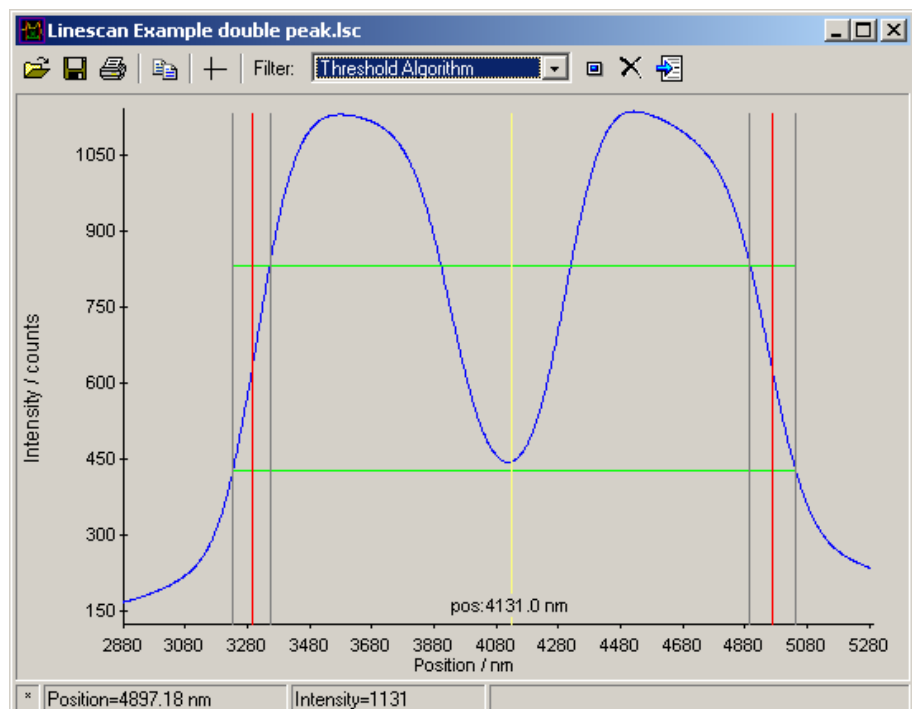
## 8.3 Evaluation algorithms

In this section the theoretical background of the various algorithms is described.

### 8.3.1 Threshold algorithm

The basis for the peak detection, the edge detection, or the pitch detection is a threshold algorithm. The idea of the threshold algorithm is that in all three cases the intensity has to go through two levels or thresholds. Within Figure 60 these two thresholds are indicated by two green lines. The usage of two levels makes the algorithm more robust because simple outliers can be filtered out by setting the second threshold high enough.

**Figure 60:** Linescan after applying the Threshold Algorithm to determine the center of this double peak structure.



The range between the intersections of threshold levels with the intensity slope is called an edge. The boundaries of the two edges are indicated in Figure 60 by gray lines. The actual position of an edge can be defined between these boundaries. The position is marked by red lines in Figure 60.

After detection two edges it is then possible to calculate the distance or the center between them. The distance or the center can be

interpreted for example as the width or as the position of a structure on the sample. For example the center of the double peak structure in figure is marked by a yellow line and its numerical value is given too.

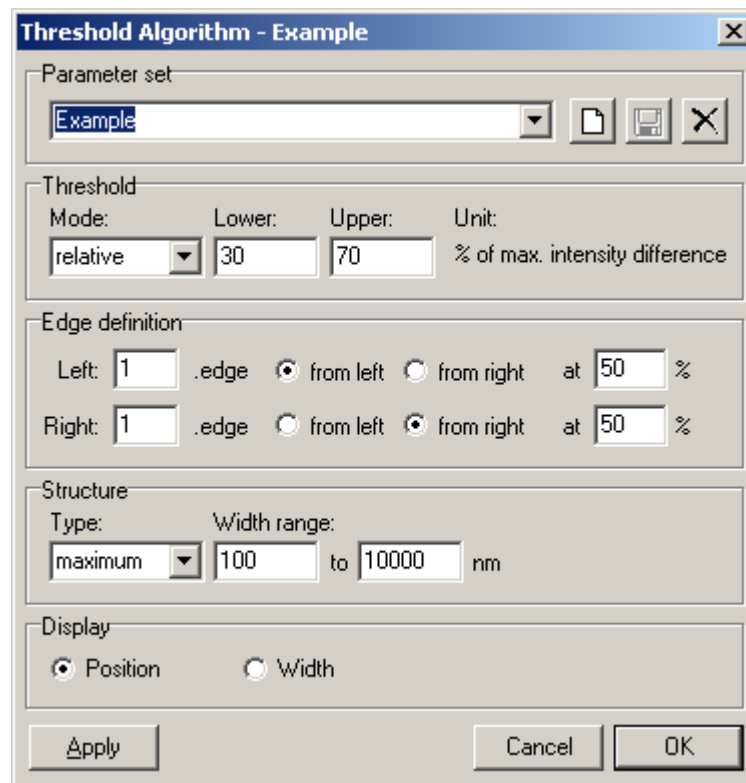
The threshold algorithm can be modified by several parameters. All these parameters together form a set which is stored under one name. In all three cases, i.e. for the peak detection, for the edge detection, and for the pitch detection, these parameters are very similar so that they are described in the following together.

### Setting up threshold algorithm

The threshold parameters can be accessed from several points within the software. The way described in the following has the advantage that different parameters can be tried out while a pre-recorded Linescan has been opened beforehand.

- STEP 1 ►** Open a pre-recorded Linescan by using **File > Open Linescan**. Some example Linescans come with the software.
- STEP 2 ►** Choose the command **Filter > Select active Filter** to select the **Threshold filter** for detecting a peak or valley, the **Edge detection** or the **Pitch detection** filter.
- STEP 3 ►** Choose the command **Filter > Apply active Filter** to open the window for setting up the parameters.

**Figure 61:** Parameter set window to define threshold algorithm for **Peak Detection**.



**STEP 4 ►** Select the name of an existing **Parameter set** or, if a set with appropriate parameters does not exist, create a new set by choosing the New icon.

**STEP 5 ►** Select the following parameters for the threshold levels, the edges and the structure type to define the measurement.

**Mode** Select a relative or absolute definition of the threshold values. Normally, relative definition is the more robust detection, because the success depends not on the signal brightness and contrast. But to discriminate out scans achieving not a certain signal level, it can make sense to use an absolute definition.

**Lower, Upper** Type in the threshold values either from 0% to 100% in the relative definition or from 0 to the maximum intensity in the absolute definition mode. Press **Apply** to see the current threshold levels as horizontal, green lines.

**Left, Right** Choose which edges are defining the structure and from which direction the algorithm is searching for these edges. This setting becomes important if more than one peak is present within the Linescan or when determining the pitch of a grating. The intersections of the intensity curve with the two threshold levels define a range on the position axis. To calculate the position of the edge within this range use the **at** parameter. A value of 50% means the edge is in the center of this range, whereas a value 0% or 100% means at the left or the right border of the range.

**Type** Select either "minimum" or "maximum" from the drop-down list box, if the structure is defined by a minimum or a maximum in the intensity slope.

**Width range** Using this setting, it is possible to reject structures which are too small or too large. This function limits the range the algorithm is searching for the second edge after finding the first edge. If the second edge is not found within this range, the algorithm sets the error flag and position of the edges as well as the center, the size, or the pitch are not calculated.

**Display** Choose this option to display the width or the center between the two edges numerically as well as by a yellow line. This option effects only what is display, but not the information which is stored in a Positionlist.

**STEP 6 ►** After finding a parameter set press **Apply** to start a measurement.

**STEP 7 ►** Choose save to store the optimum parameter set under the current name.



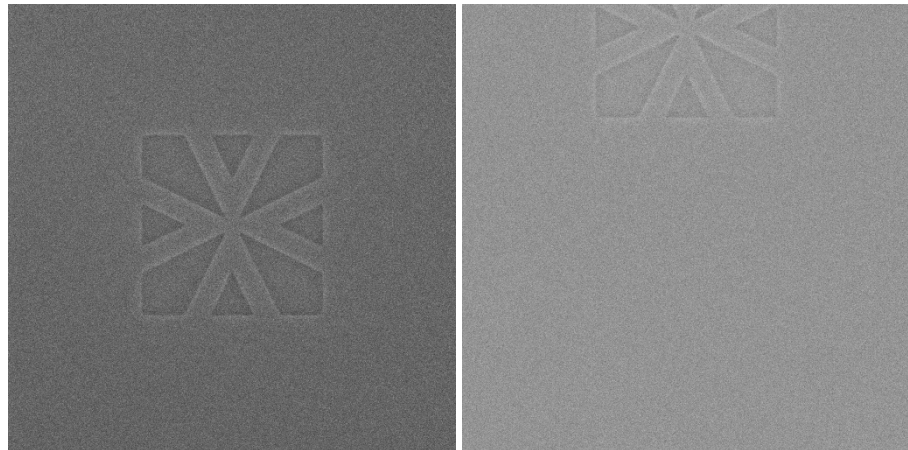
Sometimes it is very difficult to find the correct parameter set for the threshold algorithm, especially when dealing with a new Linescan. In this case it is recommended to scan first one exemplary scan, open this scan by using File > Open Linescan or by double-clicking it in a

Positionlist, and to start the Threshold algorithm by using the commands **Filter > Select active Filer** and **Filter > Apply active Filer**. In this case the **Apply** button is accessible applying the current parameters to Linescan. This makes it easy to try out various parameters and, if the right set is found, it can be stored and recalled for later usage.

### 8.3.2 2-dimensional mark detection

This algorithm compares two Images with each other. The result of the comparison is first whether a structure is present in an image and secondly how far the structures in the two images are shifted with respect to each other. Such a shifted structure and its reference are shown in Figure 62.

**Figure 62:** Two SEM images of the same structure, the reference (left) and the shifted structure (right).



A very similar algorithm is available for Linescans too. Here it is called **Cross Correlation** and its working principle is the same for Images. Thus, only the two-dimensional case is described in the following.

By comparing the images in Figure 62 the challenges for such an algorithm are clearly visible. A robust algorithm has to be able to overcome

- contrast and brightness variations,
- image distortions, like rotations and different scaling,
- visibility variations, e.g. structures might be only partially visible or even missing,
- and the background noise should not affect the comparison.

In the literature two different algorithms are discussed.

- The approach of a pure cross correlation has the disadvantage that it requires in general a pre-processing to detect larger shifts, because only small shifts are detected reliable.

- The approach of a pure deconvolution has the disadvantage to be very sensitive on noise such a careful noise-reduction is required beforehand.

In this software an implementation is used combining the advantages of both approaches meaning that it is a combination of the cross correlation as well as the deconvolution. In the following this approach is described as far as it is necessary to understand and to use the software.

The starting point is the assumption that the shifted image can be calculated by using the following equation

$$\text{"shifted image"} = \text{"reference image"} \times \delta(u-u_0, v-v_0) + \text{"noise"}.$$

Herein  $\times$  labels the convolution of two images and  $\delta(u-u_0, v-v_0)$  is the two dimensional  $\delta$ -function which is shifted by  $u_0$  and  $v_0$ . The term "noise" summarizes all sources of noise, e.g. the background noise visible in all SEM images, the different appearance of the two images can also be interpreted as noise, and the noise which comes from the fact that during the calculations periodic boundary values are used. In general, "noise" should be an image too, but for our purpose a real number representing the strength of noise is sufficient and thus making the calculation much easier.

After calculating the Fourier transformation of "shifted image" as well as "reference image" and by giving the quantity "noise" the algorithm calculates the image  $\delta(u-u_0, v-v_0)$ . It is important to understand, that the so calculated  $\delta$  depends on the "noise" and one has to search for the optimum  $\delta$  by varying the "noise". Fortunately, the here implemented algorithm depends not critically on the exact value of "noise" and a value nearby gives a sufficient result. After finding the optimum  $\delta$   $u_0$  and  $v_0$  are determined by using the coordinates of the maximum intensity in the  $\delta$  image.

When using this detection algorithm automatically, it is very important to distinguish a successful detection of a structure from unsuccessful ones. An unsuccessful might occur, when for example a structure is completely missing. In this case the real noise is much larger than that one given by the quantity "noise" and a not optimum  $\delta$  is calculated. By using the maximum intensity of  $\delta$  in comparison to the variation of the intensity values in  $\delta$  and the extension of the maximum peak a quality is calculated. Its values can be between 0.0 and 1.0 corresponding to a perfect  $\delta$ . By setting a threshold for this quality it is possible to discriminate out unsuccessful comparisons between the two images.

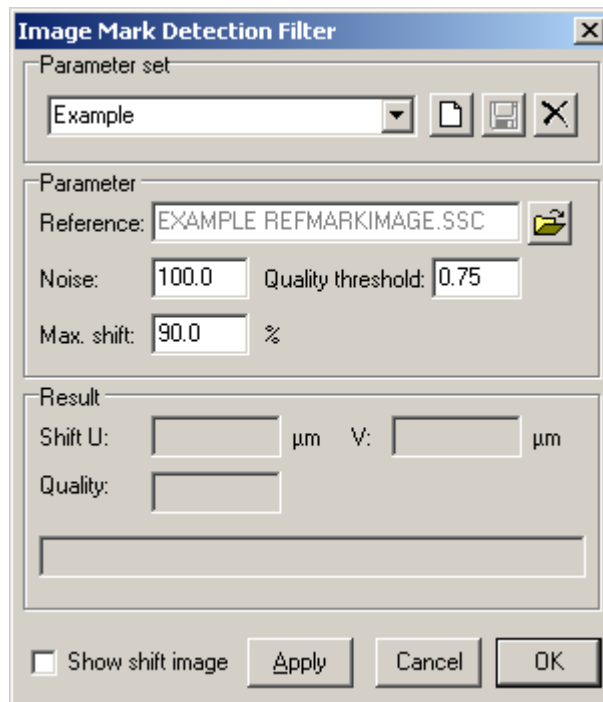
Even if the comparison of two images was successful, it might be necessary to react on a shift which is too large. In this case, it is possible to define in addition a maximum allowed shift.

## Setting up mark detection

The cross correlation parameters can be accessed from several points within the software. The way described in the following has the advantage that different parameters can be tried out while a pre-recorded Image has been opened beforehand.

- STEP 1 ►** Open a pre-recorded Image by using **File > Open image**. Some example images come with the software.
- STEP 2 ►** Choose the command **Filter > Mark detection** to open the window for setting up the parameters. Figure 63 shows this window.

**Figure 63** Window to define parameters for **Mark detection** filter.



- STEP 3 ►** Select the name of an existing **Parameter set** or, if a set with appropriate parameters does not exist, create a new set by choosing the New icon.
- STEP 4 ►** Select the reference image by using the Open Icon.
- STEP 5 ►** For the first attempt choose a **Noise** of 100.0 and **Max. shift** of 90% of the image width.
- STEP 6 ►** Select **Show shift image** and press **Apply** to calculate the  $\delta$  image its **Quality**.
- STEP 7 ►** Change **Noise** and press **Apply** again to find the largest value for the **Quality** and thus optimizing  $\delta$  and therefore the mark detection.
- STEP 8 ►** After finding the optimum value for noise, set **Max. shift**. The calculated shift is given in micrometer.
- STEP 9 ►** Choose save to store the optimum parameter set under the current name.

## 9 Scan Manager

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The Scan Manager is a supporting tool which allows to define and to locate intensity recordings. These recordings are then used during more complex tasks, like dimensional metrology jobs or write field alignments. These tasks are described in other sections: adjusting the sample to the stage is described in section [Stage to sample adjustment](#), aligning a write field is described in section [Beam to sample alignment](#) and during an exposure in section [Exposures](#). Within this chapter the focus lays on recording intensity, processing these intensities and using them for dimensional metrology jobs.

### 9.1 Main window

The various parameters can be individually stored for the various scan types. The organization of this is done in hierarchical way within the main window of the scan manager. For dimensional metrology jobs the following general scan types are available.

- Type Linescans, i.e. scans made along one direction by an electron or an ion beam. These scans are used for measurements of positions and distances between structures. But can also be used for line width measurements, if an exact line width determination is not critical.
- Type Images. These scans are used for recording images for example for off-line inspection or documentation purposes.
- Type Image Linescans. These scans are used for measurements of positions or distances in images. Hence, measurements are possible in an off-line manner.
- Type Calibration Linescans. These scans are used for measurements of line widths of structures where the exact line width determination is critical, e.g. as in CD measurements.

#### 9.1.1 Mouse commands

Clicking with the right mouse button on one of the scan types or the scans themselves opens a small menu with the same commands as given under the **Edit** menu.

### 9.1.2 Drag and Drop

Each of the scans can be placed within all UV-windows or a Positionlist by using the drag-and-drop technique. When using an UV-window as destination, the scan is stored in all open Positionlists. If no Positionlist is open, one is generated automatically.

## 9.2 Defining Linescans

A Linescan is recorded by moving the beam along one scan direction and measuring the intensity at each point. This scan direction is called the main direction. It can be along U- or V-direction as well as under an angle. In addition it is possible to average the intensity of several beam movements by defining a scan size perpendicular to the scan main direction. In the end, a Linescan is a single waveform showing the measured intensity versus a scan direction.

After recoding the intensity it is possible to perform a post-processing, for example noise reduction, as well as a subsequent evaluation, for example peak detection.

Starting from the scratch the first step is to define a new parameter set.

### 9.2.1 Basic settings

- STEP 1 ►** Select type Linescans and choose menu command **Edit > New** to create a new parameter set. Alternatively use the right mouse menu.
- STEP 2 ►** In the following properties window define the name for this Linescan using the corresponding input field.
- STEP 3 ►** Choose the tab **Main** to set the following Linescan parameters.
- Main Direction** Select the primary scan orientation to be either in horizontal, i.e. U-direction, or vertical, i.e. V-direction.
- Scan Size** Enter the length of the scan in  $\mu\text{m}$ . In general the scan size in the main direction is larger than in the averaging direction. **Keep aspect** ensures that if one of the scan sizes is changed the other is automatically scaled, such that the ratio between is constant. Please note, that for an finite scan size **No. of Pixels** must be larger than 1. Maximum scan size in is the current write field size.
- Step size** It is possible to define the distance between two points in  $\mu\text{m}$ . For the main direction the step size defines then the minimum resolution of the Linescan. For the averaging direction this defines the distance between two separate beam movements which are then summed up for averaging. **Step size** is a multiple of **Basic Step size** which is defined in **Exposure > Details**.



**No of pixels** It is possible to define the number of pixel along the main as well as the averaging direction. Maximum scan size in pixel is 4096 minus the number of pixels used to compensate dynamic effects. In addition, **No of pixels** has to be a value which can be divided by 4 without a remainder, because in such a way images are handled internally within Windows.

**Scan size**, **Step size**, and **No. of Pixels** depend on each other because the Scan size is the product of the two others. Consequently, the third value can be calculated after setting the two other quantities. Use the calculator button behind the value to perform the calculation. A message indicates, if these three values fit to each other. If this is the case, it is possible to confirm these settings by pressing **OK**.



**Scan size** and **Step size** are quantities, which are normally given by the scan task itself, and therefore should be defined first. **No of pixels** can then be calculated. Because of the restriction that **No of pixels** is equal to **Scan size / Step size**, it can be necessary to calculate the other quantities in the following.

**Point average** This parameter allows signal averaging by measuring the intensity at the same position several times. Therefore it is used to enhance the signal-to-noise ratio.

**Angle** Choose the angle to record a Linescan under a certain angle. The angle is defined relatively to the main scan so that it can only be varied in the range between  $\pm 45^\circ$ .

## 9.2.2 Advanced settings

### STEP 1 ►

Choose the tab **Advanced** to add additional parameters.

**Attribute** Enter a character to be added to the column "Attribute" of the Positionlist when dropping the scan into a target window. Please note that some characters have a special meaning and can not be used. By default the character L is used assuring that the scan is defined as a Linescan and the character N marks it as a new one. If other characters shall be used in addition make sure that also L and N are used.

**Position** This parameter defines the addressing mode of the scan. **Absolute** means that the stage drives to the position of the scan when dropped into a Positionlist. **Relative** means that the addressing is done with respect to the current stage position and the beam is deflected within the write field without driving the stage. If this mode is selected it is under the responsibility of the operator to type in the distance for the stage movement in U and V-direction.

**Options** Within this input field it is possible to define some options for the execution of the scan. For a typical Linescan the stay option is the only important one. Please not this option is placed automatically when selecting **stay at position**.

- stay at position** Choose this option to prevent the stage from driving. This option can be used in connection with relative positioning.
- halt before closing** Choose this option to halt execution which is useful for debugging purposes through the operator.
- save scan before closing** Choose this option to save the scan for example for documentation or off-line evaluation.
- STEP 2 ►** Choose **OK** button to quit the scan property definition and to save the new parameter set.

### 9.2.3 Processing Linescans

Very often not only a recording but also a processing is required. The setup of these parameters is described in the following.

- STEP 1 ►** Select one Linescan.
- STEP 2 ►** Choose the menu command **Edit > Properties** to open the property window or alternatively double click the scan using the left mouse button. Select the tab **Post Processing**.
- STEP 3 ►** Choose **Noise reduction**, **Offset correction**, **Derivate** to modify the Linescan directly after recording it. The functionality is described in section [Post-processing filters](#).
- STEP 4 ►** Choose **OK** button to quit the scan property definition and to save the new parameter set.

### 9.2.4 Evaluating Linescans

After recording and optionally post-processing, Linescans can be evaluated also for line width, position, and distance measurements.

- STEP 1 ►** Select one Linescan.
- STEP 2 ►** Choose the menu command **Edit > Properties** to open the property window or alternatively double click the scan using the left mouse button. Select the tab **Evaluation**.
- STEP 3 ►** Choose **Check Amplitude**, **Peak detection**, **Edge detection**, **Pitch detection**, **Cross correlation**, **Check detected width** to evaluate some of the Linescan properties. The functionality is described in section [Finding structures](#). When using **Peak detection**, **Edge detection** or **Pitch detection** it is possible to determine which quantity is stored by selection either **Store position** or **Store width**. The position is the center between the two edges whereas the width is the distance between the two edges.

- STEP 4 ►** Choose **OK** button to quit the scan property definition and to save the new parameter set.

## 9.3 Defining Images

An Image is recorded by moving the beam along two scan directions and measuring the intensity at each point. At each point it is possible to average the intensity by measuring the intensity several times.

After recoding the intensity it is possible to perform a post-processing, for example noise reduction, as well as a subsequent evaluation, for example peak detection.

Starting from the scratch the first step is to define a new parameter set.

### 9.3.1 Basic settings

- STEP 1 ►** Select type Image and choose menu command **Edit > New** to create a new parameter set. Alternatively use the right mouse menu.

- STEP 2 ►** In the following properties window define the name for this image using the corresponding input field.

- STEP 3 ►** Choose the tab **Main** to set the following Image parameters.

**Scan Size** Enter the size of the scan in  $\mu\text{m}$ . This size is used for both directions. Please note, that for a finite scan size **No. of Pixels** must be larger than 1. Maximum scan size in is the current write field size.

**Step size** It is possible to define the distance between two points in  $\mu\text{m}$ . The step size defines then the minimum resolution of the Image. **Step size** is a multiple of **Basic Step Size** defined in **Exposure > Details**.

**No of pixels** It is possible to define the number of pixel. Maximum scan size in pixel is 4096 minus the number of pixels used to compensate dynamic effects.

**Scan size**, **Step size**, and **No. of Pixels** depend on each other because the Scan size is the product of the two others. Consequently, the third value can be calculated after setting the two other quantities. Use the calculator button behind the value to perform the calculation. A message indicates, if these three values fit to each other. If this is the case, it is possible to confirm these settings by pressing **OK**.



**Scan size** and **Step size** are quantities, which are normally given by the scan task itself, and therefore should be defined first. **No of pixels** can then be calculated. Because of the restriction that **No of pixels** is equal to **Scan size / Step size**, it can be necessary to calculate the other quantities in the following.

**Point average** This parameter allows signal averaging by measuring the intensity at the same position several times. Therefore it is used to enhance the signal-to-noise ratio.

**Average** Choose either **Line-by-Line** or **Frame-By-Frame** for signal averaging by multiple scans. If **Line-by-Line** is chosen, each line is scanned as often as defined as defined by **Average Count** before applying the average algorithm. If **Frame-by-Frame** is chosen, the entire image is scanned as often as defined by **Average Count** before applying the average algorithm.

### 9.3.2 Advanced settings

**STEP 1 ►** Choose the tab **Advanced** to add additional parameters.

**Attribute** Enter a character to be added to the column "Attribute" of the Positionlist when dropping the Image into a target window. Please note that some characters have a special meaning and can not be used. By default the character I is used assuring that the scan is defined as an Image and the character N marks it as a new one. If other characters shall be used in addition make sure that also IN are set.

**Position** This parameter defines the addressing mode of the Image. **Absolute** means that the stage drives to the position of the scan when dropped into a Positionlist. **Relative** means that the addressing is done with respect to the current stage position and the beam is deflected within the write field without driving the stage. If this mode is selected it is under the responsibility of the operator to type in the distance for the stage movement in U- and V-direction.

**Options** Within this input field it is possible to define some options for the execution of the scan. For a typical Image the stay option is the only important one. Please not this option is placed automatically when selecting **stay at position**.

**stay at position** Choose this option to prevent the stage from driving. This option can be used in connection with relative positioning.

**halt before closing** Choose this option to halt execution which is useful for debugging purposes through the operator.

**save scan before closing** Choose this option to save the scan for example for documentation or off-line evaluation.

**STEP 2 ►** Choose **OK** button to quit the scan property definition and to save the new parameter set.

### 9.3.3 Post-processing Images

Very often not only a recording but also a processing is required. Several functions to process images are implemented and the parameters of these functions are described in the following.

- STEP 1 ►** Select one Imagescan.
- STEP 2 ►** Choose the menu command **Edit > Properties** to open the property window. Select the tab **Post Processing**.
- STEP 3 ►** Choose **Image filter** to modify the Image directly after recording it. The functionality is described in section [🌐 Imagescan window](#).
- After recording and optionally post-processing, it is possible to detect within an image a structure and to determine the deviation of a structure with respect to a reference structure.
- STEP 4 ►** Choose **Mark detection filter**. The functionality is described in section [🌐 2-dimensional mark detection](#).
- STEP 5 ►** Choose **OK** button to quit the scan property definition and to save the new parameter set.



## 10 Stage to sample adjustment

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It is typical for nearly all application tasks to find a specific location on a sample and then for example to expose at this location a GDSII structure. To find this location it is very convenient to apply a coordinate system to the sample. Finding this location is then in general simply a drive command within this coordinate system. In reality the success depends on the accuracy of the applied transformation, on the accuracy of the stage and last but not least on the required accuracy.

The various possible coordinate systems turn out to be a difficult topic. To give an overview, the first part of this chapter introduces the various coordinates systems and transformations between them.

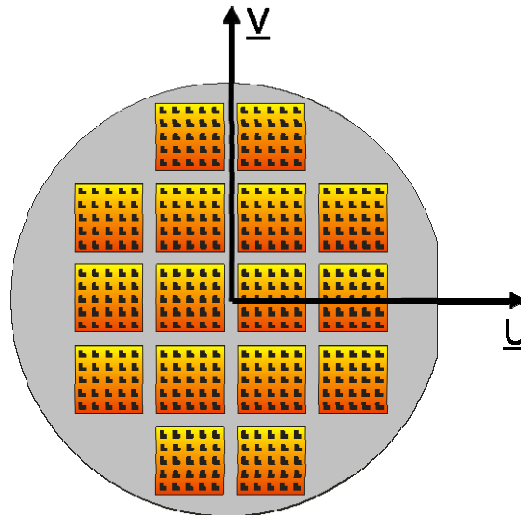


Please note that throughout the software and manuals the terms "adjust" or "adjustment" are used only in connection with the transformation between stage and sample. The term "alignment" is used in connection with the transformation between sample and beam.

### 10.1 Coordinate systems and transformations

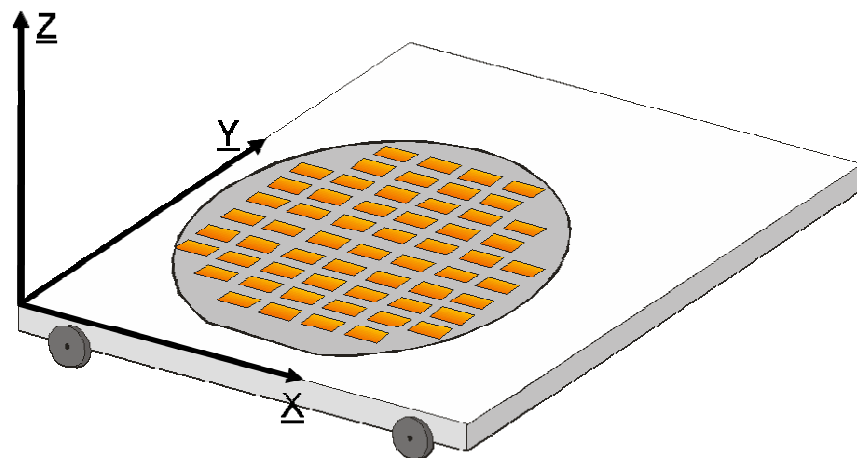
To find a location it is very convenient to apply a coordinate system to the sample. For example the center of a wafer is (0, 0) and an axis of this coordinate system is pointing towards the flat. Within the Raith software this sample coordinate system is labeled with U, V, and W.

**Figure 64:** As an example, the sample coordinates  $\underline{U}$ ,  $\underline{V}$  defined on a wafer.



On the other side the stage of the system is moving in another coordinate system. The directions of the stage movements define this coordinate system. The directions of this coordinate system are labeled throughout this manual and the software by X, Y, and Z. These coordinates are oriented perpendicular to each other. Normally (0, 0) of this system is the center of the travel range and the X axis is then arbitrarily selected as one of the motor axis.

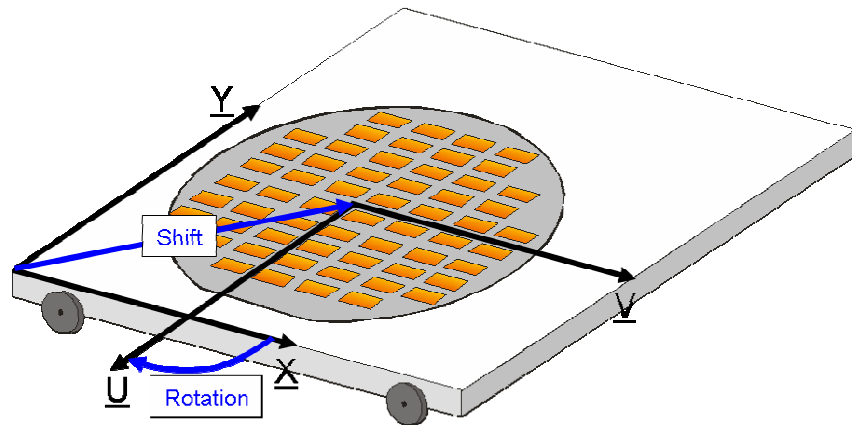
**Figure 65:** Sketch of stage coordinates  $\underline{X}$ ,  $\underline{Y}$ ,  $\underline{Z}$ .



In the most cases these two coordinate systems are not identical. The two coordinate systems may have different origins, causing an offset vector. Additionally, the U, V, W system may be rotated against the X, Y, Z system and the systems may have different scales.

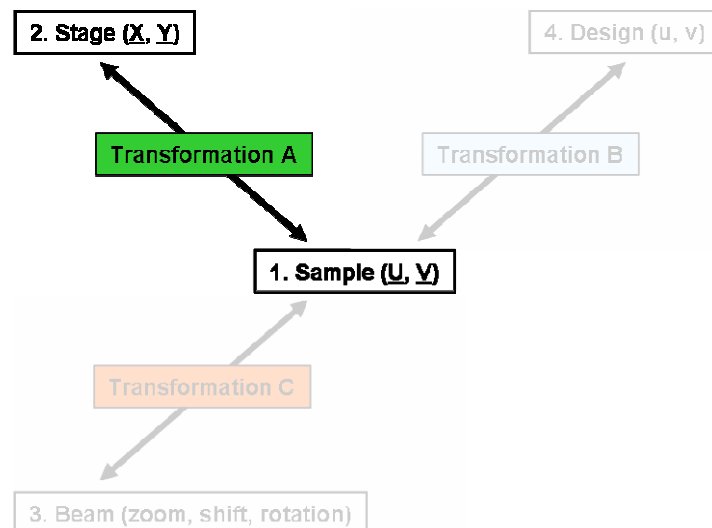


**Figure 66:** Stage sample coordinates transformation.



In conclusion, a coordinate transformation has to be calculated, so that it is possible to drive to a specific location on a sample. How this transformation fits into the scheme of coordinate systems is shown in **Figure 67**.

**Figure 67:** Stage sample coordinates transformation A.

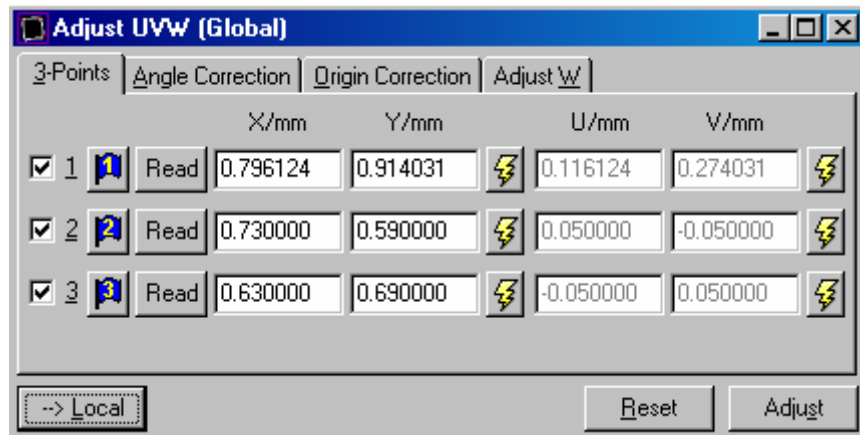


But not all applications require a full transformation with two scaling factors, one shift vector, and two angles. Therefore, it is possible to use the coordinate transformation in several degrees of complexity. It is now absolutely important to know which application requires which coordinate transformation and to understand how the various functions work. The Adjust UVW (see **Figure 68**) contains all commands to setup and establish the various transformations between the  $X, Y, Z$  system and the  $U, V, W$  system.


After defining some term, this chapter describes two applications with increasing complexity as a guideline.

## 10.2 Adjust UVW window

**Figure 68:** Part of the Adjust UVW window used to calculate the transformation between  $\underline{U}$ ,  $\underline{V}$ ,  $\underline{W}$  and  $\underline{X}$ ,  $\underline{Y}$ ,  $\underline{Z}$ .



### Reset

Choose this command to reset the transformation to the identity transformation. Alternatively, choose the  button in the symbol bar.

### Adjust

Choose to calculate and establish the coordinate transformation.

### Read

Choose this button to read the current  $\underline{X}$ ,  $\underline{Y}$  coordinates and store them in the corresponding input fields.



Choose this action button to drive to the corresponding position.



Choose the blue flags to read the  $\underline{X}$ ,  $\underline{Y}$  coordinates from a UV window. To do so, open a calibrated image, choose the corresponding flag, and drop it into the image.



## 10.3 Global and local transformations

Within the Raith software two different transformations exist. The first one is called global transformation and the second one local transformation. To motivate the introduction of two different transformations, it is intuitively to look for example at a wafer application. When working on wafers it is very convenient to use two independent coordinate transformations. The first coordinate transformation can be attached to the wafer itself whereas the second transformation serves for navigation within a chip.

The global and local transformations are defined only between the  $\underline{X}$ ,  $\underline{Y}$ ,  $\underline{U}$ , and  $\underline{V}$ . There is neither a global nor local transformation between  $\underline{Z}$  and  $\underline{W}$ .

### --> Local, --> Global

Choose this commands in the Adjust UVW window to switch between the global transformation and the local transformation at any time. In addition it is possible to switch between them by choosing the related

buttons   in the icon bar. The icons as well as the window title display the current status.

For both global and local transformation a complete set of transformation parameters are stored. In addition, these sets include also the locations of for the marks which were used to calculate the transformations. Switching between global and local activates one of these sets.

But the global and local transformations are not independently from each other. The following relationships exist between them.

- Any action performed while the global transformation is active effects also the local transformation with the same action.
- Any action performed while the local transformation is active has no impact on the global transformation.


#### Example

Switching to the global transformation and pressing than **Adjust** calculates also the local transformation with same transformation parameters. Switching to the local transformation would then make no difference.

Changing then some coordinates and pressing **Adjust**, calculates a new local transformation totally independent from the global one. After switching back to the global transformation it is possible to use the global one again.

## 10.4 Transformation with 1, 2, or 3 points

Again the following information applies to the transformation between X, Y, U and V only.

In general, a coordinate transformation can be established using 3 points, 2 points, or 1 point only. How many points are adequate, depends on the application. To select the number of points, use the tick boxes in front of each blue flag within the Adjust UV window (see  **Figure 68**).

- Using 1 point only. By defining X, Y, U and V at one location on the sample it is possible to calculate the shift between the two systems. Other transformation variables are not affected. An alternative is using the **Origin Correction** tab. On this tab one has to specify U and V only and when pressing **Adjust** the current X and Y coordinates are used.
- Using 2 points. By defining X, Y, U and V at two locations on the sample it is possible to calculate the shift, one rotation angle and one scaling factor between the two systems. The rotation angle and the scaling factor are applied to both axis in the same way, i.e.

both axis are rotated and scaled by the same amount. An alternative is using the **Angle Correction** tab, but the functionality is quit the same. At each point  $\underline{X}$  and  $\underline{Y}$  are defined assuming that both locations lie on the  $\underline{U}$  axis. Thus only one rotation angle can be calculated which is applied to both axis. The other transformation parameters are not affected.

- Using 3 points. By defining  $\underline{X}$ ,  $\underline{Y}$ ,  $\underline{U}$  and  $\underline{V}$  at three locations on the sample it is possible to calculate the shift, two rotation angles and two scaling factors between the two systems. The rotation angles and the scaling factors are applied to each axes individually, i.e. the axis are rotated and scaled by different amounts.

The following table summarizes this behavior.

**Table 32:** Possible coordinate transformations and their results.

| <b>transformation</b>    | <b>transformation variables</b>  |
|--------------------------|--|
| 1 point                  | New shift.<br>Scaling factors for both axes unchanged.<br>Rotation angle for both axes unchanged.      |
| <b>Origin Correction</b> | New shift.<br>Scaling factors for both axes unchanged.<br>Rotation angle for both axes unchanged.      |
| 2 points                 | New shift.<br>One new scaling factor for both axes.<br>One new rotation angle for both axes.           |
| <b>Angle Correction</b>  | Shift unchanged.<br>Scaling factors unchanged.<br>One new rotation angle for both axes.                |
| 3 points                 | New shift.<br>Two new scaling factors one for each axis.<br>Two new rotation angles one for each axis. |

## 10.5 An un-patterned, small sample

In this case no pattern exists on the sample which can serve as a reference and the sample itself is not a complete wafer maybe only a fraction of it with at least one straight edge.

This Adjustment consists of two tasks. One task is to assign a certain point on the sample specific coordinates whereas the other task is to define the U-direction on the sample. The sequence between these two tasks does not matter. It is also possible to do them at the same time, for example when one point is used to define the point as well as the angle.

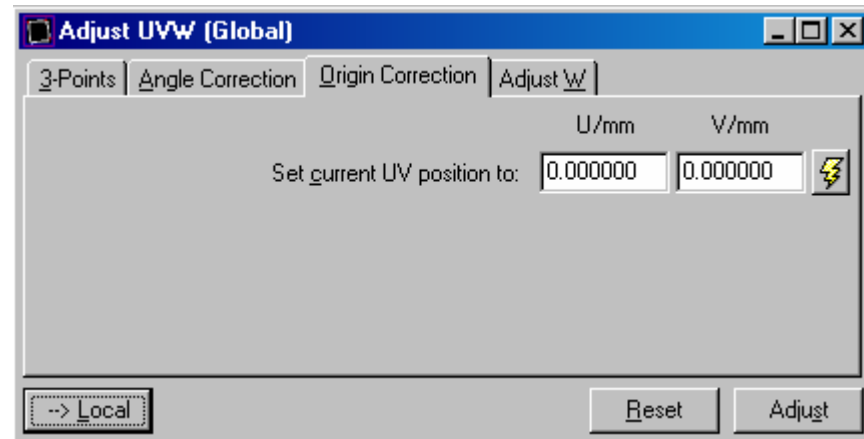
Before starting these two tasks one should switch to global or local transformation. Normally, for simple tasks the global one is the best

choice. Then one should press Reset to make sure that the scaling factors as well as all other parameters set to the identity transformation.

### 10.5.1 Origin correction

The Origin Correction tab serves to determine the shift vector between the origin of the X, Y system and the origin of the U, V system.

**Figure 69:** Tab **Origin Correction** to calculate the shift between X, Y system and U, V system.



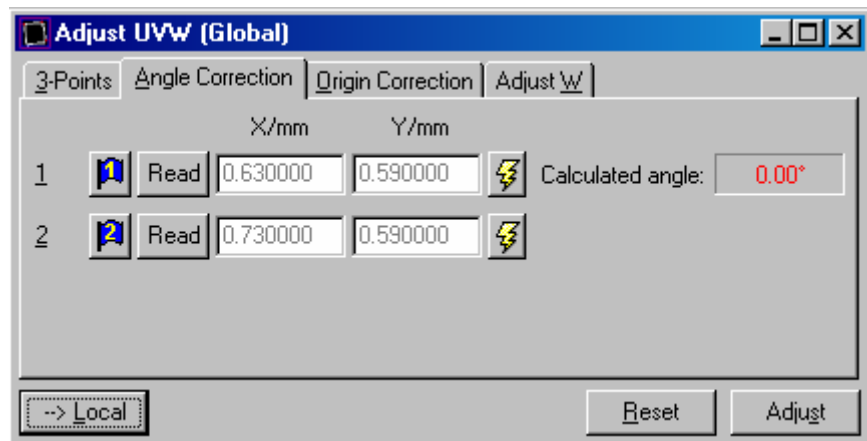
#### Defining an origin correction

- STEP 1 ►** Locate a reference structure on the sample such as the lower left corner of the sample.
- STEP 2 ►** Use the appropriate control, e.g. a joystick, to place this reference structure in the center of the field of view, e.g. a SEM screen.
- STEP 3 ►** Switch to global or local transformation before pressing **Adjust** to calculate the shift for that transformation.

### 10.5.2 Angle correction

The Angle Correction tab offers the capability to adjust the angle between X axis and U axis. To calculate this transformation it is necessary to read in the X and Y of two different points along the U-axis of the sample. Naturally, the degree of accuracy of the angle is related to the accuracy of the positioning as well as the distance between these two points. If the distance is larger, it is more accurate.

**Figure 70** Tab: Angle Correction to calculate the angle between X axis and U axis.



### Defining an angle correction

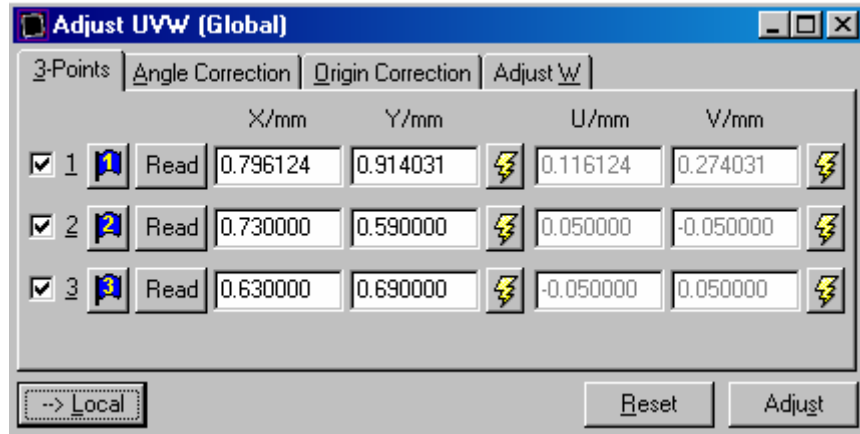
- STEP 1** ▶ Locate an extended reference structure which can serve as the U axis, e.g. the lower edge of the sample.
- STEP 2** ▶ Use the appropriate control, e.g. a joystick, to place on point of this reference structure in the center of the field of view, e.g. a SEM screen.
- STEP 3** ▶ Choose **Read** in line 1 to use the corresponding X, Y coordinates for the angle calculation.
- STEP 4** ▶ Use the control to place another point of the reference structure in the center of the field of view. This second point should be separated by a few mm, e.g. 10 mm, from the first one.
- STEP 5** ▶ Choose **Read** in line 2 to use now this X, Y coordinates for the angle calculation. After pressing **Read** the **Calculated angle** is given on the same tab as information in red. Please verify that the calculated number makes sense especially that the sign is correct which means that the U axis is pointing into the right direction.
- STEP 6** ▶ Choose **Adjust** to use the so defined U direction. The angle between U and X is given now in green.

## 10.6 A patterned sample

If already a pattern exists on a sample, for example made in a previous process step, and one has to navigate on this sample, for example to find a specific structure, it is absolutely necessary to adjust the U, V coordinates to this pattern. This situation becomes clearer when assuming the pattern was defined in a previous step by a mask plate with a scaling error. To find then a specific structure the Raith software has to use the same scaling factor. In addition and very common the pattern is rotated against a reference direction, e.g. a wafer flat, due to poor alignment. Of course is a mask plate of high

fidelity and a good mask aligner or a good stepper is used, the rotation angles are very small, the scaling factors are near 1.0, and the adjustment procedure consists mainly in defining the origin. But in the following it is assumed that one has to do the full adjustment procedure meaning to use three points.

**Figure 71:** Tab 3-Points to calculate a full transformation.



### Defining a full transformation

#### STEP 1 ►

Type in the U, V coordinates of the three reference structures into the corresponding U, V fields. The easiest way is to get them from the GDSII design. Here it is possible to use the green flags.

#### STEP 2 ►

Locate one of the three reference structures, e.g. the first one. Choose **Read** to automatically update the corresponding X, Y coordinates.



This task is normally the trickiest one. In this case it is very helpful to do first a course adjustment using only an origin and an angle correction using the global coordinate system. This coordinate system can then be used to find the first reference structure. The following fine adjustment using three points is then done in local coordinate system. Therefore it is possible to switch at each point back to global one to find the next structure or to repeat previous steps.

#### STEP 3 ►

Place the tick in front of the corresponding coordinates. This tick means that the X, Y, U, V values will be used to calculate the corresponding transformation.

#### STEP 4 ►

Locate the second structure of the three reference structures. Choose **Read** and place the corresponding tick.


#### STEP 5 ►

Locate the last structure of the three reference structures. Choose **Read** and place the corresponding tick.

#### STEP 6 ►

To calculate and to activate the transformation, choose **Adjust**.



If the coordinate transformation differs not too much from the identity or a global transformation is used (see previous hint), the task to find the second and the third structure can be speeded up by pressing 

behind the corresponding U, V coordinates.

## 10.7 Defining a new adjustment procedure

The main task of a predefined adjustment procedure is to automate the adjustment on wafers (global adjustment) and their chips (local adjustment). If one work with the same wafer layout every day, the adjustment procedures will simplify and speedup this task.

The adjustment procedure executes the following steps. The stage drives to all specified UV-position of the marks and records an Imagescan or a Linescan at each position. From the deviation between actual and reference position a new coordinate transformation is calculated and applied. The case that a manual procedure is executed the operator has to define the deviation using the **Control** key and left mouse button.



The position of each mark is specified in U and V. Thus a coarse UV-adjustment has be executed or applied to sample before using a procedure. This can be a Preadjustment or an unpatterned wafer adjustment. Than an adjustment procedure can be used for a fine adjustment.

Within the Scan Manager three sorts of adjustment procedures are available: Manual, Automatic with Linescans and Automatic with Images. The Manual and Automatic with Images procedures use images and perform 2-dimensional mark detections to determine the shift at each mark. The Automatic with Linescans procedure uses Linescans in U- and V-direction and requires a cross-shaped mark.

The details how to configure Imagescans used for the procedures **Manual** and **Automatic with Images** can be found in section [Defining Images](#). Refer to the corresponding section [Defining Linescans](#) to learn how to configure Linescans used for the Automatic with Linescans procedures. In the following only the deviation from these settings are described.

### 10.7.1 Main settings

In the case of an Automatic with Linescans procedure two Linescans are defined to determine the deviation in U- and V-direction at each mark. Thus the selection of a Main Direction is not necessary.

### 10.7.2 Mark procedure settings

Choose the tab Mark procedure to define number and positions of the mark scans. Use the check boxes to select which marks shall be used

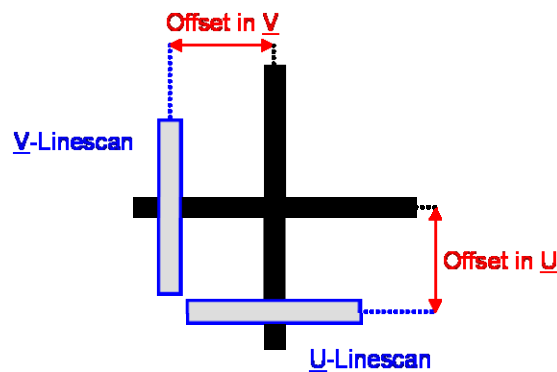


and type in the U and V coordinates in corresponding input fields. Therefore, use the check boxes to select which marks shall be used. The number of marks corresponds to an 1-, 2- or 3-point adjustment (see section [Transformation with 1, 2, or 3 points](#)). After selecting the number of marks, type in the U- and V-coordinates in the corresponding input fields.

### Offset

This parameter is used only by **Automatic with Linescans** procedure to define the placement of each Linescan with respect to the mark position. The figure below shows the principle.

**Figure 72:** Placement of Linescans with respect to a mark using the offset.



### 10.7.3 Advanced settings

It is possible to setup an Automatic with Images procedure in two different ways. If no reference image exists, select the option automatic scan with reference mark at beginning. In this case a reference image is created automatically by recording an image in the center of the write field.



The precision of an adjustment depends on how accurate is the position of the reference image. Hence, when recording the reference image it is a must-see to perform first a very accurate adjustment as well as a write field alignment.

**Adjust after every mark** Select this option to calculate and apply the coordinate transformation after every mark scan. This procedure increases the accuracy from step to step and simplifies finding the next mark scan in the sequence.

**Halt before closing** If this option is active, the automatic procedure stops execution after each mark scan. Do not select this feature, if full automatic procedure is desired.

### 10.7.4 Processing and evaluation


An automatic detection of the deviation at each mark, i.e. an evaluation algorithm, is mandatory for all automatic procedures. See the corresponding section [Evaluation algorithms](#) to configure the mark detection.

## 11 Beam to sample alignment

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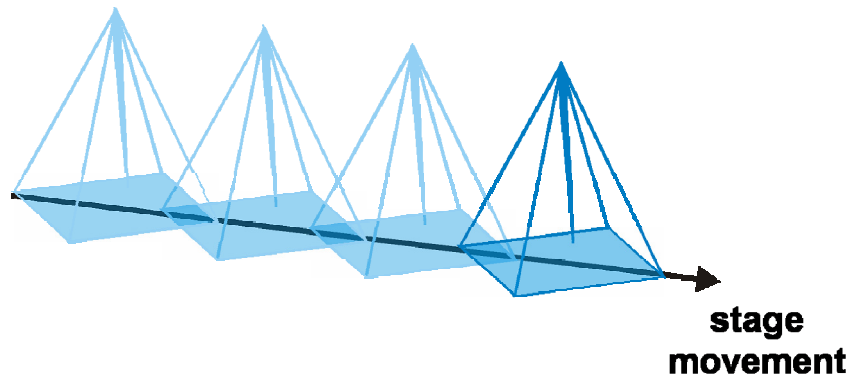
|  |            |
|--|------------|
| <b>11.1 Coordinate systems and transformations</b> | <b>156</b> |
| <b>11.2 Align Write field window</b>               | <b>157</b> |
| <b>11.3 Microscope control window</b>              | <b>158</b> |
| <b>11.4 Alignment / adjustment interrelation</b>   | <b>160</b> |
| <b>11.5 Aligning write fields</b>                  | <b>160</b> |
| <b>11.6 Defining a new alignment procedure</b>     | <b>164</b> |

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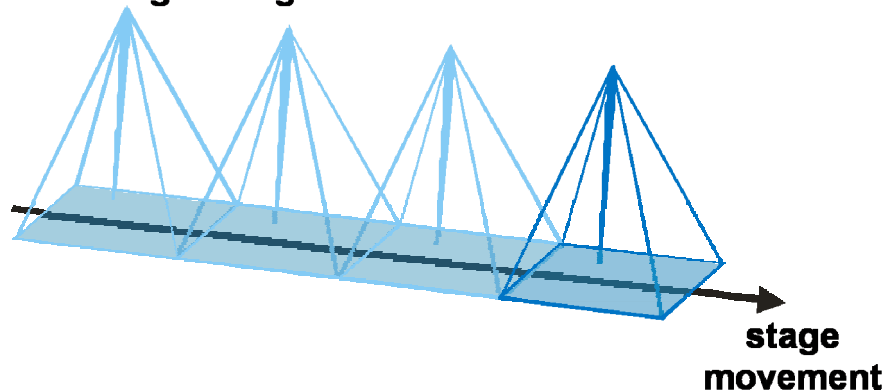
Write field alignment is a very central alignment in the process of exposing a pattern into an existing pattern or exposing large structures consisting of several smaller write fields. The first case is called "Mix-and-Match" exposure whereas the second one is called "stitching". This case is displayed in  **Figure 73**. Another case would be recording images or Linescans to determine a certain dimension ("Metrology") or exposing elements with certain widths ("CD control"). In these two cases a correct orientation of the write field might be not so important, but its size becomes crucial. From these examples, it becomes clear that the beam has to be positioned very precisely on the sample or in other words the beam positioning has to be aligned to the sample coordinate system.

**Figure 73:** Effect of write field alignment on "stitching".

### Stitching w/o Alignment



### Stitching w/ Alignment



To give an overview over the beam-to-sample coordinate transformation, the first part of this chapter introduces coordinate system of the beam and its transformation with respect to the sample.



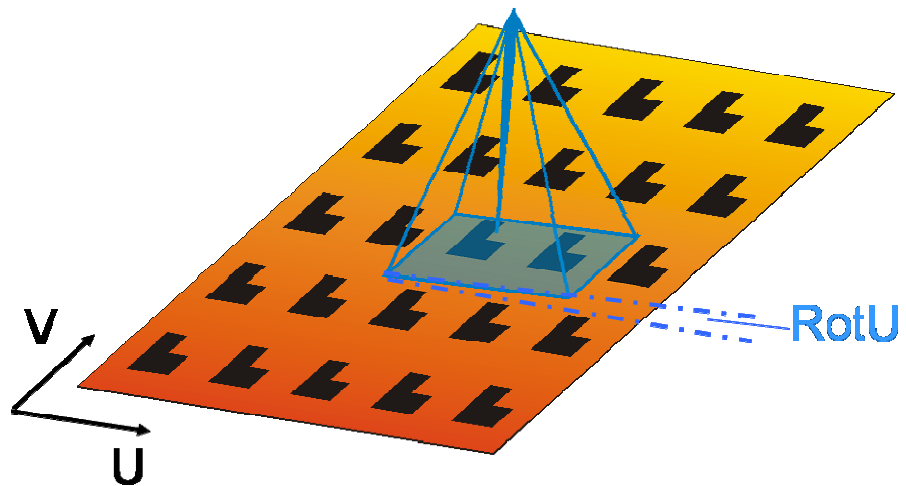
Please note that throughout the software and manuals the terms "align" or "alignment" are used only in connection with the transformation between beam and sample. The term "adjustment" is used in connection with the transformation between sample and stage.

## 11.1 Coordinate systems and transformations

In section [Stage to sample adjustment](#) the UV-coordinate systems of the sample were introduced. Thus a point on the sample can be placed underneath the beam by specifying its U- and V-coordinates. For the beam itself a different way was chosen. An additional coordinate system was not introduced; only the transformation between UV and the beam is visible. The relevant quantities are

- ZoomU and ZoomV the scaling of the beam mayor axes with respect to U- and V-axes. Zoom values are necessary for the right scaling of the beam movement. For example, if an image is scanned, the dimensions of the displayed structure shell fit to the real size of this structure.
- ShiftU and ShiftV the offset of the beam center with respect to a point in U and V. The shift is used to move the beam with respect to a reference structure on the sample. Thus, if the shift is determined correctly an overlay exposure is possible.
- RotU and RotV the rotation of the beam mayor axes with respect to U- and V-axes. The rotation values are responsible for the correct orientation of the beam movement relative to the sample coordinate system. For example, if the rotation is well aligned, stitching of write fields is possible.

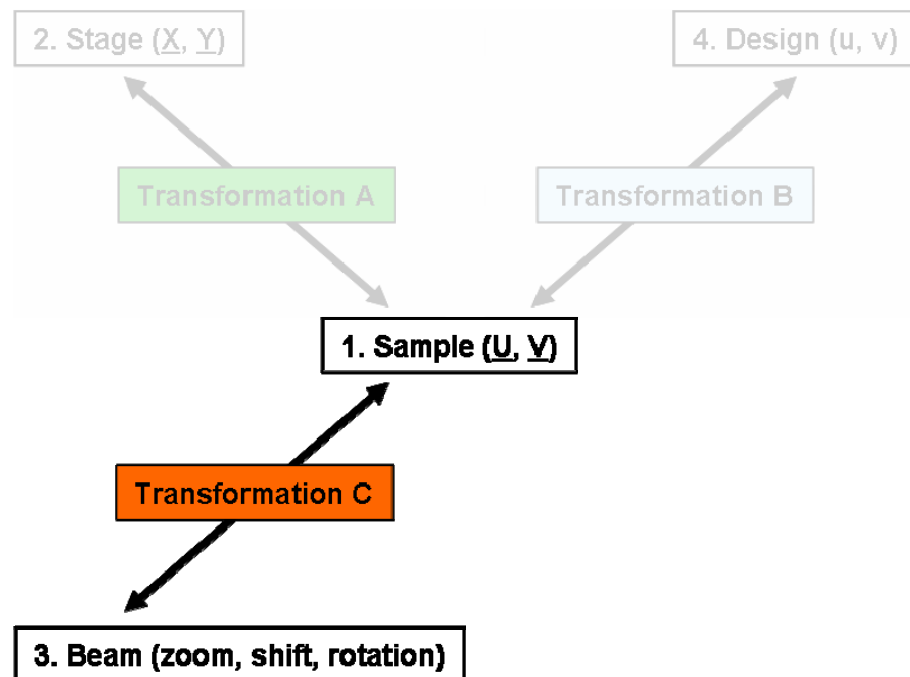
**Figure 74:** Sketch of the beam system with respect to the sample.



This reason for this way of describing the transformation is that exactly these values are sent to the Digital Pattern Generator or to the Scanboard. Then within the Pattern Generator these values are used to perform electronically the coordinate transformation.

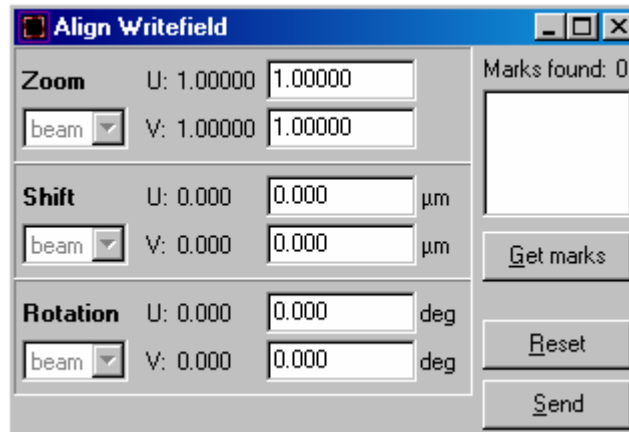
How the transformation between the sample and the beam fits into the general scheme of coordinate systems is displayed in [Figure 75](#).

**Figure 75:** Sample beam coordinates transformation C.



## 11.2 Align Write field window

The transformation quantities ZoomU ... RotV are displayed and can be changed in the **Align write field** window. In addition the window gives access to all relevant commands to handle the transformation.

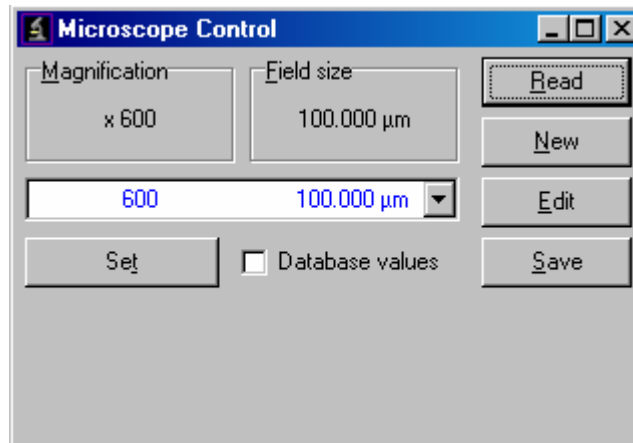
**Figure 76:** Align write field window.

|                     |  |
|---------------------|--|
| <b>Zoom</b> U/V     | Zoom for <u>U</u> -, <u>V</u> -axis scaling, value between 0 and 1   |
| <b>Shift</b> U/V    | Shift with respect to <u>U</u> -, <u>V</u> -axis, can be positive and negative. Please note Raith lithography systems compensate a shift larger than 2% of current write field (parameter can be changed) by applying the corresponding value to the transformation between sample and stage.  |
| <b>Rotation</b> U/V | Rotation relative <u>U</u> -, <u>V</u> -axis, can be positive and negative. Beam tries to compensate rotation of UV system, therefore rotation angle of UV adjustment and beam have different signs. Please note Raith lithography systems compensate a rotation larger than 1° (parameter can be changed) by sending corresponding value to the column. |
| <b>Input boxes</b>  | The values given here are the alteration of the transformation quantities. The values for zoom are multiplied and for shift and rotation are added to current values.  |
| <b>Get marks</b>    | Command calculates correction parameter from positionlist containing alignment marks. Alignment procedures called from the Scan Manager perform this command automatically.  |
| <b>Reset</b>        | Reset correction parameters to identity transformation.  |
| <b>Send</b>         | Send alteration of transformation parameters (values in input boxes) to beam control hardware.   |

### 11.3 Microscope control window

Closely connected with each other are transformation quantities of the write fields are the settings on the column or microscope. For example when setting up a write field of 100 μm, the field of view has to be larger than this 100 μm. In addition, the correct transformation quantities might depend on the beam energy, working distance, slight non-linearity while using different amplifier for different magnification regions, etc. Thus each write field must be aligned for every magnification separately. As write field size, magnification and the transformation quantities depend on each other they are stored together in one database.

**Figure 77:**  
Microscope control window.



The currently selected write field size and the magnification are displayed in the top of the dialog. If polling of the magnification is on, the magnification will be updated periodically. In this case magnification, which does not fit to selected write field, becomes red.

Use dropdown list below to select a new write field. Entries in this list are blue if corresponding alignment values in database and current alignment values in Align Writefield window are different. A new entry becomes red, if it was not stored in database. Black entries belong to parameter sets which database settings agree with current setting in the system.

**Read** Use this command to force reading current magnification from the column.

**New** Choose this command to create a new parameter set of write field size with corresponding magnification. It is possible to create several parameter sets with equal write field size but different magnifications and vice versa.



To setup a new parameter set, it helps to realize that the product of write field size and magnification should be constant. The actual value of the product itself depends on beam control hardware as well as the column.

**Edit** Choose this command to change an existing parameter set.

**Save** Choose this command to store changes of the currently selected parameter set to the database (only red and blue entries are affected).

**Set** Choose this command to activate the currently selected write field size and magnification. If **Database values** is selected the beam alignment values are read from the database before activating them. Otherwise current alignment values are still active.

## 11.4 Alignment / adjustment interrelation

As the marks used for an alignment are features on a sample, the sample orientation or dimensions on the sample are affecting the alignment itself. For Example if the sample is rotated by certain angle with respect to the stage, then after an alignment the write field will be rotated by the same angle (assuming that stage and beam are perfectly aligned to each other.) Hence, one can use the information from the UV-adjustment procedure to roughly calculate the rotation and scaling of the write field.

Starting with version 4.0 a mechanism was implemented taking this interaction into account. This mechanism consists of parts.

- Before storing the write field parameters to the database, the current UV-adjustment values are used to calculate new write field parameters which do not depend on the UV-adjustment values. Only these values are stored.
- Before setting a write field with parameters from the database, the current UV-adjustment values are used to calculate effective write field parameters. Naturally, these effective values do depend on the current UV-adjustment.

## 11.5 Aligning write fields

The principle of a write field alignment is simple. Some unique and easily recognizable features on the sample are selected as marks. The dots from focusing or the corners on a "Chessy" are good examples. Scanning now over these marks with the beam let each mark appear at a certain positions. This actual position with respect to their reference position gives now the input parameter for calculating the write field transformation.

The alignment procedure is imbedded into the general sequence as follows:

- STEP 1 ►** Focus on the sample surface.
- STEP 2 ►** Adjust UV coordinates with respect to stage XY.
- STEP 3 ►** Select desired write field size in Microscope Control window.
- STEP 4 ►** Perform write field alignment using corresponding procedures in Scan Manager.
- STEP 5 ►** Execute exposure, metrology or other job.





It is important to understand that a write field alignment depends on the current transformation between sample and stage. Therefore before starting a write field alignment, establish first the coordinate transformation between stage and sample, i.e. perform an UV-Adjustment.

Depending on equipment with laser interferometer stage two different alignment procedures are possible: alignment with and alignment without laser stage. The mix-and-match operation which is possible with and without a Laser stage is described in section [● \*Mix-and-Match Exposure\*](#).

### 11.5.1 Write field alignment without laser stage

If your system is not equipped with laser interferometer stage use precise and well structured sample. For example the "Chessy" sample. This sample serves as a measuring standard for the following write field alignment.



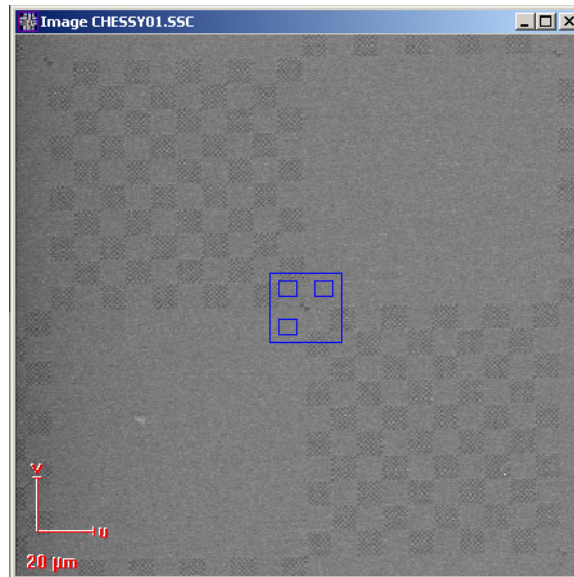
Please note it is possible to align such parameter like shift and rotation using a "Chessy" but there are two limitations which make a stitching application impossible. First, the "Chessy" and the sample must have the same UV adjustment and the same focus (exactly same height). And second, the Stage must have an accuracy of a few nm to perform stitching.

Normally, the alignment for each write field size is done once during installation before using the system. Then these values are store into the database. This makes it possible to work with these stored parameters without any alignment in the future.

The following steps are necessary to perform a "Chessy" alignment. For a more detailed description please refer to the Operation Manual.

- STEP 1 ►** Focus on a leveled sample.
- STEP 2 ►** Perform an UV-Adjustment with **Origin Correction** and **Angle Correction** using the "Chessy". See section [● \*Alignment / adjustment interrelation\*](#) to understand why this step is necessary.
- STEP 3 ►** Place the adjacent corners of two squares near to the center of the beam. Record at this position an image.
- STEP 4 ►** If an applicable alignment procedure in Scan Manager (see **Align Write Field Procedures > Manual**) exists, select this procedure and drag and drop it on to the adjacent corner in the image center. The result is displayed in [● \*\*Figure 78\*\*](#). If an applicable procedure does not exist, crated one as described in section [● \*Defining a new alignment procedure\*](#).


**Figure 78:** Image after drag-and-dropping an applicable procedure onto "Chessy".



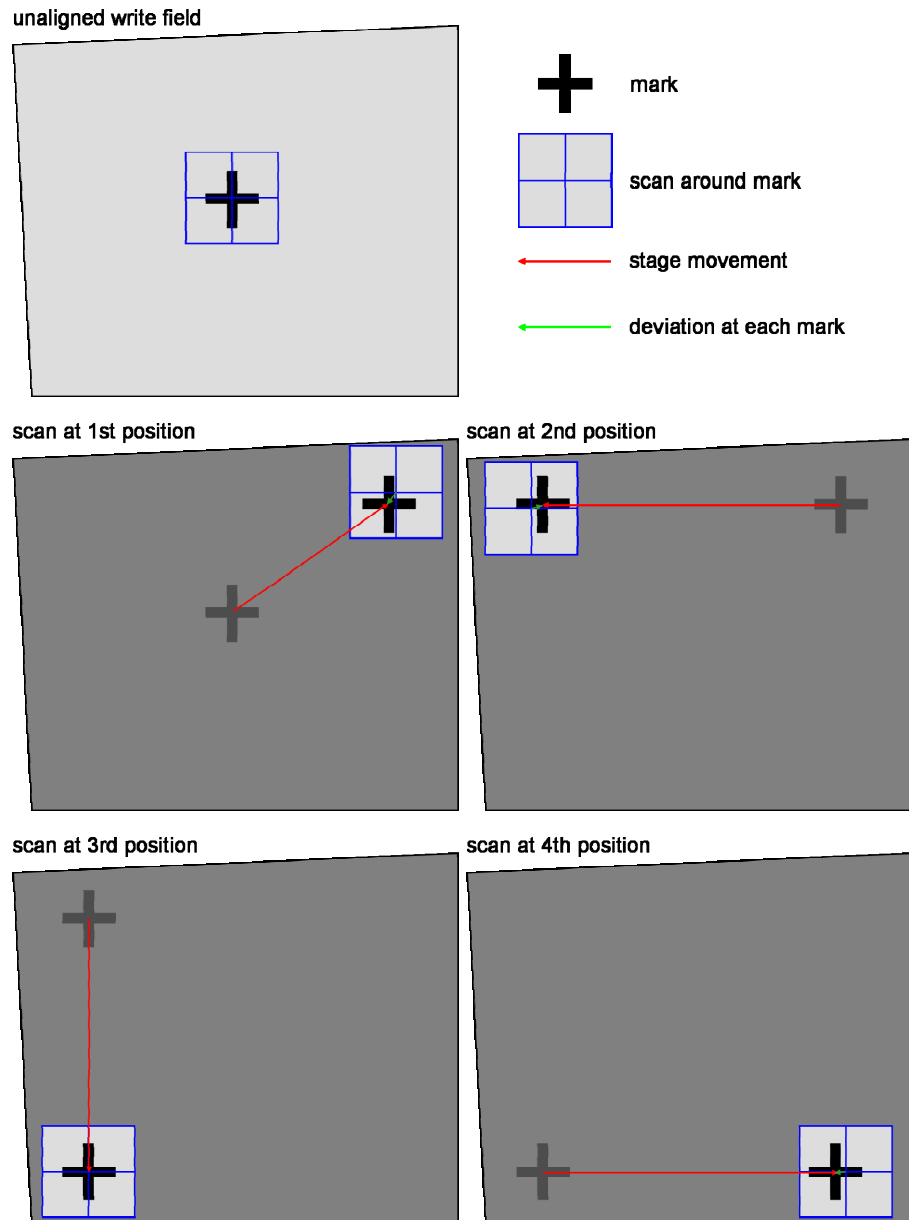
- STEP 5 ►** Select the Positionlist where the alignment procedure has been stored and scan the corresponding position.
- STEP 6 ►** In each image place the blue marker on the mark by using the **Control** key together with the left mouse button.
- STEP 7 ►** At the end of the procedure, apply correction values, if procedure was successful.

### 11.5.2 Write field alignment with laser stage

If your system is equipped with a laser interferometer stage it is possible to use the laser stage as measuring standard. The precision of the Laser stage allows a very precise alignment of the beam with respect to sample making a stitching possible.

The internal procedure is not quite the same as within the "Chessy" procedure. Here only one mark is used. The mark is moved to several positions within an unaligned write field. At each position a smaller image is recorded such that the difference between the actual and reference position can be determined. From all differences the beam alignment values are calculated.  **Figure 79** displays this procedure.

**Figure 79:** Align write field procedure used with Laser stage. One mark is moved using the Laser stage to different locations so that the same mark appears in each scan.

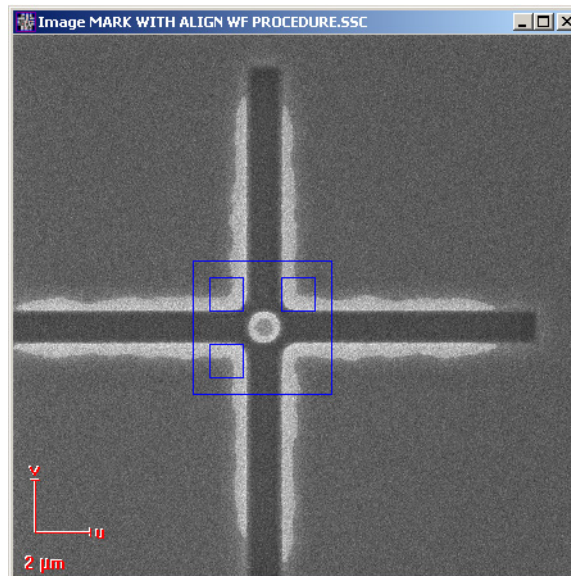


Before this procedure can be executed, the following steps are necessary.

- STEP 1** ▶ Focus on a leveled sample.
- STEP 2** ▶ Perform an UV-Adjustment with **Origin Correction** and **Angle Correction** using the sample. See section [Alignment / adjustment interrelation](#) to understand why this step is necessary.
- STEP 3** ▶ Place the mark near to the center of the beam. Record at this position an image.
- STEP 4** ▶ If an applicable alignment procedure in Scan Manager (see **Align Write Field Procedures > Manual**) exists, select this procedure and drag and drop it on to the adjacent corner in the image center. The result is displayed in [Figure 80](#). If an applicable procedure does not

exist, create one as described in section [Defining a new alignment procedure](#).

**Figure 80:** Image after drag-and-dropping an applicable procedure onto one mark.



- STEP 5** ▶ Select the Positionlist where the alignment procedure has been stored and scan the corresponding position.
- STEP 6** ▶ In each image place the blue marker on the mark by using the **Control** key together with the left mouse button.
- STEP 7** ▶ At the end of the procedure, apply correction values, if procedure was successful.
- STEP 8** ▶ Repeat this sequence with a smaller scan fields until no decrease in correction factors is observed.

## 11.6 Defining a new alignment procedure

Within the Scan Manager three sorts of write field alignment procedures are available: **Manual**, **Automatic with Linescans** and **Automatic with Images**. The **Manual** and **Automatic with Images** procedures use images and perform 2-dimensional mark detections to determine the shift at each mark. The **Automatic with Linescans** procedure uses Linescans in U- and V-direction and requires a cross-shaped mark.

The details how to configure Imagescans used for the procedures **Manual** and **Automatic with Images** can be found in section [Defining Images](#). Refer to the corresponding section [Defining Linescans](#) to learn how to configure Linescans used for the **Automatic with Linescans** procedures. In the following only the deviation from these settings are described.

### 11.6.1 Main settings

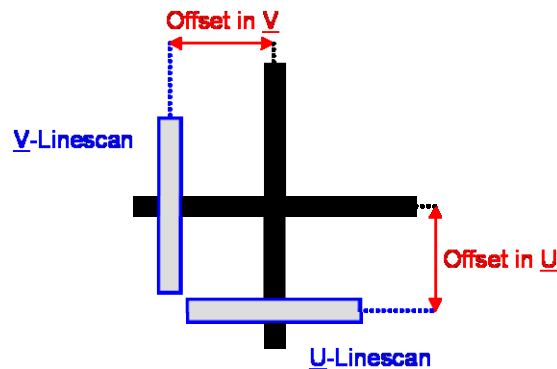
In the case of an **Automatic with Linescans** procedure two Linescans are defined to determine the deviation in U- and V-direction at each mark. Thus the selection of a **Main Direction** is not necessary.

### 11.6.2 Mark procedure settings

Choose the tab **Mark procedure** to define number and properties of mark scans.

|                      |  |
|----------------------|--|
| <b>Mark sequence</b> | Choose which marks shall be used by selecting corresponding check boxes.   |
| <b>Placement</b>     | Defines the distance between the scans and center of write field.  |
| <b>Iterations</b>    | Defines the number of repetitions the alignment procedure are repeated to achieve better results.  |
| <b>Offset</b>        | This parameter is used only by <b>Automatic with Linescans</b> procedure to define the placement of each Linescan with respect to the mark position. The figure below shows the principle. |

**Figure 81:** Placement of Linescans with respect to a mark using the offset.



### 11.6.3 Advanced settings

It is possible to setup an **Automatic with Images** procedure in two different ways. If no reference image exists, select the option **automatic scan with reference mark at beginning**. In this case a reference image is created automatically by recording an image in the center of the write field.



The precision of an adjustment depends on how accurate is the position of the reference image. Hence, when recording the reference image it is a must-see to perform first a very accurate adjustment as well as a write field alignment.

**Halt before closing** If this option is active, the automatic procedure stops execution after each mark scan. Do not select this feature, if full automatic procedure is desired.

### 11.6.4 Processing and evaluation

An automatic detection of the deviation at each mark, i.e. an evaluation algorithm, is mandatory for all automatic procedures. See the corresponding section [Evaluation algorithms](#) to configure the mark detection.

# 12 Exposures

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Normally having a certain exposure result in mind, it is very important to have some background information on how the GDSII design is transferred into an exposure and how the various exposure parameters affect the exposure.

The aim of this section is it, to provide the necessary information. To get an overview, it is useful to recall that the following steps have to be executed before an exposure.

- Create the design structures using the GDSII editor and its elements with various properties.
- Setup the column, i.e. select the acceleration voltage, the beam current, and the write field size.
- Define design parameters, i.e. the layers, the working area, and the location on the sample.
- Define your exposure parameters, i.e. step sizes, dwell times, settling times, and select between different modes.
- Start the exposure.



Within this reference manual we do not describe how to setup an exposure in a step-by-step way. To learn more about this, please consult the operation manual.

## 12.1 Exposing GDSII structures

A fast and very flexible way to expose a structure is provided in combination with the Positionlist mechanism of the Raith software. This approach becomes even more powerful when exposing multiple or repeated structures with the same or different parameters. This allows a powerful batch job type operation, especially if the stage can be driven automatically.

### 12.1.1 Preparing a Positionlist

To generate an automated exposure sequence of one or more structures at different locations on the sample,

- a GDSII database containing the structures must be loaded,
- a new Positionlist must be created choosing the command **File > New Positionlist**.

Now, select the structure to be exposed within the GDSII Database window, drag it to and drop it at any location within the Positionlist window. Using this technique, the structure will be added as a line entry into that Positionlist. To expose multiply GDSII structures, repeat this procedure or use the Positionlist filters, like Matrix Copy, to generate additional exposure tasks.

When using this drag-and-drop technique, the software stores the following settings

- the current write field size,
- the current UV position,
- the current GDSII working area, and
- if the exposure of lines and dots is switched on

within the Positionlist. To use different parameters, one has to redefine these parameters for this position. The exposure of the GDSII structure will be performed by applying these parameters.

For a quick graphical inspection of selected layers and the working area, just double-click on the line entry. This action opens automatically the GDSII viewer and displays the selected structure, layers and working areas.

The exposure of each individual structure within the Positionlist as well as of groups or of all structures can be started by the **Scan** menu commands of the Positionlist, such as **Current**, **All**, etc. Of course, the complete exposure list can be stored and recalled for use or modification at any time. For more details please refer to section [Positionlists](#).

In order to modify or only to inspect these parameters, select the related line in the Positionlist by right mouse click and choose the command **Properties** from the appearing menu. After this you have access to a dialog box as shown in **Figure 82** to set these parameters.



**Figure 82:** Dialog to set all parameters relevant for an exposure.

### Exposed layer

Choose the corresponding button to select the layers to be exposed. A dialog appears with a listing of all layers. Select the layers to be exposed. Unselect layers by an additional mouse click. Alternatively, multiple layers are separated by a comma and a range of layers is indicated by a hyphen “-“.

### Working area

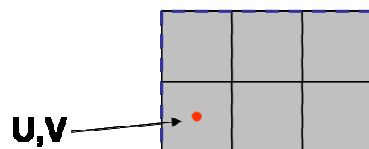
Choose the corresponding button to select the working area from a list of predefined areas. Alternatively, enter the coordinates of the lower left and upper right corner in GDSII-UV-coordinates.

### Position

Enter the location where the GDSII structure should be get exposed. The coordinates are sample-UV-coordinates. Within the design-UV-coordinates this position corresponds to the center of the first write field.


**Figure 83:** Definition of UV-position for an exposure.

**working area > write field**



**working area = write field**



If the sample coordinates are identical to the GDSII-coordinates, it is possible to use the  button to calculate the UV-position on the bases of the stored working area and current write field size. Thus, it is very important that the working area and the write field are set before using this function.



Identical sample coordinates and GDSII coordinates is typical for a mix-and-match application, i.e. mixing of an optical lithography with an e-beam exposure step.

**Exposure Parameters** Choose this button to enlarge the window to set the exposure parameters like step sizes, dwell times, etc.

**Default** Select for each parameter, if the corresponding default value should be used. The default values are defined within the Exposure window (see section [Exposure Window](#)). To edit one of these parameters unselect the **Default** option.

**Area Step Size** This parameter defines the distance between exposure spots in  $\mu\text{m}$ . It has to be an integer multiple of the basic step size (see section [Advanced Exposure Parameters](#)).

**Area Dwell Time** This parameter defines the time the beam waits at each step when exposing an area. The minimum dwell time depends on the hardware and is automatically set, if the user tries to enter a smaller value. Dwell times can be selected in steps of 1 ns and, if the user input does not fit exactly into this dwell time raster, the Raith software automatically selects the next larger value.

**Lines** Select this option to enable the exposure of single pixel lines.

**Line Step Size** This parameter defines the step size along a single pixel lines in  $\mu\text{m}$ . It has to be an integer multiple of the basic step size (see section [Advanced Exposure Parameters](#)).

**Line Dwell Time** This parameter defines the time the beam waits at each step when exposing a line. The minimum dwell time depends on the hardware and is automatically set, if the user tries to enter a smaller value. Dwell times can be selected in steps of 1 ns and, if the user input does not fit exactly into this dwell time raster, the Raith software automatically selects the next larger value.

**Dots** Select this option to enable the exposure of dots.

**Dot Dwell Time** This parameter defines the time the beam waits when exposing a dot. The minimum dwell time depends on the hardware and is automatically set, if the user tries to enter a smaller value. Dwell times can be selected in steps of 1 ns and, if the user input does not fit exactly into this dwell time raster, the Raith software automatically selects the next larger value.

**Dose Factor**

This parameter can be used to scale the applied dose for all GDSII elements by a certain factor. The dose factor is multiplied to the dwell time of areas, lines and dots.



The dose factor becomes very useful, when used for the determination of the clearing dose. On a test sample the same structure is exposed at different locations with a different dose factor. After processing of the sample and inspection of the result, the best dose is selected and used for further sample preparations. The dose factor is also supported by the Positionlist command **Matrix copy**.

**12.1.2 Exposure Parameter Calculation****Calculator**

Choose this button to calculate the exposure parameters for the doses of areas, lines and dots. Please note, the parameters for lines and dots are only visible, if the corresponding option within the Exposure window is selected. All parameters will be taken over from the Exposure Properties window, and they will be written back into it, when choosing the **OK** button.

**Figure 84:** Window to calculate exposure parameters.

**Write field size,**

**Min step size**

**Beam current**

These values are given for information purposes only.

For most systems a software module is available to read in the beam current from a current meter. Then its value is automatically given here. If such a module is not available, use an external current meter to measure the current and enter its value in nA. The same beam current is used to calculate the exposure parameter for areas, lines and dots.

The four input parameters for an area exposure show four buttons besides the related input field. One may enter the values in any three of these four fields. To calculate the fourth parameter such that all four parameters fulfill the equation

$$\text{"area dose"} = \frac{\text{"beam current"} \cdot \text{"area dwell time"}}{\text{"area step size"}^2},$$

choose the button behind it. Now that these four parameters fulfill the given equation, the corresponding title of the tab changes from red to black.

The parameters for line and dot exposures may be calculated in the same way. In this case the following equations are used to calculate the parameters for a line exposure

$$\text{"line dose"} = \frac{\text{"beam current"} \cdot \text{"line dwell time"}}{\text{"line step size"}}$$

and for a dot exposure

$$\text{"dot dose"} = \text{"beam current"} \cdot \text{"dot dwell time"}.$$

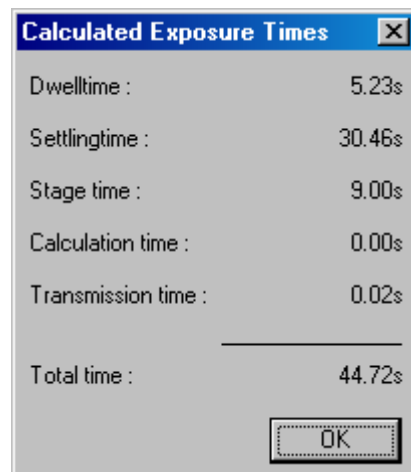
If all three parameter sets for area, line and dot exposure fulfill their corresponding equation, the OK button is enabled and the values will be written back into the Exposure window.

### 12.1.3 Estimating exposure time

#### Times

Choose this button to get information about the expected total exposure time. After calculation has finished, a message box shows the different kinds of times.

**Figure 85:** Window showing the different kinds of estimated exposure times.



| Calculated Exposure Times |        |
|---------------------------|--------|
| Dwelltime :               | 5.23s  |
| Settlingtime :            | 30.46s |
| Stage time :              | 9.00s  |
| Calculation time :        | 0.00s  |
| Transmission time :       | 0.02s  |
| <hr/>                     |        |
| Total time :              | 44.72s |
| OK                        |        |

## 12.2 Exposure window

The Exposure window allows the definition of the default parameters which are used during an exposure like step sizes, dwell times, and different exposure modes. But the actual exposure job is started from a Positionlist. The advantage is that within a Positionlist it is possible to define very flexible several additional parameters, e.g. the location on

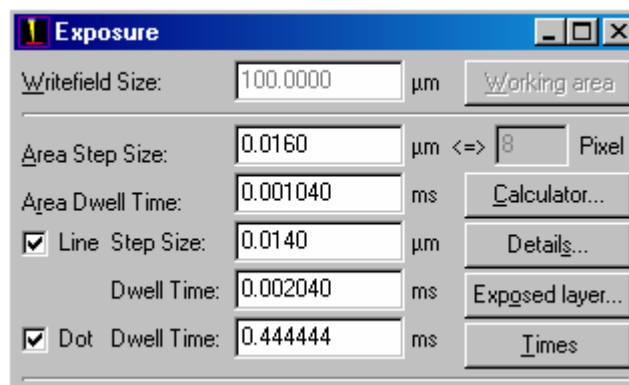
the sample where a structure should be exposed and the working area. A Positionlist can store also more than one exposure job making a kind of batch execution possible. Additionally, it is possible to use for each exposure job different exposure parameters, i.e. one can overwrite the default parameters as defined in the exposure window, which is very useful when searching for the best process parameters.



It is very important to understand that some of the exposure parameters in the **Exposure** window can be overwritten when using the Positionlist. If in doubt which setting for which parameter was used, see the protocol file.

Exposure task may be combined with overlay alignment procedures as described in section [Beam to sample alignment](#).

**Figure 86:** Exposure window to define the default exposure parameters.



#### Write field size

Information of the currently selected write field size. A squared write field is assumed so that width is equal to height.

The following exposure parameters can be edited and calculated within the **Exposure** window. An optional setting within a Positionlist is possible.

#### Area step size

The same meaning as described in section [Preparing a Positionlist](#). In addition, entering a step size value in  $\mu\text{m}$ , the related step size in **Pixel** will be calculated.

#### Area dwell time

The same meaning as described in section [Preparing a Positionlist](#).

#### Line

Select this option to enable the exposure of single pixel lines. After enabling the parameters step size and dwell time for these lines are available.

#### Line step size

The same meaning as described in section [Preparing a Positionlist](#).

#### Line dwell time

The same meaning as described in section [Preparing a Positionlist](#).

#### Dot

Select this option to enable the exposure of dots. After enabling the parameter dwell time for dots is available.

#### Dot dwell time

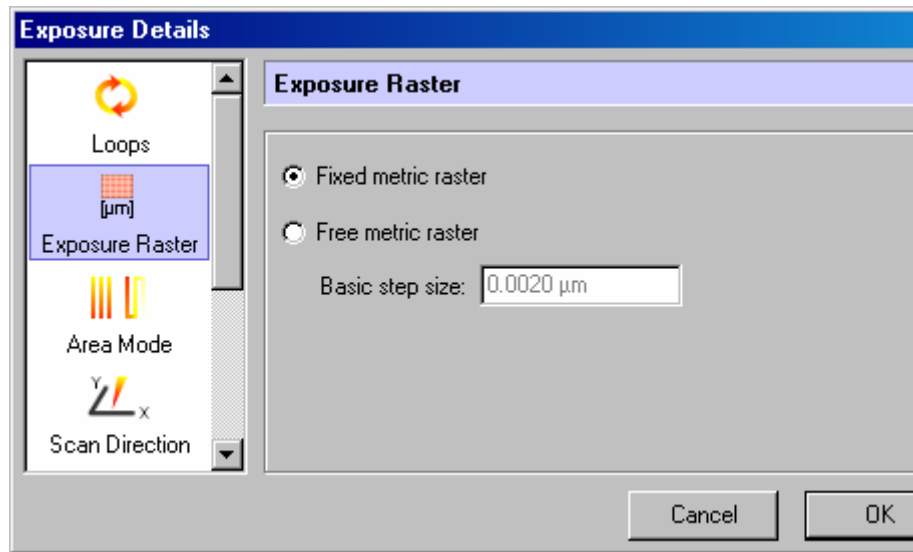
The same meaning as described in section [Preparing a Positionlist](#).

## 12.2.1 Advanced Exposure Parameters

### Details

Choose this button to set some additional exposure parameters.

**Figure 87** Dialog to set additional exposure parameters.



### Loops

The number entered within this text box defines how many times the complete structure will be exposed. Usually, a pattern is exposed just once. But it may be necessary, e.g. to avoid charging up effects, to perform the exposure in several loops with lower dose.

If this parameter is set to zero, the exposure will start an endless loop until it is stopped within the corresponding window.

### Exposure Raster

This setting is only available in connection with all digital pattern generators with version 6 or higher as well as ELPHY *Quantum* PCI-board. The software automatically detects the hardware and enables this feature.

The exposure raster determines the minimum distance between two neighboring points that can be exposed. This minimum distance is called **Basic step size**. The **Basic step size** depends on the currently used write field size. Use **Fixed metric raster** to automatically use the smallest possible **Basic step size**. Use **Free metric raster** mode to define the **Basic step size** manually. It can be any number larger than approximately  $\frac{\text{"write field size"}}{2^{\text{"number of bits"}}$ . For example the minimum Basic

step size for 100 µm write field is 1.6 nm and 0.8 nm for 50 µm write field. The Basic step size can be increased in 0.1 nm steps. Sometimes it is useful to work with free metric raster to achieve optimal exposure results.



For example, if several elements with dimension of 5 nm have to be exposed, it is best to define the Basic step size of for example 2.5 nm. This guarantees that all elements get the same number of points. If one would use for example 2 nm, it can happen that due to rounding one element would get 2 lines and another one would get 3 lines.

**Area Mode**

The filling of areas is defined here. In **Line** mode the beam exposes each line by driving the beam always from one direction. By this behavior a greater accuracy in exposure is achieved, but the exposure takes a longer time due to larger beam settling times.

In **Meander** mode the beam is moved alternates from line to line its direction. This mode results in shorter exposure times. If one wants to use this mode, one has to switch off the dynamic compensation.

**Scan Direction**

When filling an area the beam exposes this area line by line. The direction of these lines is called the scan direction.

The **Scan direction** can be set manually or automatically. If it is set automatically the longest dimension which is parallel to U or V of a trapezoid determines the scan direction. Selecting **Manual** forces the beam to expose only in the specified direction U or V.



Normally the automatic mode should be used. If the manual mode is used, e.g. set to V, and a narrow horizontal rectangles is exposed, this results in longer exposure times.

**Settling Time**

The **Settling time** is the time which the hardware waits after positioning of the beam before starting the exposure of the next trapezoid, line or dot. The **Settling time** is necessary to stabilize the column deflection unit. Therefore the beam is blanked during this time and the values depend on the column itself as well as the distance. Typical values are in the range of milliseconds.

The **Settling time** can be set manually or calculated automatically. In the case that it is calculated automatically, the software calculates the **Settling time** depending on the distance between the elements with respect to a reference value and assuming a linear dependency. The reference value has to be defined as a time per jump over such a distance. The value depends on the column.



Normally the automatic mode should be used. If the manual mode and a relatively large value for the **Settling time** is used, this results in longer exposure times.

**Flyback**

By means of the **Flyback factor**, the software calculates the time which the pattern generator waits between exposing the two lines. The actual time is calculated by multiplying the **Flyback factor** with the settling time.

The **Flyback factor** can be set manually or calculated automatically. In the case that it is calculated automatically, the software determines for each trapezoid the maximum needed flyback time which is then used for the complete trapezoid. The software calculates the **Flyback factor** depending on the distance between the start and end point with respect to a reference value and assuming a linear dependency. The reference value has to be defined as a time per jump over such a distance. The value depends on the column.



Normally the automatic mode should be used. If the manual mode and a relatively large value for the **Flyback factor** is used, this results in longer exposure times.

### Advanced Details

Two modes can be activated here. When using the **Circular mode**, circles defined in the GDSII are not fractured into trapezoids. Instead they are fractured down into concentric rings with decreasing diameter. Hence, this mode is more adapted to the circular geometry of the pattern and the exposure is of higher quality. The **Circular mode** is only available, if within the GDSII the element is defined as full and completely filled circle.

In addition, it is possible to switch off the **Dynamic compensation** applied to the beam. All Raith systems come with an algorithm to compensate dynamic effects which occur when steering the beam whereas all Raith attachments do not have this option. Thus, only at systems it is possible to switch this mode off. If **Dynamic compensation** has been switched, off much faster exposures can be expected but with a reduced placement accuracy.

### 12.2.2 Exposed layer

#### Exposed layer

Choose this button to select the layers to be exposed. A dialog appears with a listing of all layers. Select the layers to be exposed. Unselect layers by an additional mouse click.

## 12.3 Mix-and-Match Exposure

To perform mix-and-match lithography, interactive as well as automatic write field alignments can be performed.

To use this functionality one has to go through the following steps.

#### STEP 1 ►

Within the GDSII design one has to define the mark scans. These mark scans can be placed in the GDSII editor by using the commands **Add > Manual mark scan** and **Add > Auto mark scan**. The command **Add > Manual mark scan** place scans which require some interaction with the software. Within the following dialog type in the exact position of the related physical mark on the sample fabricated within a preceding process step. Define also the size of the scan field.

Up to three mark scans can be used within one write field. A shift correction is possible with just one mark. In case of using 3 marks in each writing field, a complete field alignment in (XY) scaling, rotation, rectangularity and (XY) shift can be performed. If more than 3 marks are defined, these marks are used only if a previous scan failed.





Each mark scans has to lie within one write field. Otherwise it is fractured by a write field border and part of the scan is executed within the adjacent write field.



In the case of automatic scans each U-Scan has to be followed by a V-Scan. Also when placing them within the editor. Use the command **Modify > Order** to check the element order and if required to change it. Otherwise the software can not calculate the correct transformation.

**STEP 2 ►**

Within the Scan Manager use the scans defined under **Align write field procedure > GDSII Markscans > Automatic** or **Manual** to set the corresponding parameter like number of points averaging, etc. For the automatic mark scans make sure to define the correct evaluation method. All parameters are the same as described in section [Scan Manager](#).

**STEP 3 ►**

When choosing the layers to be exposed, select layer 63 to execute the manual mark scans and layer 61 to execute the automatic scans. Then one can start the exposure task.

**STEP 4 ►**

If Manual mark scans are executed, the user has to assign for each displayed mark the true mark centers. After scanning all marks within the current write field the user is asked to confirm the correct transformation values.



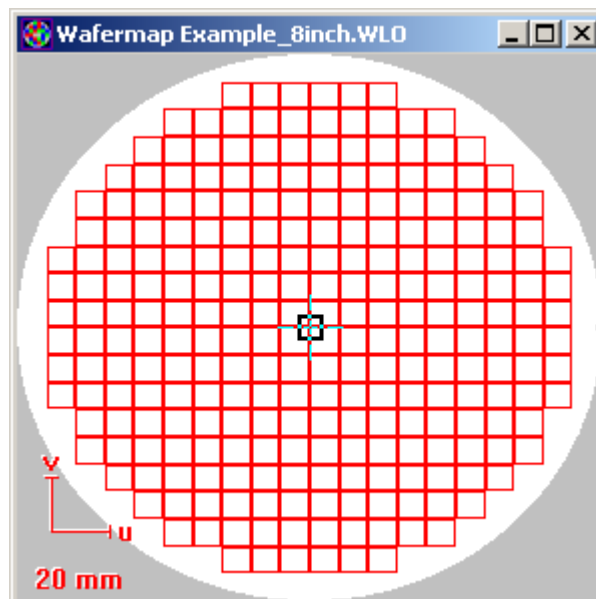
## 13 Wafermaps

|  |            |
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A Wafermap is defined and stored as an ASCII data file, which normally is indicated by extension WLO. In case of importing defect data by using the Import window, the Wafermap layouts are automatically constructed from the imported data file and stored within the subdirectory WAFER of the user's directory. For generation of customized Wafermap layouts choose the command **File > Waferlayout** as described below.

### 13.1 Wafermap window

**Figure 88:** Example of a Wafermap representing an 8" wafer.



Use one of the following ways to open a Wafermap window:

- Choose the command **File > New Wafermap**. In this case an empty Wafermap is displayed. This map can be modified using the command **File > Waferlayout** or replaced by an existing Wafermap using the command **File > Open**.
- Choose the command **File > Open Wafermap**. In this case an existing Wafermap will be loaded and displayed. Also this Wafermap can be modified or replaced by another one.


The elements of the Wafermap window are (see figure):

#### Title Bar

The title bar shows the name of the loaded Wafermap.

- Scale** The scale serves to indicate the size of your sample, graphically.
- Limits** As an overlay the software limits can be graphically indicated. Use the command **Module status > Wafermap > Show limits** to enable this feature.
- Icon bar** If a Wafermap window is activated, additional symbols, menus and menu items are available within the menu bar which will be explained in detail in the following sections.

### 13.1.1 File Menu

- Open** Choose this command to load an existing Wafermap layout. This command replaces the actually activated layout by the newly selected one.
- Save** Choose this command to save the activated Wafermap layout under its current name.
- Save as** Choose this command to save the activated Wafermap layout under a freely selectable name.
- Link positionlist** Choose this command to open a Positionlist and link it to the activated Wafermap. This relation between Wafermap and Positionlist is necessary to make use of the defect overlay feature which is not used in standard lithography applications.
- Open chipmap** Choose this command or choose the symbol button  or double-click on a chip within the Wafermap to open the related Chipmap window.
- Waferlayout** Choose this command to open a dialog for editing the currently opened Wafermap meeting your application. A dialog is preset with parameters taken from the activated Wafermap window. Editing is described in the following section in section [🌐 \*Defining wafer layouts\*](#).

## Defining wafer layouts

**Figure 89:** Dialog to for editing a Wafermap.

**Edit Waferlayout**

Filename:

**Wafer**

Shape:  Rest. Area:

Size U:  Size V:

Origin U:  Origin V:

**Coarse Alignment**

Type:  Position:

Size:

**Chip Parameter**

Size U:  Size V:

Distance U:  Distance V:

Offset U:  Offset V:

Count origin U:  Count origin V:

Count offset U:  Count offset V:

Label:  Count offset:

Count type U:  Count type V:

Count:  Chiplayout:

**Filename:** Enter a suitable name for your Wafermap layout file. The extension WLO will be added automatically. The file will be stored in the subdirectory WAFER of the user's directory.

**Shape:** Select an elliptical or a rectangular layout shape from this drop-down list box.

**Rest. Area:** Enter the width of the restriction area, i.e. the thickness of a margin restricting the chip area. Chips which are partly or completely located inside the restriction area are not drawn in the Wafermap layout, but they may be counted in the chip numbering sequence.

**Size U/V:** Enter the outer diameter of your wafer in U and in V direction.

**Origin U/V:** Enter the origin of the U/V (sample) coordinate system, i.e. the distance of the U/V origin from the lower left corner of a square enclosing the wafer layout. Typical values are either "0 / 0", i.e. U/V origin is lower left, or "Radius / Radius", i.e. U/V origin is wafer center. Set the origin according to the conventions you are using for the general sample (U/V) coordinate system.

**Type:** Use this drop-down list box to select one of the following orientation markers: **Major Flat**, **Square** or **Notch**.


**Position:** Use this drop-down list to select one of the following locations of the orientation marker: **Top**, **Right**, **Bottom** or **Left**.

**Size:** Enter the size of the orientation marker.

**Size U/V:** Enter the chip size with U = width and V = height.

**Distance U/V:** Enter the horizontal (U) distance and the vertical (V) distance between two adjacent chips.

**Offset U/V:** Enter the distance between the lower left corner of the center chip and the U/V origin of the wafer.

**Count origin U/V:** Use these drop-down list boxes to select the starting point of the chip numbering scheme, i.e. to determine the chip counting direction. To increase chip numbers from left to right use **Left** and vice versa. To increase chip numbers from bottom to top choose **Bottom** and vice versa. The numbering scheme can be displayed by choosing the  symbol button.

**Count offset U/V:** Enter the start number for the chip numbering scheme in U direction resp. in V direction. These text boxes are accessible for the numbering manners **U/V** and **V/U**, only

**Label:** Use this drop-down list to select the manner of chip numbering. **U/V** first matrix coordinate U, **V/U** first matrix coordinate V, **Number** single number.

**Count offset:** Enter the start number for the chip numbering scheme. This start number is valid for both matrix directions (U/V). This text box is accessible for the numbering manner **Number**, only.

**Count type U/V:** Use this drop-down list to select between different alphanumerical numbering manners.

**Count:** Use this drop-down list to select the manner of chip counting.  
**Chips:** The chips which are not completely located inside the chip area are not counted in the chip sequence. **Matrix:** The chips which are not completely located inside the chip area are counted in the chip sequence.

**Chip layout:** Use this text box to assign an existing chip layout file to the Wafermap layout. The specified chip layout file must be available in the subdirectory CHIP within the user's directory. It is used to overlay a substructure on the Chipmap. If no chip layout is available or required leave this text box free.

To modify the waferlayout on-line on a chipwise base, point to the chip of interest, press and hold the **Shift** key and click the left mouse button. This operation opens the **Edit Wafer Element** dialog for the

selected chip which can be used to modify chip representations or to delete the complete chips from the wafer.

**Figure 90:** Dialog for editing the properties of a selected chip.

Select the element **Type** from the drop-down list box. Available types are **ELLIPSE**, **BOX**, **CHIP**, **TEXT**. The **Text** field is used only for the elements **CHIP** and **TEXT** but is ignored for **ELLIPSE** and **BOX**.

Select **Frame** color, **Fill** color and **Text** color for the specified element from the related drop-down list boxes. For the element **TEXT**, fill color and text color are ignored, but the frame color is used instead. For the element **CHIP**, frame color and fill color are ignored, but the color coding defined by the command **Chip Colors** is used instead.

Enter the coordinates of the lower left corner (**U1**, **V1**) and the coordinates of the upper right corner (**U2**, **V2**) of the specified element within the related text boxes.

Choose **Delete** to delete the specified element completely from the wafer layout.




The element will be deleted at once without further query. An undo function is not implemented.

### 13.1.2 Edit Menu

#### Delete

Choose this command to delete the selected chips.

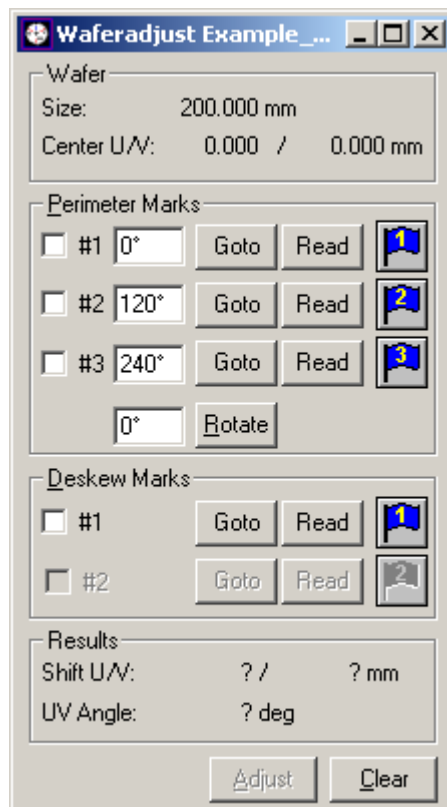
#### Preadjustment

Choose this command or choose the icon  to set up an open the Automatic Adjustment dialog showing information about the transformation parameters. Choose the **OK** button to perform the

preadjustment. These values are stored together with the Wafermap file and are imported when the corresponding file is opened.

**Unpatterned wafer adjustment** The adjustment procedure for an unpatterned or blank wafer requires a different approach compared to that for other samples, as in this case there are no easy to recognize regular structures for which the sample coordinates are known. To overcome this disadvantage, the adjustment procedure determines the center of the wafer and its angular orientation by using its perimeter and its flat or notch. It requires no additional input information such as precise wafer size or a set of known coordinates.

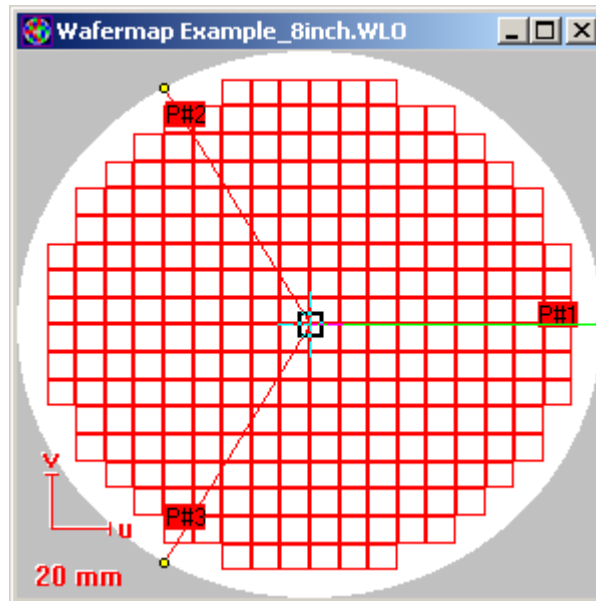
**Figure 91:** Dialog to perform preadjustment procedure.



The corresponding dialog offers a toolbox and calculator for the alignment routine. In parallel, there is an overlay displayed on the Wafermap which indicates the selected sites within the alignment procedure.



**Figure 92:**  
Visualization of  
preadjustment  
procedure within  
Wafermap.



The dialog box has the following functionality:

**Wafer:** This section displays information already available to the program from the import of the Wafermap, such as wafer diameter and wafer center in UV coordinates.

**Perimeter Marks:** This section is the interactive part which allows also configuring the marks to be used for alignment. Three perimeter marks have to be set and used for determining the exact center of the wafer. The ideal locations of the marks are displayed in parallel on the Wafermap as "P#1 – P#3". Each of these marks can be assigned with a dedicated angular position or all marks together can be rotated stepwise on the Wafermap, if the default settings are not suitable for the instrument or application. Use **Goto** followed by the **Read** buttons (or the blue flags for reading coordinate data from UV windows) to read current stage position when at the corresponding mark at the perimeter.



The procedure of determining the wafer center has to be completed before the angular orientation can be measured within the section **Deskew Marks**.

**Deskew Marks:** This section allows measuring the angular orientation of a blank wafer by aligning to the wafer notch or flat. From the information in the Wafermap, the program automatically determines whether the wafer has a flat or a notch. The procedure differs for these two cases. In the case of a flat, two marks are used, which are along the flat of the wafer. In the case of a notch, only one mark is used. For both case, only the angular orientation is calculated. Use the **Goto** buttons followed by the **Read** buttons (or the blue flags for reading coordinate data from UV windows) to read current stage position when at the corresponding mark at flat or notch.

**Results:** In this section the results of the adjustment actions are displayed.

The results of the alignment procedure become active after choosing the **Adjust** button. The button can only be applied, if a complete set of angular and lateral wafer alignment steps has been performed.

As results, the UV offset value of the wafer center and the calculated rotation is displayed.

The individual adjustment steps can be repeated and changed independent from each other.

Choose **Clear** to reset the coordinate transformation back to the identity transformation.

### Performing an adjustment routine

- STEP 1 ►** Open the Wafermap and apply the preadjustment routine.
- STEP 2 ►** Get access to the unpatterned wafer alignment window by choosing the command **Edit > Unpatterned wafer adjustment**.
- STEP 3 ►** Set the 3 perimeter marks into those locations which can be easily accessed by your wafer stage. For this, you can vary the individual angular locations of the marks and the angle of the set commonly.
- Begin with the adjustment of the exact wafer center by using the perimeter marks.
- STEP 4 ►** Choose for mark #1 the **Goto** button, and the stage will automatically move close to the wafer boundary under the specified angular orientation.
- STEP 5 ►** After the stage has reached its destination, move the stage manually in such a way that you can see the wafer boundary crossing the center of your SEM screen displaying e.g. an SE image. For this it is not important that you keep or take care on the angular orientation. If necessary, perform a backlash operation and readjust. Then choose the **Read** button.
- STEP 6 ►** Alternatively, if a image is available, use the **Blue Flag** and drag it onto the wafer boundary within the image. The first check box gets a tick mark, which means that this mark has been processed.
- STEP 7 ►** Repeat these steps for mark #2 and #3.
- Now perform the deskew procedure which is explained here for a wafer flat.
- STEP 8 ►** Choose the **Goto** button of deskew mark #1. The stage will move to that location based on the current adjustment.

**STEP 9 ►** After the stage has reached its destination, move the stage manually in such a way that you can see the wafer boundary crossing the center of your SEM screen displaying e.g. an SE image. For this it is not important that you keep or take care on the exact position along the flat. If necessary, perform a backlash operation and readjust. Then choose the **Read** button.

**STEP 10 ►** Alternatively, if an image is available, use the **Blue Flag** and drag it onto the wafer boundary within the Image. The first check box gets a tick mark, which means that this mark has been processed.

**STEP 11 ►** Repeat these steps for deskew mark #2.

**STEP 12 ►** Choose the Adjust to apply this new UV-Adjustment.


Please note that after this adjustment procedure the particles should be in reach of the stage. In some cases, a 3 point alignment at found particles or a post-alignment can be useful to improve accuracy and speed of the review procedure. However, this depends strongly on the precision of both: the stage and the defect inspection tool, delivering the coordinate set (Positionlist).

**Adjustment** Command common to all UV windows, described in section [UV Windows](#). Please note the resulting mark location depends on the actual catch status.

**Measure** Command common to all UV windows, described in section [UV Windows](#).

### 13.1.3 View menu

**Chip text** Choose this command or icon  to display the chip labeling.

**Defect marker** Choose this command or icon  to display the defect positions.

**Redraw** Choose this command to refresh the graphical representation of the Wafermap due to layout changes.





**Zoom** Command common to all UV windows, described in section [UV Windows](#).

**Overlay** Command common to all UV windows, described in section [UV Windows](#).

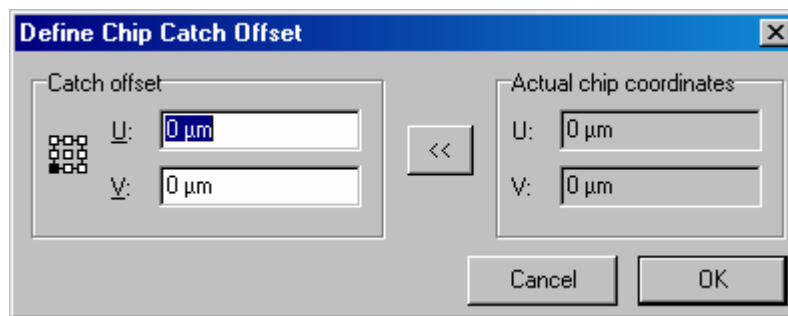
**Toolbox** Command common to all UV windows, described in section [UV Windows](#).

### 13.1.4 Options menu

#### Catch mode

The catch mode defines how a location within a chip is addressed, for example when a chip is the target for a drag-and-drop action. Three different modes exist: **None**, **Offset** and **Position**. If the catch status is **None**, the exact pointer position is used for **UV** addressing. If the catch status is **Offset**, the **Chip Catch Offset** setting with the chip is used. Choose the command **Chip Catch Offset** to define this offset. If the catch status **Position**, the existing position located nearest to the mouse pointer is used. The Catch mode status is displayed also the the following icons:  for **None**,  for **Offset** and  for **Position**. The icons can also be used to toggle between the modes. The **Chip Catch Offset** can also be defined using the  icon.

**Figure 93:** Dialog to define the catch offset for each chip.




#### Chip colors

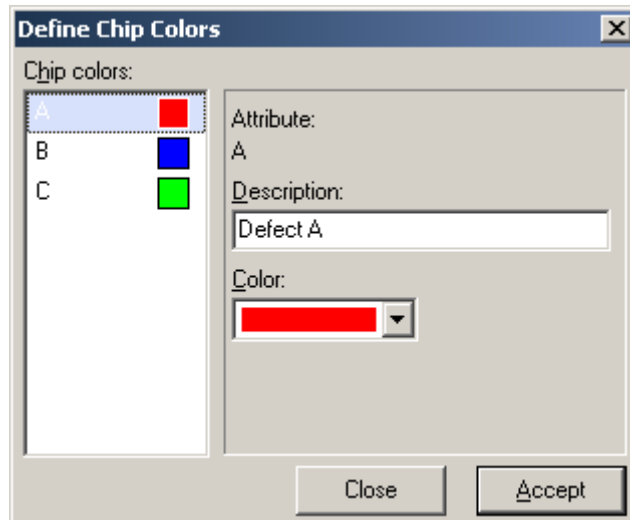
Some chips containing one or more positions from an associated Positionlist can be color coded and thus give an overview in which chips are which kinds of defects.



A Positionlist must be opened and linked to the Wafermap. Otherwise this command is not possible.

Choose this command or choose the symbol button  to modify the assignment of the chip color coding within the Wafermap layout to the defect attributes in the related Positionlist.

**Figure 94:** Dialog to define the color coding for each chip depending on the Position it contains.



On the left hand side, the **Chip colors** list box shows the current assignment for all attributes of the associated Positionlist. Select the current color assignment to be modified within that list box. Then select the new color to be assigned and choose **Accept**. In addition, you may enter a description of the attribute.

**Same aspect ratio**

Command common to all UV windows, described in section [UV Windows](#).

**Cursor grid**

Command common to all UV windows, described in section [UV Windows](#).

**UV Display ...**

Command common to all UV windows, described in section [UV Windows](#).

## 13.2 Mouse Commands

The table below gives a summary of all available mouse commands within an activated Wafermap window.

**Table 33:** Mouse commands in Wafermap window.

| Action       | Key(s) + Mouse Button | Functionality                              |
|--------------|-----------------------|--|
| Single click | <b>Shift</b> + left   | Opens <b>Edit Wafer Element</b> dialog.    |
| Single click | none + right          | Drives the stage to the selected position. |
| Double click | none + left           | Opens the related Defectmap window.        |

### 13.3 Interaction with Other Modules

A summary of drag and drop operations involving a Wafermap is listed below.

**Table 34:** Wafermap drag and drop functionality.

| Source         | Object          | Target                                | Action  |
|----------------|-----------------|---------------------------------------|---|
| GDSII Database | Structure       | Wafermap with associated Positionlist | GDSII structure is placed in Wafermap and stored in Positionlist. |
| Positionlist   | Position        | Wafermap with associated Positionlist | Redefines location of object.                                     |
| Scan Manager   | Scan Definition | Wafermap with associated Positionlist | Scan task is placed in Wafermap and stored in Positionlist.       |
| Automation     | Script or Macro | Wafermap with associated Positionlist | Macro file is placed in Wafermap and stored in Positionlist.      |

# 14 Chipmaps

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## 14.1 Chipmap window 191

## 14.2 Mouse Commands 193

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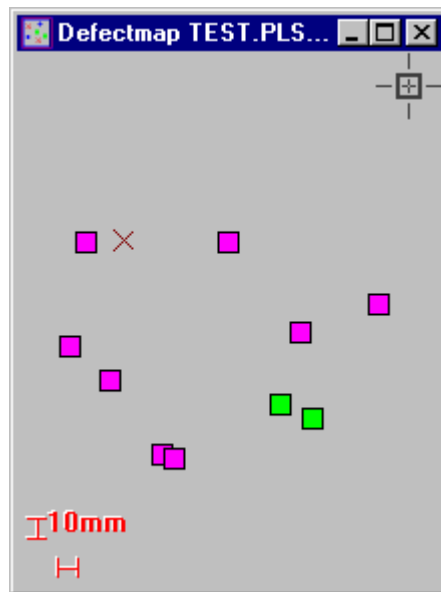
The Wafermap representation and addressing is very convenient on a large scale wafer level. For more precise addressing inside a chip, use the Chipmap representation which contains a zoomed chip from a Wafermap.

### 14.1 Chipmap window

First activate a Wafermap module window, and then use one of the following ways to open a Chipmap module window:

- Choose the command **File > Open Chipmap** and select the chip of interest within the appearing dialog box.
- Double-click on the chip of interest.

**Figure 95:** Example Chipmap with same defects.



The elements of a Chipmap window are.

#### Title Bar

The title bar shows the name of the related Positionlist and the number of the chip within the related Wafermap.

#### Position Cursor

The position cursor graphically indicates the actual location of the electron beam on the sample. In addition, the global wafer coordinates, the local chip coordinates and the stage coordinates XY of the current location are displayed within the status bar.

#### Scale

The scale bars indicate the size of the sample.

**Defects**

The defects are graphically indicated by colored rectangles, circles or crosses.

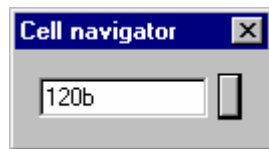
If a Chipmap module window is activated, additional menus, menu items and symbols are available within the Program Desktop which will be explained in detail in the following.

**14.1.1 File menu****Open ...**

Choose this command to load a chip layout file to be overlaid within the Chipmap module window. Chip layout files (extension CLO) are commonly used to define a Bitmap design.

**14.1.2 Edit menu****Cell navigator**

This command is only available, if a chip layout file was selected. Choose this command or use the hot keys **Ctrl + n** to open the memory cell navigator dialog box. After finishing navigation work, use the **Esc** key to close this dialog box.



The cell navigator allows entering drive commands digitally on the bit line and word line level, similar to the handling of the Command window.

The following commands are available:

**Table 35:** Commands available within **Cell navigator** dialog.

| Command | Functionality                               | Example |                                 |
|---------|---|---------|---------------------------------|
| <n>B    | Relative drive command over <n> bit lines.  | -1B     | Moves 1 bit line down.          |
| <n>b    | Absolute drive command to bit line <n>.     | 120b    | Moves to bit line number 120.   |
| <n>W    | Relative drive command over <n> word lines. | 4W      | Moves 4 word lines up.          |
| <n>w    | Absolute drive command to word line <n>.    | 8191w   | Moves to word line number 8191. |



The small button on the right hand side of the text box allows repeating the last command.



**Adjustment** Command common to all UV windows, described in section [UV Windows](#).

**Measure** Command common to all UV windows, described in section [UV Windows](#).

### 14.1.3 View menu

**Chip layout level** Choose this command to change the hierarchy level of the displayed Chip layout by one step upwards or one step downwards: from array to segment to block to quadrant. Alternatively, use the icons  .





**Redraw** Command common to all UV windows, described in section [UV Windows](#).


**Zoom** Command common to all UV windows, described in section [UV Windows](#).

**Overlays** Command common to all UV windows, described in section [UV Windows](#).

**Toolbox** Command common to all UV windows, described in section [UV Windows](#).

### 14.1.4 Options menu

**Catch Mode** Command described in section [Wafermaps](#). Alternatively, use icons    .

**Defect Marker** Command described in section [Wafermaps](#). Alternatively, use icon .

**Same aspect ratio** Command common to all UV windows, described in section [UV Windows](#).

**UV Display...** Command common to all UV windows, described in section [UV Windows](#).

## 14.2 Mouse Commands

The table below gives a summary of all available mouse commands within an activated Chipmap module window.

**Table 36:** Mouse commands in Chipmap window.

| <b>Action</b> | <b>Key(s) + Mouse Button</b> | <b>Functionality</b>   |
|---------------|------------------------------|--|
| Single click  | <b>Control</b> + right       | Drives the stage to the selected position.   |
| Double click  | none + left                  | Opens "Edit Position" dialog box for the defect located near to the selected position. |