

# Medical Imaging Interaction Toolkit: The Movie Maker View

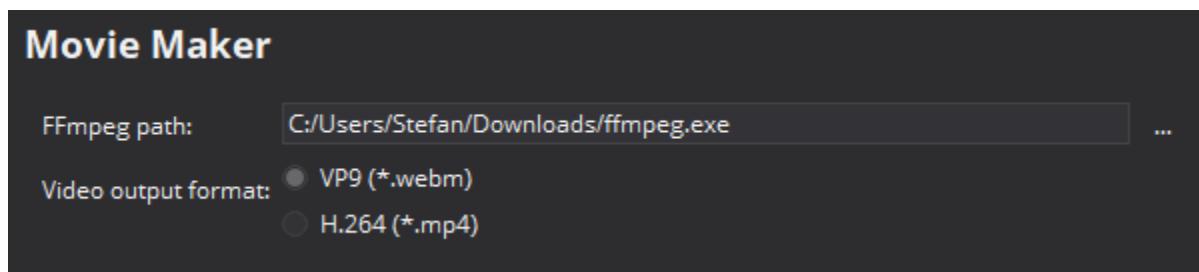
Icon of the Movie Maker Plugin.

## Overview

The Movie Maker View allows you to create basic animations of your scene and to record them to video files. Individual animations are arranged in a timeline and can be played back sequentially or in parallel.

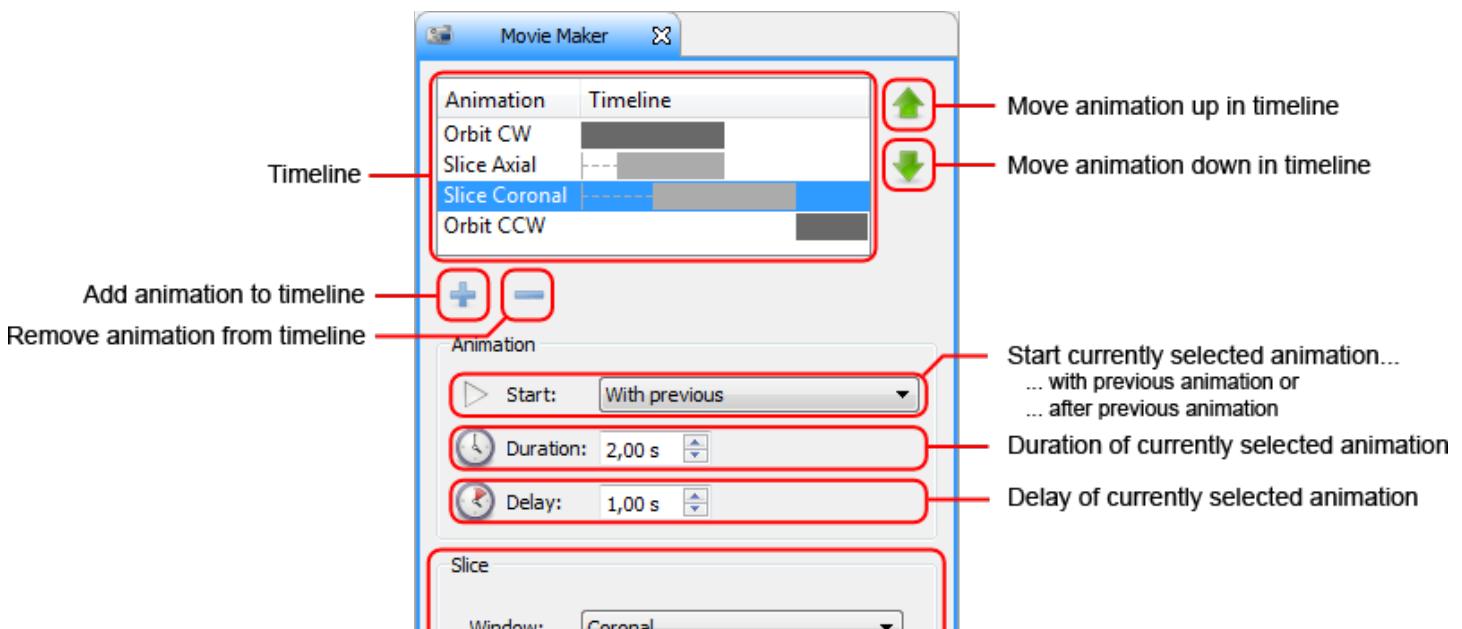
The Movie Maker View uses the external FFmpeg command-line application to write compressed video files.

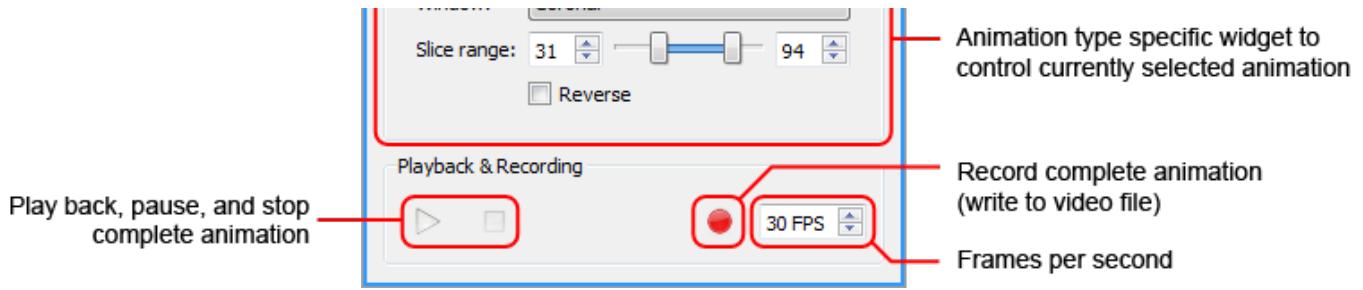
**You must install FFmpeg and set its corresponding path in the "Movie Maker" preferences (Ctrl+P) to be able to record your movies to video files.**



The Movie Maker preferences page.

## Usage





## The Movie Maker View.

To create a movie, add an animation to the timeline by clicking the "Add animation" button. You can choose between the available types of animations, e.g., Orbit or Slice.

The buttons surrounding the timeline allow you to arrange, remove, or add further animations to your movie.

Each animation can be set to either begin with the previous animation, i.e., run in parallel, or to start after the previous animation, i.e., run sequentially. In combination with delays, rather complex animation arrangements are possible.

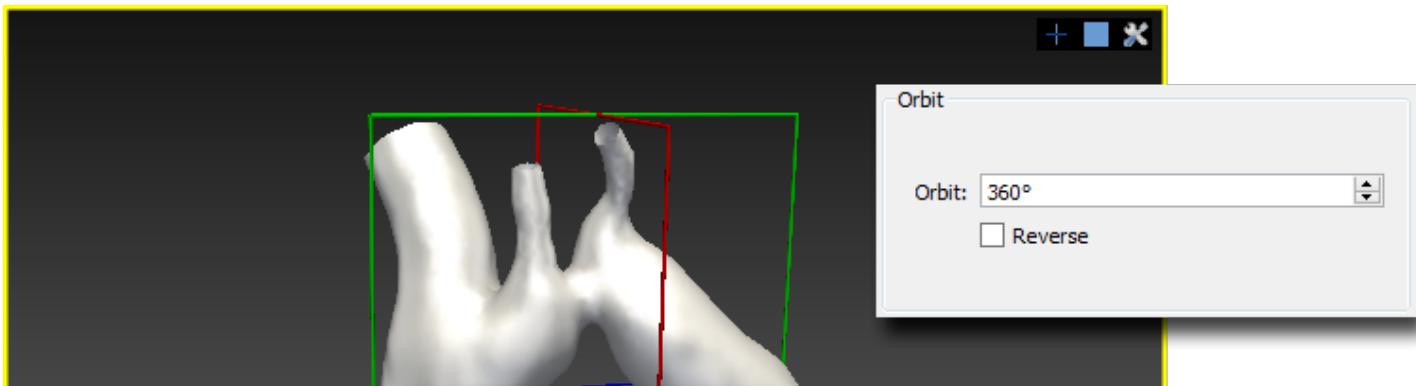
To set animation specific parameters, select the corresponding animation in the timeline first.

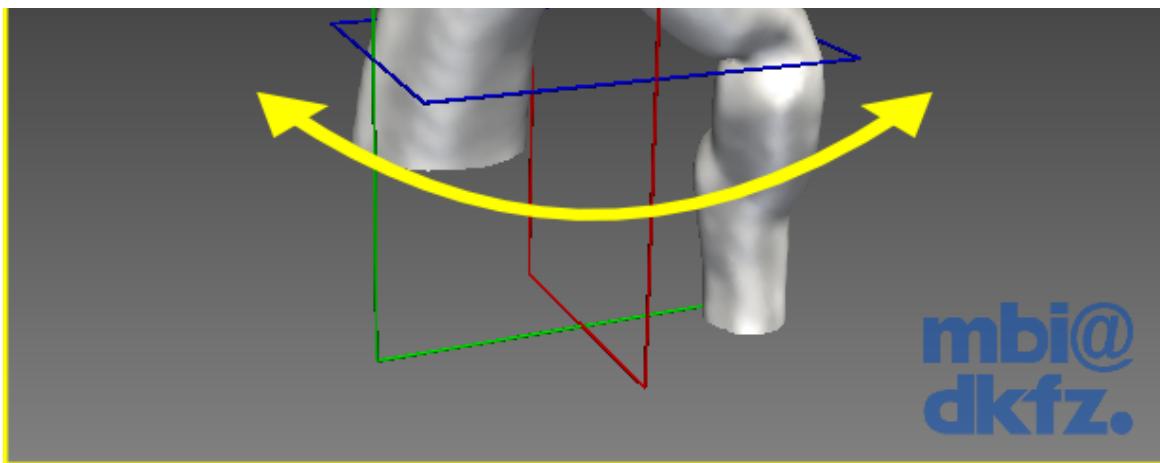
You can play back, pause and stop your movie with the controls at the bottom of the Movie Maker View. Click the "Record" button to finally record your movie to a video file with the specified frame rate resp. number of frames per second. Choose the render window that you want to record.

By default, movies are recorded into \*.webm files using the open and royalty-free VP9 video codec. You can switch to the widespread \*.mp4 file format using the non-free H.264 video codec in the Movie Maker preferences.

## Orbit Animation

The Orbit animation rotates the camera in the 3D window around the scene. Align the camera directly in the 3D window and enter the number of degrees for the orbiting. If you are planning to have a specific view in the middle of your movie you can play the movie and pause it at the specific frame of interest. Adjust the camera in the 3D window and restart the animation.

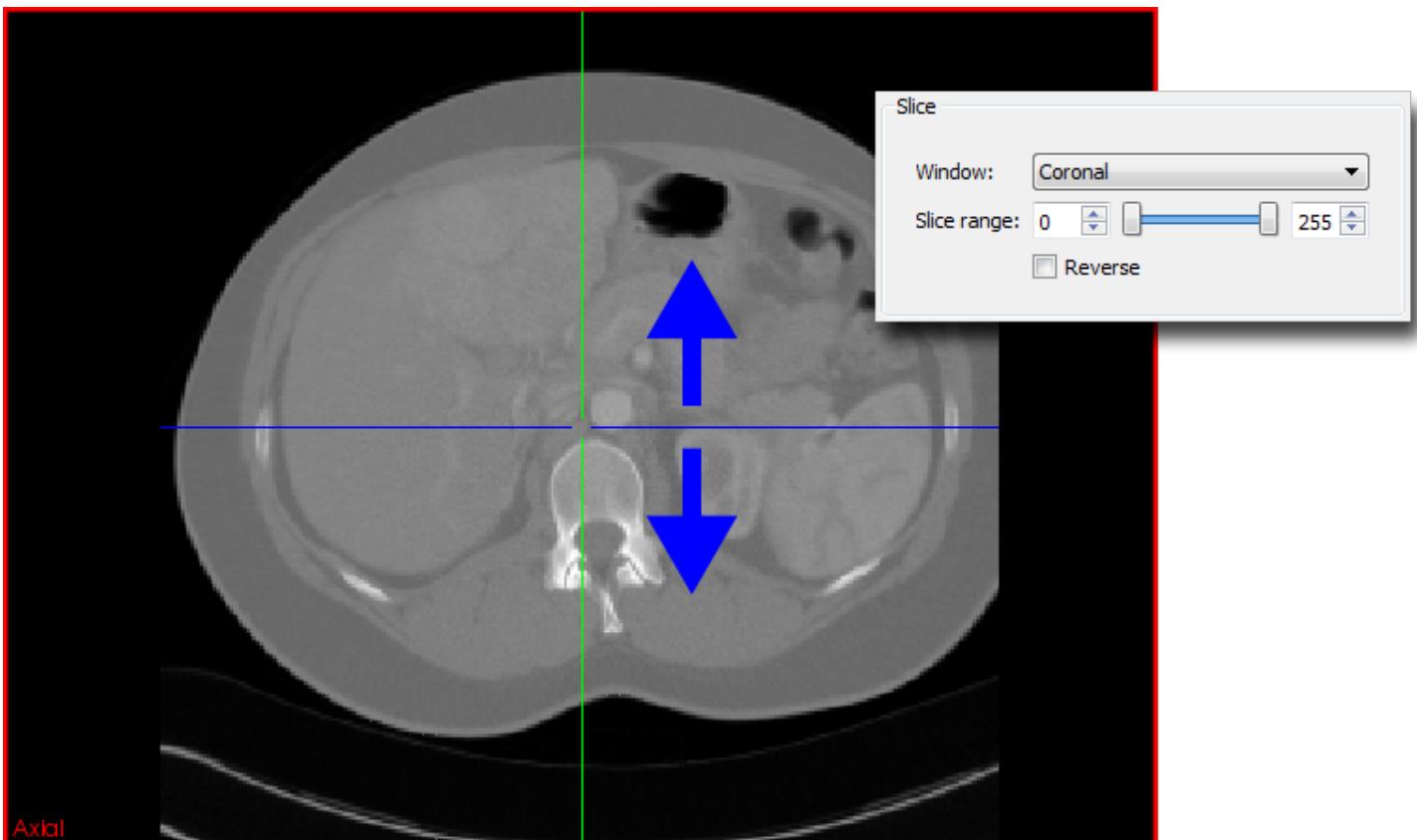




The Orbit animation.

## Slice Animation

The Slice animation slices through an image. You can choose the image plane (axial, sagittal, or coronal), as well as the start and end points of the slicing. Look at the Image Navigator View to get an idea of the desired values. Toggle "Reverse" to slice from the higher slice number to the lower slice number.



The Slice animation.

## Time Animation

The Time animation steps through the individual time steps of the current scene. You can specify the range of the animated time steps. Look at the Image Navigator View to get an idea of the desired values. Toggle "Reverse" to step from later time steps to previous time steps.



Axial

The Time animation.

# Medical Imaging Interaction Toolkit: The MxN Display

## General remark on F1 help

This is the help window of the MxN display. To display the help windows of other plugins, press F1 when the plugin of interest is active (please make sure the tab of the plugin of interest is highlighted). Alternatively, go to the *Help* menu and select *Open Help Perspective*. A help window opens from which you can select the documentation of the plugin of interest.

## Overview

The MxN display is an alternative image viewer to the Standard display. It is a more flexible, customizable approach to displaying images with a strong focus on displaying different images simultaneously but independently. Unlike than the Standard Display it allows to show a different image for each window view while also allowing independent image navigation. The number of window views can be freely chosen and anatomical view planes / view directions can be changed for each window view.

## Working with the MxN display

The following sections describe how to work with the MxN display. The MxN display can be customized and several properties can be set to modify the behavior.

## Configuration Toolbar

The MxNDisplay is initialized with a single window view and a configuration toolbar on the right side. In the toolbar you can find three icons / actions, where two buttons have an on/off state.

 Layout button	
 Synchronize button	 Desynchronize button
 MITK mode button	 PACS mode button

Layout button: Choose a layout from presets or select a custom number of available window views and their layout in a grid

Synchronization button: Enable or disable synchronized interaction across the window views

Interaction mode button: Switch between the MITK interaction mouse mode and the PACS interation mouse mode

## MxN display layout

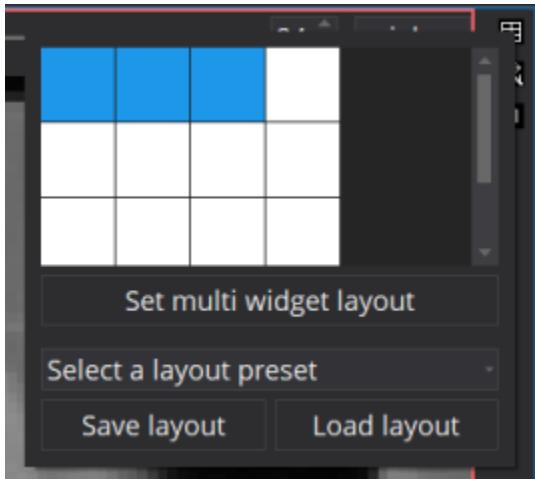
There are several options to customize the MxN display layout.

Using the layout button from the configuration toolbar allows to customize the layout the following way:

By choosing the desired amount of windows and confirming via "Set multi widget layout". The window views are arranged in a rectangular grid, as specified. Depending on the selected number of window views, existing window views will be removed or additional window views will be added. New window views will have a sagittal view direction. Window views that stay untouched will keep their settings and continue displaying their selected data.

By selecting one of the provided layout presets.

By saving / loading a custom layout, either created using the previous methods and further refinement or by handcrafting a suitable file.



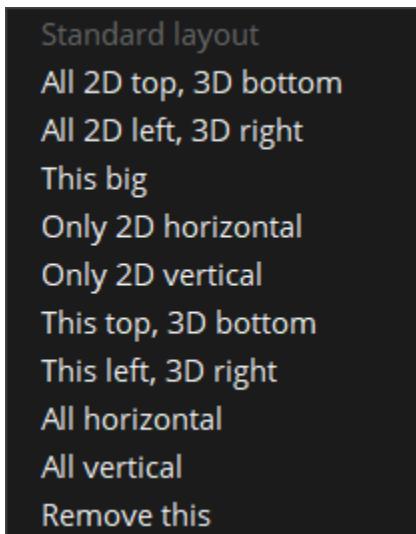
Layout widget

By moving the cursor to the upper right corner of any window you can activate the window menu. It consists of three buttons:

The crosshair button allows to toggle the crosshair and to reset the view.

The middle button expands the corresponding window to fullscreen.

The right button allows you to choose between many different arrangements of the available windows.



Layout arrangement

## Window synchronization

If data is displayed inside a window view you can interact with the window / loaded image using your mouse. As long as the interaction synchronization is disabled (), mouse interactions, such as zooming, setting the point of interest, mouse wheel scrolling etc. will affect only the window view you click in. If the interaction synchronization is enabled (, performing any of the mouse interactions inside a window view will perform the same interaction in any other visible window view.

## Mouse interaction mode

As mentioned before, you can use the mouse to interact with each window / loaded image. There are two interaction modes which can be switched between using the interaction mode button: the MITK interaction mouse mode and the PACS interaction mouse mode. If the PACS interaction mouse mode is selected, an interaction tool bar is added to the left side of the MxN display: It allows to select the action to perform for the left mouse button. The difference between the MITK and PACS mode is as follows:

MITK interaction mouse mode



left mouse button: setting the point of interest

right mouse button: zooming in and out while moving the mouse

middle mouse button / pressing mouse wheel: moving the image while moving the mouse

mouse wheel: scrolling through the displayed image slices

## PACS interaction mouse mode

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left mouse button: depending on the selected mode in the interaction tool bar

right mouse button: changing the level window for the topmost visible image under the mouse cursor

middle mouse button / clicking mouse wheel: no interaction

mouse wheel: scrolling through the displayed image slices

strg-key + right mouse button: zooming in and out while moving the mouse

shif-key + right mouse button: moving the image while moving the mouse

## Utility Menu

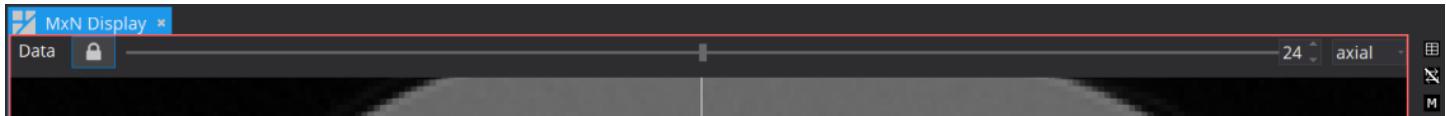
Each window view has a utility menu at the top with four UI elements that allow to perform the following actions:

Data selection button: Select which data should be selected and visible inside the window view

Lock / unlock button: Set the lock state of a window to couple / decouple the window from other windows.

Slice slider: Navigate along the view direction of this window

View direction drop down menu: Select the current anatomical view plane / view direction



Utility menu

## Data node selection

Using the data selection button of a window view you can open a data node selection dialog which shows the currently selected data nodes for the window view. "Currently selected" means that you can either decide to show all available data nodes from the data storage or - for a better data node overview - only show an individually selected subset of the available data nodes. You can either remove a node from the selection by clicking the "x" on a data node or use the "Change selection" button to individually select data nodes. The "Select all nodes" checkbox denotes which of the selection types is currently used - showing all available data nodes or showing only a subset of data nodes. Checking the checkbox will reset the selection to all available data nodes.

Selecting data nodes does not mean that this node always has to be visible in the window view

(rendered). If you want to hide a node, e.g. for temporarily inspecting underlying images, you can do so by clicking the "eye" icon for each selected data node.

If you want to reset the window view to a specific node / image, you can use the "arrow" icon. This will reset the camera to focus on the selected node, using default zoom and centered camera position. If you want to reset the camera to focus on the whole scene / all selected nodes, you can use the window menu, see [MxN display layout](#). Resetting a window only affects the corresponding window view, regardless of any synchronization / lock state.

## Lock button

So far showing / hiding nodes or removing them from a selection / changing a selection affected all window views. If you want to use individual selections for a window view, you can unlock / decouple the window view from other window views by clicking on the lock button in the utility menu. This will decouple the current window view. Changing the visibility of a node or selecting individual nodes / removing nodes using the data node selection button will affect only the current window view. This allows to show different images in each window view, e.g. by decoupling multiple window views and selecting individual nodes in each window. It is still possible to have a synchronized mouse interaction, see [Window synchronization](#) and [Mouse interaction mode](#).

## Slice selection slider

Displayed data is typically 3D data but each window view shows a 2D slice of the 3D volume. The direction in which the 3D volume is sliced is defined by the "view direction" (or "anatomical plane"). To define at which position in the view direction the 3D volume should be sliced, the slice selection slider can be used. It can either be moved using the mouse or by using the appropriate mouse interaction (see above, e.g. mouse wheel scrolling).

## View direction

Each window view "is looking in" one of the three available view directions, namely "Axial", "Sagittal" or "Coronal". You can change the view direction by switching to another anatomical plane in the view direction drop down menu. Changing the view direction will reset the camera to its default for the new view direction, meaning default zoom and centered camera position.

## The Pixel Value View

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Icon of the Pixel Value Plugin.

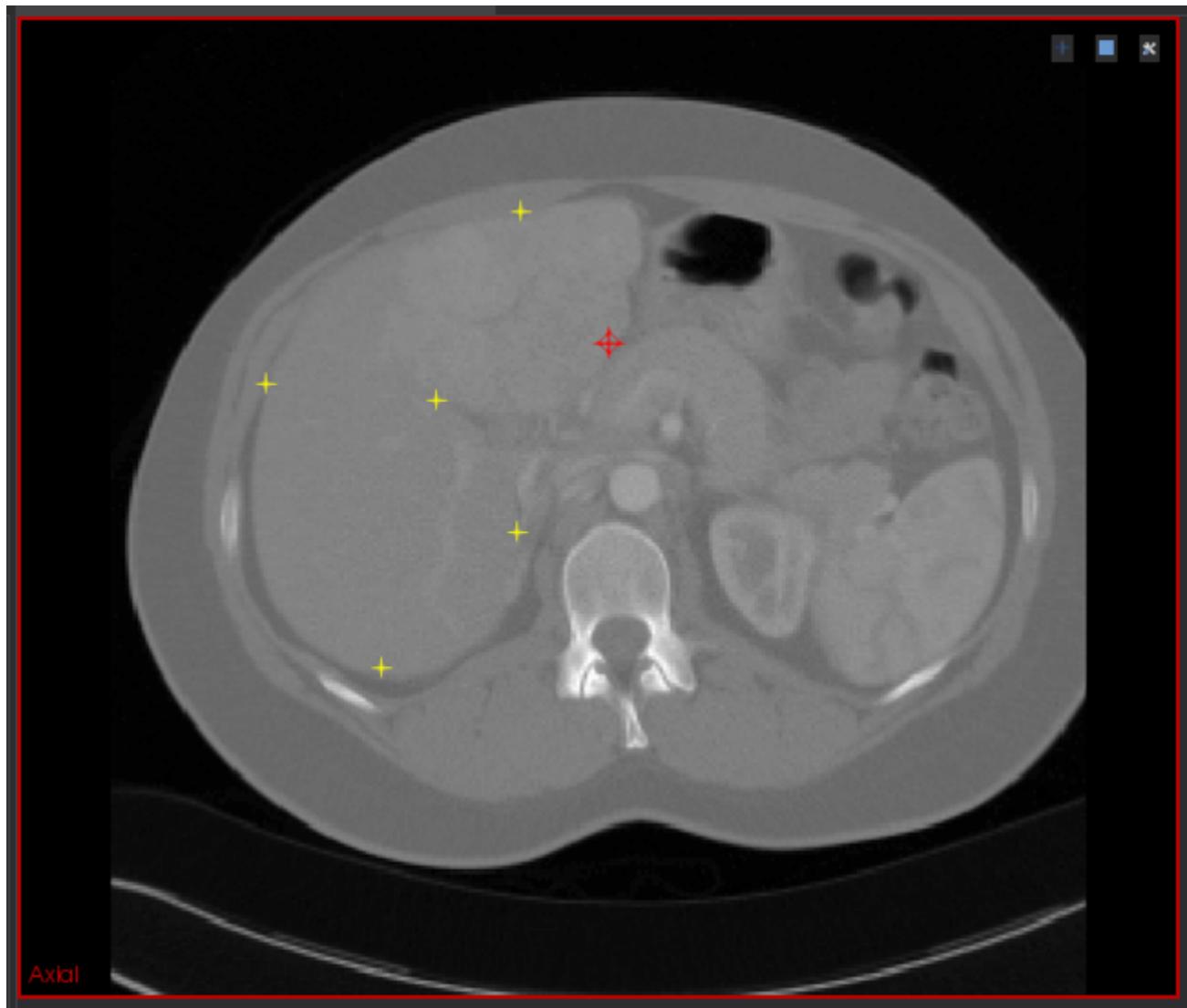
This is the pixel value plugin. It shows the value of the selected pixel in images.

# Medical Imaging Interaction Toolkit: The Point Set Interaction

Icon of the Point Set Interaction View

## Overview

This view allows you to define multiple sets of points, to fill them with points and to save them in so called PointSets.



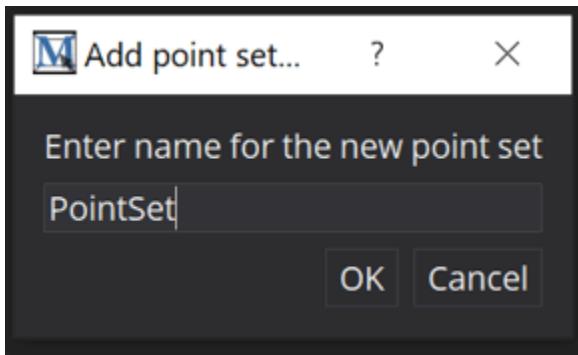
PointSet Annotations in MITK

This document will tell you how to use this view, but it is assumed that you already know how to navigate through the slices of an image using the four window view. Please read the application manual for more information.

# Usage

## Create new PointSet

First of all you have to select a PointSet to use this view. You can either select an existing PointSet in the data manager or you can create a new one. This is done by clicking the 'Add pointset...' button.



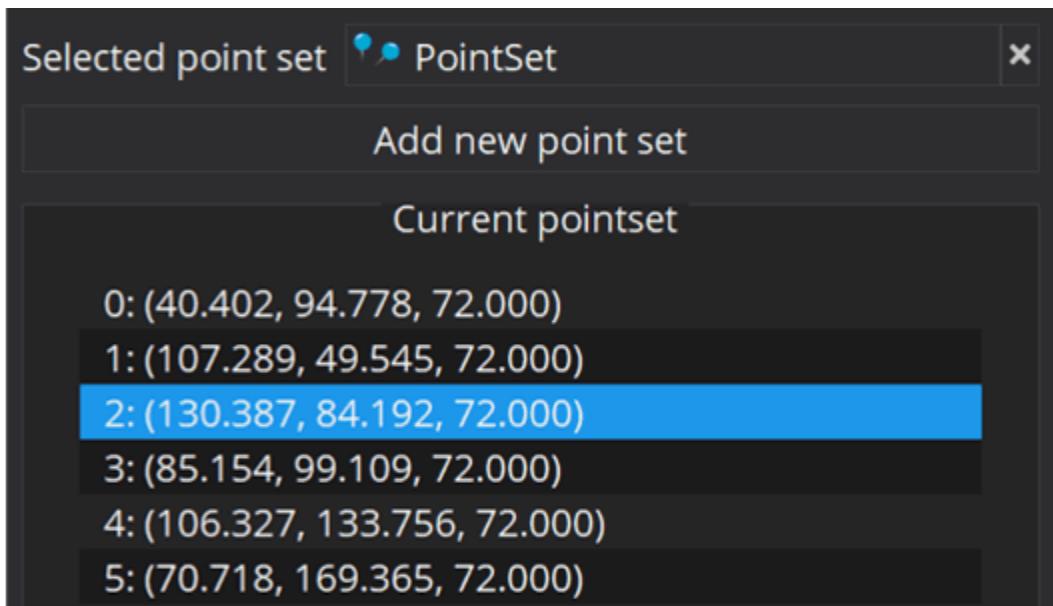
The Add pointset... dialog

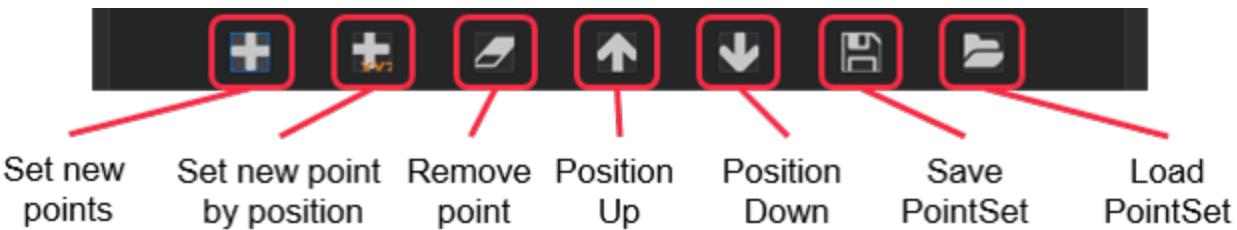
In the pop-up dialog, you have to specify a name for the new PointSet. Afterwards, it appears as a new node in the data manager.

## Add new points

To set points you have to toggle the 'Set Points' button (+), the leftmost of the seven buttons on the bottom of the view. Points can be defined by performing a left mouse button click while holding the 'Shift'-key pressed in the four window view. Alternatively, you can set a new point by pressing the button next to the left most button (+ xyz) and adding a new point location directly.

The 'Current pointset' area contains a list of all points in the current PointSet node with index and position.





## PointSet Interaction View

### Remove points

To erase a point from the list press either the third button or the delete key on your keyboard.

### Modify point position

By using the 'up' and 'down' arrow buttons, the index location of a point in the PointSet can be altered.

### Save and load a PointSet

With the two last buttons PointSets can be saved and loaded. With the 'save' button, the entire PointSet can be saved to the harddrive. The user is prompted to select a filename. PointSets are saved in XML fileformat but have to have a '.mps' file extension. A previously saved PointSet can be loaded and all of its points appear in the list and the four window view as well as a node in the data manager.

### Modify points

You can select a single point in the render window, if the 'Set Points' button is toggled. If you keep the mouse button pressed, you can move the points by moving the mouse and then releasing the mouse button. With the delete key you can remove the selected points.

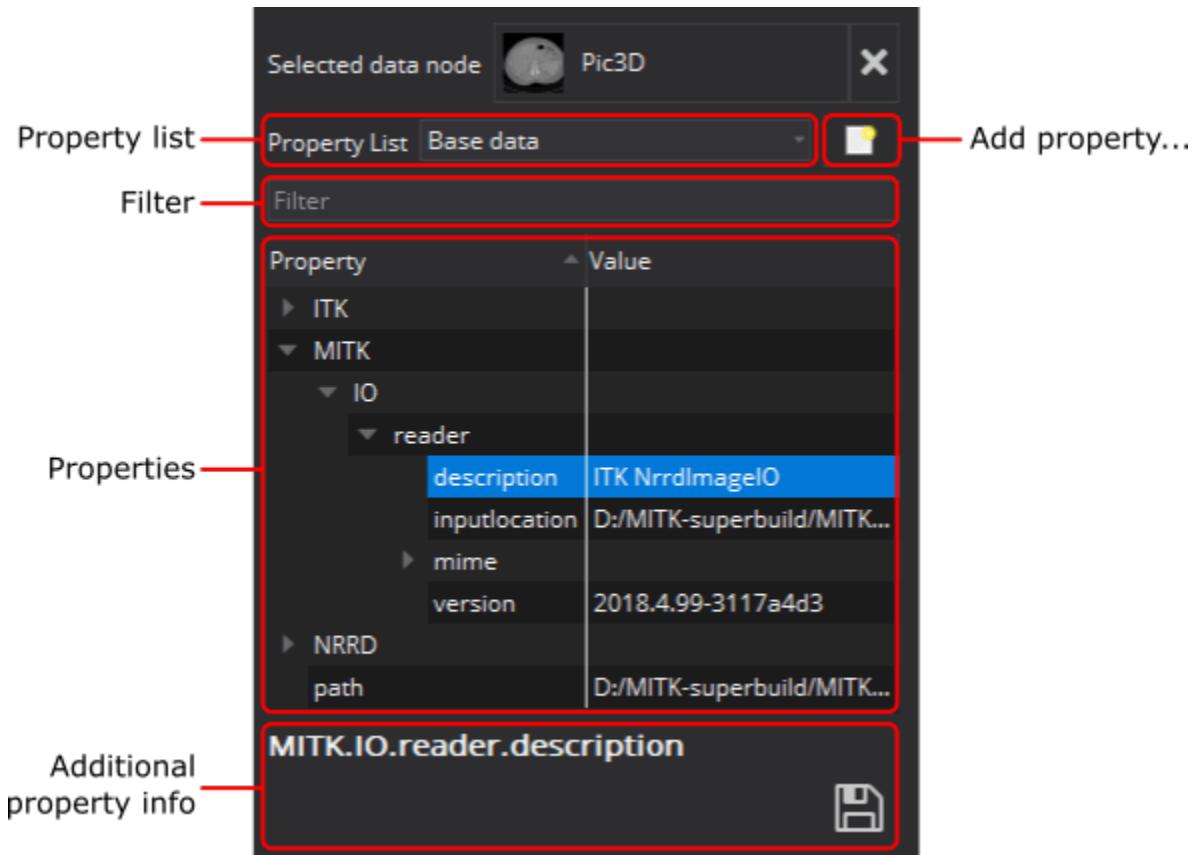
# Medical Imaging Interaction Toolkit: The Properties View

Icon of the Properties View.

## Overview

The Properties View allows you to inspect and change properties of a selected data node and its attached data. This View is only for advanced users and developers, as it is easy to alter the program state in unexpected ways. It can be considered as a complete exposure of parts of the backend that are usually supposed to be accessed only through dedicated frontend components like the color or opacity widgets in the context menu of a data node in the Data Manager View.

## Usage



The Properties View.

## Property list types

After you selected a data node, the Properties View allows you to switch between several property lists

that are attached to the selected data node and its actual data. By default, you see the common data node property list.

There are two types of property lists: data node property lists and data property lists.

Data node property lists consist of properties that the application attaches mainly for rendering settings. They are not intrinsically part of the actual data and are only persisted when saving the MITK scene as a whole. A typical example of such a property is "visible", which decides if the data should be rendered or hidden.

The common data node property list is applied to all render windows but there are also render window specific data node property lists. Any property that is found in both the common list and a render window specific list is overridden by the latter one. For example, if you want to hide an image only in the 3d render window but show it in all other render windows, you check "visible" in the common list, add the same property to the 3d render window specific list, and uncheck it there.

There is only a single data property list. It represents the true metadata of the selected data like DICOM tags of a DICOM image. When saving specific data, most data properties are written to the data file, as long as the selected file format supports metadata. A popular example is the NRRD image format that allows to save custom key value pairs in text format in the file header. Not all data properties are meant for persistence, though. To check if a certain data property will be written to a metadata-enabled file format, click on it in the properties tree view and check if there is a save icon at the bottom in the additional property info box.

## Filter

Property lists can be quite large and complex, shown as a tree structure in the Properties View. To quickly find properties of interest you can use the filter text box, which will filter the properties while you type.

## Edit properties

Most property value types like numbers, strings, boolean values, or colors can be edited by either clicking or double-clicking in the Value column. For example, to edit color properties, double-click on the colored Value cell. You can either enter a color by name like "yellow", in hex notation like "#fffffoo" (or abbreviated "#ff0"), or click on the "..." button to open a color picker dialog.

## Additional property information

Some properties have additional information attached like a description, aliases, or a persistence flag. This information is shown at the bottom of the Properties View. When no additional information is

available, the additional property info box is hidden.

# Medical Imaging Interaction Toolkit: The Remeshing View



Icon of the Remeshing Plugin.

## Decimate surfaces

Decimating surfaces effectively reduces their number of vertices and hence their number of polygons. In other words, decimating surfaces coarsens their meshes.

Vertices are successively eliminated until the desired relative number of vertices remain. During this process, the decimation algorithm tries to keep the spatial difference between original meshes and decimated meshes to a minimum.

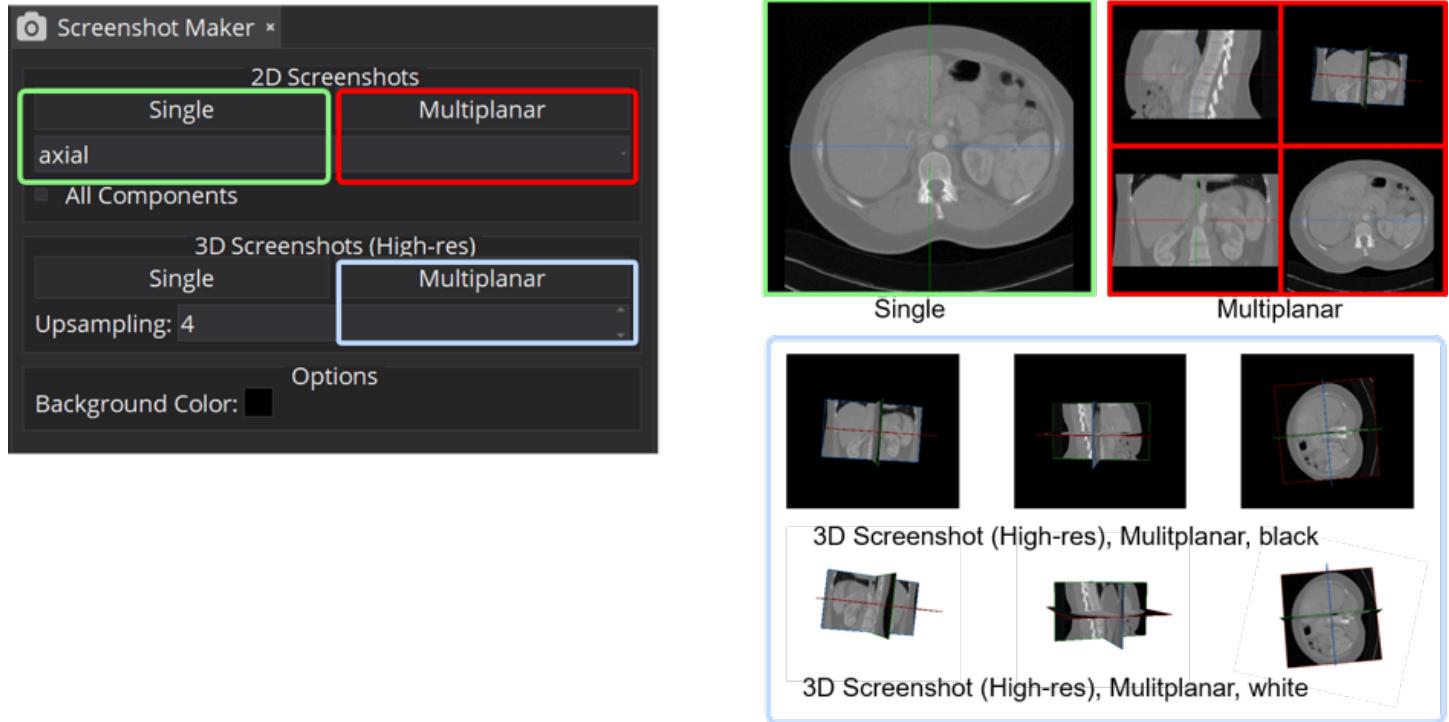
A surface may consist of multiple meshes in different time steps. The decimation is applied to all time steps.

Before the actual decimation, meshes are triangulated, i. e., polygons with more than three edges like quadrilaterals are converted to triangles. Lines and points are ignored. Resulting meshes are guaranteed to consist of triangles only.

Vertex normals can be optionally (re-)calculated for decimated meshes. To decide if you should flip normals, enable the Backface Culling property of the decimated surface in the Properties View - otherwise it is impossible to tell, as by default, both sides of polygons are shaded in MITK.

# Medical Imaging Interaction Toolkit: The Screenshot Maker View

This view provides the functionality to create and save screenshots of the data.



The Screenshot Maker User Interface

## Usage

The first section offers the option to create a screenshot of selected view plane (axial, sagittal or coronal). Upon clicking the 'Single' button in the '2D Screenshot' section, the Screenshot Maker asks for a filename in which the screenshot is to be stored. The 'Multiplanar' button asks for a folder, in which screenshots of the three 2D views will be stored with default names.

If you tick the 'All Components' checkbox, you can take a screenshot of every channel of your multi-channel image. Otherwise, only the visible channel is captured.

The '3D Screenshots (High-res)' section works the same as the simple screenshot section, aside from the fact, that the user can choose a magnification ('Upsampling') factor. The 'Single' button creates a screenshot of the current 3D render window and the 'Multiplanar' button creates three screenshots from different perspectives.

In the 'Options' section, one can choose the background color for the screenshots, default is black.

## The Segmentation Flow

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The view offers a simple way to directly save the first segmentation found in the data storage. The save location will be determined given the application argument flags (-flow.outputdir and -flow.outputextension). If no flags where set when starting the application the current working directory and "nrrd" as extensions will be used.

# The Segmentation Task List View

Icon of the Segmentation Task List View

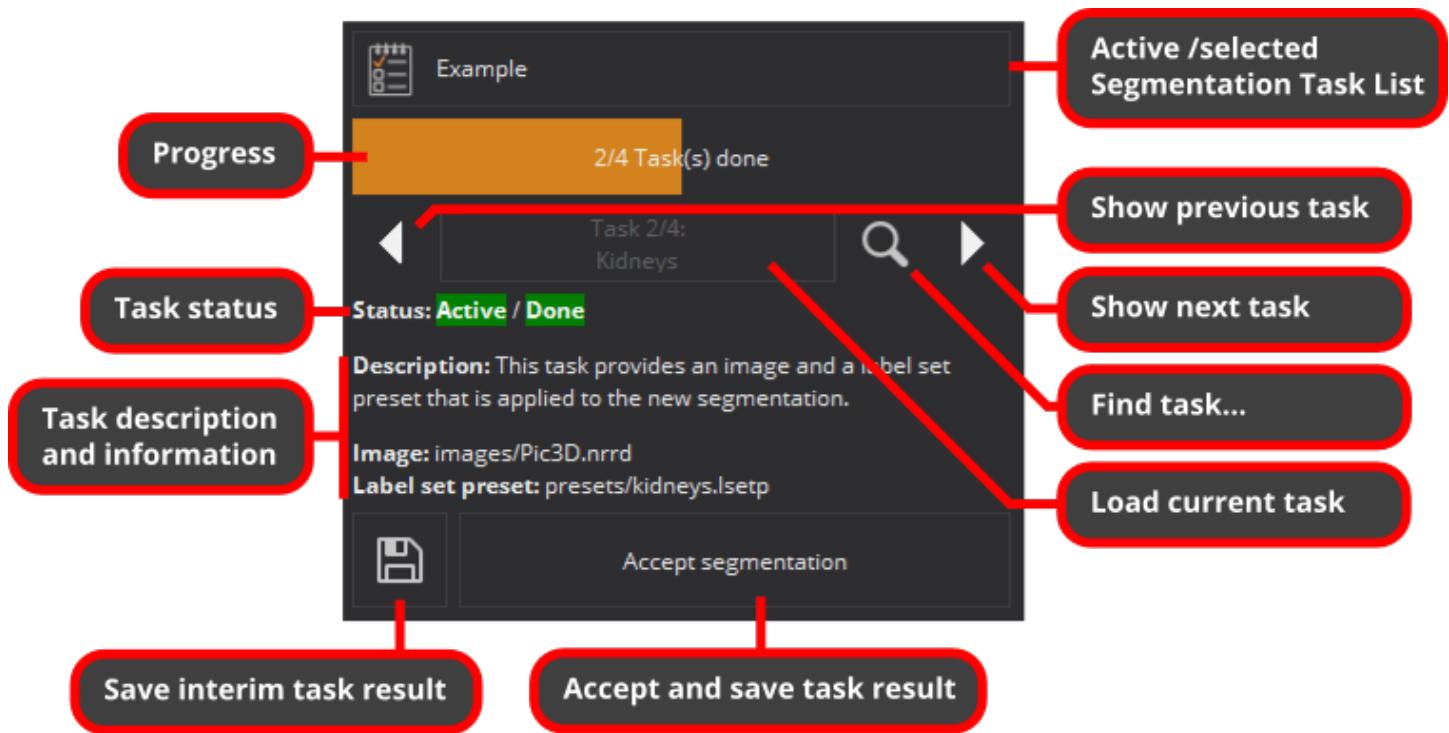
## Disclaimer

The Segmentation Task List View and MITK Segmentation Task Lists in general are still in an **experimental** stage.

While we try to minimize breaking changes in the future, we cannot give any guarantees at the moment.

We strongly advise to ignore the Data Manager regarding loading and unloading of data while using the Segmentation Task List View, as it will completely take over these operations and may run into invalid states otherwise.

## Overview



Segmentation Task List View

As the Segmentation Task List View is typically used in combination with the Segmentation View, we suggest to move the Segmentation View to the other side of the application (e.g. on top of the Data Manager), to see both views at the same time.

To unlock the Segmentation Task List View, unload everything but a single MITK Segmentation Task List. The remaining Segmentation Task List will be automatically selected.

The Segmentation Task List View shows the progress of the whole Segmentation Task List, e.g., the number of the tasks marked as *done* vs. the total number of available tasks.

Below the progress indicator you can navigate between tasks, read their descriptions and related information, as well as load/activate the currently shown task. This will unload all data from a previously active task, if any, and load all data of the current task. To prevent any accidental data loss, unsaved task data will interfere task switches and you can decide on how to proceed.

Above the task description, the status of tasks is displayed as a pair of colored labels, indicating if a task is either active or inactive and if it is considered not to be done, having unsaved changes, or to be done.

With the bottom two buttons you can either save an interim result (the task is considered not to be done), or accept and save the task result. You can still edit accepted tasks but in contrast to interim results, the task is considered to be done.

## Keyboard shortcuts

The Segmentation Task List View can be used even more efficiently with the following set of keyboard shortcuts:

**Ctrl + Alt + P:** Navigate to **previous** task

**Ctrl + Shift + P:** Navigate to **previous undone** task (or **Shift + click** on resp. button)

**Ctrl + Alt + N:** Navigate to **next** task

**Ctrl + Shift + N:** Navigate to **next undone** task (or **Shift + click** on resp. button)

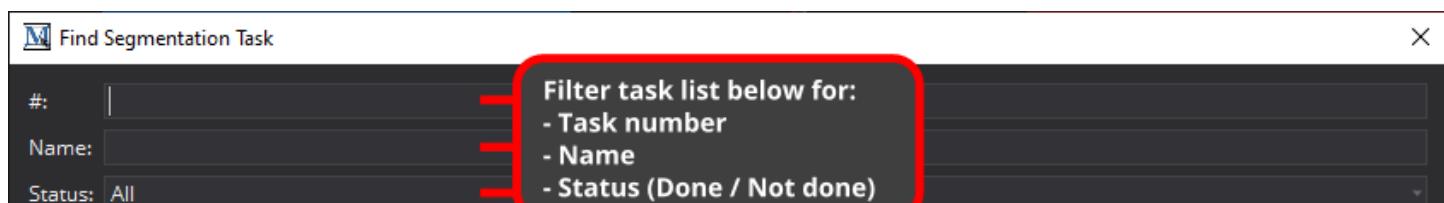
**Ctrl + Alt + L:** Load currently shown task

**Ctrl + Alt + S:** Store interim result

**Ctrl + Alt + A:** Accept task and store result

**Ctrl + F:** Find task...

## Finding tasks



#	Name	Status	Image	Segmentation	Result	Description
1	Liver	Done	images/Pic3D.nrrd		results/liver.nrrd	This task provides an image and lat
2	Kidneys	Done	images/Pic3D.nrrd		results/kidneys.nrrd	This task provides an image and a li
3	Spleen	Not done	images/Pic3D.nrrd	segmentations/spleen.nrrd	results/spleen.nrrd	This task provides an image and an
4	Surprise	Not done			results/US4DCyl.nrrd	And now for something completely

Load selected task

When closing this dialog:  
 - Load selected task above  
 - Only navigate to selected task

OK Cancel

## Find Segmentation Task dialog

To find a specific task in a segmentation task list, click on the "Find task..." button (magnifier icon) or press **Ctrl + F**. A dedicated dialog will appear for filtering and searching the current segmentation task list. Enter a task number and press **Return** to immediately load the according task or filter the shown list of tasks and double click on a result to load the task.

## MITK Segmentation Task List file format

MITK Segmentation Task List files are JSON files containing a JSON object as root. It must contain the two mandatory properties **FileFormat** and **Version**:

```
{
    "FileFormat": "MITK Segmentation Task List",
    "Version": 1
}
```

We also recommend to specify an optional **Name** that is used in the application if present instead of the plain filename of the JSON file:

```
{
    "FileFormat": "MITK Segmentation Task List",
    "Version": 1,
    "Name": "My First Task List"
}
```

## Tasks

The root object must also contain a mandatory **Tasks** array, containing JSON objects that specify the individual tasks of the task list. A minimum task object must contain **Image** and **Result** file paths.

**Image** refers to the patient image and **Result** refers to the path where the resulting segmentation is expected to be stored. Paths can be absolute or relative to the JSON file.

```
{  
  "FileFormat": "MITK Segmentation Task List",  
  "Version": 1,  
  "Tasks": [  
    {  
      "Image": "images/Pic3D.nrrd",  
      "Result": "results/liver.nrrd"  
    }  
  ]  
}
```

In addition, tasks can contain a bunch of optional properties that mainly specify a segmentation a user starts with:

**Name** (*string*): A name for the task.

**Description** (*string*): A short description/definition of the task.

**LabelName** (*string*): The name of the first label in a new segmentation that is created for the task on the fly.

**LabelNameSuggestions** (*file path*): A Label Suggestions JSON file (example in next comment) specifying names and optional colors, that are suggested to the user for new labels in the segmentation.

**Preset** (*file path*): A Label Set Preset XML file in MITK's .lsetp file format. The preset is applied to a new segmentation that is created for the task on the fly. We recommend to use the Segmentation plugin of the MITK Workbench to create such label set preset files as described in its {key F1} user guide.

**Segmentation** (*file path*): A pre-segmentation that a user can start with or has to refine for example.

**Dynamic** (*boolean*): In case **Image** refers to a dynamic (3d+t) image, specifies whether the segmentation should be static (*false*), i.e. equal for all time steps, or dynamic (*true*), i.e. individual for each time step.

## Task defaults / common properties

If a task list contains multiple tasks with common properties, they do not have to be specified for each and every task again and again. Instead, the root object can contain an optional `Defaults` object that is identical in format to the tasks specified above. As the name indicates, default properties can still be overridden by individual tasks if they are specified explicitly.

There is a single exception, though: A `Defaults` object must not contain a `Result` file path, since result files of tasks must be distinct by definition.

### Example

The following example is a complete showcase of the properties and features listed above. It specifies 4 tasks. 3 tasks refer to the same patient image so it is specified as default.

Remember that the only task property required to be distinct is `Result` so you are pretty free in your task design. For simplicity, we chose to define tasks around organs for this example and named the tasks accordingly:

```
{
  "FileFormat": "MITK Segmentation Task List",
  "Version": 1,
  "Name": "Example Segmentation Task List",
  "Defaults": {
    "Image": "images/Pic3D.nrrd"
  },
  "Tasks": [
    {
      "Name": "Liver",
      "LabelName": "Liver",
      "LabelNameSuggestions": "suggestions/label_suggestions.json",
      "Description": "This task provides an image and label name suggestions for new labels. The segmentation will start with an empty label named Liver.",
      "Result": "results/liver.nrrd"
    }
  ]
}
```

```

},
{
  "Name": "Kidneys",
  "Description": "This task provides an image and a label set preset that is applied to the new segmentation.",
  "Preset": "presets/kidneys.lsetp",
  "Result": "results/kidneys.nrrd"
},
{
  "Name": "Spleen",
  "Description": "This task provides an image and an initial (pre-)segmentation.",
  "Segmentation": "segmentations/spleen.nrrd",
  "Result": "results/spleen.nrrd"
},
{
  "Name": "Surprise",
  "Description": "And now for something completely different. This task overrides the default Image and starts with an empty static segmentation for a dynamic image.",
  "Image": "images/US4DCyl.nrrd",
  "Result": "results/US4DCyl.nrrd",
  "Dynamic": false
}
]
}

```

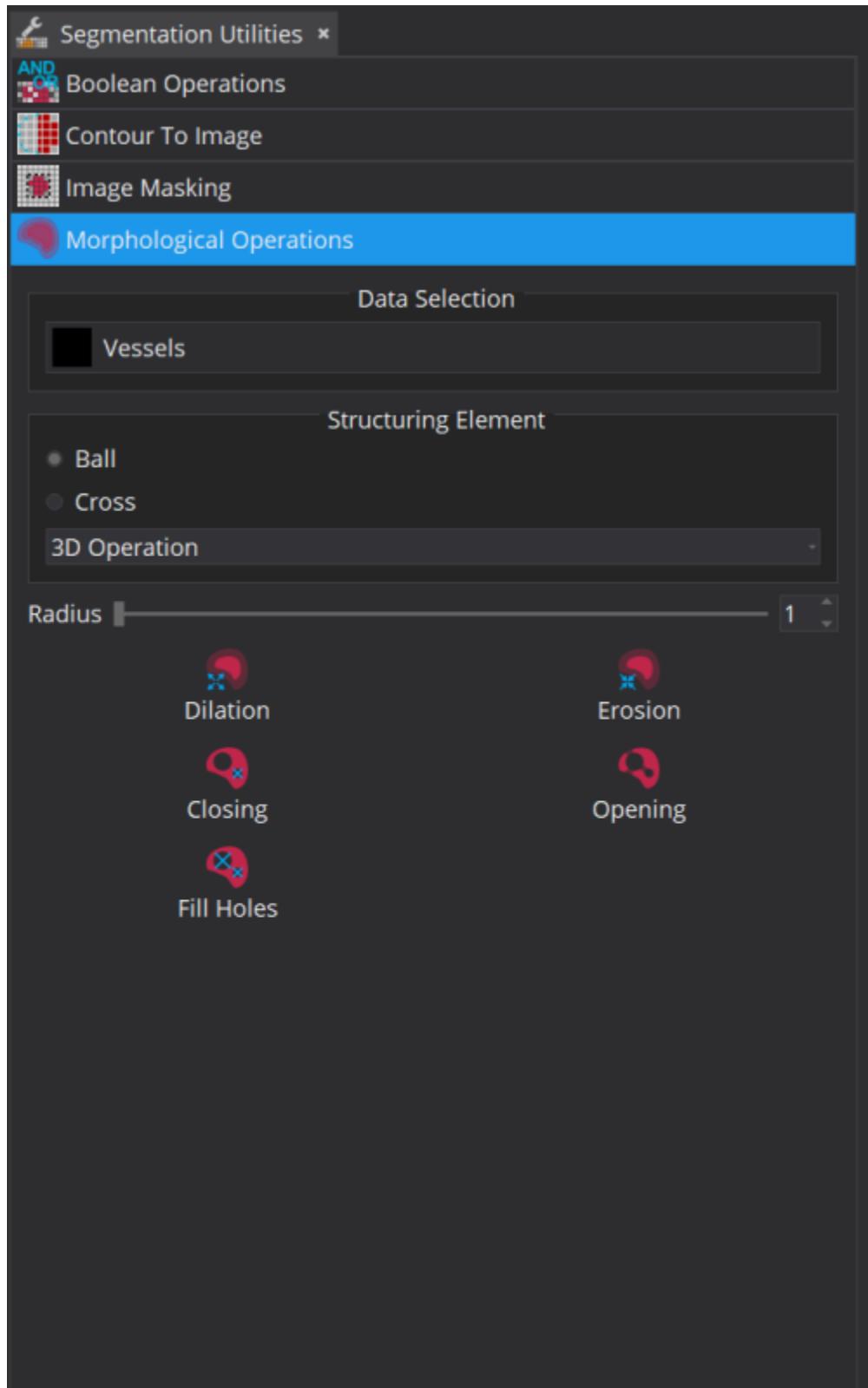
## MITK Label Suggestions file format

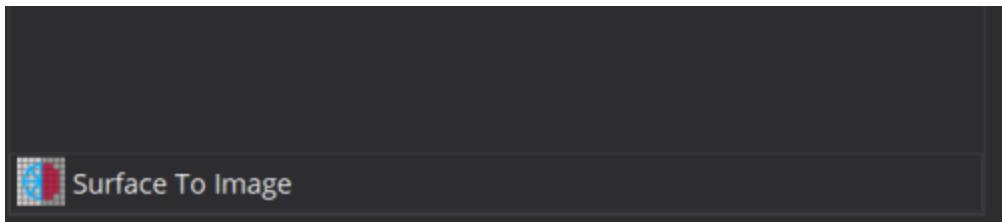
The Label Suggestions JSON file format mentioned above to specify a list of suggested names and optional colors for new labels is as follows:

```
[  
 {  
   "name": "Abdomen",  
   "color": "red"  
 },  
 {  
   "name": "Lung",  
   "color": "#ooffoo"  
 },  
 {  
   "name": "Heart"  
 },  
 {  
   "name": "Aortic Valve",  
   "color": "CornflowerBlue"  
 }]  
 ]
```

# Medical Imaging Interaction Toolkit: The Segmentation Utilities View

Icon of the Segmentation Utilities View





The Segmentation Utilities View

## Overview

The **Segmentation Utilities View** allows to postprocess existing segmentations. Currently five different operations exist:

[Boolean operations](#)

[Contour to image](#)

[Image masking](#)

[Morphological operations](#)

[Surface to image](#)

## Data Selection

All postprocessing operations provide one or more selection widgets, which allow to select the data for the operation.

## Boolean operations

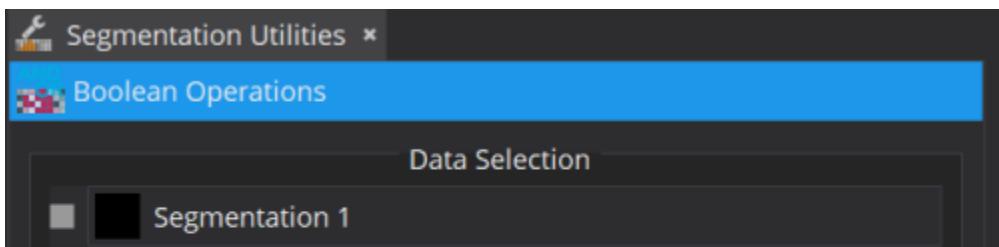
Boolean operations allows to perform the following fundamental operations on two segmentations:

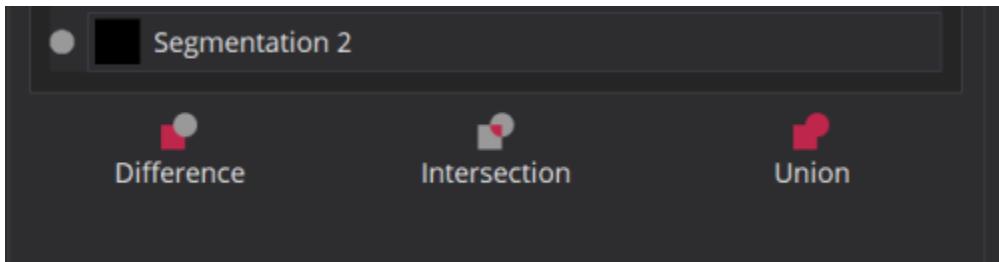
**Difference:** Subtracts the second segmentation from the first segmentation.

**Intersection:** Extracts the overlapping areas of the two selected segmentations.

**Union:** Combines the two existing segmentations.

The selected segmentations must have the same geometry (size, spacing, ...) in order for the operations to work correctly. The result will be stored in a new data node as a child node of the first selected segmentation.

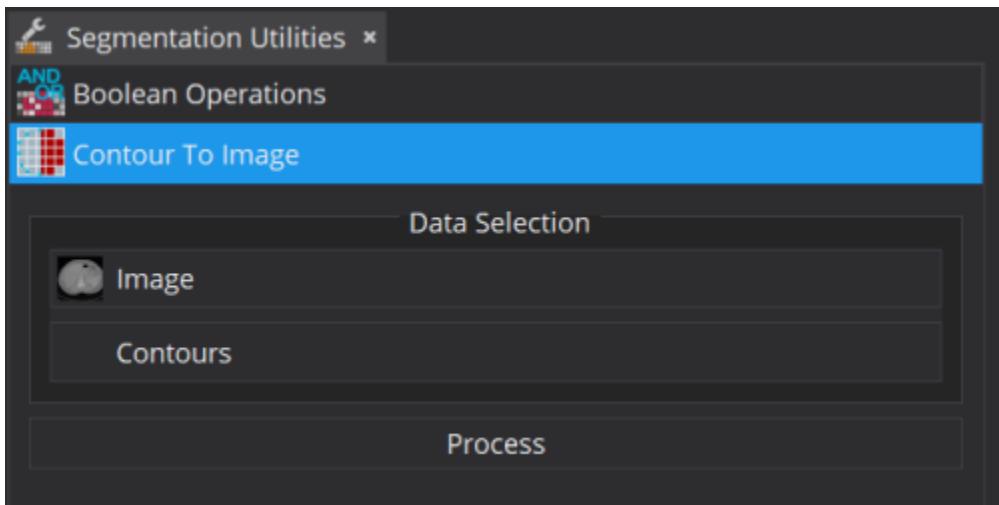




Boolean operations

## Contour to image

Contour to image allows to create a segmentation out of a given contour-model. The operation requires a contour model set and a reference image. The created segmentation image will have the same geometrical properties like the reference image (dimension, size and Geometry3D).

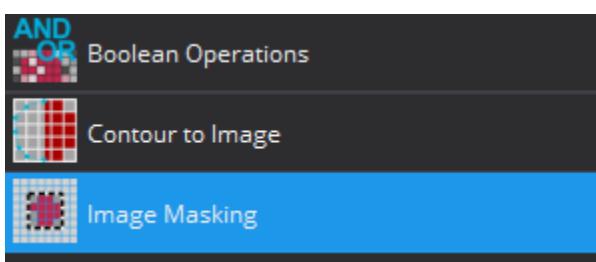


Contour to image

## Image masking

Image masking allows to mask an image with either an existing segmentation or a surface. The operation requires an image and a segmentation or a surface. The result will be an image containing only the pixels that are covered by the respective mask.

The default background pixel value is zero. It can be changed to the minimum existing pixel value of the image or to a custom pixel value. If the custom pixel value is out of the valid bounds of the pixel type, it is optionally clamped accordingly.



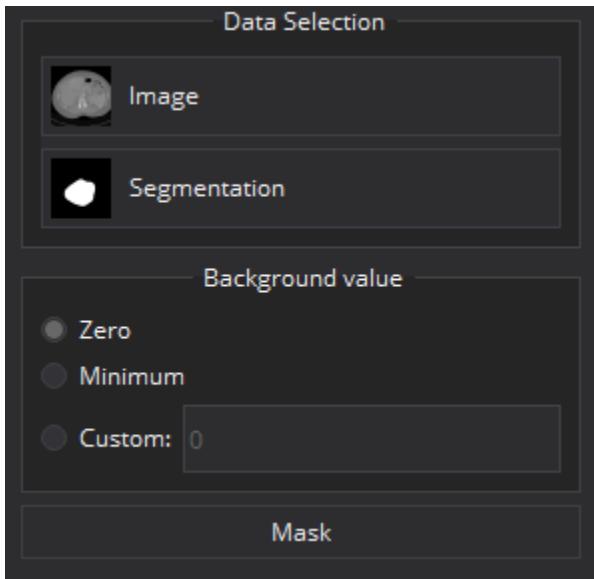


Image masking

## Morphological operations

Morphological operations are applied to a single segmentation image. Based on a given structuring element the underlying segmentation will be modified. The plugin provides a **ball** and a **cross** as structuring elements. The follow operations are available:

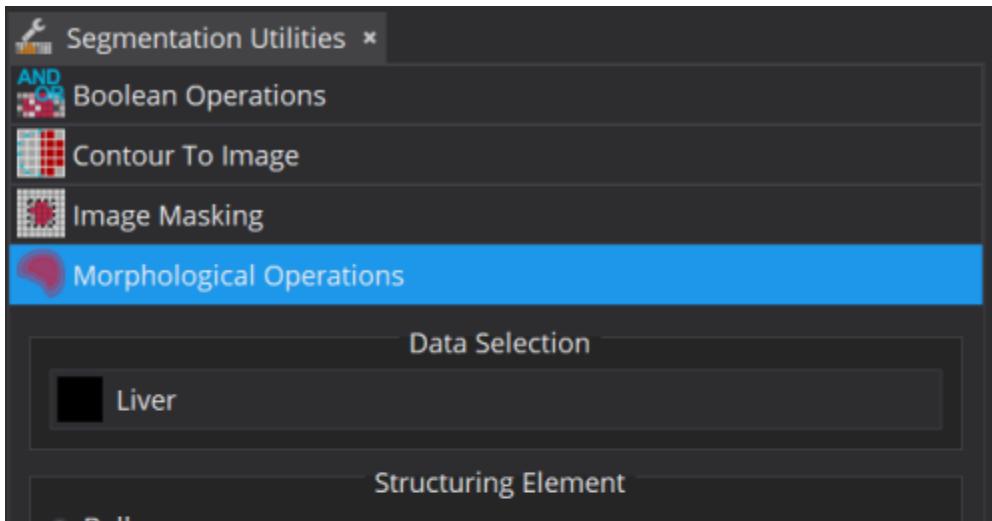
**Dilation:** Each labeled pixel within the segmentation will be dilated based on the selected structuring element.

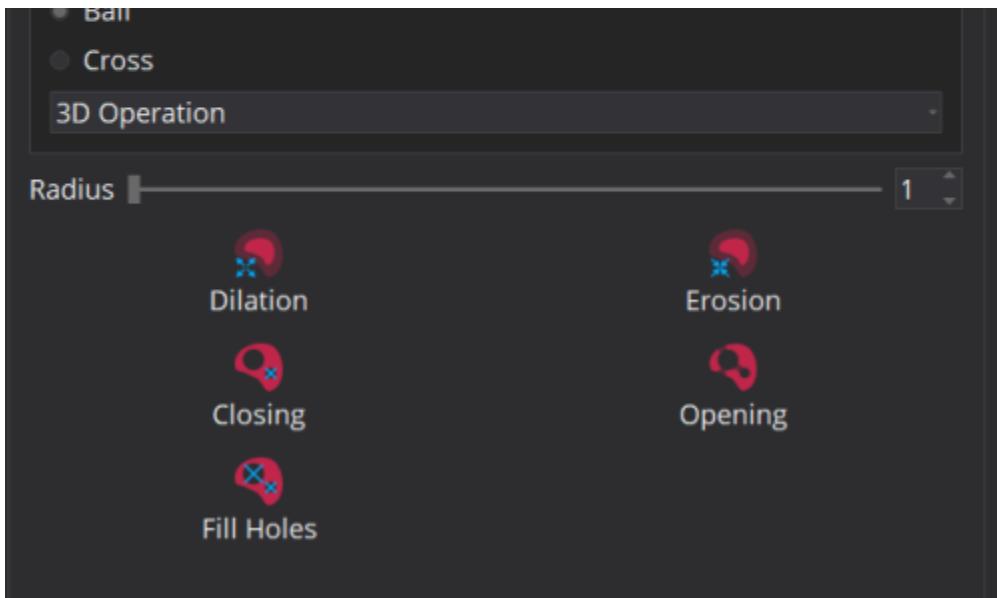
**Erosion:** Each labeled pixel within the segmentation will be eroded based on the selected structuring element.

**Opening:** A dilation followed by an erosion, used for smoothing edges or eliminating small objects.

**Closing:** An erosion followed by an dilation, used for filling small holes.

**Fill Holes:** Fills bigger holes within a segmentation.

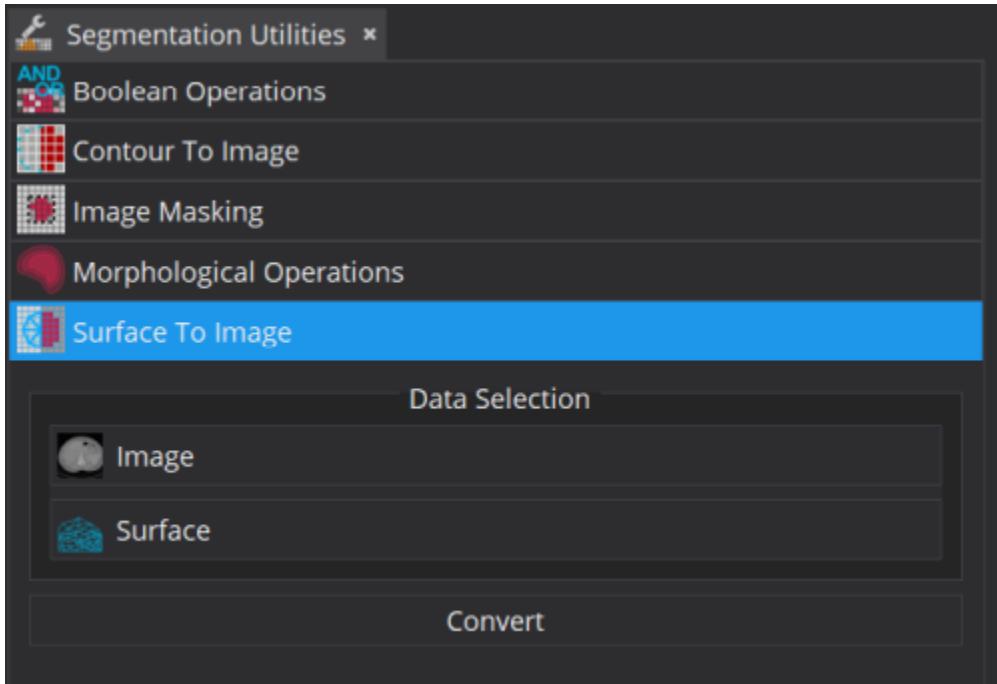




Morphological operations

## Surface to image

Surface to image allows to create a segmentation out of a given surface. The operation requires a surface and a reference image. The created segmentation image will have the same geometrical properties like the reference image (dimension, size and Geometry3D).



Surface to image

# Medical Imaging Interaction Toolkit: The Segmentation View

Icon of the Segmentation View

## Overview

Segmentation is the act of separating an image into foreground and background subsets by manual or automated delineation, while the foreground is defined to be part of the segmentation. Such a segmented image subset is also called a label as it typically labels a specific region of interest. A multilabel segmentation may contain multiple labels organized in distinct groups. You can create multiple labels for different regions of interest contained within a single segmentation image. Labels in the same group cannot overlap each other but labels from different groups may overlap.

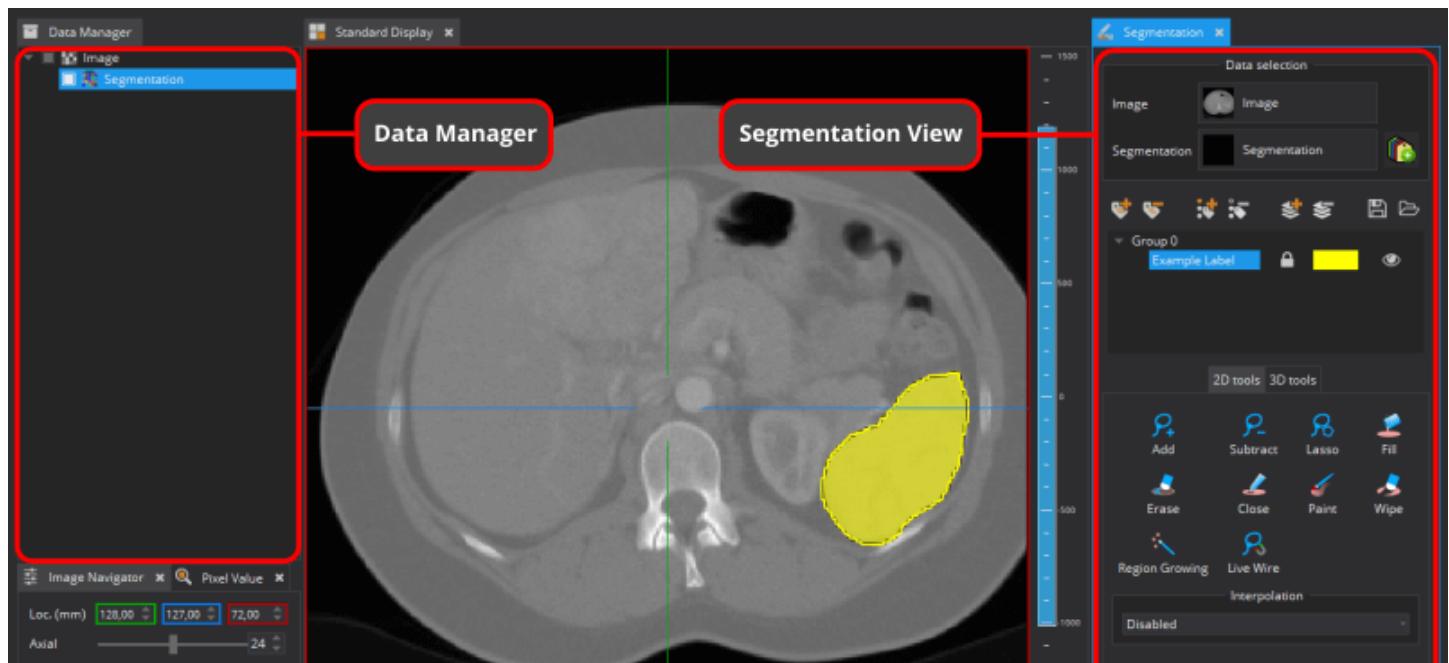
The MITK **Segmentation Plugin** allows you to create multilabel segmentations of anatomical and pathological structures in medical images. The plugin consists of three views:

**Segmentation View:** Manual and (semi-)automatic segmentation

[The Segmentation Utilities View](#) : Post-processing of segmentations

[The Segmentation Task List View](#) : Optimized workflow for batches of segmentation tasks based on a user-defined task list

In this user guide, the features of the **Segmentation View** are described. For an introduction to the Segmentation Utilities or Segmentation Task List, refer to the respective user guides.





Segmentation View

## Image and segmentation prerequisites

The Segmentation View has a few prerequisites regarding segmentations and their reference image:

Images must be two or three-dimensional and may be either static or dynamic, e.g., are time-resolved resp. have different pixel values for different time steps.

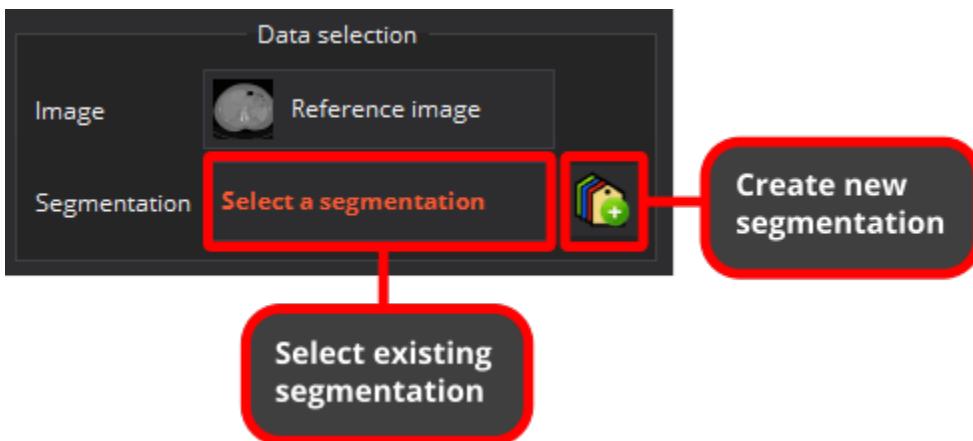
Images must be single-valued, i.e. CT, MRI or ultrasound. Images from color doppler or photographic (RGB) images are only partially supported (please be aware that some tools might not be compatible with this image type).

Segmentations must be congruent to their reference images.

## Image selection and creating new segmentations

To select a reference image for a new segmentation, click on the *Image* widget in the Data selection section at the very top of the Segmentation View. Choose an image from the displayed list of Data Manager images. Once an image is selected, a new segmentation for this reference image can be created by clicking the button right next to the *Segmentation* widget in the Data selection section. A new multilabel segmentation with an initial, empty label is automatically generated if not set otherwise in the preferences. The new segmentation will be added to the Data Manager as a child node of its reference image node. It is automatically selected and can be edited in the Segmentation View right away.

Instead of creating a new segmentation, an existing segmentation can be selected and edited as well. The selection list of existing segmentations for a certain reference image consists of matching/congruent segmentations only.



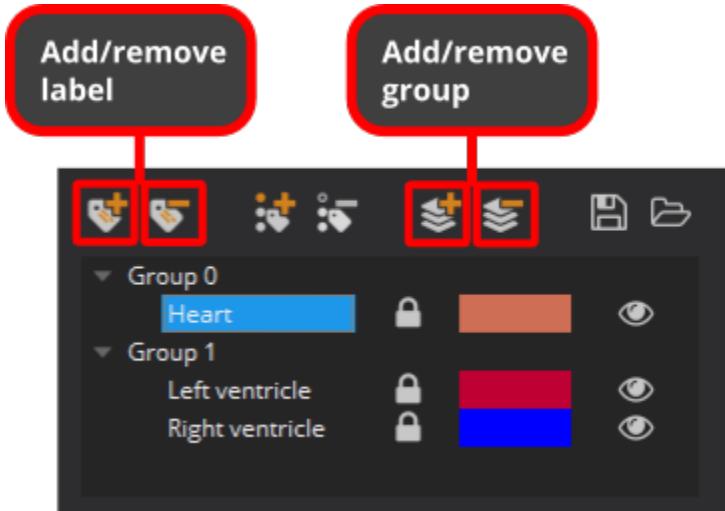
Data selection and creating new segmentations

## Groups

Segmentation images consist of at least a single group called "Group 0" in which the first default label is created. More groups can be added and removed but there will always be at least a single group. Labels of the same group cannot overlap each other. Labels of different groups may overlap each other.

For example, you could segment the whole heart as "Heart" label in "Group 0", add "Group 1" and create multiple labels of the anatomical details of the heart in that group. Naturally, all these labels lie within the extents of the "Heart" label of "Group 0" but in principle they are completely independent of "Group 0". Some pixels are now labelled twice, e.g., as "Heart" and "Left ventricle". Since the labels of "Group 1" cannot overlap each other, it is impossible to accidentally label a pixel as both "Left ventricle" and "Right ventricle".

If you would like to segment even more details you could create "Group 2" to have up to three labels per pixel. Nevertheless, groups are technically a flat data structure and cannot contain nested groups. It is all about possibly overlapping labels from distinct groups and spatially exclusive, non-overlapping labels within the same group.



Groups

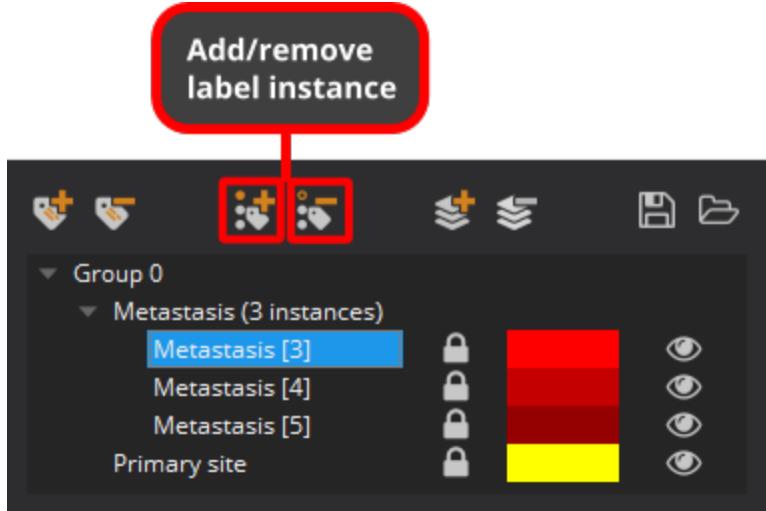
## Labels vs. label instances

The Segmentation View supports label instances. That is, segmenting multiple distributed entities of the same thing like metastases for example.

A label, as we used the term before, is already a single instance of itself but it may consist of multiple label instances.

If a label consists of multiple label instances, they each show their own distinct pixel value in square brackets as a clue for distinction and identification.

It is important to understand that this number is not a separate, consecutive index for each label. It is just the plain pixel value of the label instance, which is unique across all label instances of the whole segmentation.



Label instances

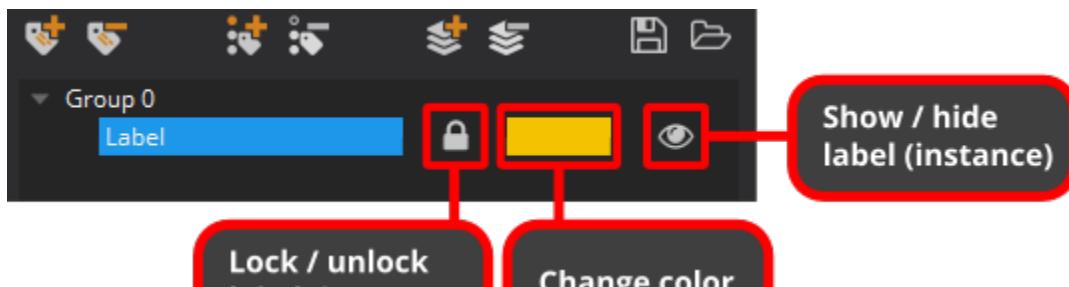
## Unlocking, changing color of, and hiding label instances

Label instances are locked by default: label instances from the same group cannot accidentally override pixels from other label instances. Locked label instances behave like cookie cutters for other label instances of the same group. You can unlock label instances to remove that protection from other label instances of the same group. Their pixel contents can then be overridden by other label instances of the same group.

Remember that label instances from distinct groups do not interact with each other. They can always overlap (not override) each other.

You can also change the color of label instances as well as show (default) or hide their pixel contents. The icons at the right side of the rows of the groups and labels widget reflect their state in all these regards.

Renaming of labels and label instances can be found in their content menu as shown further below.



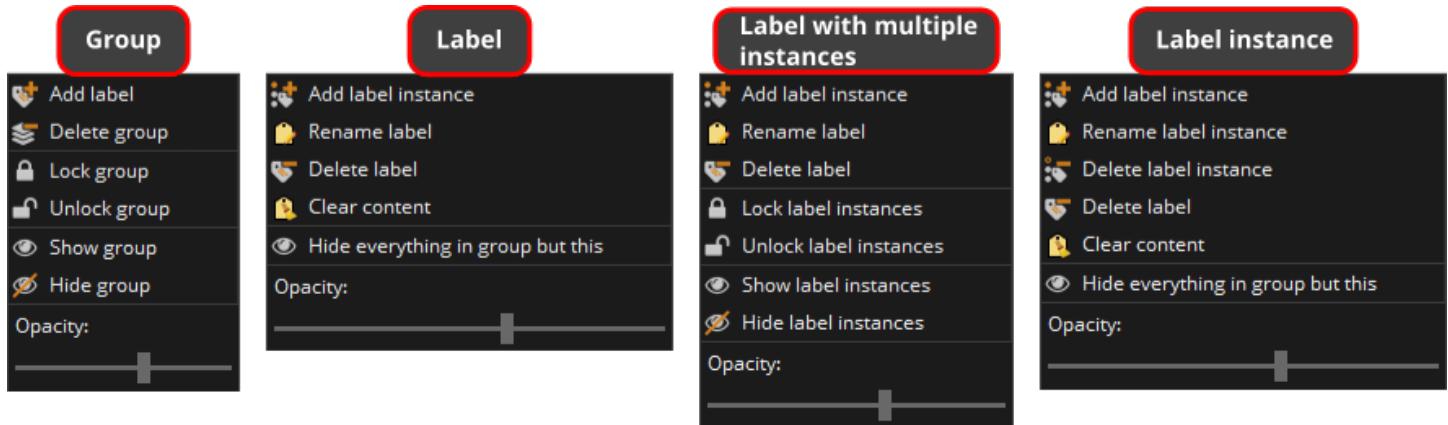
**label (instance)**

**Change color**

Unlocking, changing color of, and hiding label instances

## Context menus

Actions for organization of groups, labels, and label instances (as well as other operations) can be also found in their right-click context menus.



Context menus of groups, labels, and label instances

Most actions available in these context menus are self-explanatory or were already described above by other means of access like the tool button bar for adding and removing groups, labels, and label instances.

Labels and label instances can be **renamed**, while groups have fixed names. Note that renaming a label instance will make a separate label out of it, since all instances of the same label share a single common name.

**Clear content** only clears the pixels of a label instance but won't delete the actual label instance.

Groups can be **locked** and **unlocked** as a whole from their context menu, while label instances can be directly locked and unlocked outside the context menu as described further below.

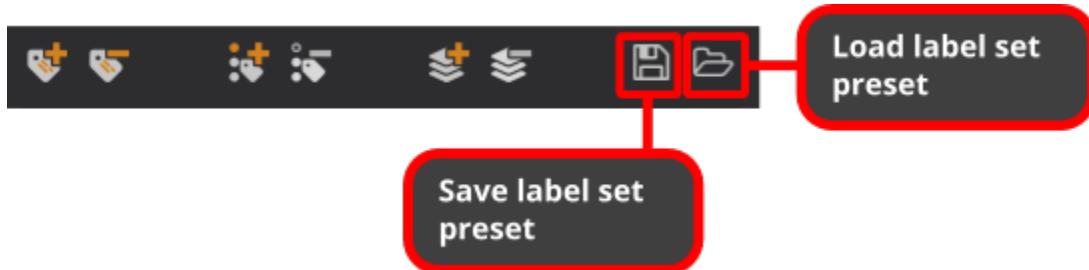
## Label name and color suggestions

When renaming label instances or creating new label instances with enforced manual naming in the Segmentation preferences, entering names is supported by auto-completion for common label names. The list of predefined label names and colors for the auto-completion feature can be either extended or replaced by a custom list of label name and color suggestions. This custom list must be specified as a JSON file, just containing an array of objects, each with a mandatory "name" string and an optional "color" string. The JSON file can be set in the Segmentation preferences as well as a few options on how to apply these suggestions.

## Saving and loading label set presets

Label set presets are useful to share a certain style or scheme between different segmentation sessions or to provide templates for new segmentation sessions.

The properties of all label instances in all groups like their names, colors, and visibilities are saved as a label set preset by clicking on the 'Save label set preset' button. Label set presets are applied to any segmentation session by clicking on the 'Load label set preset' button. If a label instance for a certain value already exists, its properties are overridden by the preset. If a label instance for a certain value does not yet exist, an empty label instance with the label properties of the preset is created. The actual pixel contents of label instances are unaffected as label set presets only store label properties.



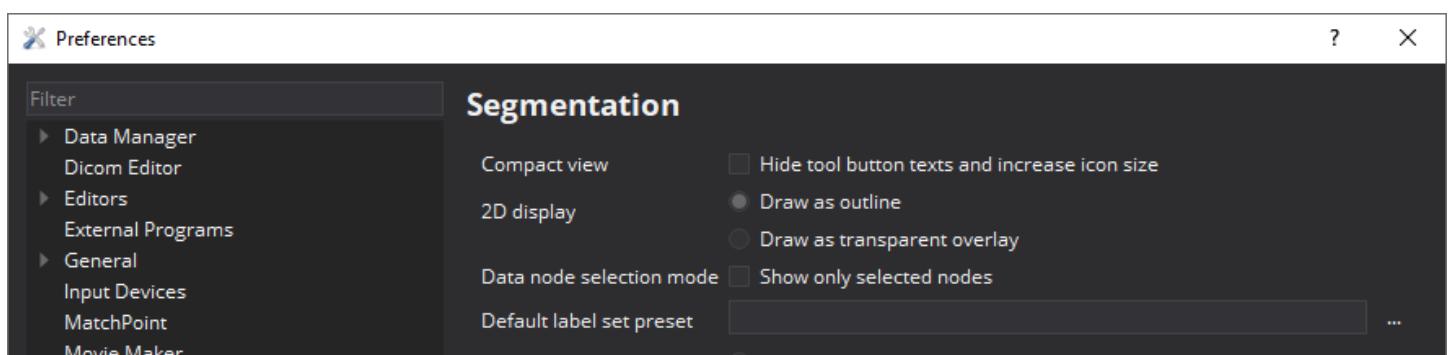
### Saving and loading label set presets

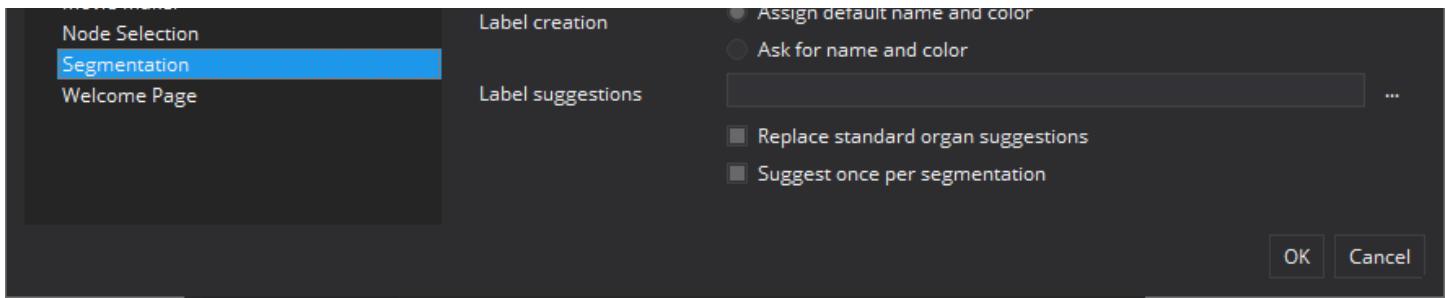
If you work on a repetitive segmentation task, manually loading the same label set preset for each and every new segmentation can be tedious. To streamline your workflow, you can set a default label set preset in the Segmentation preferences (Ctrl+P). When set, this label set preset will be applied to all new segmentations instead of creating the default red "Label 1" label instance.

If you work on a repetitive segmentation task, manually loading the same label set preset for each and every new segmentation can be tedious. To streamline your workflow, you can set a default label set preset in the Segmentation preferences (Ctrl+P). When set, this label set preset will be applied to all new segmentations instead of creating the default red "Label 1" label instance.

## Preferences

The Segmentation Plugin offers a number of preferences which can be set via the MITK Workbench application preferences (Ctrl+P):





## Segmentation preferences

**Compact view:** Hide the tool button texts to save some space on screen (6 instead of 4 buttons per row)

**2D display:** Draw segmentations as outlines or transparent overlays

**Data node selection mode:** Hide everything but the selected segmentation and its reference image

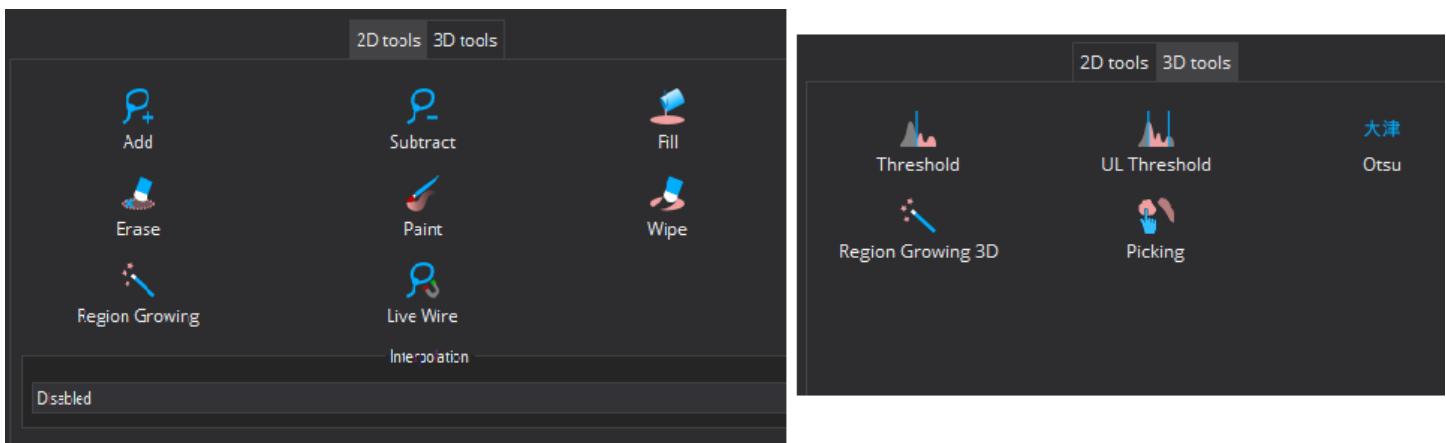
**Default label set preset:** Start a new segmentation with this preset instead of a default label

**Label creation:** Assign default names and colors to new label instances or ask users for name and color

**Label suggestions:** Specify custom suggestions for label names and colors

## Segmentation tool overview

MITK offers a comprehensive set of slice-based 2D and (semi-)automated 3D segmentation tools. The manual 2D tools require some user interaction and can only be applied to a single image slice whereas the 3D tools operate on the whole image. The 3D tools usually only require a small amount of user interaction, i.e. placing seed points or setting / adjusting parameters. You can switch between the different toolsets by selecting the 2D or 3D tab in the segmentation view.



An overview of the existing 2D and 3D tools in MITK.

## 2D segmentation tools

With 2D manual contouring you define which voxels are part of the segmentation and which are not. This allows you to create segmentations of any structures of interest in an image. You can also use manual contouring to correct segmentations that result from sub-optimal automatic methods. The drawback of manual contouring is that you might need to define contours on many 2D slices. However, this is mitigated by the interpolation feature, which will make suggestions for a segmentation.

To start using one of the editing tools, click its button from the displayed toolbox. The selected editing tool will be active and its corresponding button will stay pressed until you click the button again. Selecting a different tool also deactivates the previous one.

If you have to delineate a lot of images, shortcuts to switch between tools becomes convenient. For that, just hit the first letter of each tool to activate it (A for Add, S for Subtract, etc.).

All of the editing tools work by the same principle: using the mouse (left button) to click anywhere in a 2D window (any of the orientations axial, sagittal, or coronal), moving the mouse while holding the mouse button and releasing the button to finish the editing action. Multi-step undo and redo is fully supported by all editing tools by using the application-wide undo / redo buttons in the toolbar.

*Remark:* Clicking and moving the mouse in any of the 2D render windows will move the crosshair that defines what part of the image is displayed. This behavior is disabled as long as any of the manual segmentation tools are active - otherwise you might have a hard time concentrating on the contour you are drawing.

## Add and subtract tools



Add and subtract tools

Use the left mouse button to draw a closed contour. When releasing the mouse button, the contour will be added (Add tool) to or removed (Subtract tool) from the current segmentation. Adding and subtracting voxels can be iteratively repeated for the same segmentation. Holding CTRL / CMD while drawing will invert the current tool's behavior (i.e. instead of adding voxels, they will be subtracted).

## Lasso tool



Lasso tool

The tool is a more advanced version of the add/subtract tool. It offers you the following features:

Generating a polygon segmentation (click left mouse button to set anchor point)

Freehand contouring (like the add tool; press left mouse button while moving the mouse)

Move anchor points (select an anchor point, press left mouse button while moving the mouse)

Add new anchor points (press CTRL while click left mouse to add an anchor to the contour)

Delete an anchor point (press Del while anchor point is selected)

Segmentation can be added to the label (Add mode) or subtracted (Subtract mode)

To start a segmentation double left click where the first anchor point should be. To end the segmentation double left click where the last anchor point should be. Please note that:

feature 3-6 are only available, if auto confirm is *not* activated

feature 3-5 is not available for freehand contour segments

## Paint and wipe tools



Paint and wipe tools

Use the *Size* slider to change the radius of the round paintbrush tool. Move the mouse in any 2D window and press the left button to draw or erase pixels. Holding CTRL / CMD while drawing will invert the current tool's behavior (i.e. instead of painting voxels, they will be wiped).

## Region growing tool



Region growing tool

Click at one point in a 2D slice widget to add an image region to the segmentation with the region growing tool. Region Growing selects all pixels around the mouse cursor that have a similar gray value as the pixel below the mouse cursor. This allows to quickly create segmentations of structures that have a good contrast to surrounding tissue. The tool operates based on the current level window, so changing the level window to optimize the contrast for the ROI is encouraged. Moving the mouse up / down is different from left / right: Moving up the cursor while holding the left mouse button widens the range for the included grey values; moving it down narrows it. Moving the mouse left and right will shift the range. The tool will select more or less pixels, corresponding to the changing gray value range.

## **Fill tool**



Fill tool

Left-click inside a region/segmentation to flood fill all connected pixels that have the same label with the active label. This tool will only work on regions of unlocked labels or on regions that are not labeled at all.

## **Erase tool**



Erase tool

This tool removes a connected part of pixels that form a segmentation. You may use it to remove single segmented regions (left-click on specific segmentation) or to clear a whole slice at once (left-click at the non-labeled background). This tool will only work on regions of unlocked labels or on regions of the active label.

## **Close tool**



Close tool

Left-click inside the region/segmentation to fill all "holes" (pixels labelled with another label or no label) inside the region. Therefore this tool behaves like a local closing operation. This tool will not work, when a non-labeled region is selected and holes of locked labels will not be filled.

## **Live wire tool**



Live wire tool

The Live Wire Tool acts as a magnetic lasso with a contour snapping to edges of objects.





### Steps for using the Live Wire Tool

The tool handling is the same like the Lasso tool (see for more info), except it generates live wire contours instead of straight lines.

## Segment Anything Tool



Segment Anything tool

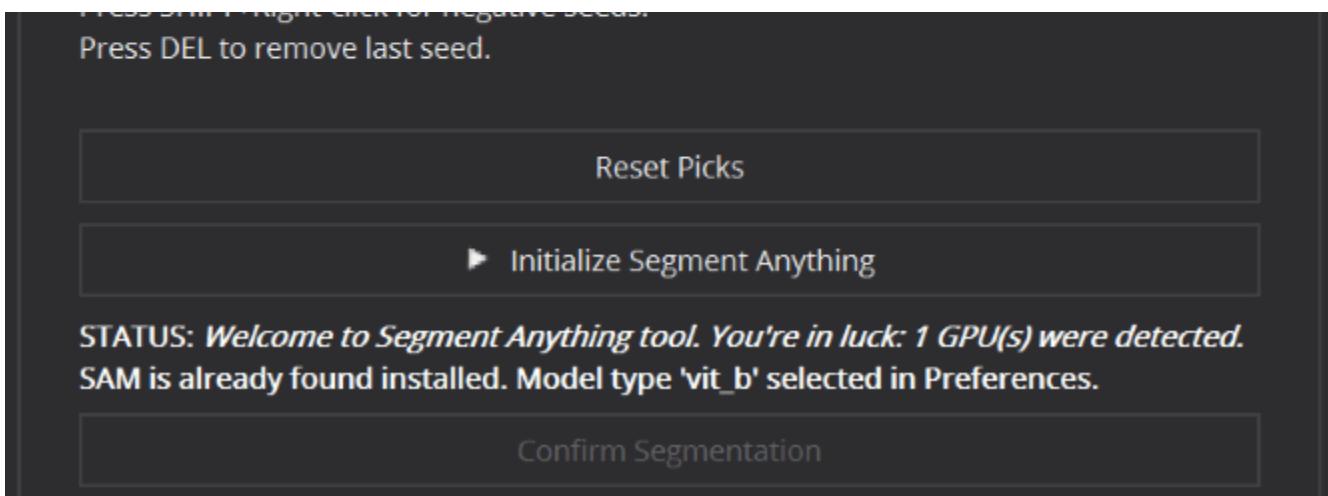
[2D tools](#) [3D tools](#)

Welcome to Segment Anything Model (SAM) tool in MITK. [Experimental]

Please note that this is only an interface to SAM. MITK does not ship with SAM. Make sure to have a working internet connection to install Segment Anything Model via MITK.

Refer to <https://segment-anything.com> to learn everything about the Segment Anything Model.

Press SHIFT+Left-click for positive seeds.  
Press SHIFT+Right-click for negative seeds



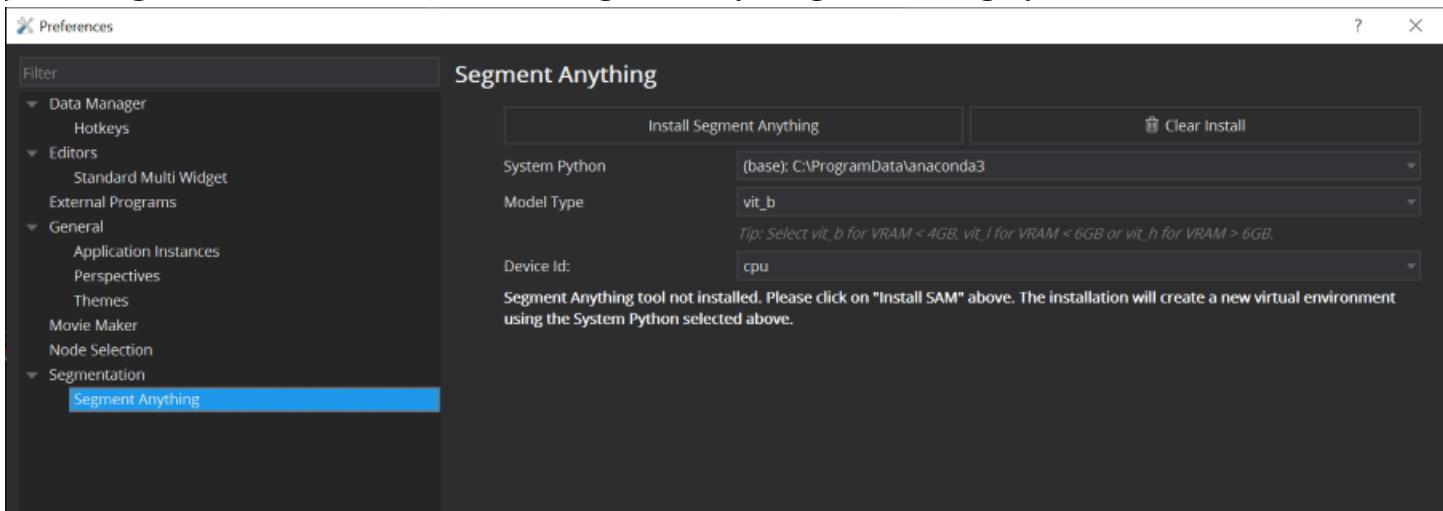
## Segment Anything tool

The Segment Anything Tool is a deep learning-based interactive segmentation tool. Originally created by MetaAI, MITK presents this model for medical image segmentation tasks. The tool requires that you have Python 3 installed and available on your machine. Note: On Debian/Ubuntu systems, you need to install git, python3-pip, python3-venv package using the following command: `apt install git python3-pip python3-venv`. For best experience, your machine should be ideally equipped with a CUDA-enabled GPU. For a detailed explanation of what this algorithm is able to, please refer to <https://ai.facebook.com/research/publications/segment-anything/>

Any adjustments to the [Levelwindow](#) setting impacts the segmentation. However, any applied color maps are ignored.

## Workflow:

Install Segment Anything: Goto Preferences (Cntl+P) > Segment Anything and click "Install Segment Anything" to install Segment Anything (version: 1.0). The installation process implicitly creates a python virtual environment using the Python located in "System Python" in an MITK maintained directory. Make sure you have a working internet connection. This might take a while. It is a one time job, though. Once installed, the "Install Segment Anything" button is grayed out.





## Segment Anything Preferences

Note: If Python is not listed by MITK in "System Python", click "Select..." in the dropdown to choose an unlisted installation of Python. Note that, while selecting an arbitrary environment folder, only select the base folder, e.g. "/usr/bin/". No need to navigate all the way into "../usr/bin/python3", for example.

Select a specific model type in the "Model Type" dropdown. The default is "vit\_b" for low memory footprint. However, more larger models "vit\_l" and "vit\_h" are also available for selection.

Select inference hardware, i.e. any GPU or CPU. This is internally equivalent to setting the **CUDA\_VISIBLE\_DEVICES** environment variable.

Click "OK" to save the preference settings.

Goto Segmentation View > 2D tools > Segment Anything.

Click "Initialize Segment Anything" to start the tool backend. This will invoke downloading of the selected model type from the internet. This might take a while. It is a one time job, though.

Once the tool is initialized, Press SHIFT+Left Click on any of the 3 render windows to start click guided segmentation on that slice.

Press SHIFT+Right Click for negative clicks to adjust the preview mask on the render window.

## 2D and 3D Interpolation

Creating segmentations using 2D manual contouring for large image volumes may be very time-consuming, because structures of interest may cover a large range of slices. The segmentation view offers two helpful features to mitigate this drawback:

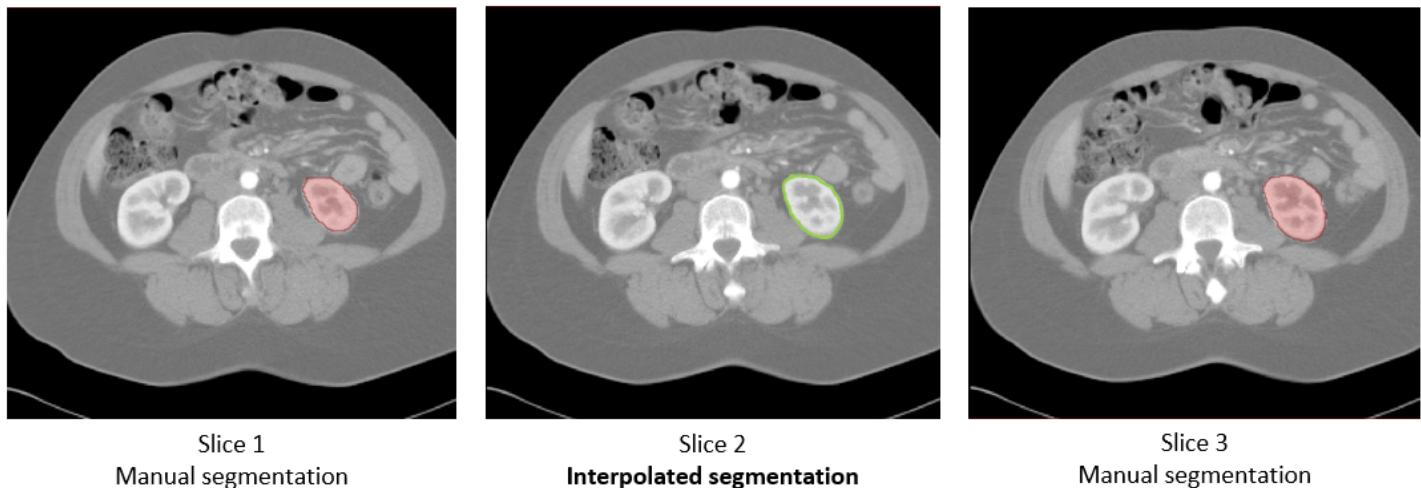
2D Interpolation

3D Interpolation

The **2D Interpolation** creates suggestions for a segmentation whenever you have a slice that

has got neighboring slices with segmentations (these do not need to be direct neighbors but could also be a couple of slices away) AND

is completely clear of a manual segmentation, i.e. there will be no suggestion if there is even only a single pixel of segmentation in the current slice.

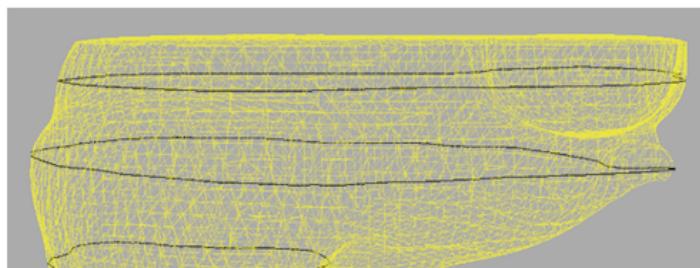


## 2D interpolation usage

Interpolated suggestions are displayed as outlines, until you confirm them as part of the segmentation. To confirm single slices, click the *Confirm for single slice* button below the toolbox. You may also review the interpolations visually and then accept all of them at once by selecting *Confirm for all slices*.

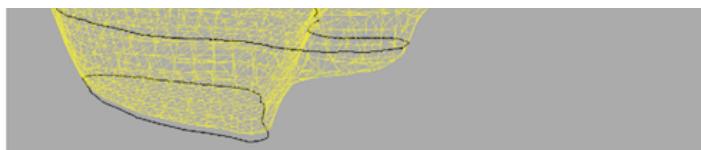
The **3D interpolation** creates suggestions for 3D segmentations. That means if you start contouring, from the second contour onwards, the surface of the segmented area will be interpolated based on the given contour information. The interpolation works with all available manual tools. Please note that this is currently a pure mathematical interpolation, i.e. image intensity information is not taken into account. With each further contour the interpolation result will be improved, but the more contours you provide the longer the recalculation will take. To achieve an optimal interpolation result and in this way a most accurate segmentation you should try to describe the surface with sparse contours by segmenting in arbitrary oriented planes. The 3D interpolation is not meant to be used for parallel slice-wise segmentation, but rather segmentations in i.e. the axial, coronal and sagittal plane.

**Wrong**



**Right**





Parallel slice-wise segmentation



Segmentation in arbitrary slices

### 3D interpolation usage

You can accept the interpolation result by clicking the *Confirm*-button below the tool buttons. In this case the 3D interpolation will be deactivated automatically so that the result can be post-processed without any interpolation running in the background.

Additional to the surface, black contours are shown in the 3D render window, which mark all the drawn contours used for the interpolation. You can navigate between the drawn contours by clicking on the corresponding *position* nodes in the data manager which are stored as sub-nodes of the selected segmentation. If you do not want to see these nodes just uncheck the *Show Position Nodes* checkbox and these nodes will be hidden.

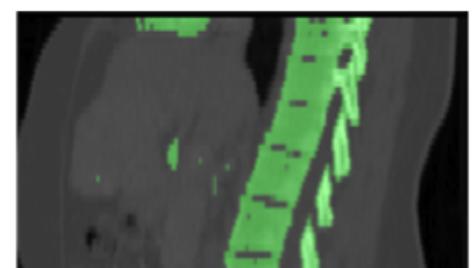
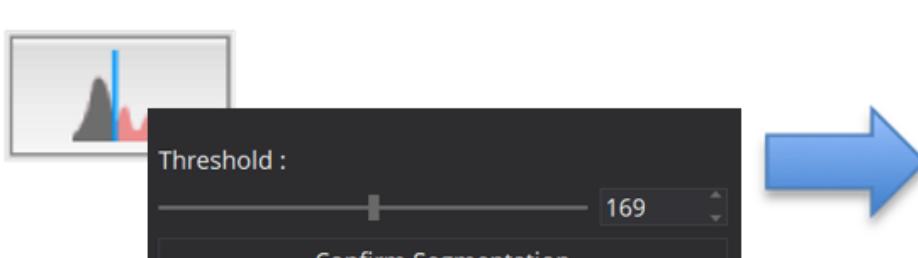
If you want to delete a drawn contour we recommend to use the Erase-Tool since undo / redo is not yet working for 3D interpolation. The current state of the 3D interpolation can be saved across application restart. For that, just click on save project during the interpolation is active. After restarting the application and load your project you can click on "Reinit Interpolation" within the 3D interpolation GUI area.

## 3D segmentation tools

The 3D tools operate on the whole image and require usually a small amount of interaction like placing seed-points or specifying certain parameters. All 3D tools provide an immediate segmentation feedback, which is displayed as a transparent green overlay. For accepting a preview you have to press the *Confirm* button of the selected tool. The following 3D tools are available:

### 3D Threshold tool

The thresholding tool simply applies a 3D threshold to the patient image. All pixels with values equal or above the selected threshold are labeled as part of the segmentation. You can change the threshold by either moving the slider or setting a certain value in the spinbox.

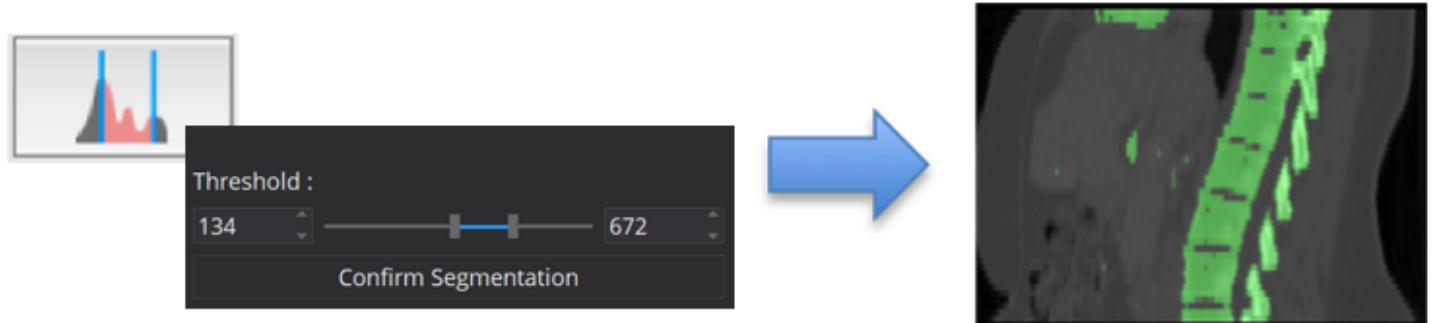




3D Threshold tool

### 3D upper / lower threshold tool

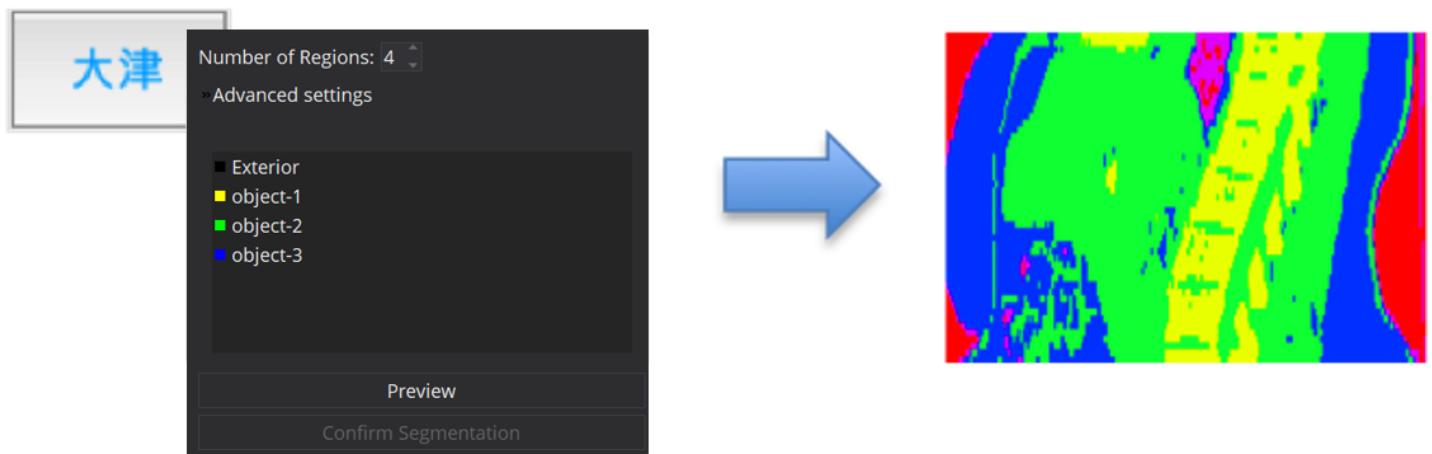
The Upper/Lower Thresholding tool works similar to the simple 3D threshold tool but allows you to define an upper and lower threshold. All pixels with values within this threshold interval will be labeled as part of the segmentation.



3D upper / lower threshold tool

### 3D Otsu tool

The 3D Otsu tool provides a more sophisticated thresholding algorithm. It allows you to define a number of regions. Based on the image histogram the pixels will then be divided into different regions. The more regions you define the longer the calculation will take. You can select afterwards which of these regions you want to confirm as segmentation.

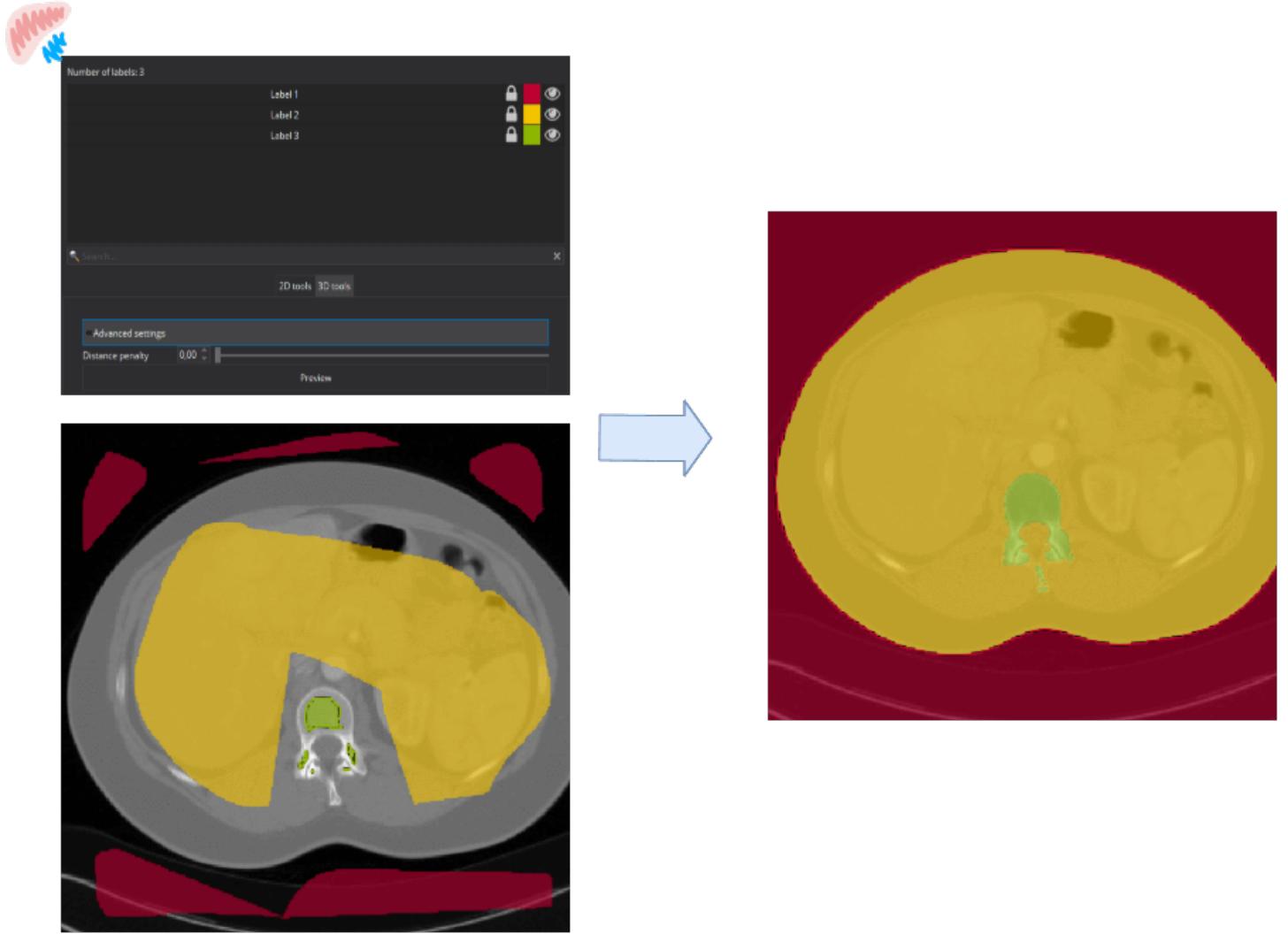


3D Otsu tool

### 3D GrowCut tool

The 3D GrowCut tool uses previously created segmentation labels (e.g. by the "Add"-tool) stored in

the segmentation layer  $o$ . The GrowCut tool will use these segmentation labels to create a seedimage that will serve as input to the algorithm. As an advanced setting option, a Distance penalty can be set, which increases the cohesion in the immediate surroundings of the initial labels. Based on the seedimage and the Distance penalty, a growing is started, which includes all areas that are not initially assigned to a specific label. During this process, initially unassigned areas are assigned to the best fitting labels. After the segmentation process, the user can decide which newly generated labels should be confirmed.



3D GrowCut tool

## Picking Tool

The Picking tool offers two modes that allow you to manipulate "islands" within your segmentation. This is especially useful if e.g. a thresholding provided you with several areas within your image but you are just interested in one special region.

**Picking mode:** Allows you to select certain "islands". When the pick is confirmed, the complete content of the active label will be removed except the pick. This mode is beneficial if you have a lot

segmentation noise and want to pick the relevant parts and dismiss the rest. Hint: You can also pick from other labels, but this will only work if these labels are unlocked.

Relabel mode: Allows you to select certain "islands". When the pick is confirmed, it will be relabeled and added to the active label content. Hint: This mode ignores the locks of other labels, hence you do not need to unlock them explicitly.



Picking tool

## nnU-Net Tool (Ubuntu only)



nnUNet tool

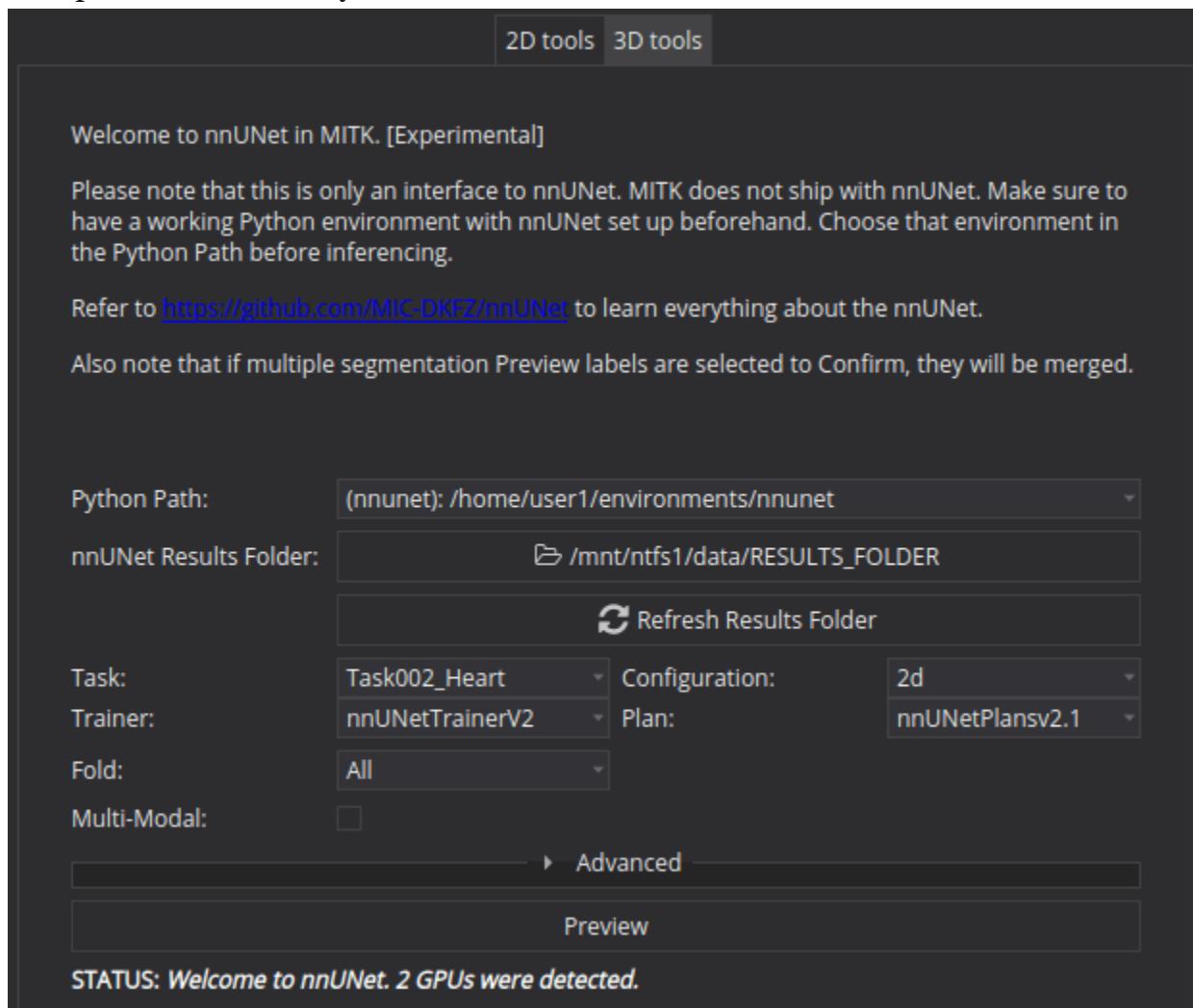
This tool provides a GUI to the deep learning-based segmentation algorithm called the nnU-Net v1. With this tool, you can get a segmentation mask predicted for the loaded image in MITK. Be ready with the pre-trained weights (a.k.a **RESULTS\_FOLDER**) for your organ or task concerned, before using the tool. For a detailed explanation of the parameters and pre-trained weights folder structure etc., please refer to <https://github.com/MIC-DKFZ/nnUNet>.

Remark: The tool assumes that you have a Python3 environment with nnU-Net v1 (pip) installed. Your machine should be also equipped with a CUDA enabled GPU.

## Workflow:

Select the "Python Path" drop-down to see if MITK has automatically detected other Python environments. Click on a fitting environment for the nnUNet inference or click "Select" in the dropdown to choose an unlisted python environment. Note that, while selecting an arbitrary environment folder, only select the base folder, e.g. "myenv". No need to select all the way until "../myenv/bin/python", for example.

Click on the "nnUNet Results Folder" directory icon to navigate to the results folder on your hard disk. This is equivalent to setting the **RESULTS\_FOLDER** environment variable. If your results folder is as per the nnUNet required folder structure, the configuration, trainers, tasks and folds are automatically parsed and correspondingly loaded in the drop-down boxes as shown below. Note that MITK automatically checks for the **RESULTS\_FOLDER** environment variable value and, if found, auto parses that directory when the tool is started.

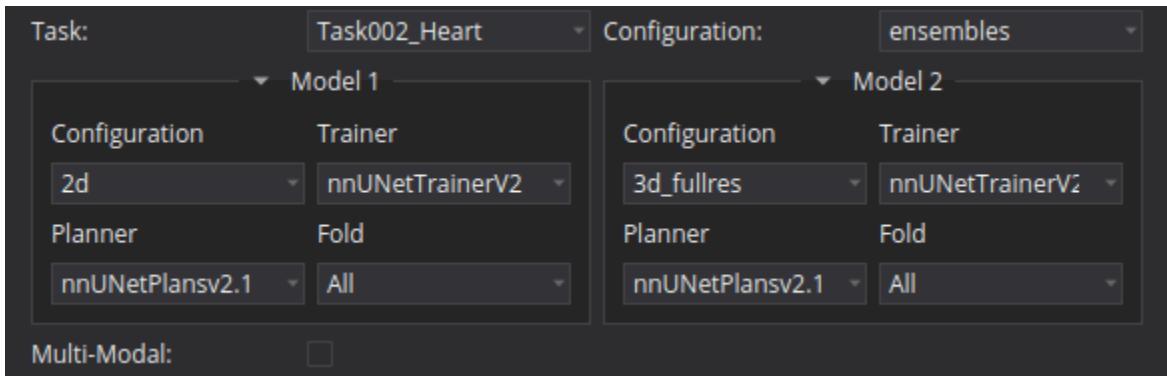


## nnUNet Segmentation Settings

Choose your required Task-Configuration-Trainer-Planner-Fold parameters, sequentially. By default, all entries are selected inside the "Fold" dropdown (shown: "All"). Note that, even if you uncheck all entries from the "Fold" dropdown (shown: "None"), then too, all folds would be considered for inferencing.

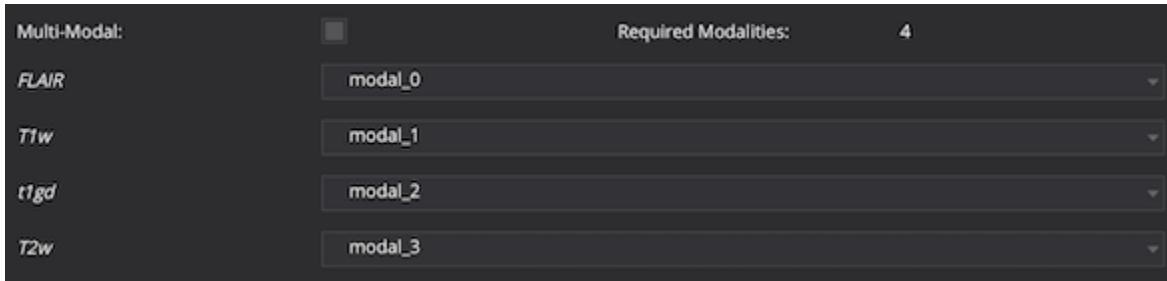
For ensemble predictions, you will get the option to select parameters irrespective on postprocessing files available in the ensembles folder of **RESULTS\_FOLDER**. Note that, if a postprocessing json file exists for the selected combination then it will be used for ensembling, by default. To choose not to,

unchecked the "Use PostProcessing JSON" in the "Advanced" section.



### nnUNet Segmentation Settings

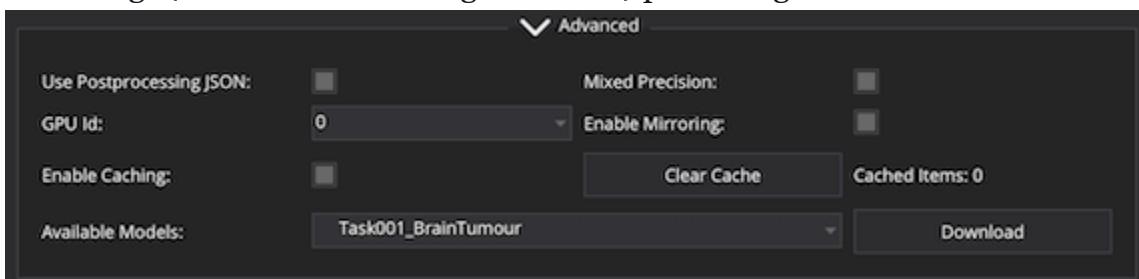
If your task is trained with multi-modal inputs, then "Multi-Modal" checkbox is checked and the no.of modalities are preloaded and shown next to "Required Modalities". Instantly, as much node selectors with corresponding modality names should appear below to select the Data Manager along including a selector with preselected with the reference node. Now, select the image nodes in the node selectors accordingly for accurate inferencing.



### nnUNet Multi Modal Settings

Click on "Preview".

In the "Advanced" section, you can also activate other options like "Mixed Precision" and "Enable Mirroring" (for test time data augmentation) pertaining to nnUNet.



### nnUNet Advanced Settings

Use "Advanced" > "GPU Id" combobox to change the preferred GPU for inferencing. This is internally equivalent to setting the **CUDA\_VISIBLE\_DEVICES** environment variable.

Every inferred segmentation is cached to prevent a redundant computation. In case, a user doesn't wish to cache a Preview, uncheck the "Enable Caching" in the "Advanced" section. This will ensure that the current parameters will neither be checked against the existing cache nor a segmentation be loaded from it when Preview is clicked.

You may always clear all the cached segmentations by clicking "Clear Cache" button.

### Miscellaneous:

In case you want to reload/reparse the folders in the "nnUNet Results Folder", eg. after adding new tasks into it, you may do so without reselecting the folder again by clicking the "Refresh Results Folder" button.

The "Advanced" > "GPU Id" combobox lists the Nvidia GPUs available by parsing the `nvidia-smi` utility output. In case your machine has Nvidia CUDA enabled GPUs but the `nvidia-smi` fails for some reason, the "GPU Id" combobox will show no entries. In such a situation, it's still possible to execute inferencing by manually entering the preferred GPU Id, eg. 0 in the combobox.

The "Advanced" > "Available Models" lists the available pre-trained tasks for download. Make sure you have internet connection. Then, choose a Task from the dropdown and click the Download button. The pre-trained models for the selected Task will be downloaded and placed to the **RESULTS\_FOLDER** directory automatically.

In the **RESULTS\_FOLDER** directory, inside the trainer-planner folder of every task, MITK keeps a "mitk\_export.json" file for fast loading for multi-modal information. It is recommended not to delete this file(s) for a fast responsive UI. Tip: If multi-modal information shown on MITK is not correct for a given task, you may modify this JSON file and try again.

## TotalSegmentator Tool

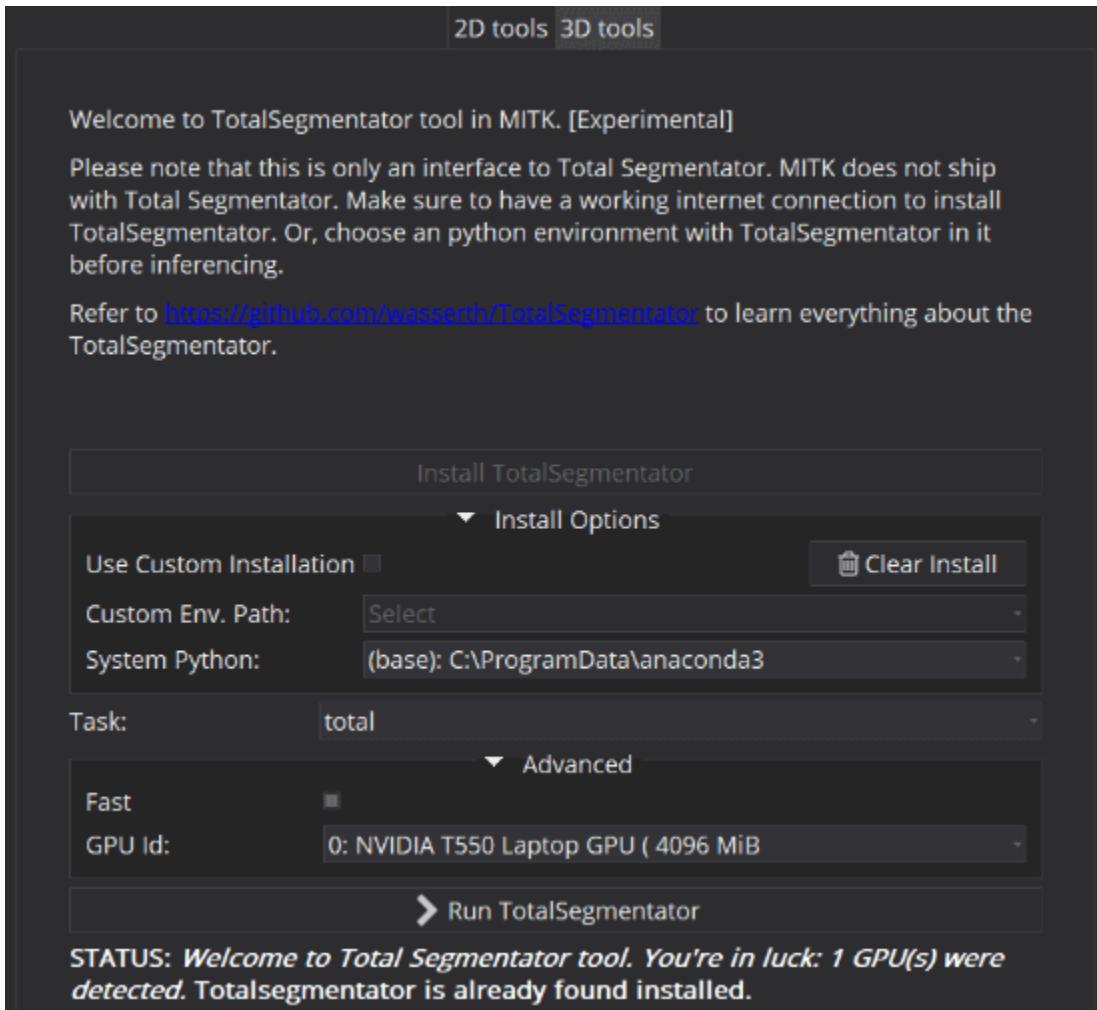


TotalSegmentator tool

This tool provides a GUI to the deep learning-based segmentation algorithm called the TotalSegmentator (v2). With this tool, you can get a segmentation mask predicted for 117 classes in CT images, loaded in MITK. For a detailed explanation on tasks and supported classes etc., please refer to <https://github.com/wasserk/TotalSegmentator>

The tool assumes that you have Python >= 3.9 installed and available on your machine. We

recommend to install TotalSegmentator via MITK. The "Install TotalSegmentator" action implicitly creates a python virtual environment in an MITK maintained directory. Note: on Debian/Ubuntu systems, you need to install the python3-venv package using the following command: `apt install python3-venv`. For best results, your machine should be ideally equipped with a CUDA-enabled GPU.



## TotalSegmentator Settings

### Workflow:

Install TotalSegmentator: Click "Install TotalSegmentator" to install TotalSegmentator (version: 2.0.5) in a virtual environment. Make sure you have a working internet connection. This might take a while. It is a one time job, though. Once installed, the "Install TotalSegmentator" button is grayed out.

If Python is not found by MITK goto "Install Options" & select the "System Python Path" drop-down to see if MITK has automatically detected other Python environments. Click on a fitting Python installation for TotalSegmentator to use or click "Select" in the dropdown to choose an unlisted installation of Python. Note that, while selecting an arbitrary environment folder, only select the base folder, e.g. "/usr/bin/". No need to navigate all the way into "../usr/bin/python3", for example.

Select a specific subtask in the "Tasks" drop-downs. The default is "total" for non-specific total segmentation.

Click on "Run TotalSegmentator" for a preview.

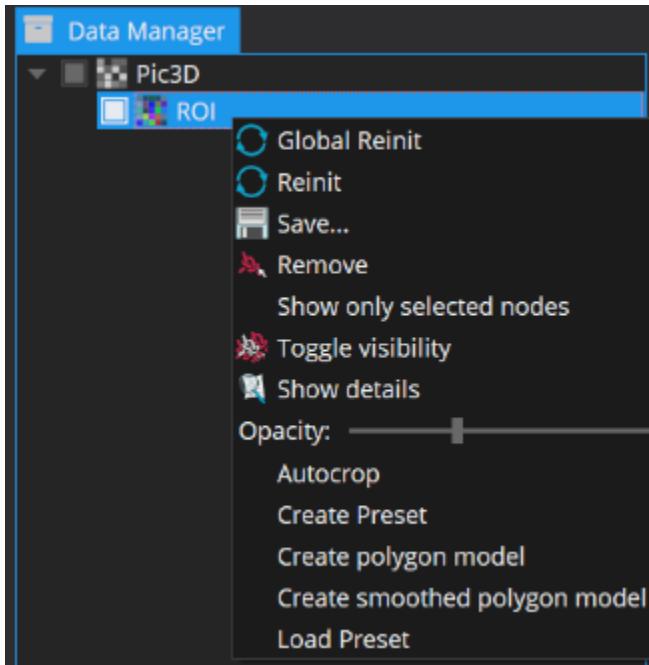
In the "Advanced" section, you can also activate other options like "Fast" for faster runtime and less memory requirements. Use "Fast" if you only have a CPU for inferencing.

Use "Advanced" > "GPU Id" combobox to change the preferred GPU for inferencing. This is internally equivalent to setting the **CUDA\_VISIBLE\_DEVICES** environment variable.

In case you want to use your own virtual environment containing TotalSegmentator, goto "Install Options" & check "Use Custom Installation" checkbox. Then, select the environment of your choice by using "Custom Env. Path".

## Additional things you can do with segmentations

Segmentations are never an end in themselves. Consequently, the segmentation view adds a couple of "post-processing" actions, accessible through the context-menu of the data manager.



Context menu items for segmentations

**Create polygon model** applies the marching cubes algorithm to the segmentation. This polygon model can be used for visualization in 3D or other applications such as stereolithography (3D printing).

**Create smoothed polygon model** uses smoothing in addition to the marching cubes algorithm, which creates models that do not follow the exact outlines of the segmentation, but look smoother.

**Autocrop** can save memory. Manual segmentations have the same extent as the patient image, even if the segmentation comprises only a small sub-volume. This invisible and meaningless margin is removed by autocropping.

## Segmentation of 3D+t images

For segmentation of 3D+t images, some tools give you the option to choose between creating dynamic and static masks.

Dynamic masks can be created on each time frame individually.

Static masks will be defined on one time frame and will be the same for all other time frames.

In general, segmentation is applied on the time frame that is selected when execution is performed. If you alter the time frame, the segmentation preview is adapted.

## Technical information for developers

For technical specifications see [Technical design of QmitkSegmentation](#) and for information on the extensions of the tools system [How to extend the Segmentation view with external tools](#).

# Medical Imaging Interaction Toolkit: The Standard Display

## General remark on F1 help

This is the help window of the standard display. To display the help windows of other plugins, press F1 when the plugin of interest is active (please make sure the tab of the plugin of interest is highlighted). Alternatively, go to the *Help* menu and select *Open Help Perspective*. A help window opens from which you can select the documentation of the plugin of interest.

## Four Window View

### Overview

The four window view is the heart of the MITK image viewing. The standard layout is three 2D windows and one 3D window, with the axial window in the top left quarter, the sagittal window in the top right quarter, the coronal window in the lower left quarter and the 3D window in the lower right quarter. The different planes form a crosshair that can be seen in the 3D window.

Once you select a point within the picture, information about it is displayed at the bottom of the screen.

### Navigation

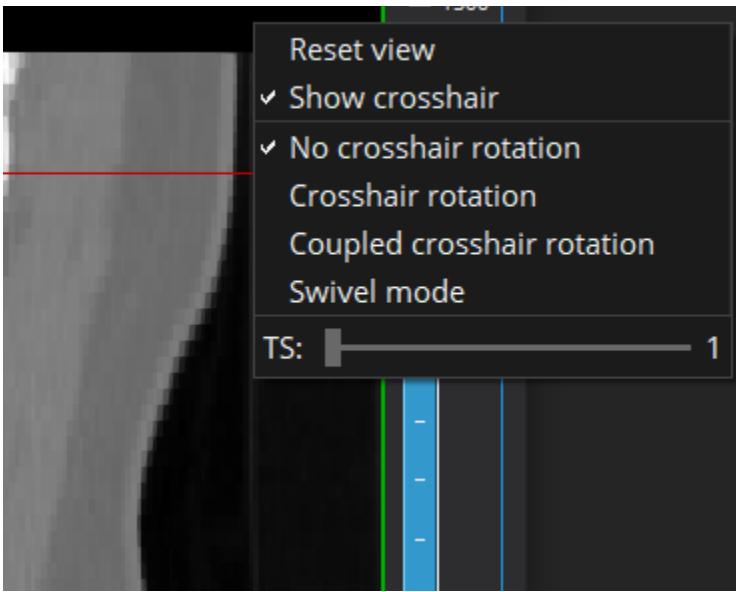
Left click in any of the 2D windows centers the crosshair on that point. Pressing the right mouse button and moving the mouse **zooms** in and out. By scrolling with the mouse wheel you can **navigate through** the slices of the active window and pressing the mouse wheel while moving the mouse **pans** the image section.

In the 3D window you can **rotate** the object by pressing the left mouse button and moving the mouse, **zoom** either with the right mouse button as in 2D or with the mouse wheel, and **pan** the object by moving the mouse while the mouse wheel is pressed. Placing the cursor within the 3D window and holding the "F" key allows **free flight** into the 3D view.

### Customizing

By moving the cursor to the upper right corner of any window you can activate the window menu. It consists of three buttons.





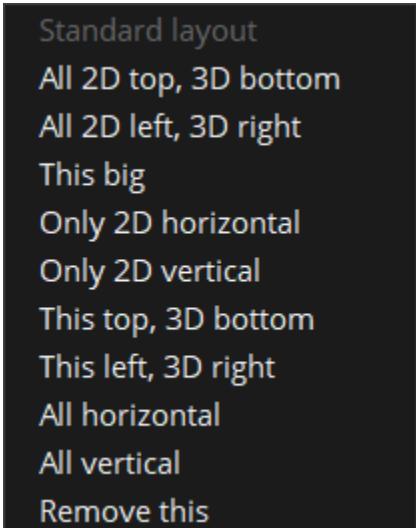
## Crosshair

The crosshair button allows you to toggle the crosshair, reset the view and change the behaviour of the planes.

Activating either of the rotation modes allows you to rotate the planes visible in a 2D window by moving the mouse cursor close to them and click and dragging once it changes to indicate that rotation can be done.

The swivel mode is recommended only for advanced users as the planes can be moved freely by clicking and dragging anywhere within a 2D window.

The middle button expands the corresponding window to fullscreen within the four window view.



## Layout Choices

The right button allows you to choose between many different layouts of the four window view to use the one most suited to your task.

## **Levelwindow**

Once an image is loaded the levelwindow appears to the right hand side of the four window view. With this tool you can adjust the range of grey values displayed and the gradient between them. Moving the lower boundary up results in any pixels having a value lower than that boundary to be displayed as black. Lowering the upper boundary causes all pixels having a value higher than it to be displayed as white.

The pixels with a value between the lower and upper boundary are displayed in different shades of grey. This way a smaller levelwindow results in higher contrasts while cutting off the information outside its range whereas a larger levelwindow displays more information with a higher detail level at the cost of contrast.

You can pick the levelwindow with the mouse to move it up and down, while moving the mouse cursor to the left or right to change its size. Picking one of the boundaries with a left click allows you to change the size symmetrically. Holding CTRL and clicking a boundary adjusts only that value.

With line edit fields below you can directly adjust the levelwindow. The upper field describes the center of the levelwindow, the bottom the span of the window around the center. By selecting one of fields and typing any number you can set these two parameters.

# Medical Imaging Interaction Toolkit: The View Navigator



Icon of the view navigator

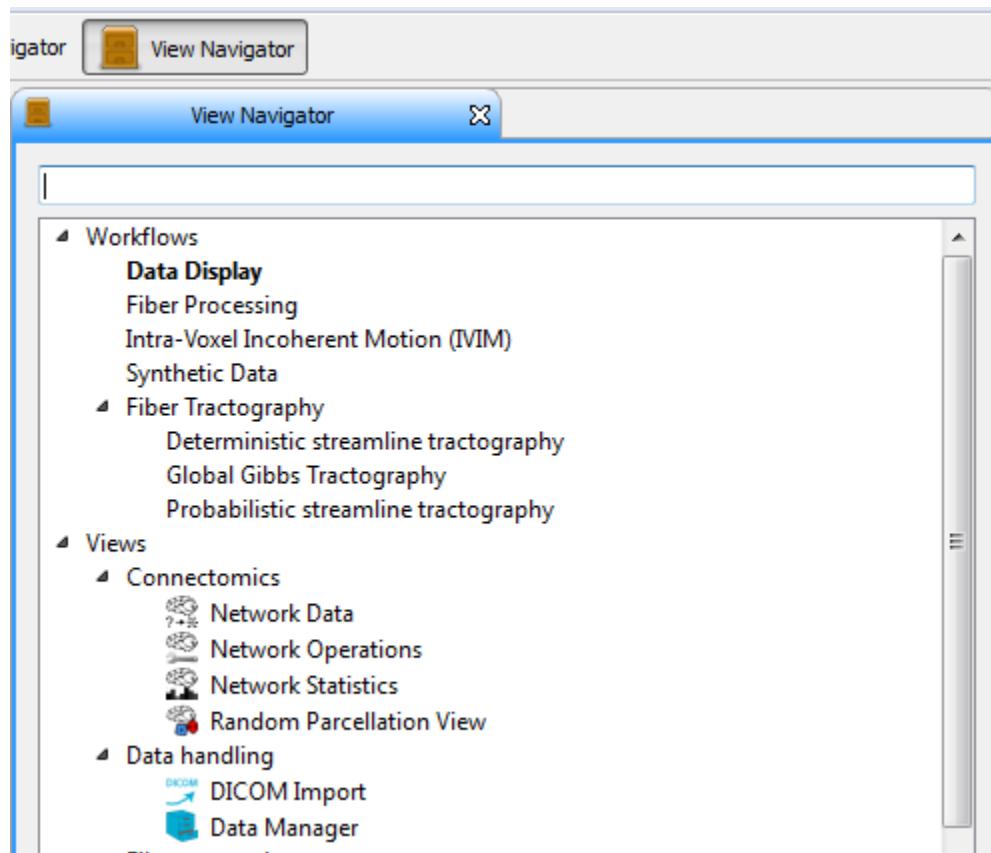
## Overview

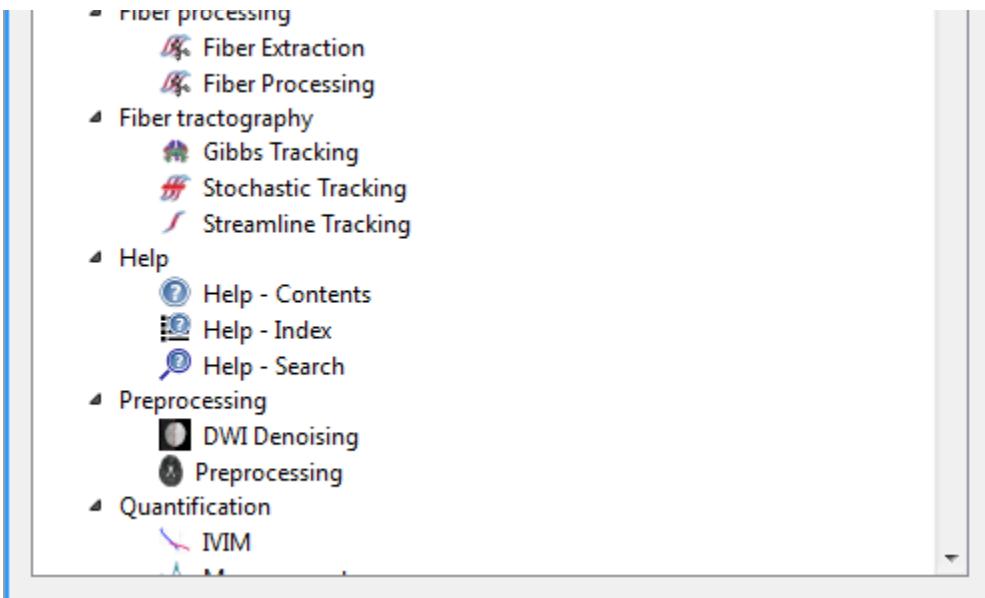
This view allows for the easy navigation of the available views.

You can select which view to open by double-clicking the name of the view in the view navigator. It provides a keyworded, grouped and searchable list of views.

## Usage

You can toggle the View Navigator on and off by clicking on its icon in the menu bar. Alternatively it is also available via the Window->Show Views dialog.





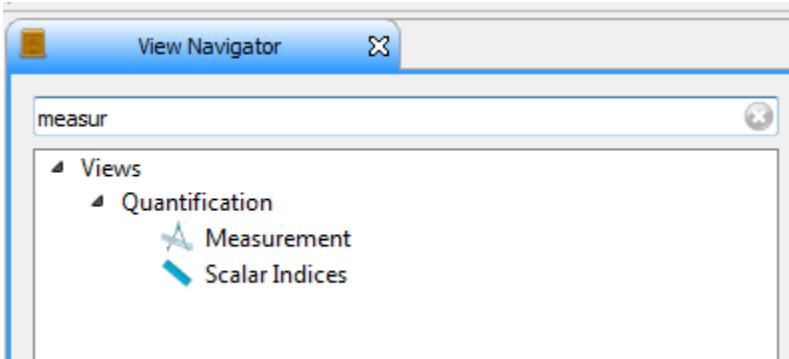
## The View Navigator GUI

Once the View Navigator has been opened you will see a list divided in workflows/perspectives and views. Via this list you can access any view or perspective provided by the application. They are further organized based on their associated category.

An entry on the list is opened by a double left-click.

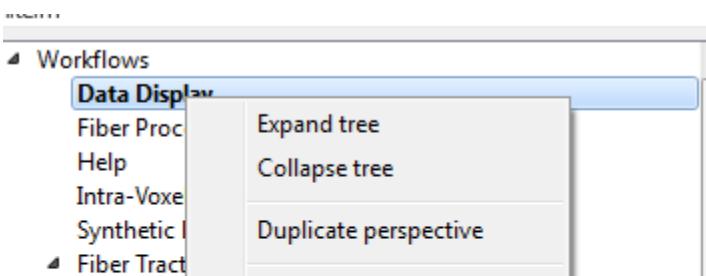
## Search

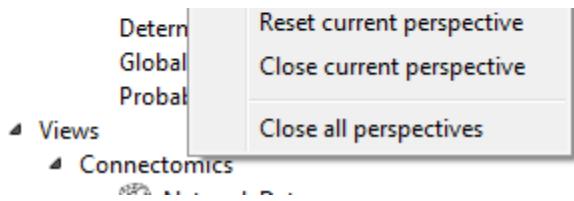
You can search the lists for view/workflow names, keywords or categories.



Search the View Navigator

## Custom Workflows



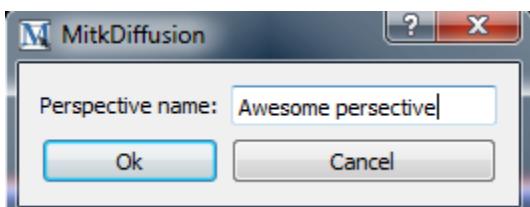


### The workflow context menu

A right click on a workflow opens a context menu that allows you to copy that workflow to create your own custom one.

#### Note

The duplicated workflow will look like the basic state of the original workflow. Any changes to the original workflow will not be copied.

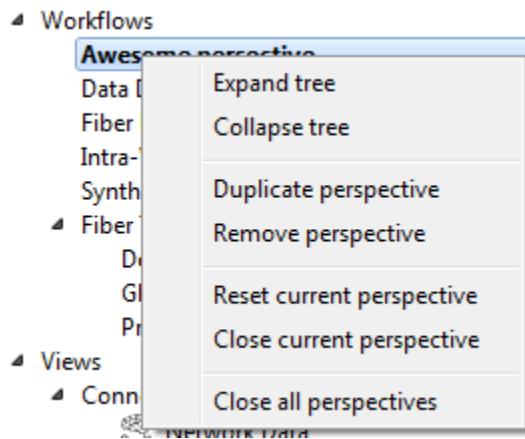


### Custom workflow creation dialog

Your new workflow will appear in the list and you can modify it independently of the original workflow. Any changes will be stored for future sessions unless the workflow is deleted.

#### Note

Resetting a custom perspective will return it to the original state after duplicating.



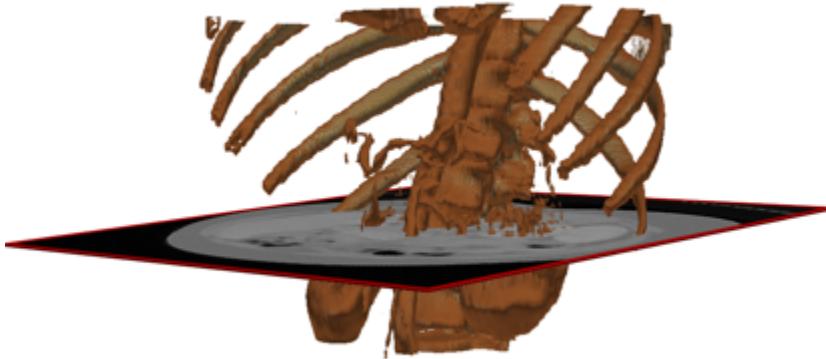
### Custom workflow context menu

# Medical Imaging Interaction Toolkit: The Volume Visualization Plugin

Icon of the Volume Visualization Plugin

## Overview

The **Volume Visualization Plugin** is a basic tool for volume rendering of three dimensional medical images. MITK provides generic transfer function presets for medical CT and MRT data. These functions that map the gray-value to color and opacity can be interactively edited. Additionally, there are controls to quickly generate commonly used transfer function shapes like the threshold and bell curve to help identify a range of grey-values.



## Volume Rendering

### Select an image and enable volume rendering

Select an image on top of the view and click on the checkbox left of 'Volume rendering'.

#### Note

Volume Visualization imposes following restrictions on images:

- It has to be a 3D scalar image, that means e.g. a CT or MRT image.
- 3D+t images are supported for rendering, but the histograms are not computed.
- Also be aware that volume visualization requires a huge amount of memory. Very large images may not work unless you use the 64bit version.

## Dropdown menu for the blend modes

Two dropdown menu is located right next to the 'Volume rendering' checkbox. It allows you to select a blend mode (Composite, Maximum intensity, Minimum intensity, Average intensity, and Additive intensity).

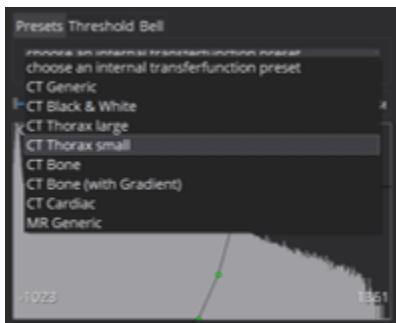
Blend modes define how the volume voxels, intersected by the rendering rays, are pooled. The 'Composite' mode specifies standard volume rendering, for which each voxel contributes equally with opacity and color. Other 'blend' modes visualize the voxel of the maximum or minimum intensity or average or add the intensities along the rendering ray.

## Applying premade presets

### Internal presets

There are some internal presets given that can be used with normal CT data (given in Houndsfield units). A large set of medical data has been tested with those presets, but they may not suit some special cases.

Click on the 'Preset' tab for using internal or custom presets.



'CT Generic' is the default transfer function that is first applied.

'CT Black&White' does not use any colors for the volume visualization as it may be distracting on some data.

'CT Cardiac' is well-suited for CT images containing the heart.

'CT Bone' emphasizes bones and shows other areas more transparent.

'CT Bone (Gradient)' is like 'CT Bone' but shows only the surface from other organs by using the gradient.

'MR Generic' is the default transfer function that can be used on MRT data (which is not normalized like CT data).

'CT Thorax small' is useful if only a proportion of the thorax is selected to emphasize details.

'CT Thorax large' is useful if a large proportion or the entire thorax is selected to emphasize details.

## Saving and loading custom presets

After creating or editing a transfer function (see [Customize transfer functions in detail](#) or [Interactively create transfer functions](#)), the custom transfer function can be stored and later retrieved on the filesystem. Click 'Save' (respectively 'Load') button below the preset selection to save (load) the threshold-, color- and gradient function combined in a single .xml file.

## Interactively create transfer functions

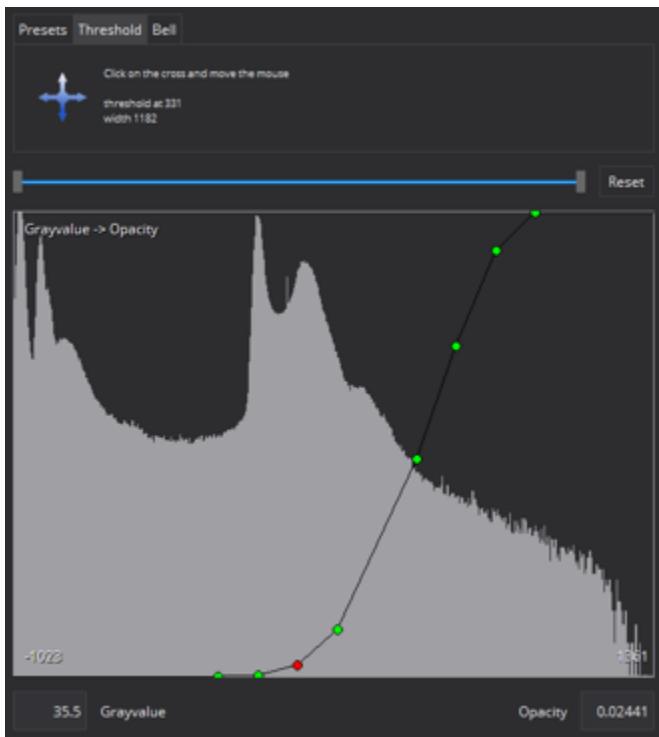
Besides the possibility to directly edit the transfer functions ([Customize transfer functions in detail](#)), the plugin provides two commonly known shapes to quickly generate transfer functions with a few clicks. Both generators have two parameters that can be modified by first clicking on the cross and then moving the mouse up/down and left/right.

The first parameter 'center' (controlled by horizontal movement of the mouse) specifies the gray value where the center of the shape will be located.

The second parameter 'width' (controlled by vertical movement of the mouse) specifies the width (or steepness) of the shape.

## Threshold

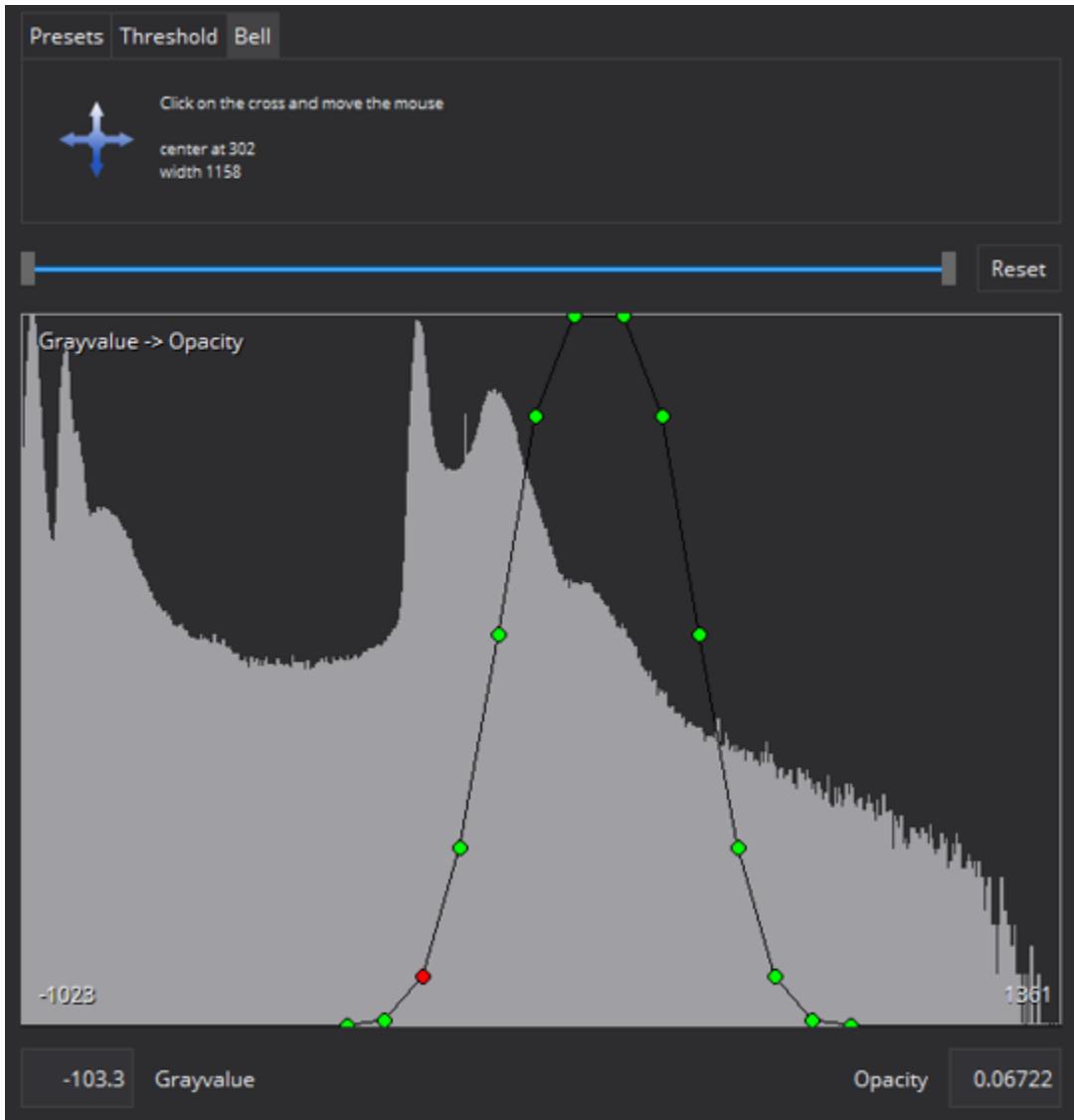
Click on the 'Threshold' tab to activate the threshold function generator.



A threshold shape begins with zero and raises to one across the 'center' parameter. Lower widths result in steeper threshold functions.

## Bell

Click on the 'Bell' tab to activate the bell-shaped threshold function generator.



A threshold shape begins with zero and raises to one at the 'center' parameter and then lowers again to zero. The 'width' parameter corresponds to the width of the bell.

## Customize transfer functions in detail

### Choosing gray value interval to edit



To navigate across the gray value range or to zoom in some ranges use the 'range'-slider.

All three function editors have in common following:

By left-clicking a new point is added.

By right-clicking a point is deleted.

By left-clicking and holding, an existing point can be dragged.

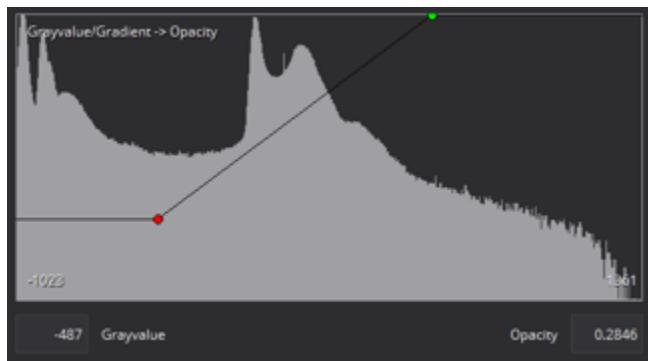
By pressing arrow keys, the currently selected point is moved.

By pressing the 'DELETE' key, the currently selected point is deleted.

Between points the transferfunctions are linear interpolated.

There are three transfer functions to customize:

## Grayvalue -> Opacity



Gray values will be mapped to opacity.

An opacity of 0 means total transparent, an opacity of 1 means total opaque. The opacity editor allows changing the opacity for all gray values independently. You can alter the position of control points using your mouse. You can add control points by left-clicking on the graph. To remove a control point again you can right-click on the respective point.

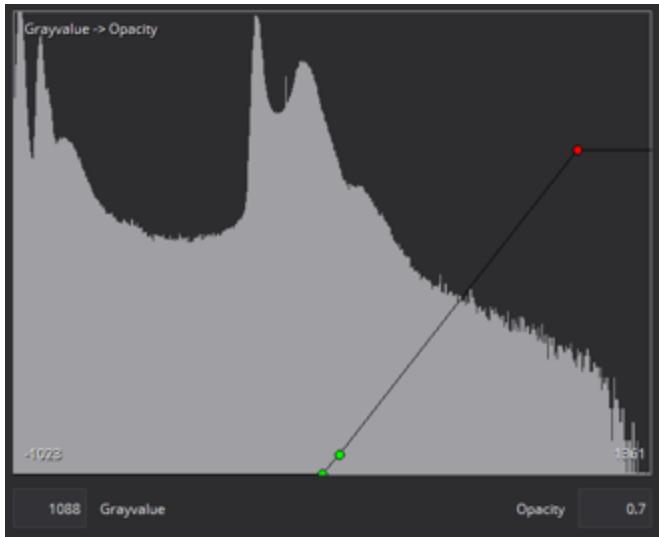
## Grayvalue -> Color



Gray values will be mapped to color.

The color transfer function editor also allows you to change its color by double-clicking a point. You can add color control points by left-clicking on the color bar. To remove a control point again right-click on the respective point.

## Grayvalue and Gradient -> Opacity



The gradient editor allows you to change the gradient influence for all gray values independently. You can move the existing control points using your mouse. Additionally, you can add control points by left-clicking on the graph. To remove a control point again, right-click on the respective point.

# MITK Plugin Manuals

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The plugins and bundles provide much of the extended functionality of MITK. Each encapsulates a solution to a problem and associated features. This way one can easily assemble the necessary capabilities for a workflow without adding a lot of bloat, by combining plugins as needed.

- [The Basic Image Processing](#)
- [The Data Manager View](#)
- [The Dicom Browser Plugin](#)
- [The DICOM Inspector](#)
- [The Image Cropper](#)
- [The Image Navigator](#)
- [The Pixel Value View](#)
- [The Logging Plugin](#)
- [The MatchPoint Algorithm Browser View](#)
- [The MatchPoint Algorithm Control View](#)
- [The MatchPoint Registration Evaluation View](#)
- [The MatchPoint Frame Correction View](#)
- [The MatchPoint Registration Manipulator View](#)
- [The MatchPoint Image Mapper View](#)
- [The MatchPoint Registration Visualizer View](#)
- [The Measurement Toolbox](#)
  - [The Measurement View](#)
  - [The Image Statistics View](#)
- [The Movie Maker View](#)
- [The Point Set Interaction](#)
- [The Python Plugin](#)
- [The Remeshing View](#)
- [The Screenshot Maker View](#)
- Segmentation
  - [The Segmentation View](#)
  - [The Segmentation Utilities View](#)
  - [The Segmentation Task List View](#)
- [The Standard Display](#)
- [The MxN Display](#)
- [The Clipping Plane View](#)
- [The View Navigator](#)
- [The Volume Visualization Plugin](#)
- [The Properties View](#)
- [The Flow application](#)
- [The Segmentation Flow](#)
- [The Anisotropic Iterative Closest Point Registration Plugin](#)

- The CEST View
- The DCE Concentration Curve Converter View
- The DCE MR Perfusion DataFit View
- The Dynamic PET DataFit View
- The MITK Examples
- The Geometry Tools
- The IGT Examples
- The IGT Tracking Plugin
- The IGT Tracking Semi Automatic Measurement
- The Fit Generator Demo View
- The Model Fit Generic Fitting View
- The Model Fit Inspector View
- The OpenCV Examples
- The Overlay Manager Plugin
- The Preprocessing and Resampling
- The Perfusion Curve Description Parameters View
- The Perfusion Data Simulation View
- The Surface Material Editor
- The ToF Tutorial
- The Object Browser
- The Ultrasound Plugin
- The XNAT Plugin

# Medical Imaging Interaction Toolkit: MITK User Manual

To get an introduction to the usage of any MITK based application please read [The MITK Workbench](#). It will give you an overview of most of the common questions, such as how to load or save data or navigate within it. This is a good starting point for first questions.

For more specific information on how a plugin operates you can find the plugin documentation in [MITK Plugin Manuals](#). The Plugin documentation usually explains the functionality in depth and should solve most problems you might encounter with the plugin. Depending on the application you are using you might have only some or all of the listed plugins available.

Lastly, if your question is not answered here, please use our [Mailinglist](#) to let us know about your problem. Alternatively, you can [contact us directly](#).

## List of topics

- [The MITK Workbench](#)
- [MITK Plugin Manuals](#)
- [Advanced MITK user topics](#)

# Medical Imaging Interaction Toolkit: The Basic Image Processing



Icon of the Basic Image Processing Plugin

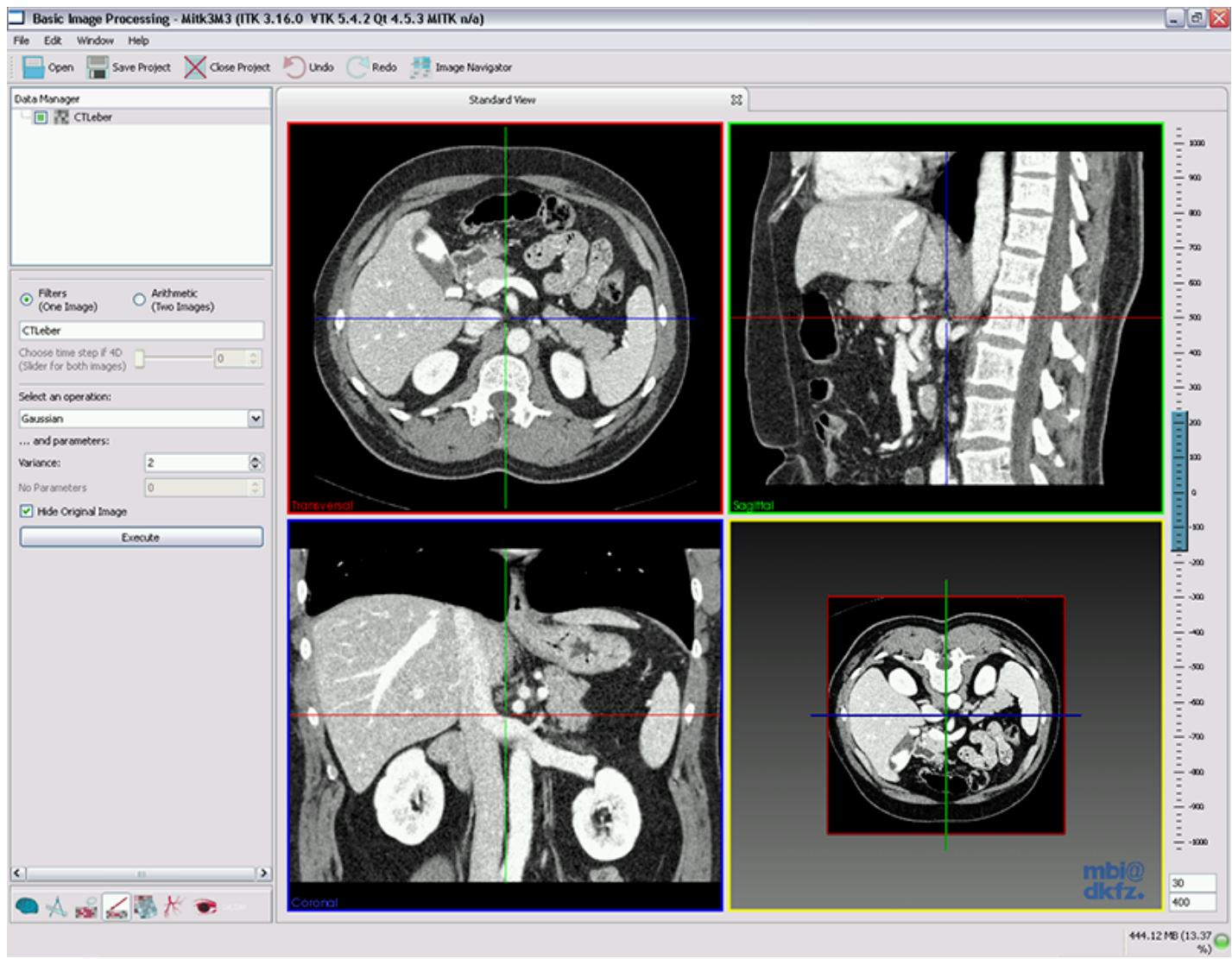
## Summary

This view provides an easy interface to fundamental image preprocessing and enhancement filters. It offers filter operations on 3D and 4D images in the areas of noise suppression, morphological operations, edge detection and image arithmetics, as well as image inversion and downsampling.

Please see [Overview](#) for more detailed information on usage and supported filters. If you encounter problems using the view, please have a look at the [Troubleshooting](#) page.

## Overview

This view provides an easy interface to fundamental image preprocessing and image enhancement filters. It offers a variety of filter operations in the areas of noise suppression, morphological operations, edge detection and image arithmetics. Currently the view can be used with all 3D and 4D image types loadable by MITK. 2D image support will be added in the future. All filters are encapsulated from the Insight Segmentation and Registration Toolkit (ITK, [www.itk.org](http://www.itk.org)).



## MITK with the Basic Image Processing view

This document will tell you how to use this view, but it is assumed that you already know how to use MITK in general.

## Filters

This section will not describe the fundamental functioning of the single filters in detail, though. If you want to know more about a single filter, please have a look at <https://itk.org/Doxygen/html/index.html> or in any good digital image processing book. For total denoising filter, please see Tony F. Chan et al., "The digital TV filter and nonlinear denoising".

Available filters are:

## Single image operations

- **Noise Suppression**
  - Gaussian Denoising
  - Median Filtering
  - Total Variation Denoising
- **Morphological Operations**

- Dilation
- Erosion
- Opening
- Closing

- **Edge Detection**

- Gradient Image
- Laplacian Operator (Second Derivative)
- Sobel Operator

- **Misc**

- Threshold
- Image Inversion
- Downsampling (isotropic)

## **Dual image operations**

- **Image Arithmetics**

- Add two images
- Subtract two images
- Multiply two images
- Divide two images

- **Binary Operations**

- Logical AND
- Logical OR
- Logical XOR

## **Usage**

All you have to do to use a filter is to:

- Load an image into MITK
- Select it in data manager
- Select which filter you want to use via the drop down list
- Press the execute button

A busy cursor appears; when it vanishes, the operation is completed. Your filtered image is displayed and selected for further processing. (If the checkbox "Hide original image" is not selected, you will maybe not see the filter result imideately, because your filtered image is possibly hidden by the original.)

For two image operations, please make sure that the correct second image is selected in the drop down menu, and the image order is correct. For sure, image order only plays a role for image subtraction and division. These are conducted ( $\text{Image1} - \text{Image2}$ ) or ( $\text{Image1} / \text{Image2}$ ), respectively.

Please Note: When you select a 4D image, you can select the time step for the filter to work on via the time slider at the top of the GUI. The 3D image at this time step is extracted and processed. The result will also be a 3D image. This means, a true 4D filtering is not yet supported.

## **Troubleshooting**

**I get an error when using a filter on a 2D image.**

2D images are not yet supported...

**I use a filter on a 4D image, and the output is 3D.**

When you select a 4D image, you can select the time step for the filter to work on via the time slider at the top of the GUI. The 3D image at this time step is extracted and processed. The result will also be a 3D image. This

means, a true 4D filtering is not supported by now.

### **A filter crashes during execution.**

Maybe your image is too large. Some filter operations, like derivatives, take a lot of memory. Try downsampling your image first.

### **All other problems.**

Please report to the MITK mailing list. See [https://www.mitk.org/wiki/MITK\\_Mailinglist](https://www.mitk.org/wiki/MITK_Mailinglist) on how to do this.

# Medical Imaging Interaction Toolkit: The CEST View

## Overview

This view gives the option to explore and analyze CEST data. You can select a CEST data set together with either a segmentation or a point set in the datamanager. If a segmentation was selected (make sure the segmentation is the same in each time step, you can use the button at the top of the view to copy the first time step to all subsequent ones) a statistic for the selected region is shown. If a point set was selected each points grey value is plotted.

## Data Loading

CEST dicom data can be loaded either via file open or drag and drop. When a dicom file is loaded via MITK and it contains CEST meta information the CEST Dicom Reader is offered as an option. Selecting it will parse the CEST data as follows:

An initial parsing determines whether the provided string belongs to CEST data at all. If the "tSequenceFileName" is of the format "{WHATEVER}CEST\_Rev####" it is assumed that the data is indeed CEST data and was taken with revision #### (not limited to four digits).

Which custom parameters to save and to which property name can be controlled by a json file. This file can be either provided as a resource for the MitkCEST module during compilation or placed next to the MitkCEST library in your binary folder.

The expected format for the file "REVISIONNUMBER.json":

```
{  
  "REVISIONNUMBER" : "revision_json",  
  "sWiPMemBlock.alFree[1]" : "AdvancedMode",  
  "sWiPMemBlock.alFree[2]" : "RetreatMode"  
}
```

where :

REVISIONNUMBER is the revision number of this json parameter mapping (files with non digit characters in their name will be ignored)

sWiPMemBlock.alFree[1] is the name of one parameter in the private dicom tag

AdvancedMode is the name of the property the content of sWiPMemBlock.alFree[1] should be saved to

If the sampling type is list it will try to access LIST.txt at the same location as the dicom files read the offsets.

## **Creating a segmentation**

You can use the segmentation view to create a segmentation for the CEST data. Drawing a segmentation will by default only add it to the first timestep. For more information check the help of the segmentation view.

You can copy the segmentation on the first timestep to all following ones by using the copy timestep button in this view.

## **Creating a point set**

You can use the point set interaction view to create a point set for the CEST data. For more information check the help of the point set interaction view.

## **Normalizing the CEST data**

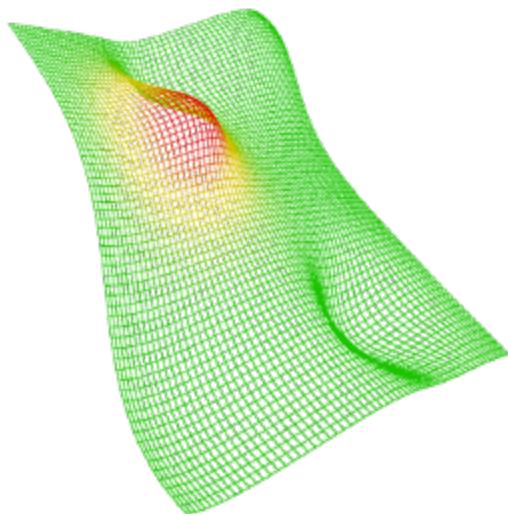
Select the CEST image in the datamanager and hit the normalize button to create a new, normalized image.

## **Investigate CEST meta data**

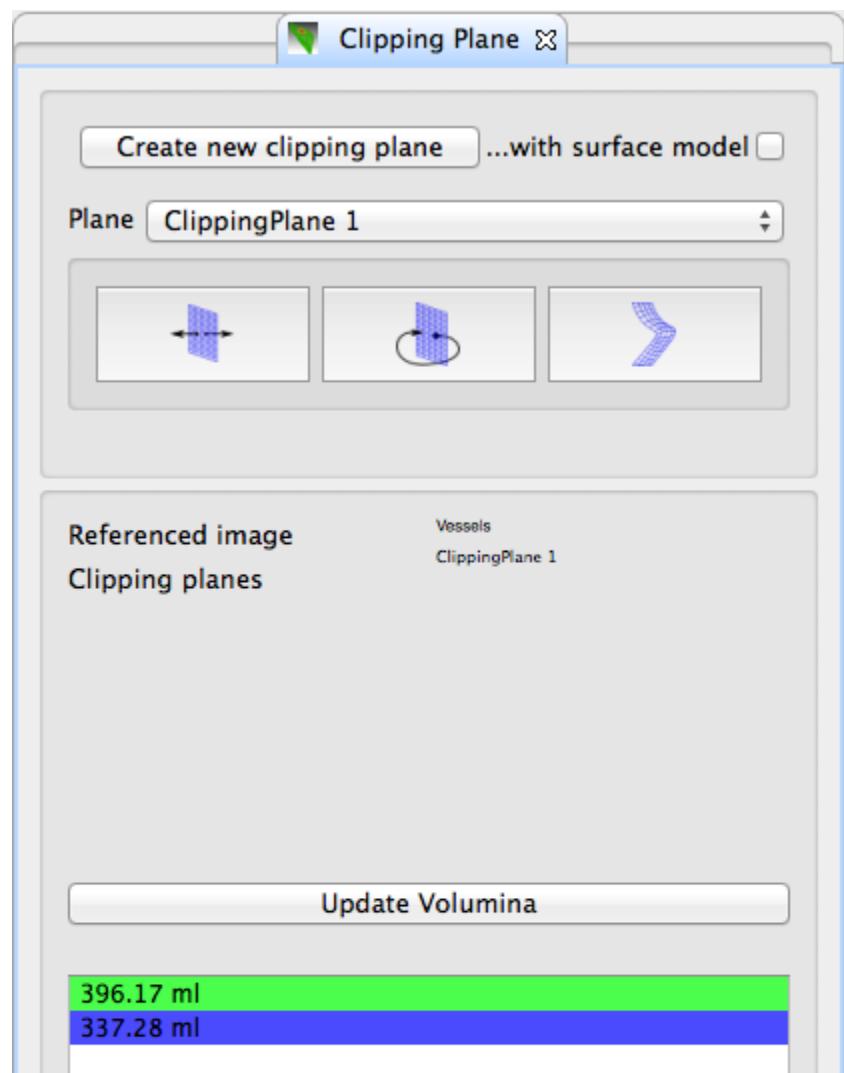
You can inspect the CEST meta data with the properties view. You need to enable the developer mode in the "Window->Preferences" Properties menu. When selecting a data node in the data manager with the properties view active you can change the Property List from "Data node: common" to "Base data".

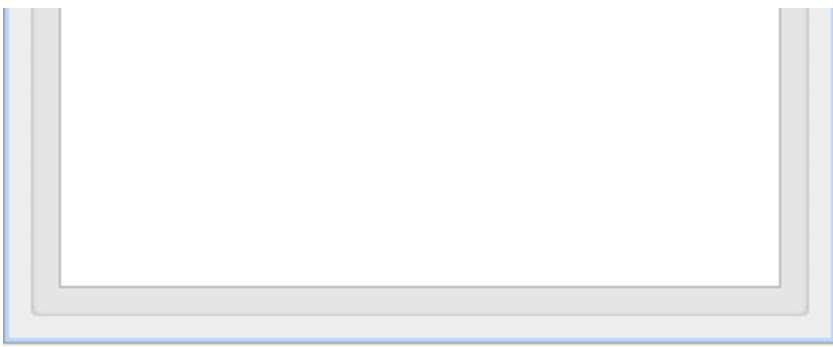
The cest meta data is grouped under CEST.

# Medical Imaging Interaction Toolkit: The Clipping Plane View



Icon of the Clipping Plane Plugin





Clipping Plane view

## Overview

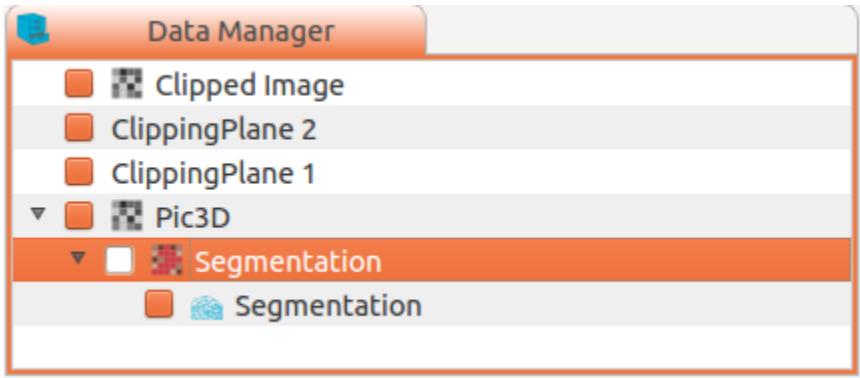
The **Clipping Plane view** allows you to create clipping planes and calculate the volumina of the divided parts.

## Technical Issue

To use the Update Volumina function your image should be binary.

## Image Selection

The Clipping Plane view makes use of the Data Manager view to give you an overview of all images, segmentations and clipping planes.



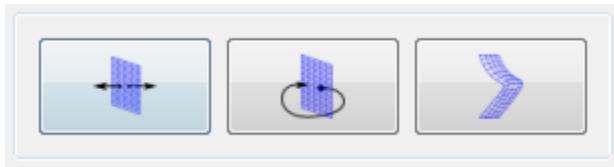
Data Manager is used for selecting the current clipping plane. The reference plane is selected in the drop down box of the control area.

To select the reference plane use the drop down box in the control area of the Clipping Plane view or the Data Manager. The clipping plane selected in the Data Manager is displayed below the drop down box. If no clipping plane exists or none is selected create a new clipping plane by using the "Create new clipping plane" button. Some items of the graphical user interface might be disabled when no plane is selected. In any case, the application will give you hints if a selection is needed.

## Creating New Clipping Plane

If you want to create a new clipping plane select an image from the Data Manager and press the button "Create new clipping plane". Optionally you can enable the "...with surface model" option.

## Interaction with the planes



The interaction buttons

You have different options to interact with the clipping planes:

### Translation

In Translation mode you can change the position of the clipping plane.

Click the Translation Button

Move mouse over the selected clipping plane (the plane changes its color from blue to green)

Hold mouse-left button and move the mouse orthogonally to the plane

### Rotation

In Rotation mode you can change the angle of the clipping plane.

Click the Rotation Button

Move mouse over the selected clipping plane (the plane changes its color from blue to green)

Hold mouse-left button and move the mouse in the direction it should be rotated

### Deformation

In Deformation mode you can change the surface of the clipping plane.

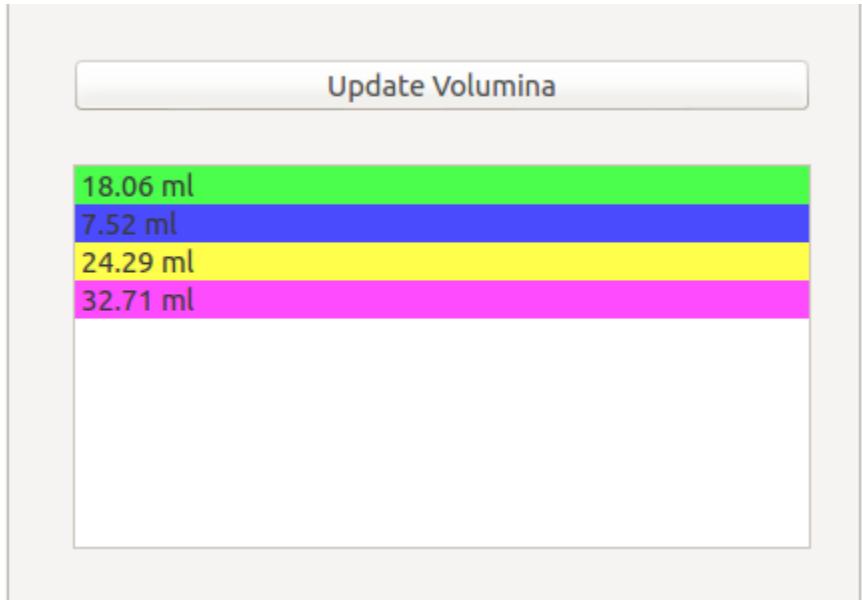
Click the Deformation Button

Move mouse over the selected clipping plane (the plane changes its color from blue to green). The deformation area is highlighted in red and yellow.

On mouse-scrolling you can change the size of the deformation area (Scroll-Down = smaller / Scroll-Up = bigger).

Hold mouse-left button and move the mouse orthogonally to the plane to deformate the plane

## Update Volumina



The 'Update Volumina' button

Calculating the volumina of the segmentation parts, which are divided by the clipping plane(s).

Create a segmentation (see Segmentation-Manual)

Create one or more clipping plane(s)

Use the interaction buttons (Translation, Rotation, Deformation) to adjust the clipping plane for intersecting the segmentation

(You can decide which planes shouldn't be included for the calculation by changing their visibility to invisible)

Click button "Update Volumina" button

The intersected parts are displayed in different colors and their volumina are shown beneath the "Update Volumina" button

# Medical Imaging Interaction Toolkit: The Data Manager View

## Introduction

The Datamanager is the central component to manage medical data like images, segmentation masks, registrations, surfaces, point sets, annotations, measurements, etc..

After loading data into the Datamanager the data is shown in the four-view window, the so-called *Standard Display*. The user can now start working on the data by interacting with the data inside the *Standard Display*, by using the MITK-plugins such as *Segmentation* or *Basic Image Processing* or by using the context menu inside the data manager.

## Loading Data

There are several ways of loading data into the Datamanager as so-called *data nodes*:

drag and drop data (e.g. from a file explorer or desktop) into the Datamanager

drag and drop data (e.g. from a file explorer or desktop) into one of the four windows of the *Standard Display*

use the keyboard shortcut *Ctrl + o*

use the *Open File* Button in the left upper corner and use the *Open Dialog*

use *File -> Open File...* from the top menu

A lot of file-formats can be loaded into MITK, for example:

2D-images / 3D-volumes with or without several time steps (\*.dcm, \*.ima, \*.nrrd, ...)

Surfaces (\*.stl, \*.vtk, ...)

Point sets (\*.mps)

and many more

The user can also load a series of 2D images (e.g. image001.png, image002.png ...) to a MITK 3D volume. To do this, just drag and drop one of those 2D data files into the Datamanager by holding the ALT key. *Note: What really happens is that the data nodes are stored inside a "Data storage" and the Datamanager is just a visual representation of the data inside the "Data storage". That's why the documentation sometimes uses the term "Data storage" instead of "Datamanager".*

## Saving Data

There are several ways of saving data from the Datamanager:

use the keyboard shortcut *Ctrl + s* on a single data node

use the keyboard shortcut *Ctrl + s* on multiple data nodes

use the context menu *right-click -> Save* on a single data node

use the context menu *right-click -> Save* on multiple data nodes

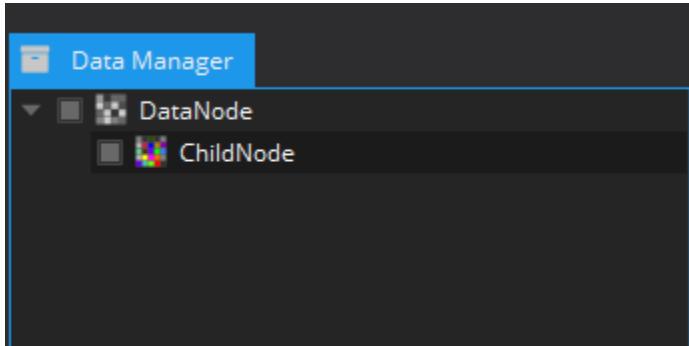
use *File -> Save...* from the top menu on a single data node

use *File -> Save...* from the top menu on multiple data nodes

## Working with the Datamanager

After loading data into the Datamanager the data appears as data nodes in a sorted list inside the Datamanager. The user can change the order of the data nodes manually by dragging one or multiple data nodes and dropping them at any position inside the Datamanager. Data nodes can also be sorted hierarchically as a parent-child-relation. For example after using the *Segmentation-Plugin* to create a segmentation on *DataNode*, the result is created as *ChildNode*, which is a child of *DataNode* (see [Parent-Child-Relation](#) screenshot).

A parent-child-relation can be changed by dragging a child of a data node and dropping it onto another data node. For this the Property *Allow changing of parent nodes* needs to be enabled (see [Preferences](#)).



Parent-Child-Relation

## Visibility of data nodes

By default all loaded data nodes are visible in the *Standard Display*. The visibility is indicated by the checkbox in front of the data node name in the Datamanager. If a data node is visible, the checkbox is filled - an empty checkbox indicates a hidden data node (see [Parent-Child-Relation](#) screenshot). Hint: *The data nodes are rendered on top of each other, such that the topmost visible data node is always*

*displayed on top of other data nodes. By hiding the topmost visible data node the next data node becomes the topmost visible data node and the hidden data node is not rendered anymore. Note: "Visible" does not mean that the node is correctly displayed inside the render windows. The user might have to re-initialize a data node to have it correctly displayed.*

## Selection of data nodes

Some MITK-plugins contain widgets to control the data nodes that are used for plugin-specific data processing. These widgets can be configured such that they listen to the current selection of the Datamanager. Having such a plugin active each selection change of data nodes inside the data manager will change the respective selection of the plugin. The data node selection widgets can have specific node predicates, which means that only specific data nodes can be controlled by the widgets. It might happen that a selected data node will not be represented in such a selection widget or that the selection widget will be emptied.

## Renaming data nodes

There are two ways of changing the name of a data node inside the Datamanager:

use the *F2* key on a single data node

double-click on a single data node

In both cases the new name can be accepted by hitting *Enter* or by clicking somewhere else.

## Context Menu

The Datamanager provides a context menu for each data node that can be opened by right-clicking on a data node. An example of the context-menu can be seen in the [Context menu](#) screenshot. The context menu allows to quickly perform common actions on data nodes. These actions differ according to the data type. Some of these actions are described here. For more actions see the respective modules and plugins (e.g. `QmitkCreatePolygonModelAction` inside the `org_mitk_gui_qt_segmentation`-plugin).

*Global Reinit:* Re-initializes the render windows to the common bounding box of all data nodes of the data storage that

have not set "includeInBoundingBox" to false

are "visible".

In this case it does not matter on which node this action is performed.

*Reinit:* Re-initializes the render windows to the common bounding box of all selected data nodes of

the data storage that  
have not set "includeInBoundingBox" to false  
are "visible".

*Save:* see [Saving Data](#) section

*Remove:* Removes all selected data nodes from the data storage.

*Show only selected nodes:* Enables the visibility of all selected data nodes and hides all other data nodes.

*Toggle visibility:* Shows / hides each selected data node according to each node's current visibility state.

*Show details:* Opens a pop-up window with detailed information about each node, like data type, geometry, DICOM information, file path etc.

*Opacity:* Sets the opacity via a slider for the rendering of the selected data node.

*Color:* Opens a pop-up window that allows to pick an arbitrary color for the rendering of all selected data nodes.

*Colormap:* Opens another submenu with a list of different colormaps that can be chosen for the rendering of all selected data nodes.

*Component:* Sets the currently visible data component for the rendering of this particular component of the selected data node.

*Texture Interpolation:* Smooths the data visualization for rendering of a selected data node.

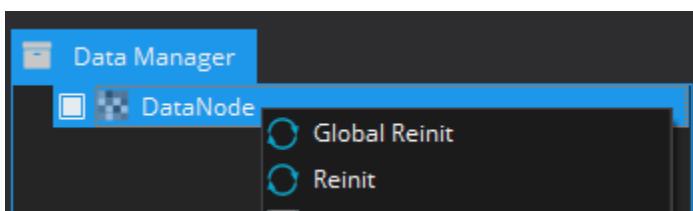
*Surface Representation:* Opens another submenu with the following entries:

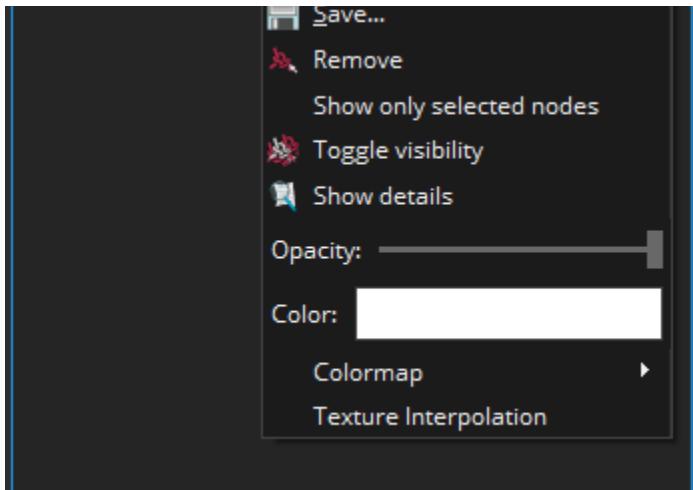
*Points:* Visually represents a surface (a data type) as a set of points.

*Wireframe:* Visually represents a surface (a data type) as a wireframe model.

*Surface:* Visually represents a surface (a data type) as a solid surface.

As the description of the actions showed, it is possible to open / use the context menu with a single data node or with a set of selected data nodes. If the data types of multiple selected data nodes differ, the actions might not appear / work as expected. Also some actions are not available for a set of selected data nodes.





Context menu

## Preferences

The MITK Workbench provides a *preference page* for specific plugins. The preference page provided for the Datamanager can be seen in the [Preference page](#) screenshot. The user can open the preference page by

using the keyboard shortcut *Ctrl + p*

using *Window -> Preferences...* from the top menu.

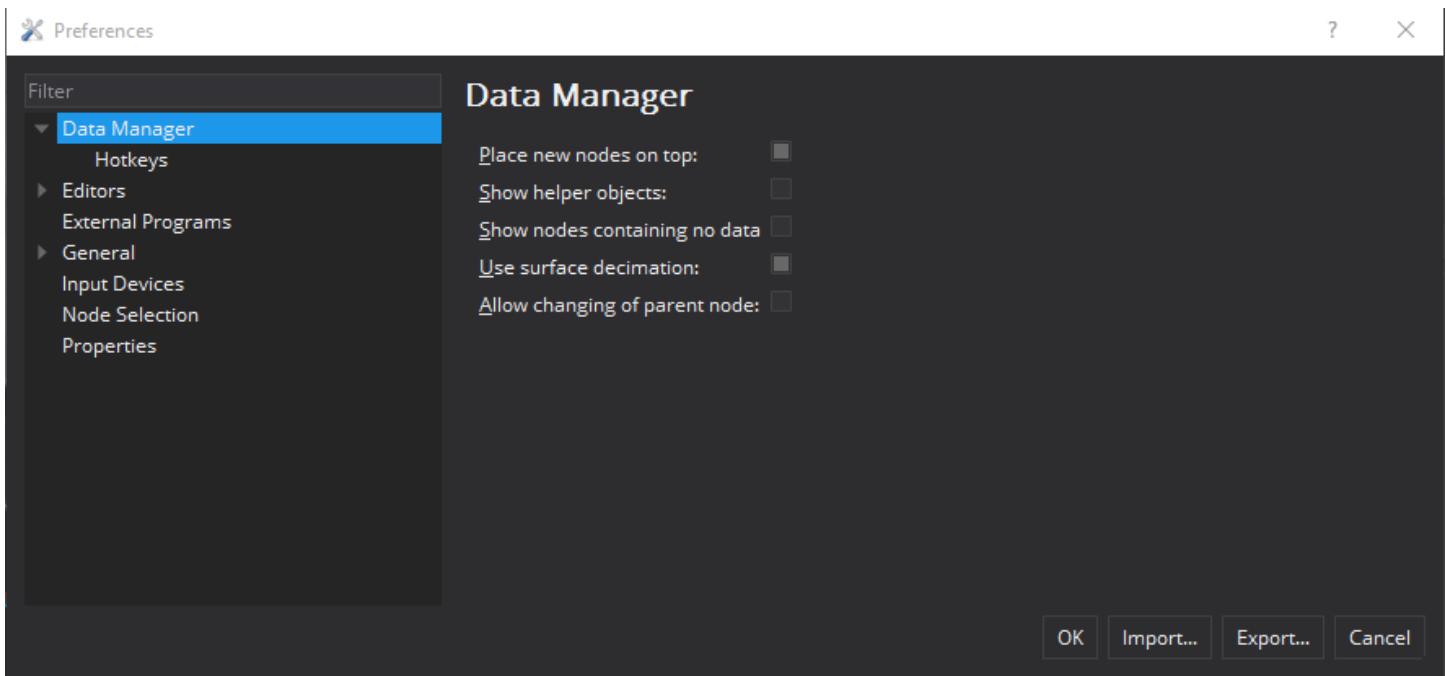
It allows to set the following preferences for the Datamanager, which define the behavior of the Datamanager:

*Place new nodes on top:* If enabled, newly added data nodes will be inserted at the top of the list of data nodes inside the Datamanager. If disabled, newly added nodes will be inserted at the bottom of the list.

*Show helper objects:* If enabled, data nodes that have set "helper object" to true will be displayed in the Datamanager. If disabled, data nodes that have set "helper object" to true will not be visible in the Datamanager.

*Show nodes containing no data:* If enabled, data nodes that have no underlying base data defined will be displayed in the Datamanager. If disabled, data nodes that have no underlying base data defined will not be visible in the Datamanager. If disabled, the surface will have its original number of triangles in the triangle mesh.

*Allow changing of parent node:* If enabled, the user can change the hierarchy of the data nodes manually by dragging one or multiple data nodes and dropping them at any position inside the Datamanager (see [Working with the Datamanager](#)) for changing the order of the data nodes manually).



Preference page

## Hotkeys

The MITK Workbench provides hotkeys for specific plugins. The hotkeys provided for the Datamanager can be seen in the [Hotkeys](#) screenshot. They allow to expedite common operations in relation to data nodes or the Datamanager. The user can customize the hotkeys by accessing the *preference page*:

using the keyboard shortcut *Ctrl + p*

using *Window -> Preferences...* from the top menu

*Delete selected nodes* Removes all selected data nodes from the data storage.

*Global reinit* Re-initializes the render windows to the common bounding box of all data nodes of the data storage that

have not set "includeInBoundingBox" to false

are "visible"

In this case it does not matter on which node this action is performed.

*Make all nodes invisible* Hides all data nodes of the data storage.

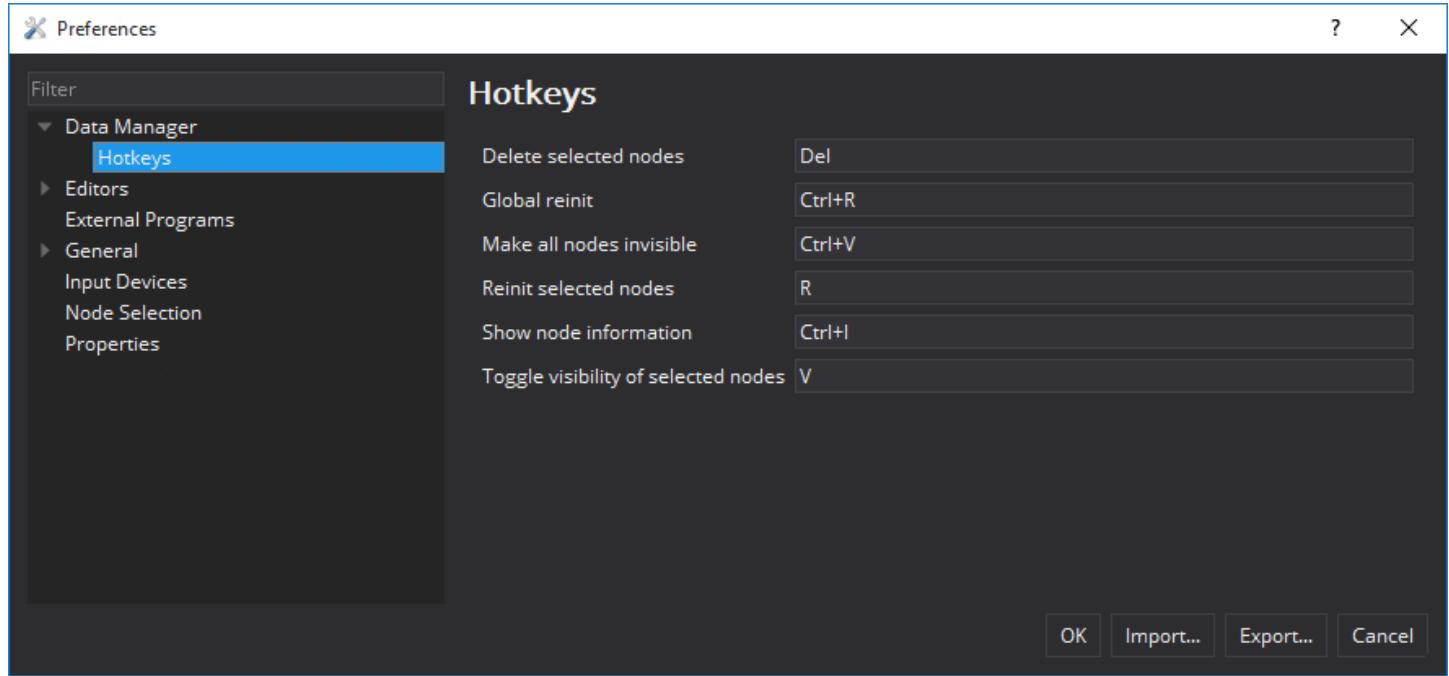
*Reinit selected nodes* Re-initializes the render windows to the common bounding box of all selected data nodes of the data storage that

have not set "includeInBoundingBox" to false

are "visible"

*Show node information* Opens a pop-up window with detailed information about each node, like data type, geometry, DICOM information, file path etc.

*Toggle visibility of selected nodes:* Shows / hides each selected data node according to each node's current visibility state.



Hotkeys

# The DCE Concentration Curve Converter View

Icon of the DCE Concentration Curve Converter View

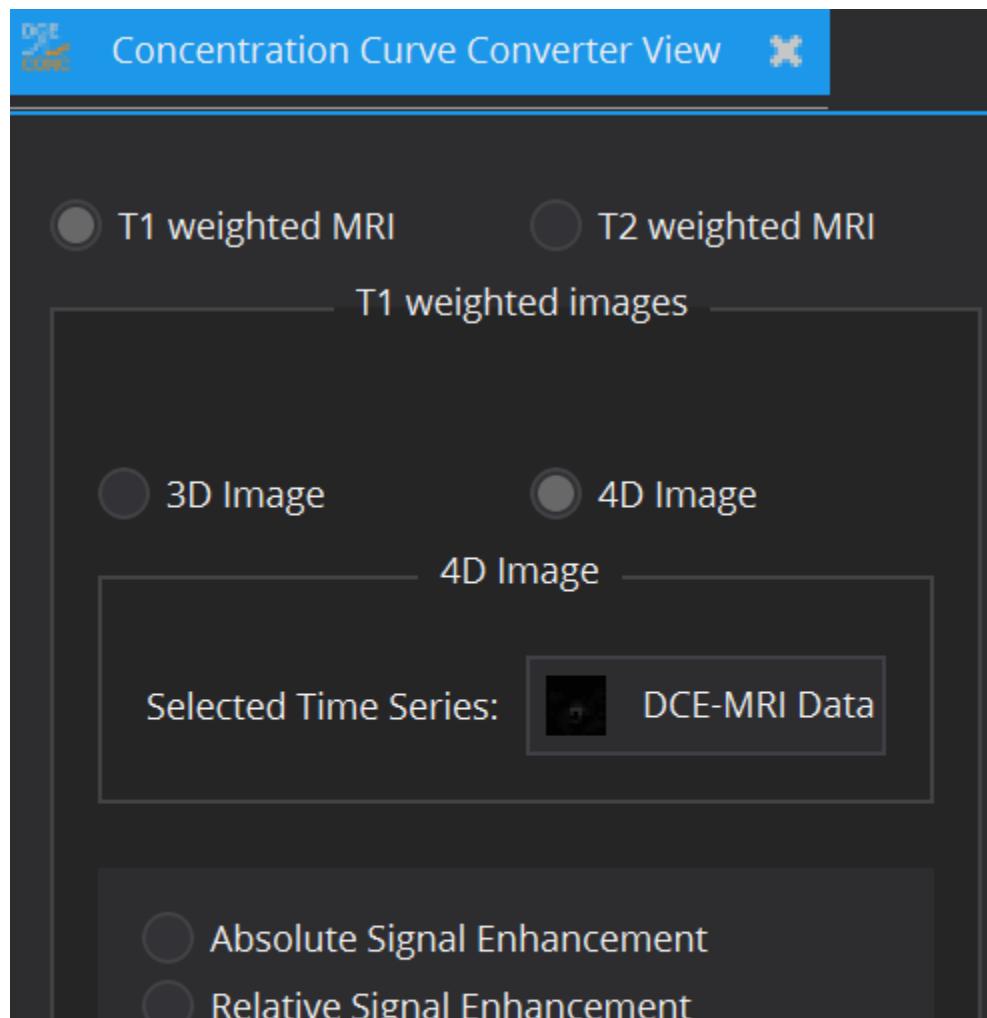
## Overview

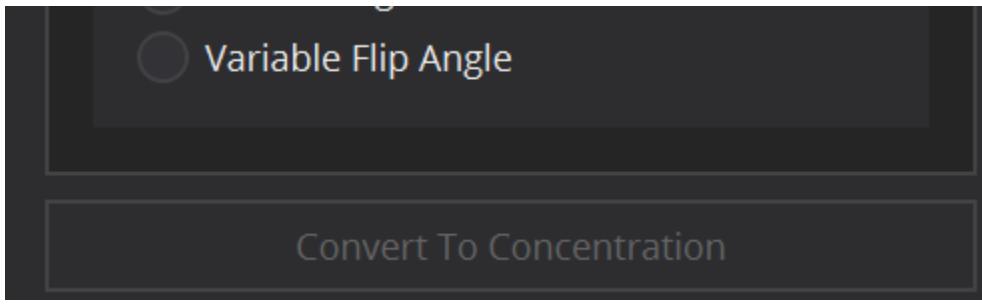
This view offers a dedicated tool for the conversion of DCE MR image signal intensities to contrast agent (CA) concentration. It contains a subset of the conversion tools for T1-weighted signal intensities, which are also a part of the DCE MR Perfusion Datafit View. Additionally, it allows for the conversion between T2-weighted MR signal intensities and contrast agent concentration.

## Contact information

If you have any questions, need support, find a bug or have a feature request, feel free to contact us at [www.mitk.org](http://www.mitk.org).

## Conversion of T1-weighted MRI data





Example screenshot of the conversion of T1-weighted MR images

The view offers the choice between a *3D Image* and a *4D image*. If a 4D image is selected, the *Selected Time Series* needs to be specified. For 4D images, for all conversion methods which require a baseline value, the range of the time points which are part of the baseline can be specified. The baseline signal  $S_{BL}$  will be averaged between the signal of the time points within this range. If not specified, the baseline signal  $S_{BL}$  is set as the signal of the first time point image of the time series. In case of a 3D image to be converted, additionally to the selected 3D image a *Baseline Image (without CA)* has to be specified.

The following types of conversion can be chosen:

*Absolute Signal Enhancement*: The dynamic contrast agent concentration  $C(t)$  is calculated according to the formula:  $C(t) = k*(S(t)-S_{BL})$ , where  $S(t)$  is the dynamic T1-weighted signal intensity,  $S_{BL}$  the baseline signal and  $k$  a user-defined conversion factor.

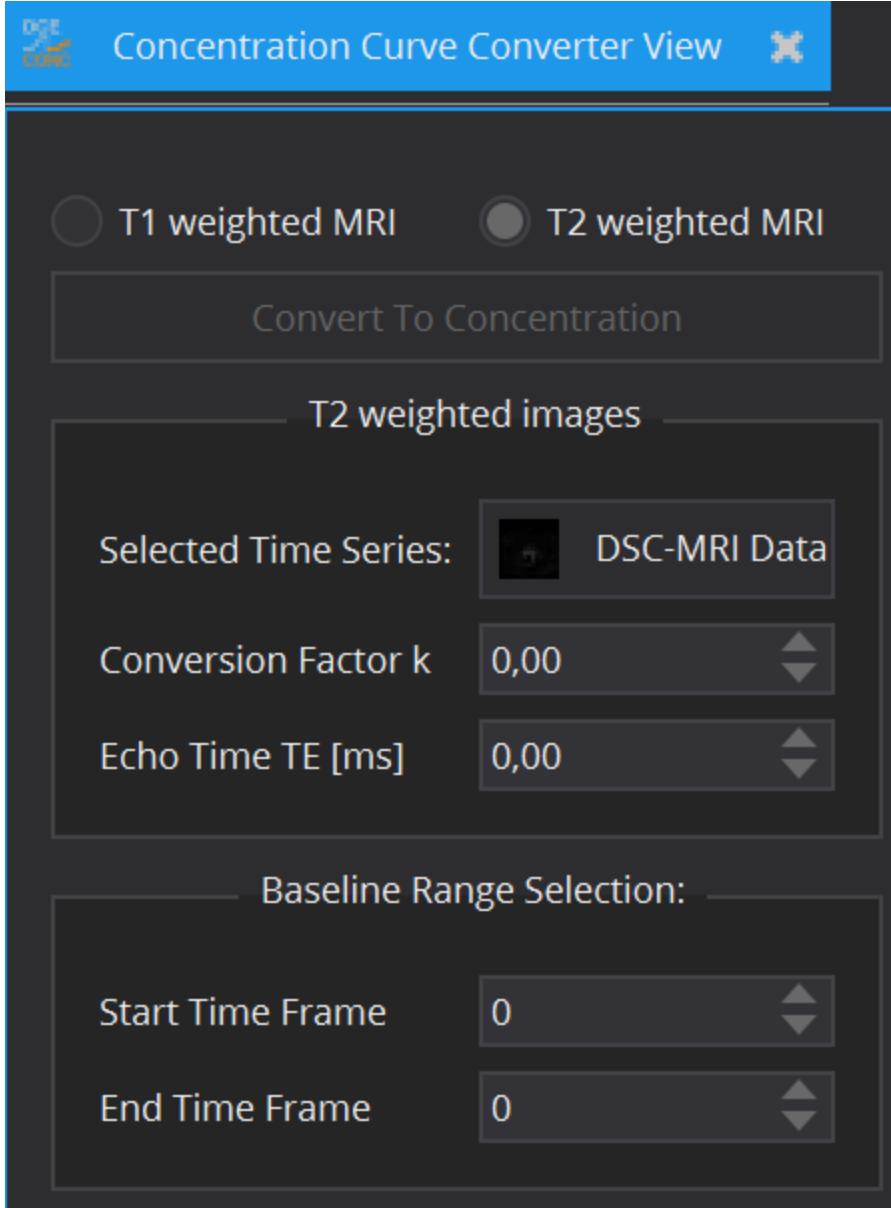
*Relative Signal Enhancement*: The dynamic contrast agent concentration  $C(t)$  is calculated according to the formula:  $C(t) = k*(S(t)-S_{BL})/S_{BL}$ , where  $S(t)$  is the dynamic T1-weighted signal intensity,  $S_{BL}$  the baseline signal and  $k$  a user-defined conversion factor.

*Variable Flip Angle*: This conversion uses the method described in [1]. As additional input to the dynamic time series, a proton density weighted (PDW) image is provided, which has been acquired pre-contrast with the same sequence parameters as for the dynamic image but a smaller flip angle. Both flip angles are provided by the user. Furthermore, the repetition time  $TR$  and the longitudinal relaxivity  $r_1$  are required as input.

It is assumed that the MR data has been acquired according to the spoiled gradient recalled echo model. The sequence formulas for the PDW image signal and for the baseline signal of the dynamic time series are two equations with two unknowns: the pre-contrast  $R_1$ -relaxation rate  $R_{10}$  and the signal scaling factor  $S_O$ . These are calculated by solving the system of equations.

With the knowledge of  $S_O$ , the dynamic contrast-enhanced relaxation rate  $R_1(t)$  is computed. Finally, the concentration is calculated by inverting the linear model:  $R_1(t)=R_{10}+r_1*C(t)$ .

## Conversion of T2-weighted MRI data



Example screenshot of the conversion of T2-weighted MR images

The dynamic contrast agent concentration  $C(t)$  is calculated according to the formula:  $C(t) = -k/TE * \ln(S(t)/S_{BL})$ , where  $S(t)$  is the dynamic T2-weighted signal intensity,  $S_{BL}$  the baseline signal,  $k$  a user-defined conversion factor and  $TE$  the echo time of the employed sequence. In practice, the factor  $k$  is often set to unity.

## References/Literature

- [1] Wang, H. Z., Riederer, S. J., and Lee, J. N. (1987). Optimization the precision in T1 relaxation estimation using limited flip angles. Magn Reson Med, 5:399–416.

# The DCE MR Perfusion DataFit View

Icon of the DCE MR Perfusion View

## Introduction

In dynamic contrast-enhanced (DCE) MRI, pharmacokinetic (PK) modeling can be used to quantify tissue physiology. Parameters describing the tissue microvasculature can be derived by fitting a pharmacokinetic model, e.g. a compartment model, to the dynamic data. This view offers a comprehensive set of tools to perform pharmacokinetic analysis.

## Contact information

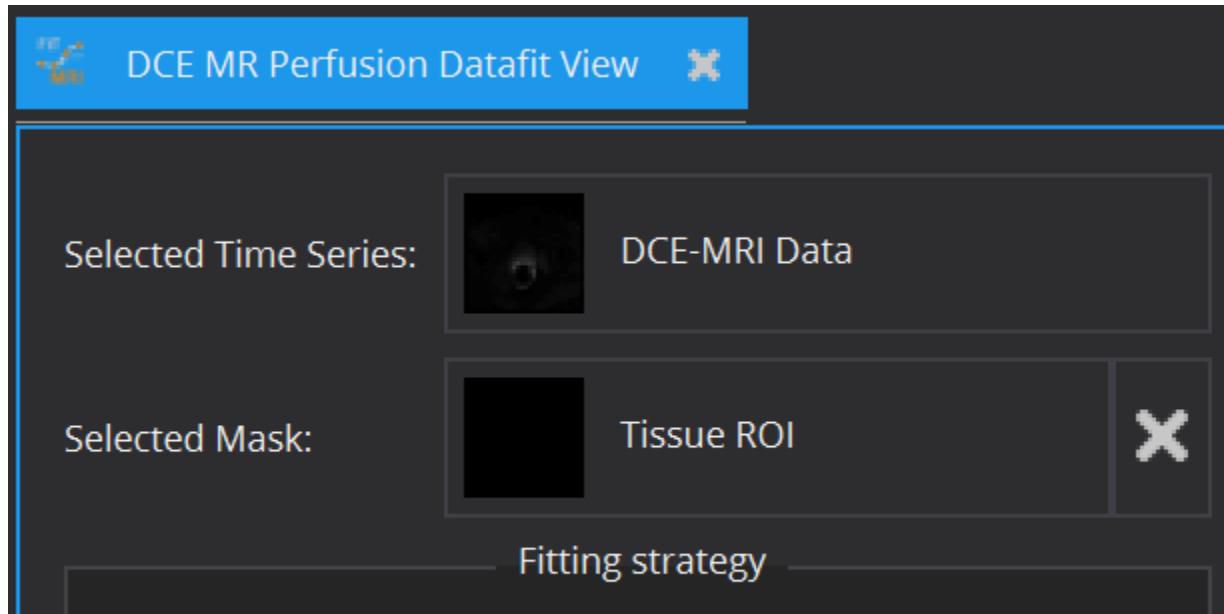
If you have any questions, need support, find a bug or have a feature request, feel free to contact us at [www.mitk.org](http://www.mitk.org).

## Citation information

If you use the view for your research please cite our work as reference:

Debus C and Floca R, Ingrisch M, Kompan I, Maier-Hein K, Abdollahi A, Nolden M, *MITK-ModelFit: generic open-source framework for model fits and their exploration in medical imaging – design, implementation and application on the example of DCE-MRI*. <https://doi.org/10.1186/s12859-018-2588-1> (BMC Bioinformatics 2019 20:31)

## Time series and mask selection





Time series and mask selection.

In principle, every model can be fitted on the entire image. However, for model configuration reasons (e.g. AIF required) and computational time cost, this is often not advisable. Therefore, apart from the image to be fitted (*Selected Time Series*), a ROI segmentation can be defined (*Selected Mask*), within which model fitting is performed. The view currently offers *Pixel based* and/or *ROI based* averaged fits of time-varying curves. The *ROI based* fitting option becomes enabled, if a mask is selected.

## Supported models

Currently the following pharmacokinetic models for gadolinium-based contrast agent are available:

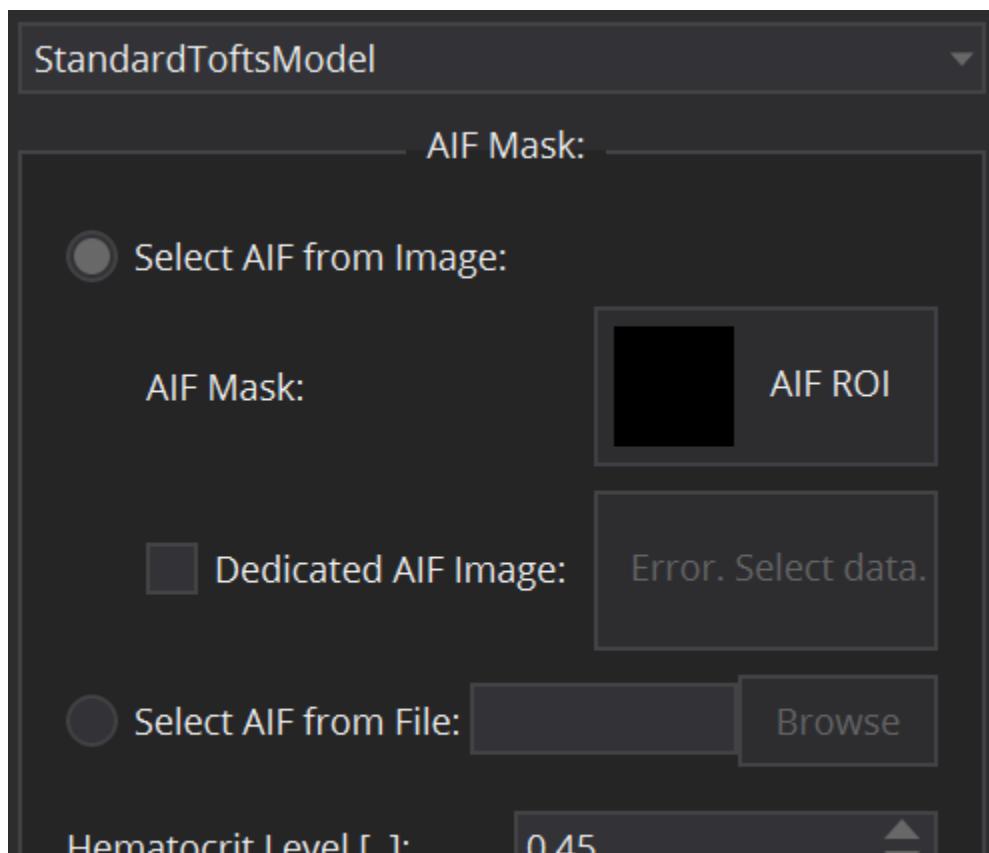
The descriptive Brix model [\[1\]](#)

The standard Tofts model [\[2\]](#)

The extended Tofts model [\[3\]](#)

The two compartment exchange model (2CXM) [\[4..5\]](#)

## Model settings





Model settings of the view for the standard Tofts model.

## Model specific settings

Selecting one of the [supported models](#) will open below tabs for further configuration of the model.

The descriptive Brix model requires only definition of the duration of the bolus, i.e. the overall time of the injection (*Injection Time [min]*).

The standard Tofts model, the extended Tofts model and the 2CXM are compartment models that require the input of the concentration time curve in the tissue feeding artery, the arterial input function (AIF). In the DCE MR Perfusion Datafit View, the arterial input function can be defined in several ways. For patient individual image derived AIFs, select the radio button *Select AIF from Image*. In that case, a segmentation ROI for the artery has to be selected. This can be done by clicking on the *AIF Mask* selection widget and selecting a suitable AIF segmentation from the data loaded in the Data Manager. In cases where the respective artery does not lie in the same image as the investigated tissue (e.g. in animal experiments, where a slice through the heart is used for AIF extraction), a dedicated AIF image can be selected using the corresponding *Dedicated AIF image* selection widget. An alternative option is to define the AIF via an external file by selecting *Select AIF from File* (e.g. for population derived AIFs or AIFs from blood sampling). By clicking the *Browse* button, one can select a csv file that holds the AIF values and corresponding timepoints (in tuple format (Time, Value)). Caution: the file must not contain a header line, but the first line must start with Time and Intensity values. Furthermore, the *Hematocrit Level* has to be set (from 0 to 1) for conversion from whole blood to plasma concentration. It is set as default to the literature value of 0.45.

## Start parameter

Start parameter		
Enter Fit Starting Parameters		
Parameters	Type	Value
K <sup>trans</sup>	scalar	15
v_e	scalar	0,5

Example screenshot for start parameter settings.

In cases of noisy data it can be useful to define the initial starting values of the parameter estimates, at which optimization starts, in order to prevent optimization results in local optima. Each model has default scalar values (applied to every voxel) for initial values of each parameter, however these can be adjusted. Moreover, initial values can also be defined locally for each individual voxel via starting value images. To load a starting value image, change the *Type* from *scalar* to *image*. This can be done by double-clicking on the type cell. In the *Value* column, selection of a starting value image will be available.

## Constraints settings

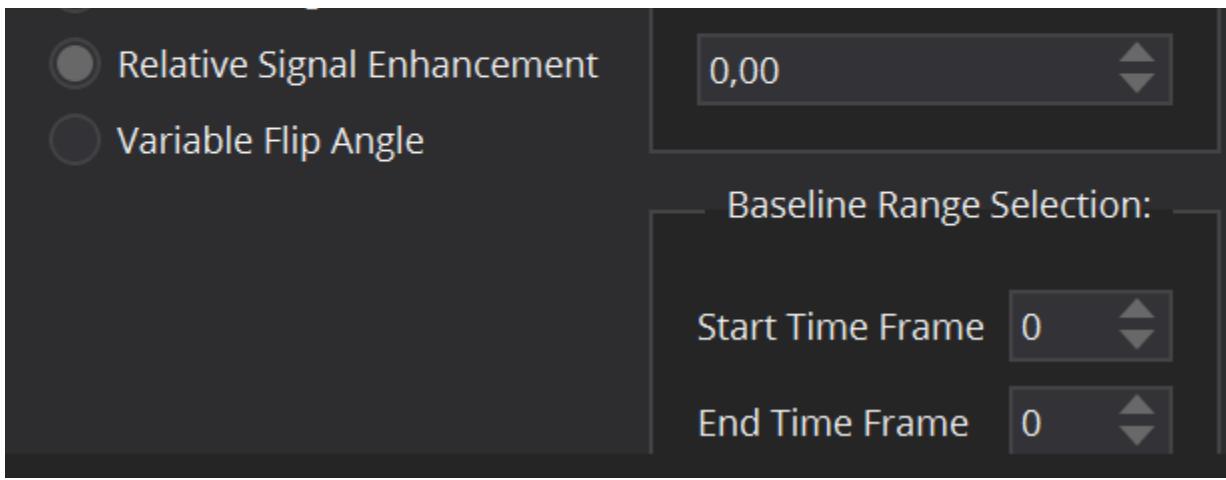
Constraints			
<input type="checkbox"/> Enter Constraints for Fit Parameters			
Parameters	Type	Value	Width
v_e	lower	0	0.0001
v_e	upper	1	0.0001

Example screenshot for constraints settings.

To limit the fitting search space and to exclude unphysical/illogical results for model parameter estimates, constraints to individual parameters as well as combinations can be imposed. Each model has default constraints, however, new ones can be defined or removed by the + and – buttons in the table. The first column specifies the parameter(s) involved in the constraint (if multiple parameters are selected, their sum will be used) by selection in the drop down menu. The second column *Type* defines whether the constraint defines an upper or lower boundary. *Value* defines the actual constraint value, that should not be crossed, and *Width* allows for a certain tolerance width.

## Signal to concentration conversion settings

Conversion: Signal to Concentration	
<input checked="" type="radio"/> No Signal Conversion	
<input type="radio"/> Absolute Signal Enhancement	Conversion Factor k:



Example screenshot for concentration conversion settings.

Most models require contrast agent concentration values as input rather than raw signal intensities (i.e. all compartment models). The DCE MR Perfusion DataFit View offers a variety of tools for the conversion from signal to concentration: by means of relative and absolute signal enhancement and via a T1-map calculated by the variable flip angle method. A more detailed description of these conversion methods can be found here: [The DCE Concentration Curve Converter View](#). For the conversion methods, a baseline image prior to contrast agent arrival is required. In many dynamic data sets, multiple images are part of the baseline. The *Baseline Range Selection* allows for selection of a range of time frames, from which the average image (along the time dimension) is calculated and set as baseline input image. Remark: The number of the first time frame is 0.

## Executing a fit

In order to distinguish results from different model fits to the data, a *Fitting name* can be defined. As default, the name of the model and the fitting strategy (pixel/ROI) are given. This name will then be appended by the respective parameter name.

For development purposes and evaluation of the fits, the option *Generate debug parameter images* is available. Enabling this option will result in additional parameter maps displaying the status of the optimizer at fit termination. In the following definitions, an *evaluation* describes the process of cost function calculation and evaluation by the optimizer for a given parameter set.

*Stop condition:* Reasons for the fit termination, i.e. criterion reached, maximum number of iterations,...

*Optimization time:* The overall time from fitting start to termination.

*Number of iterations:* The number of iterations from fitting start to termination.

*Constraint penalty ratio:* Ratio between evaluations that were penalized and all evaluations. 0.0

means no evaluation was penalized; 1.0 all evaluations were. Evaluations that hit the failure threshold count as penalized, too.

*Constraint last failed parameter:* Ratio between evaluations that were beyond the failure threshold. 0.0 means no evaluation was a failure (but some may be penalized).

*Constraint failure ratio:* Index of the first (in terms of index position) parameter, which failed the constraints in the last evaluation.

After all necessary configurations are set, the button *Start Modelling* is enabled, which starts the fitting routine. Progress can be seen in the message box on the bottom. Resulting parameter maps will afterwards be added to the Data Manager as sub-nodes of the analyzed 4D image.

## References/Literature

- [1] Brix G, Semmler W, Port R, Schad LR, Layer G, Lorenz WJ. Pharmacokinetic parameters in CNS Gd-DTPA enhanced MR imaging. *J Comput Assist Tomogr.* 1991;15:621–8.
- [2] Tofts PS, Kermode AG. Measurement of the blood-brain barrier permeability and leakage space using dynamic MR imaging. 1. Fundamental concepts. *Magn Reson Med.* 1991;17:357–67.
- [3] Sourbron SP, Buckley DL. On the scope and interpretation of the Tofts models for DCE-MRI. *Magn Reson Med.* 2011;66:735–45.
- [4] Brix G, Kiessling F, Lucht R, Darai S, Wasser K, Delorme S, et al. Microcirculation and microvasculature in breast tumors: Pharmacokinetic analysis of dynamic MR image series. *Magn Reson Med.* 2004;52:420–9.
- [5] Sourbron, Buckley. Tracer kinetic modelling in MRI: estimating perfusion and capillary permeability - pdf. *Phys Med Biol.* 2012. <https://iopscience.iop.org/article/10.1088/0031-9155/57/2/R1/pdf>. Accessed 1 May 2016.

# Medical Imaging Interaction Toolkit: The Dicom Browser Plugin

## Note

This article requires a basic knowledge of the DICOM Standard.

## Overview

The DICOM editor is an experimental editor which allows for loading of DICOM images as well as server communication. It features a highly experimental query/retrieve (you need to configure your PACS correspondingly) as well as a DICOM browser. The DICOM browser allows you to navigate the DICOM folder/cd depending on its metadata (patient/study/series) and import selected series for viewing in your MITK based application. It also allows you to store your dicom data in an internal database so you can easily access often used dicom images.

It is based on the [commonTK \(CTK\) DICOM functionality](#).

## Data handling

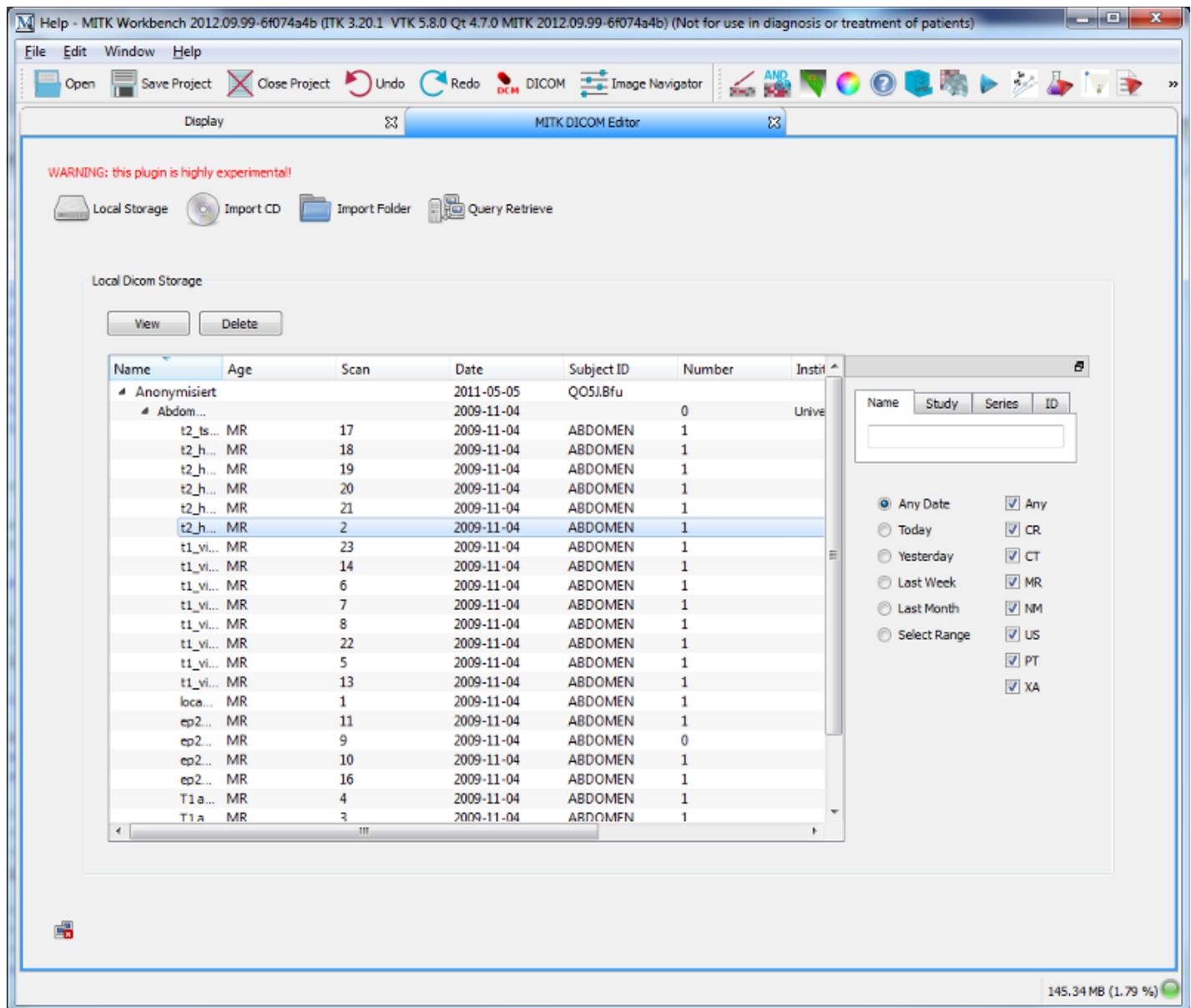


The dicom Plugin controls

In the image above you see the start page of the dicom plugin. On top of the start page you see four buttons. The Local Storage, the Import CD, the Import Folder and the Query Retrieve button. If you press one of these buttons, the dicom plugin will switch to your local dicom image storage or will start importing dicom images from CD or a folder on your hard drive or it will open the query retrieve screen.

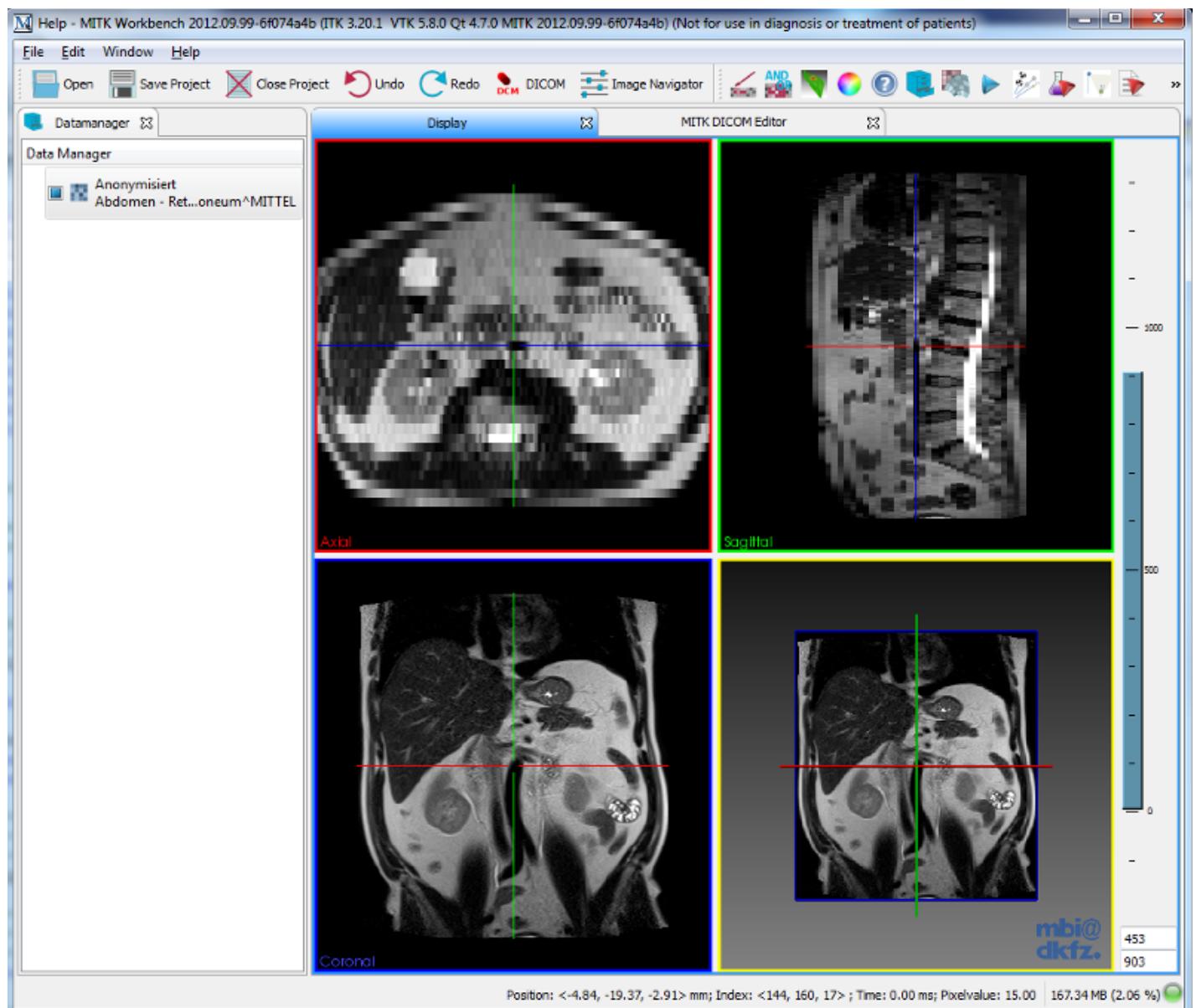
- Click the 'Local Storage' button to open the local storage screen.
- Click the 'Import CD' button to import DICOM data from a CD.
- Click the 'Import Folder' button to import DICOM date from a directory.
- Click the 'Query Retrieve' button to open the query retrieve screen.

## Data storage



## The DICOM data storage

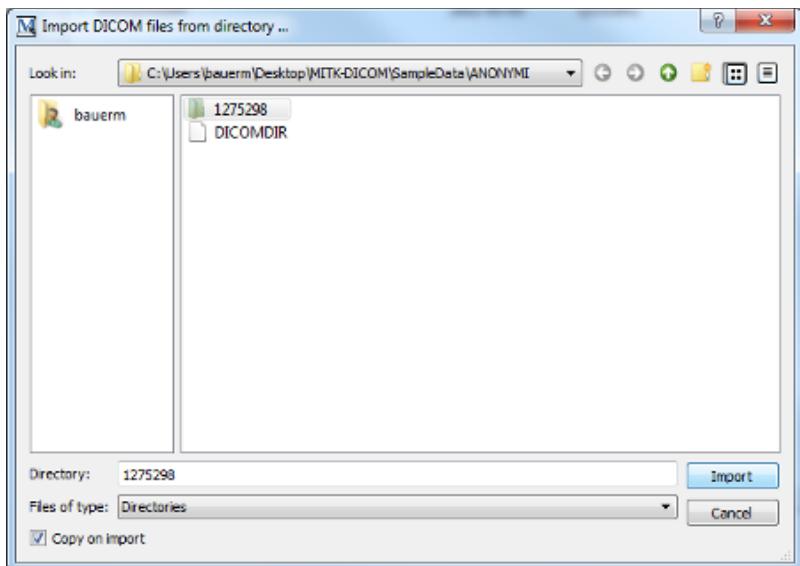
If you open the dicom plugin the dicom data storage will be displayed. You are able to see all your stored dicom image data. You can browse your data by clicking on the left arrow beside the name of your data. There are three levels available. The first level is the patient level where you can see the patient data. On the second level you can see the dicom studies for the patient. on the third level you can see all available series referring to its study. You can delete the data by selecting it and pressing the delete button. Be careful if you have selected a patient or a study all referring data be deleted. So if you delete a patient the patient and all studies and series referred to the patient will be deleted. If you delete a study all series of the study will be deleted. If you want to view the dicom data you have to select a series and click on the View button. The data will appear in the DataManager and will be displayed.



Viewed image

- Click on the arrow on the left of your data to expand or hide dicom data levels.
- Click the 'Delete' button to delete selected DICOM data.
- Click the 'View' button to view DICOM data.

## Data import



The import dialog checked

There are two different ways to import DICOM data. The First one is to directly import it into your DICOM data storage. To achieve this you should toggle the checkbox 'Copy on import'. The second approach is, to have a look at the data first before importing it. To do that you simply don't check 'Copy on import'. This will lead you to the 'External Dicom Data' screen which provides you a preview of the data containing in you're chosen folder. You can import the data here by selecting it and pressing the 'Download' button. It is also possible to view DICOM series directly in Mitk by selecting it here and pressing the 'View' button.

- Click 'Import Folder' or 'Import CD' button to open the import dialog.
  - Enable the 'Copy on import' checkbox and choose a folder to import into data storage directly.
  - Disable the 'Copy on import' checkbox to get to the 'External Dicom Data' screen.
    - Click on the arrow on the left of your data to expand or hide dicom data levels.
    - Click the 'Download' button to download selected DICOM data to your DICOM data storage.
    - Click the 'View' button to view DICOM data.

## Query/Retrieve

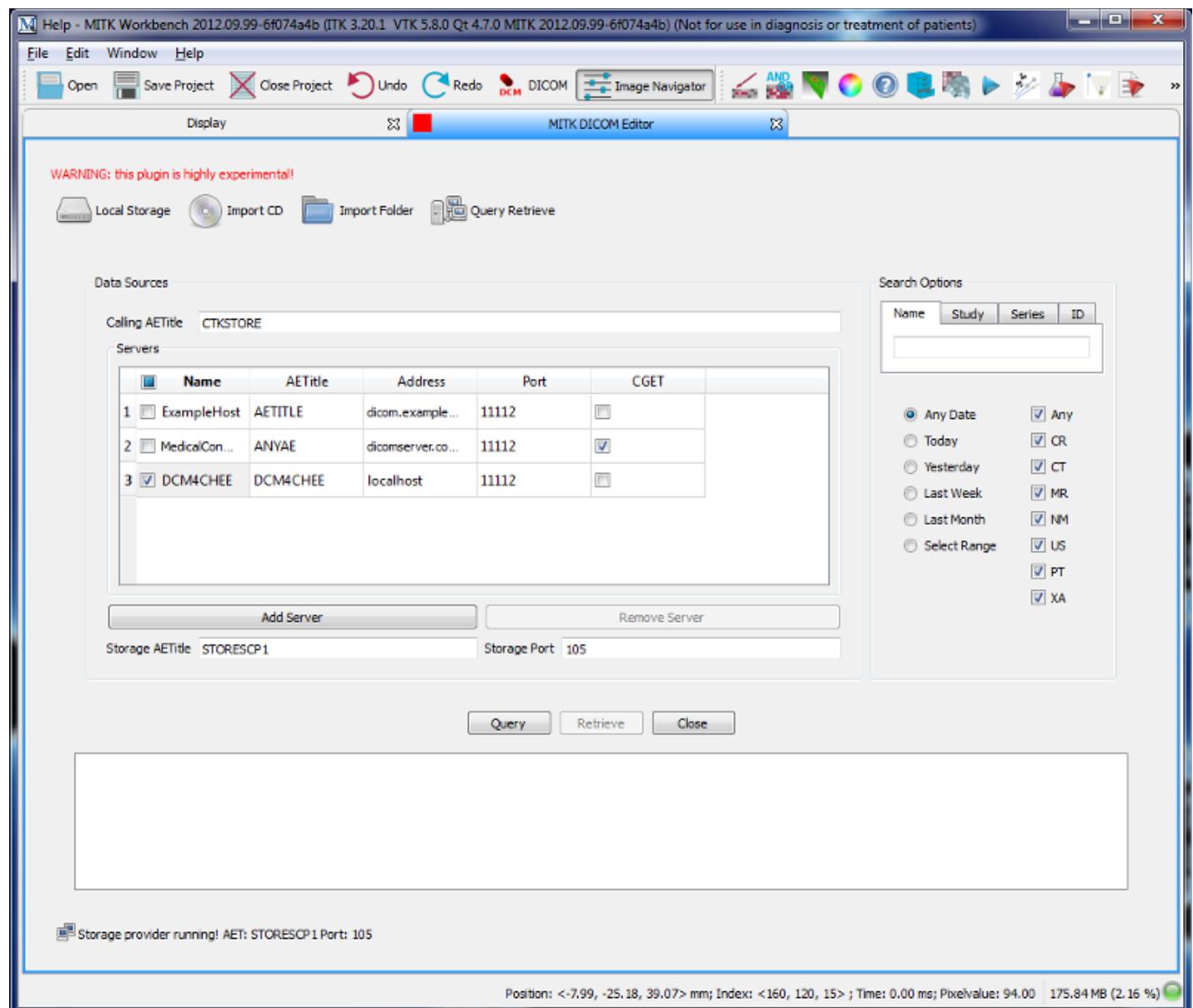
### Warning

This plugin is experimental and not all of the described features behave as expected.

### Note

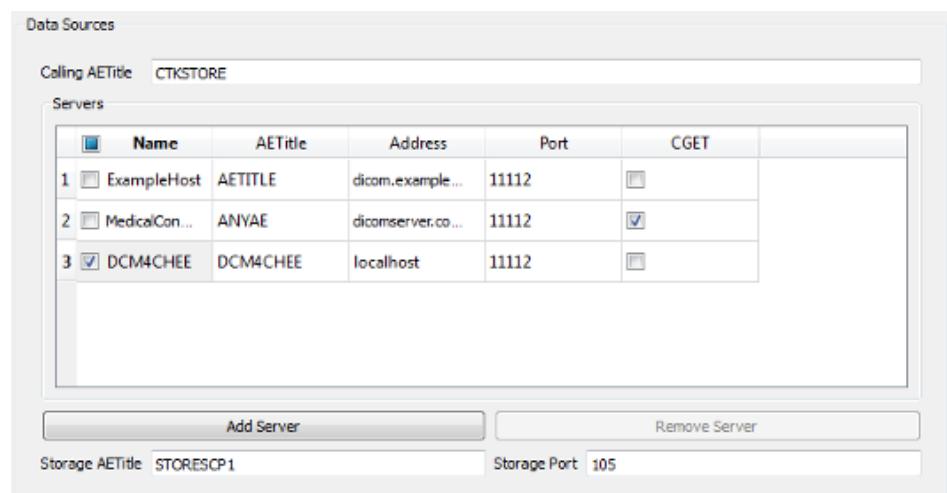
The query retrieve plugin only works if the PACS you are calling knows your machine settings. There are also issues when you are running a firewall.

The query retrieve workflow allows you to get DICOM data from a server.



The query retrieve screen

## Query



## The DICOM network configuration

By performing a DICOM query you will ask a server for it's DICOM data. This requires to setup the DICOM network configuration of your system and the server. By clicking on 'Add Server' a new plain server field will appear. Now you can give it a name of your choice. Fill the servers "DICOM name" the AETitle. Type in it's url, it's port and the specific DICOM protocol you want to use for image transfer.

### Note

I recommend not to use CGET because most of the PACS systems (Image Servers) don't support that protocol.

You can configure the DICOM network configuration of your machine by editing the 'Calling AETitle', the 'Storage AETitle' and The 'Storage Port' text fields. But normally you don't have to change your configuration.

The DICOM search options

After you have finished your network configuration and before you start the query you should use the 'Search Options' to specify your query. Otherwise all data on the server will be queried and you will have to wait for a long time. You can specify your query by searching for a specific patient name or a study or a serie or a specific DICOM object by it's id. You are allowed to include or exclude DICOM modalities from your query and you can specify a specific time in which the DICOM images you are searching for might been captured. When you finished that you can click the query button and the queried DICOM data will appear.

- Click on the 'Add Server' button.
  - Edit 'Name' field.
  - Edit 'AETitle' field.
  - Edit 'Address' field.
  - Edit 'Port' field.
- Set search options.
- Click on 'Query' button.

## Retrieve

Name	Age	Scan	Date	Subject	Number	Institution	Referrer
Anonymisiert			2011-05-05	QOSJ....			
Abdomen - Retroperitoneum^MITTEL		MR	2009-11-04	0			
t1_vibe_fs_tra_p2_bh_30° 10 min	MR	14	2009-11-04	0			
t1_vibe_fs_tra_p2_bh_20° 20 min	MR	22	2009-11-04	0			
t1_vibe_fs_tra_p2_bh_30° 20 min	MR	23	2009-11-04	0			

The queried DICOM data.

After the query you are able to select the queried data and click the 'Retrieve' button. This will store the queried DICOM data into your DICOM storage. Click on the 'Local Storage' button and work with your new data.

- Click on the 'Retrieve' button to retrieve the data to your DICOM storage.
- Click on the 'Local Storage' button.

## The DICOM Inspector

---



Icon of DICOM Inspector

This is a simple view that displays all DICOM properties of the data of the currently selected node. DICOM properties are all properties that have a property name starting with "DICOM". The plugin will show the dicom values corresponding to the currently selected time point and z slice. E.G. the value of "acquisition time" will change with changing the time step of 3d+t image or the value of "slice position" will change with changing the current z slice of the image.

# The Dynamic PET DataFit View

Icon of the DCE MR Perfusion View

## Overview

Pharmacokinetic analysis of concentration time curves is also of interest in the context of dynamic PET acquisition over the accumulation of a radioactive tracer in tissue.

## Contact information

This plug-in is being developed by Charlotte Debus and the SIDT group (Software development for Integrated Diagnostics and Therapy) at the German Cancer Research Center (DKFZ). If you have any questions, need support, find a bug or have a feature request, feel free to contact us at [www.mitk.org](http://www.mitk.org).

## Citation information

If you use the view for your research please cite our work as reference:

Debus C and Floca R, Ingrisch M, Kompan I, Maier-Hein K, Abdollahi A, Nolden M, MITK-ModelFit: generic open-source framework for model fits and their exploration in medical imaging – design, implementation and application on the example of DCE-MRI (arXiv:1807.07353)

## General information

All models require definition of the arterial tracer concentration, i.e. the AIF. For AIF definition see section 3. Instead of the hematocrit level, the whole blood to plasma correction value needs to be specified. The literature value commonly used is 0.1 Since PET images are already in concentration units of activity per volume ([Bq/ml], translates to number of nuclei per volume), no conversion of signal intensities to concentration is offered in the plugin. If, however, conversion of the 4D images to standard uptake values (SUV) is desired, this can be performed with the separate PET SUV calculation plugin. Start parameters and parameter constraints can be defined in the same manner as for the DCE tool.

## Supported models

The PET dynamic plugin works in analogy to the DCE MRI perfusion plugin. It currently supports the following compartmental models:

One tissue compartment model (without blood volume VB)

Extended one tissue compartment model (with blood volume VB)

Two tissue compartment model (with blood volume)

Two tissue compartment model for FDG (without back exchange k<sub>4</sub>)

## Model Settings

### Start parameter

In cases of noisy data it can be useful to define the initial starting values of the parameter estimates, at which optimization starts, in order to prevent optimization results in local optima. Each model has default scalar values (applied to every voxel) for initial values of each parameter, however these can be adjusted. Moreover, initial values can also be defined locally for each individual voxel via starting value images.

### Constraint settings

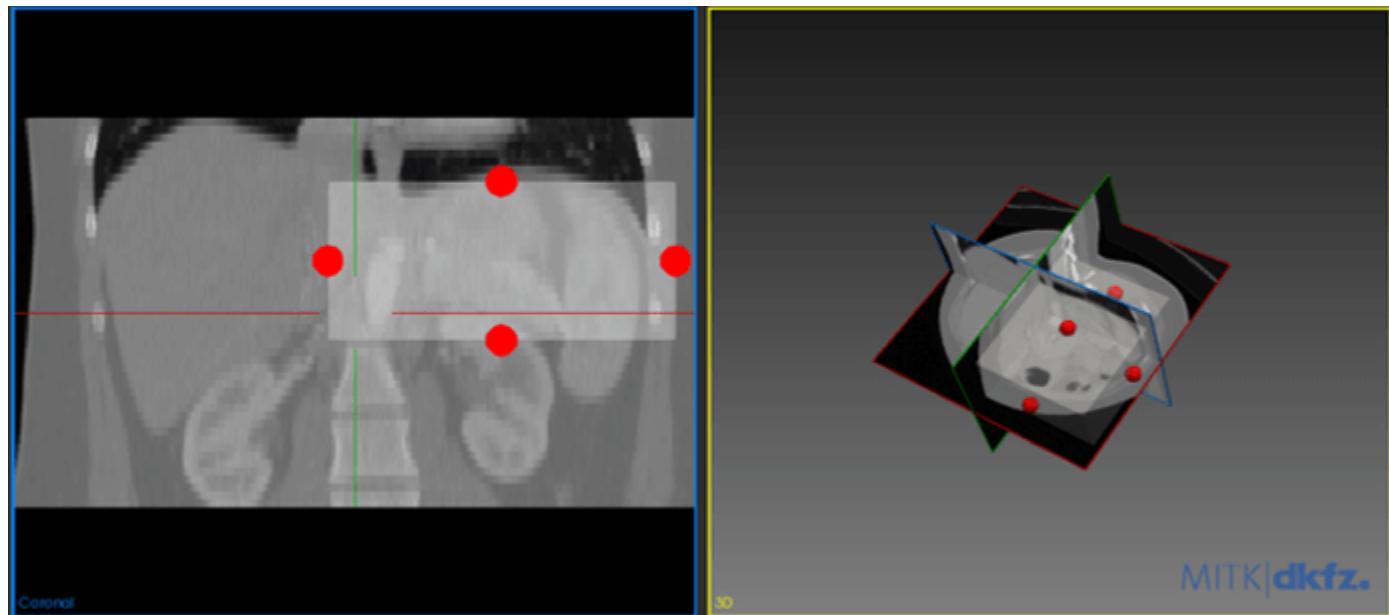
To limit the fitting search space and to exclude unphysical/illogical results for model parameter estimates, constraints to individual parameters as well as combinations can be imposed. Each model has default constraints, however, new ones can be defined or removed by the + and – buttons in the table. The first column specifies the parameter(s) involved in the constraint (if multiple selected, their sum will be used) by selection in the drop down menu. The second column defines whether the constraint defines an upper or lower boundary. Value and Width define the actual constraint value, that should not be crossed, and a certain tolerance width.

# Medical Imaging Interaction Toolkit: The Image Cropper

Icon of the Image Cropper Plugin.

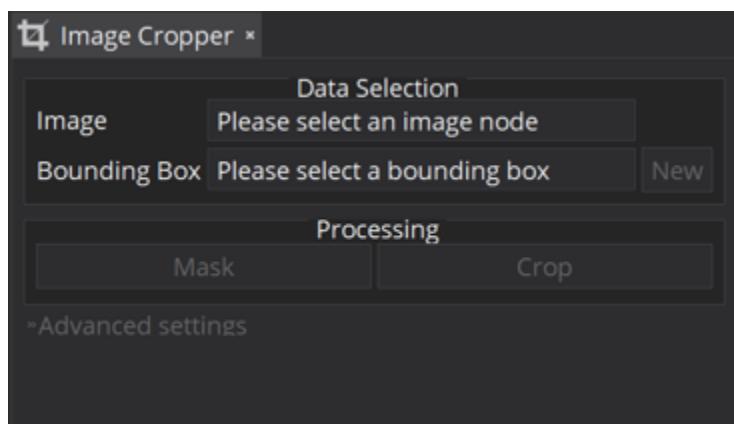
## Usage

The Image Cropper Plugin allows to crop and mask subvolumes out of the original image volume by defining a cubic bounding box.



Bounding Shape.

A new bounding box can be created by selecting an image and pressing the 'New' button. The bounding box appears as a child node in the data manager. Alternatively, an existing bounding box can be selected.



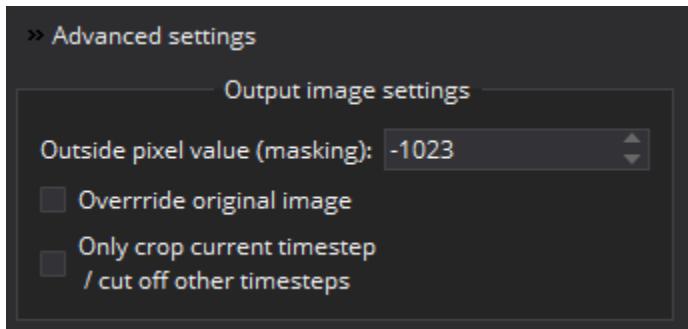
Basic Settings.

This bounding box can be placed at an arbitrary position in the volume and can be easily adjusted by using the handles on each of the faces. When activated, the handles are shown in red, otherwise, they are colored white. Hovering over either the box or a single handle allows modifying the bounding box. Moving the handles changes the respective extent of the bounding box, whereas moving the box itself changes its position.

As soon as the bounding box is placed at the desired position, pressing the button 'Crop' creates a new image assigned to the original image as a child node containing only the selected subvolume. The size of the subvolume equals the size of the bounding box. Pressing the 'Mask' button keeps the original image size but masks out the area not contained within the bounding box. In the case of 3D+t images, the whole time series is cropped by default.

## Advanced settings

In the advanced settings view you find additional features:



Advanced Settings.

## Mask with outside pixel

Assigns the value of the voxels outside of the bounding box when 'Mask' is used.

## Overwrite original image

By enabling this checkbox the image is replaced by the cropped subvolume. Be careful to use this option since there is no undo action available.

## Crop current time step only

If you have an xD + t image, the whole time series (all timesteps) is cropped by default. In this case, the 'time geometry' of the current time step is used.

If the checkbox 'Only crop current time step' is ticked, the xD + t image is reduced to an xD image (e.g., 3D+t --> 3D) with the current time step only. That can be useful if you want to extract a single image or its corresponding subvolume of the time series.

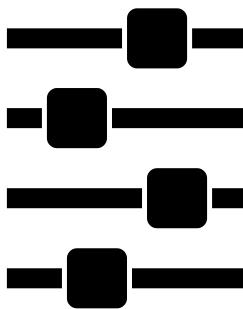
## Current issues

Cropping 2D images is not supported unless they are 3D images containing only a single slice. The user will be notified by a warning and the input is handled as a single label image.

Right now changing the rotation of the bounding box is not supported.

Furthermore, a warning appears when the bounding box is not aligned with the image. In this case, the handles can not be used correctly and get deactivated. You can continue to alter them by performing a 'Reinit' on the image.

# The Image Navigator



Icon of the Image Navigator

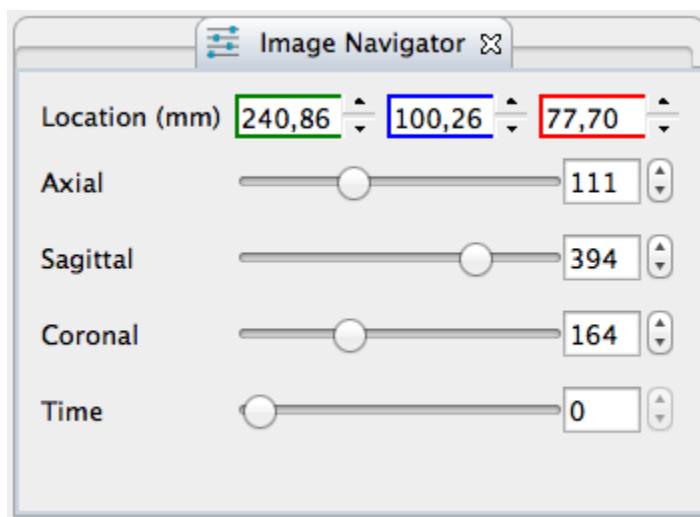


Image Navigator

Fast movement through the available data can be achieved by using the Image Navigator. By moving the sliders around you can scroll quickly through the slides and timesteps. By entering numbers in the relevant fields you can jump directly to your point of interest.

The "Show detail" checkbox enables you to see the world coordinates in millimetres and the index/voxel coordinates. These may be edited to jump to a specific location.

# Medical Imaging Interaction Toolkit: The Image Statistics View

Icon of the Image Statistics View

## Summary

This view provides an easy interface to quickly compute some features of a whole image or a region of interest.

This document will tell you how to use this view, but it is assumed that you already know how to use MITK in general.

Please see [Details](#) for more detailed information on usage and supported filters.

## Details

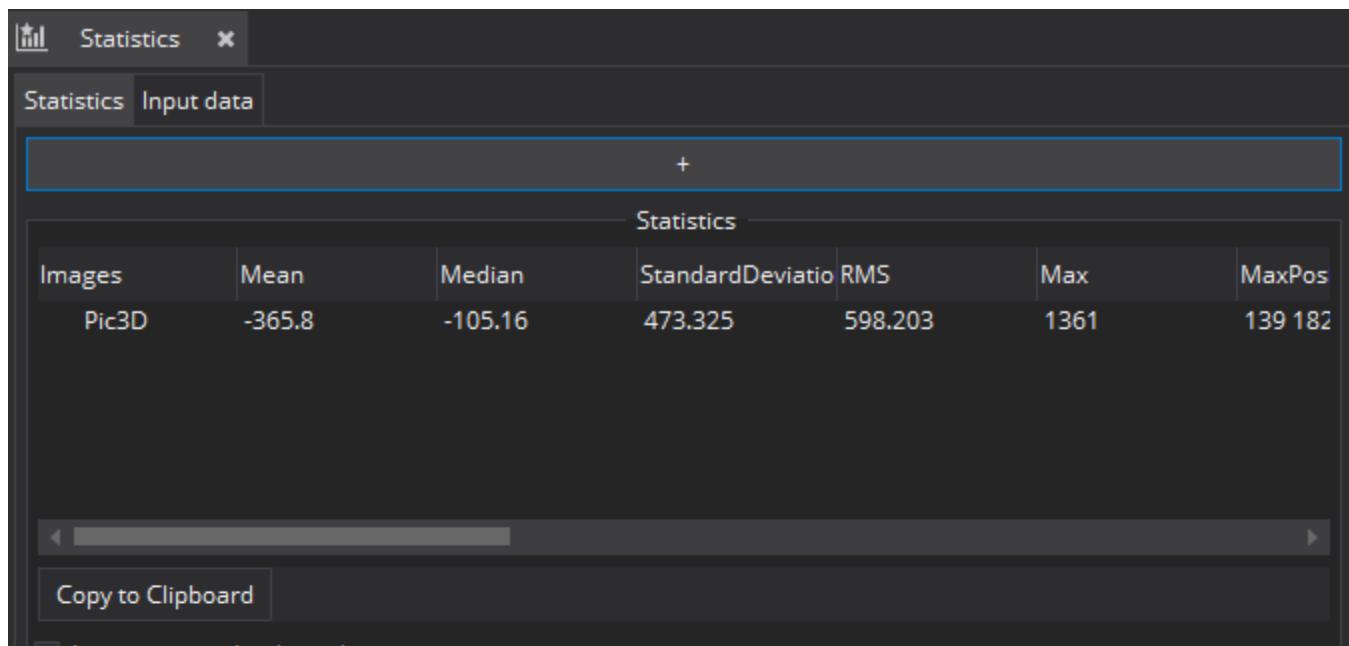
Manual sections:

[Overview](#)

[Usage](#)

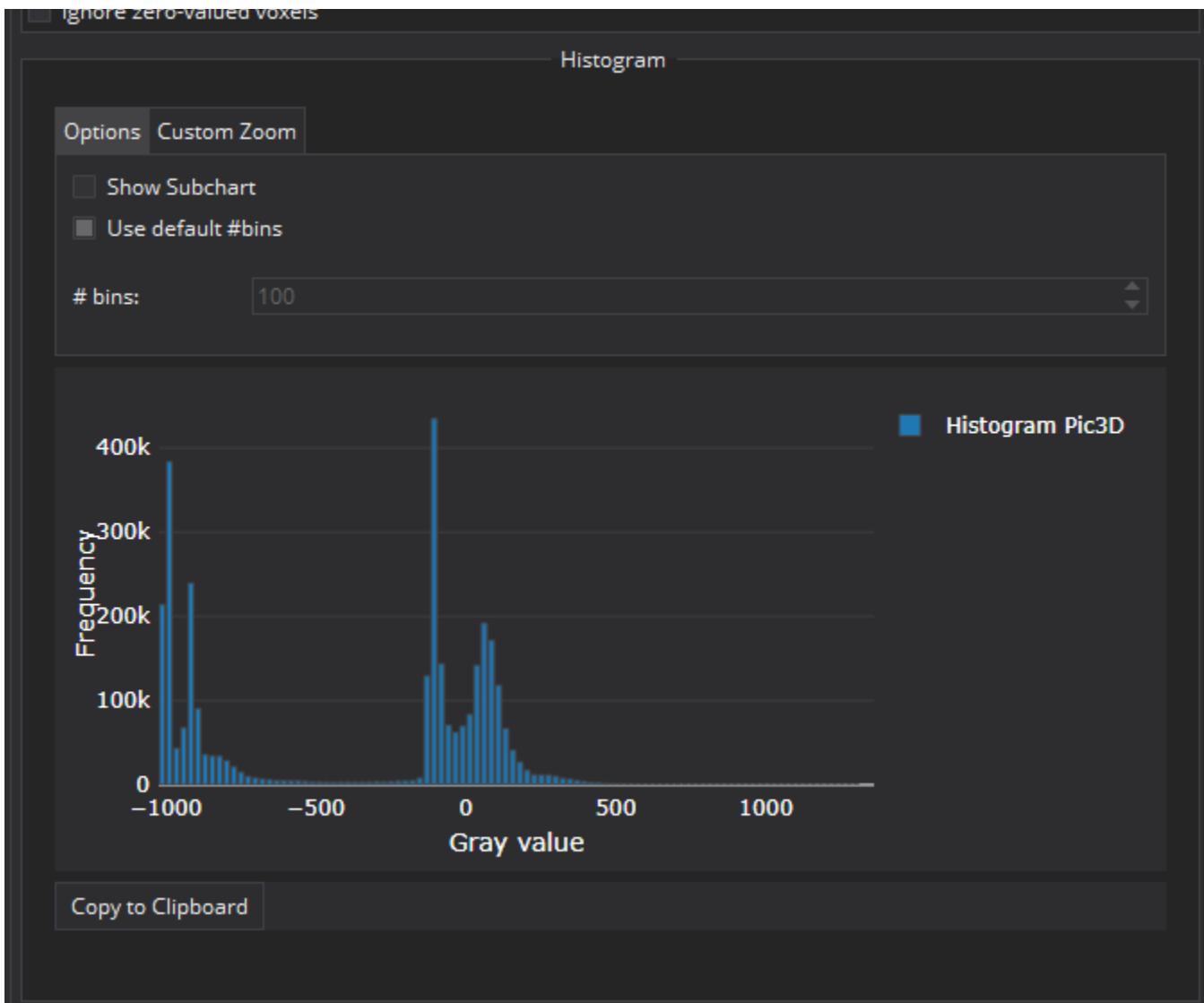
## Overview

This view provides an easy interface to quickly compute some features of a whole image or a region of interest.



The screenshot shows the 'Statistics' view window. At the top, there's a toolbar with a 'Statistics' button and a close ('x') button. Below the toolbar, a tab bar has 'Statistics' selected (it's highlighted in blue) and 'Input data' is another tab. In the main area, there's a large input field with a '+' button above it. Below this is a table titled 'Statistics'. The table has columns: 'Images', 'Mean', 'Median', 'StandardDeviation', 'RMS', 'Max', and 'MaxPos'. A single row is shown for 'Pic3D': Mean is -365.8, Median is -105.16, StandardDeviation is 473.325, RMS is 598.203, Max is 1361, and MaxPos is 139 182. At the bottom of the table, there's a 'Copy to Clipboard' button.

Statistics						
Images	Mean	Median	StandardDeviation	RMS	Max	MaxPos
Pic3D	-365.8	-105.16	473.325	598.203	1361	139 182



The interface

## Usage

To select the input data, either use the quick selection button (labeled "+"), or select the input data via the "Input Data" tab.



Select the input data via the "Input Data" tab (marked red) or via the quick selection button (marked yellow)

After selection of an image or a binary mask as input data, the image statistics are calculated and displayed in the "Statistics" section. If masks (ROIs: segmentations, planarfigures, ...) are selected, the statistics for these masks are shown. For time data the statistics for each time step are calculated correspondingly.

An example of parts of the calculated statistical features (Mean, Median, StandardDeviation, RMS, Max, MaxPosition, Min, MinPosition, Voxel, Volume [mm<sup>3</sup>], Skewness, Kurtosis, Uniformity, Entropy, MPP, UPP and Variance) for different timesteps and different masks is pictured below.

Statistics						
Images/Masks/Timesteps	Mean	Median	StandardDeviation	RMS	Max	Min
▼ Pic2DplusT						
▼ Circle						
[0] 0 ms	-488.559	-777.415	409.666	637.587	914	32
[1] 1 ms	-488.559	-777.415	409.666	637.587	914	32
[2] 2 ms	-488.559	-777.415	409.666	637.587	914	32
▼ Rectangle						
[0] 0 ms	226.281	234.17	59.504	233.974	369	16
[1] 1 ms	226.281	234.17	59.504	233.974	369	16
[2] 2 ms	226.281	234.17	59.504	233.974	369	16

Example of parts of the statistics for different masks and timestamps

Check "Ignore zero-valued voxels" to hide voxels with grayvalue zero.

## Histogram

Beneath the statistics window is the histogram window, which shows the histogram of the current selection.

The histogram window is currently only available for a single image and no or one ROI: When selection multiple images and/or multiple masks, the histogram window is deactivated!

Draw a rectangular window with a pressed left button to zoom in on the histogram. With a double click in the view area you can zoom out to the default viewport. You can also pan the view in horizontal or vertical direction by dragging with the left mouse button in the respective direction. Additionally, different options like "Custom Zoom", to set the maximum and minimum value, or by adjusting the number of bins, can be used to modify the view.

If the mask is not a closed planar figure or a segmentation an intensity profile is created instead of the histogram.

A tooltip is available by hovering over one of the bins.

## Copy to Clipboard

At the bottom of each view is a "Copy to Clipboard" button, allowing to copy the respective data in csv format to the clipboard. Be aware of the following information regarding this functionality:

The values are separated by tabulator.

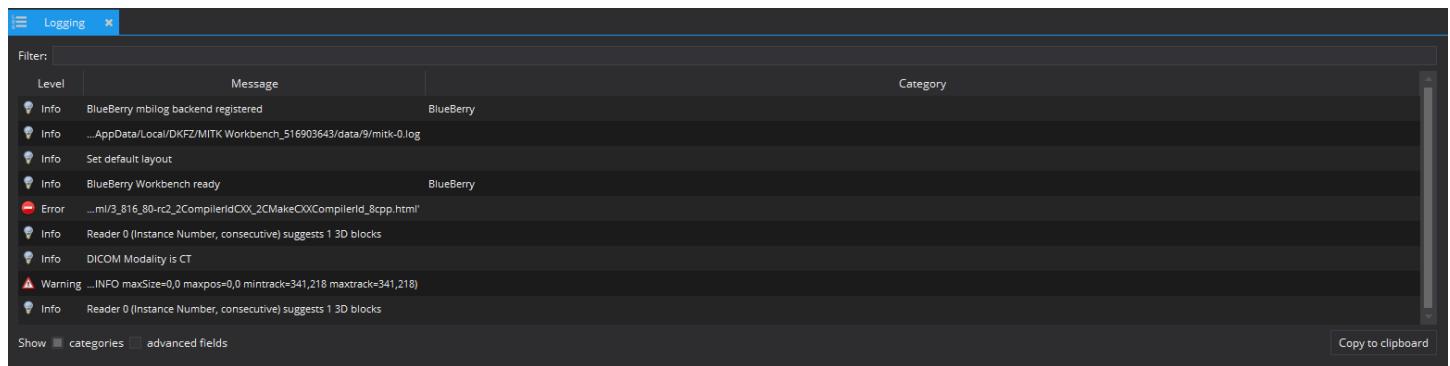
Numeric values will be converted using the system language (e.g. with German as system language the decimal separator will be ",", with English it will be '.').

One can directly copy'n'paste into Excel (and alike) as long as Excel supports/is configured to the system language

# Medical Imaging Interaction Toolkit: The Logging Plugin

## Icon of the Logging Plugin

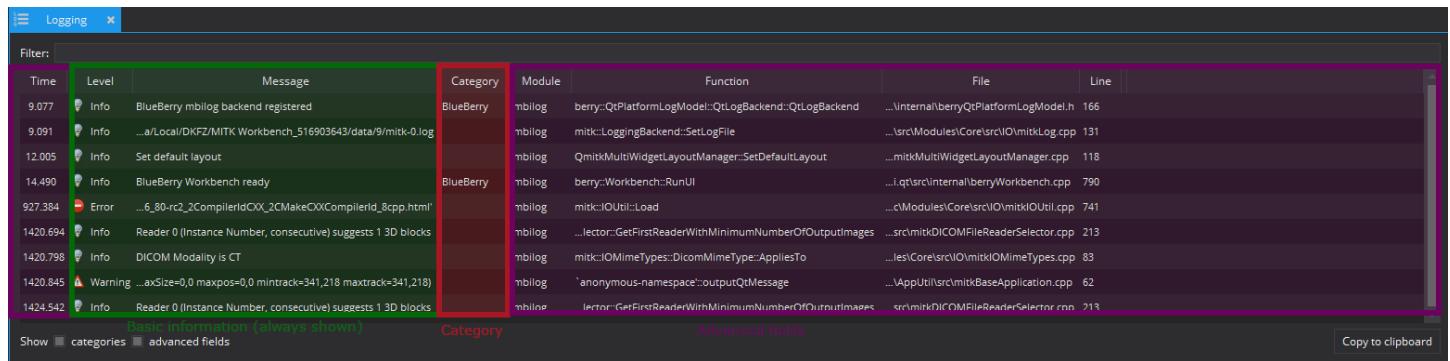
This plug-in records all logging output of events and progress as specified in the source code with time of occurrence, level of importance (Info, Warning, Error, Fatal, Debug), the message given and the origin of the message (source code section).



## Screenshot of the Logging Plugin

There are different features available in the view. The 'Filter' text field provides the possibility to search for all log events containing a certain substring. The 'Copy to clipboard' button allows you to copy the current content of the logging view to your clipboard. This enables you to insert the logging information to any text processing application.

In the simple logging view, you'll see logging messages and logging levels. A brief description of the logging levels can be found in the [logging concept documentation](#). With two checkboxes more information on every logging message can be activated. The checkbox 'categories' adds a column for the category. The checkbox 'advanced fields' additionally displays the time from application start to the log message entry and the function, filename and line number of the logging message origin.



## Details on the Visualized Logging Information

# The MatchPoint Algorithm Browser View

Icon of the MatchPoint Algorithm Browser

## Introduction

This view offers the user a way to search for available registration algorithms and select them for further usage by other views (e.g. [The MatchPoint Algorithm Control View](#)).

## Usage

The basic idea of the browser is that you can use this view as central place to search for suitable registration algorithms. If an algorithm is selected, all other views (e.g. [The MatchPoint Algorithm Control View](#)) which use registration algorithms will be notified and allow to choose the selected algorithm for usage. If you select an algorithm you can see its profile in the lower part of the view.

MatchPoint Algorithm Browser \*

Available registration algorithms:

rigid

Name	Namespace	Version
RigidICP.3D.default	org.mitk	1.0.0
RigidClosedForm.3D.default	org.mitk	1.0.0
RigidClosedForm.3D.default	de.dkfz.matchpoint.common	1.0.1
Rigid3DMattesMIAlgorithm.3D.slabbedHead	de.dkfz.matchpoint.common	1.0.1
Rigid3DMattesMIAlgorithm.3D.Head2HeadNeck	de.dkfz.matchpoint.common	1.0.2
Rigid2DMattesMIAlgorithm.2D.default	de.dkfz.matchpoint.common	1.1.0
MultiModal.rigid.default	org.mitk	1.0.0

↑  
List of available algorithms

Selected algorithm information:

**Identification**

Namespace: org.mitk  
Name: RigidICP.3D.default  
Version: 1.0.0  
BuildTag: Aug 11 2020 10:38:01; MAP 0.13.0; ITK 4.13.2  
Location: C:\MITK-build\MITK-build\bin\Release\mdra-0-13\_MITK\_Rigid\_ICP\_default.dll

**Description**

Simple 3D rigid (translation and euler angles) registration algorithm using point sets and the iterative closed points scheme. It tries to minimize the minimal point distance errors (no point pairs are assumed). Remark: at least 6 points per point sets are needed

**Keywords**

basic; point sets; ICP; rigid

**Characteristics**

data number      Points

Profile/Details of the selected algorithm

↓

View of the browser with the list of available algorithms and the profile area

## Profile info

In the following, a short description of the properties classified in the profile is given.

## Identification

- **Namespace** Namespace in which the registration name is defined.
- **Name** Identifies the name of the registration algorithm. The name is unique within the specified namespace.
- **Version** Specifies the version of the registration algorithm.

- **BuildTag** Additional information specifying the build (e.g. the build-date and -time of the so-/dll-file, the Matchpoint and the ITK version).
- **Location** Specifies the path where the so-/dll-file of the registration implementation can be found.

## Description

A short description of the chosen registration algorithm.

## Keywords

Typical keywords associated with the selected algorithm. They can i.e. be used in the search field.

## Characteristics

- **Data type(s)** The type(s) of date which is used by the algorithm to determine the registration, e.g. image, point set, contour or surface.
- **Computational style** Specifies if the registration is determined by an iterative optimization process or analytically (e.g. closed form solution).
- **Deterministic** Specifies if the algorithm is deterministic (same input -> same output) or stochastic (e.g. by sampling the image while determining the registration). Results of stochastic algorithm may vary (slightly) because of their random aspect.
- **Resolution style** Defines if the algorithm uses a multi resolution/scale approach.
- **Moving dim** Number of dimensions of the frame of reference within which the data is defined that should be registered.
- **Moving modality** Modality of the moving entity (image). Thus the frame of reference where the registration should map from, e.g. CT, MRI, PET.
- **Target dim** Number of dimensions of the frame of reference into which the data should be mapped.
- **Target modality** Modality of the target entity (image). Thus the frame of reference where the registration should map into, e.g. CT, MRI, PET.
- **Subject** Defines if the algorithm was developed to register data of the same subject (intra-subject), to register two subjects (inter-subject) or to register onto an atlas.
- **Object** Specifies which "part" of the anatomy the algorithm was developed for.
- **Transformation model** Specifies the type of transformation used by the algorithm, e.g. affine, b-spline, non-rigid.
- **Transformation domain** Defines if the transformation operates globally (e.g. Matrix) or locally (e.g. vector field).
- **Metric** The cost function/metric that is used by the optimizer (if an optimizer is used).
- **Optimization** The used optimization strategy (if an optimizer is used).
- **Interaction** Style of interaction. Currently only fully automatic registration algorithms are supported by MITK.

## Contact & Usage

- **Contact** Name of the author(s) that has (have) developed the algorithm and an email address for further questions regarding the algorithm.
- **Terms** Terms of usage for the algorithm.
- **Citation** Reference to the literature that contains information about the algorithm and

should be used to cite the algorithm.

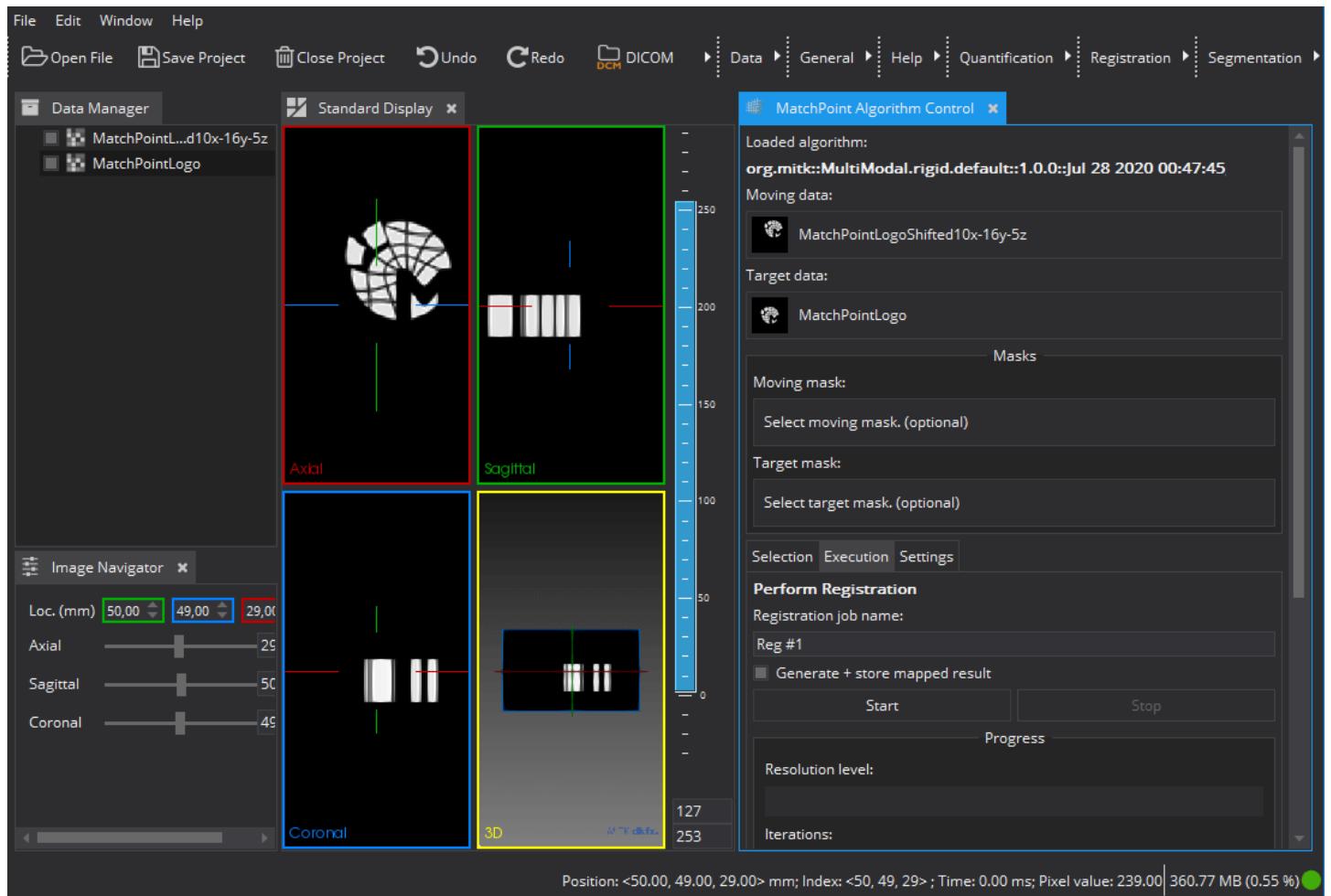
# The MatchPoint Algorithm Control View

Icon of the MatchPoint Algorithm Control

## Introduction

This plugin offers the user a way to register data (images or point sets) in order to establish a spatial correlation/mapping (stored as registration object in the data storage). To determine a registration the user has to select a registration algorithm. For the selection of an algorithm please see MatchPoint Algorithm Browser ([The MatchPoint Algorithm Browser View](#)).

## Usage

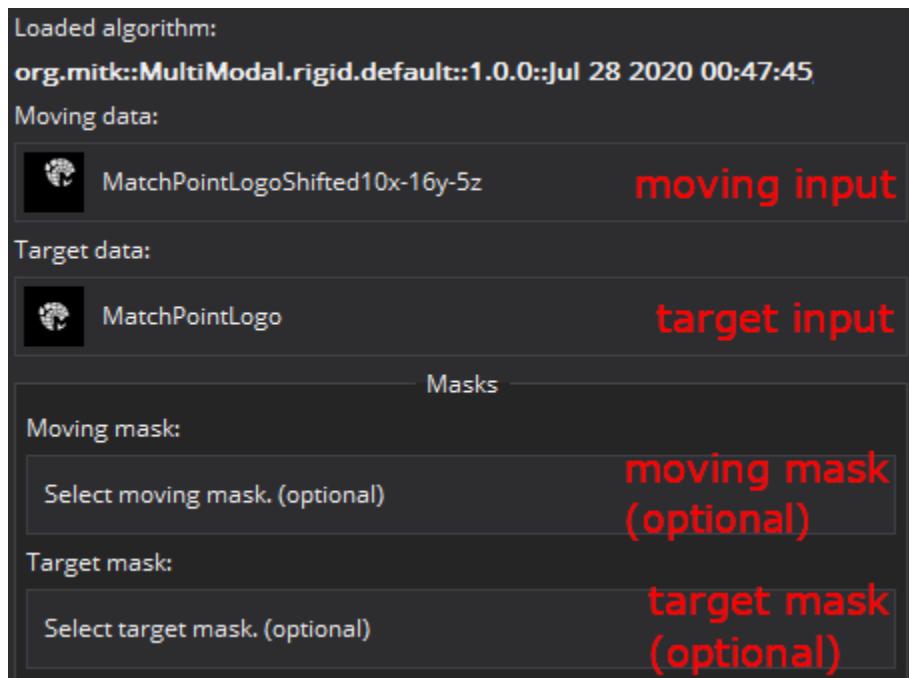


Example screenshot showing the control plugin in use.

To use the plugin a registration algorithm must be loaded and moving data as well as target data must be selected.

The type of data supported depends on the chosen algorithm. Basically the plugin supports the registration of images and point sets. The moving data is registered onto the target data. Thus in case of images, the result is a mapped input image in the geometry (field of view, orientation, spacing) defined by the target image.

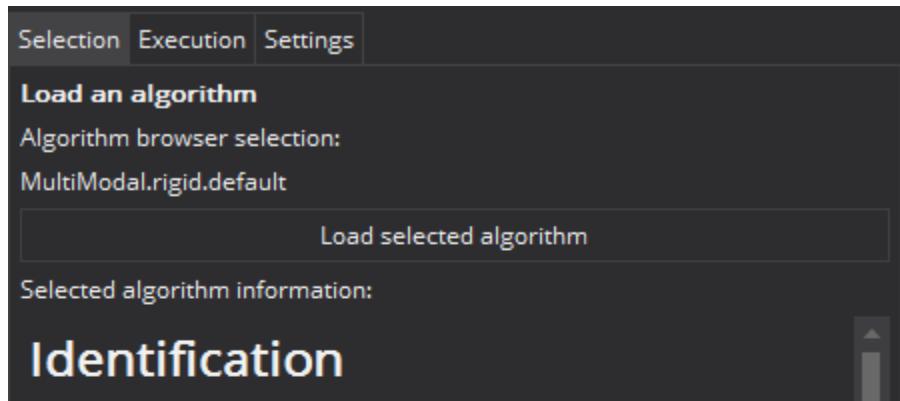
All inputs that should be used for the registration are selected via the respective selection widgets shown in the image below. The box with the mask input selectors are only shown if the chosen algorithm supports masks. It is also optional to set only one or both masks. (Remark: implications of which mask to set may depend on the specific algorithms; e.g. sometimes it is computationally more efficient to set at least the moving mask if possible.)



Input selections for the registration. Moving and target inputs are mandatory. Moving and target masks are only available if the algorithm supports them and are optional.

If an algorithm is loaded and inputs are selected, the plugin will automatically switch to the "Execution" tab.

## Selection tab



**Namespace:** org.mitk  
**Name:** MultiModal.rigid.default  
**Version:** 1.0.0  
**BuildTag:** Jul 28 2020 00:47:45; MAP 0.13.0; ITK 4.13.2  
**Location:** D:\Dev\MITK\bDoc\MITK-build\bin\Release\mdra-0-13\_MITK\_MultiModal\_rigid\_default.dll

## Description

Algorithm is used as default solution for multimodal rigid problem statements in DIPP. Uses 3 Resolution levels. By default initializes via image centers.

## Keywords

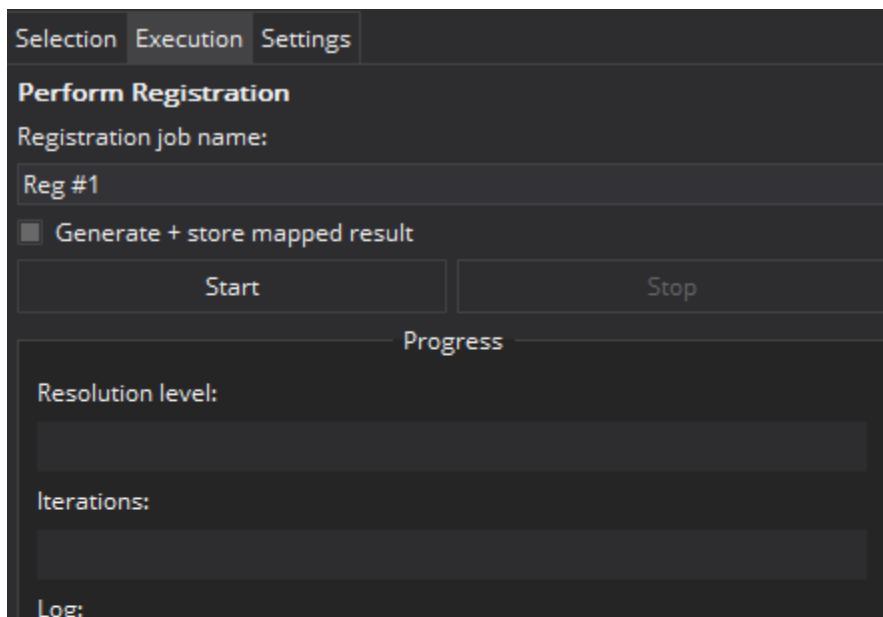
basic; pre initialization; multimodal; rigid; generic; multipurpose

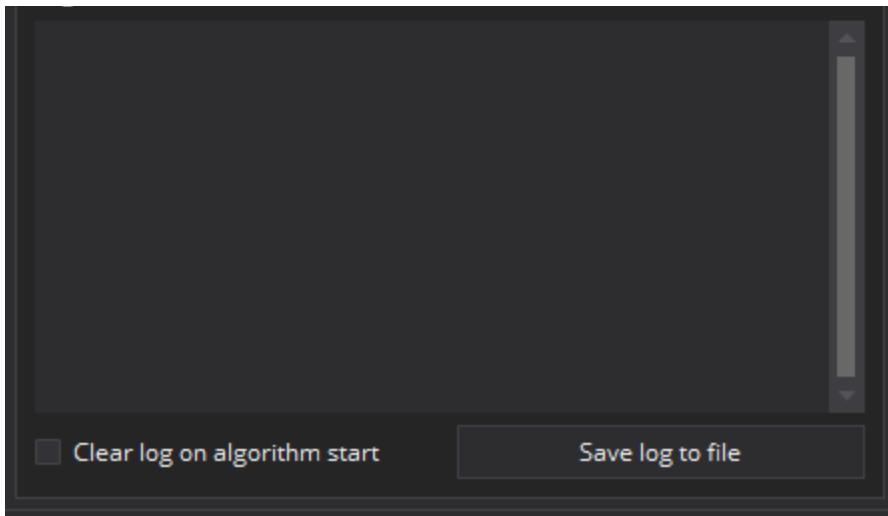
## Characteristics

Details of the selection tab.

In this tab registration algorithms that are selected in the MatchPoint Algorithm Browser can be chosen. In the tab you see the ID of the algorithm selected by the browser and its profile information. If you press the button "Load selected algorithm", the algorithm will be used by the control plugin. The name of the algorithm occurs in the text field "Loaded algorithm" (at the top of the plugin view). At this point, it has no effect if you change the selection in the browser. The control plugin will keep the loaded algorithm until you choose to load another one.

## Execution tab





Details of the execution tab.

In this tab you can specify a name for the registration job (this will determine the names of the result nodes in the Data Manager View and the data selection widgets).

You can also choose to "store registration" (which is normally the goal of the whole process, because this is the very result of the algorithm ;).

Additionally you can choose "Generate + store mapped result". This is a convenience feature which often saves you the time to use the mapper plugin afterwards. It will do the same like using the mapper plugin with the moving and target image, setting padding value "0" and using "linear interpolation". If you need other settings, skip the convenience generation and use the MatchPoint mapper plugin directly.

"Start" will trigger the registration process. Some algorithms can be stopped while processing takes place. In those cases, there is a "Stop" button enabled, as soon as the registration process starts.

## Settings tab

A screenshot of the Settings tab. At the top, there are three tabs: 'Selection', 'Execution' (which is selected), and 'Settings'. Below the tabs is a section titled 'Configure algorithm parameters' with two tabs: 'Properties' (selected) and 'Multi resolution'. A table lists various properties and their values:

Property	Value
UseAllPixels	true
TransformPar...	Error. Cannot offer MetaProperty because of ...
Scales	Error. Cannot offer MetaProperty because of ...
ResolutionLevels	3
RelaxationFactor	0,8
PreinitTransfo...	true

PreinitByCente...	false
NumberOfSpa...	0
NumberOflter...	200
NumberOfHist...	30
MinimumStep...	0,5
MaximumStep...	3
GradientMagn...	0,0001
CropInputImag...	true

Details of the settings tab.

In this tab, you can change the parametrization of the loaded algorithm (before it starts), if it offers any possibility to do so.

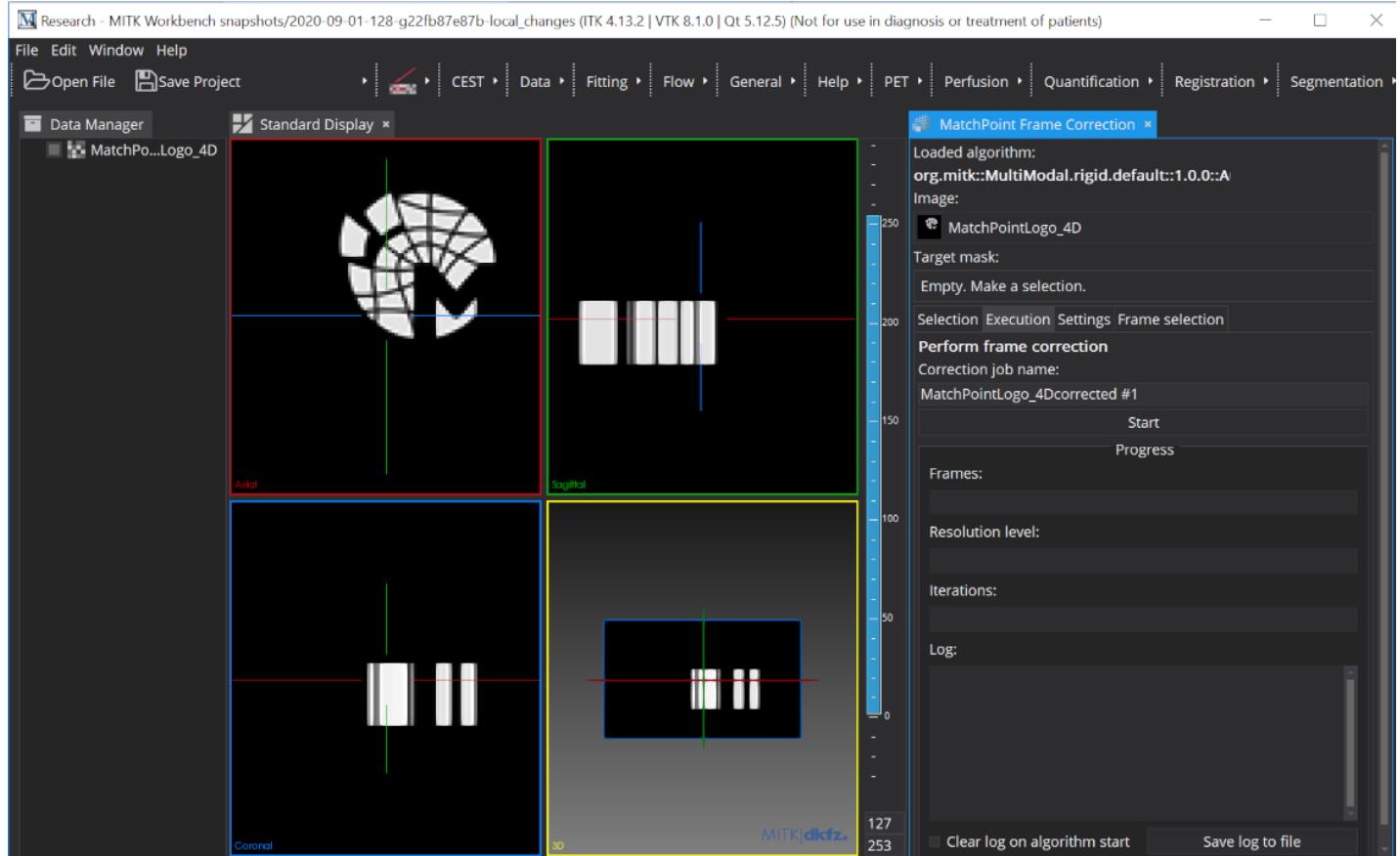
# The MatchPoint Frame Correction View

Icon of the MatchPoint Algorithm Control

## Introduction

This view offers the user a way to use a selected registration algorithm in order to apply a frame correction to a selected 3D+t image. This is for example useful if you have a dynamic image with motion artifacts in some time points and you want to reduce/remove these motion artifacts.

## Usage



Example screenshot of the view.

To use the view, a 3D+t image must be selected and a registration algorithm must be loaded. For the selection of an algorithm please see [The MatchPoint Algorithm Browser View](#).

The correction is performed such that every time frame of the image is registered to the first time frame. And the corrected time frames are mapped to the same geometry as the first frame.

If an algorithm is loaded and an input images is selected, the view will automatically switch to the *Execution* tab.

## Algorithm selection tab

Selection Execution Settings Frame selection

**Load an algorithm**

Algorithm browser selection:  
MultiModal.rigid.default

Selected algorithm information:

## Identification

Namespace: org.mitk  
Name: MultiModal.rigid.default  
Version: 1.0.0  
BuildTag: Aug 13 2020 10:16:45; MAP 0.13.0; ITK 4.13.2  
Location: C:\MITK-build\MITK-build\bin\Release\mdra-0-13\_MITK\_MultiModal\_rigid\_default.dll

## Description

Algorithm is used as default solution for multimodal rigid problem statements in DIPP. Uses 3 Resolution levels. By default initializes via image centers.

## Keywords

basic; pre initialization; multimodal; rigid; generic; multipurpose

## Characteristics

data type(s): Image  
computation style: unknown / not defined  
deterministic: no  
resolution style: 3 (multi res)  
moving dim: 3D  
moving modality: any  
target dim: 3D  
target modality: any  
subject: any  
object: any

Details of the algorithm selection tab.

In this tab, you can load the algorithm selected in the MatchPoint Algorithm Browser. In the area below the selection button the profile information of the registration algorithm is displayed. For a detailed description of the profile characteristics the user is referred to [The MatchPoint Algorithm Browser View](#). When clicking the *Load selected algorithm* button, the selected algorithm will be used by the view for the frame correction and the name of the algorithm will be displayed in the text field *Loaded algorithm* at the top of the view. At this point, it has no effect if you change the the selection in the algorithm browser. The view will keep the loaded algorithm until you choose to load another one.

## Execution tab

Selection Execution Settings Frame selection

**Perform frame correction**

Correction job name:  
Reg #1

Frames:

Resolution level:

Iterations:

Log:

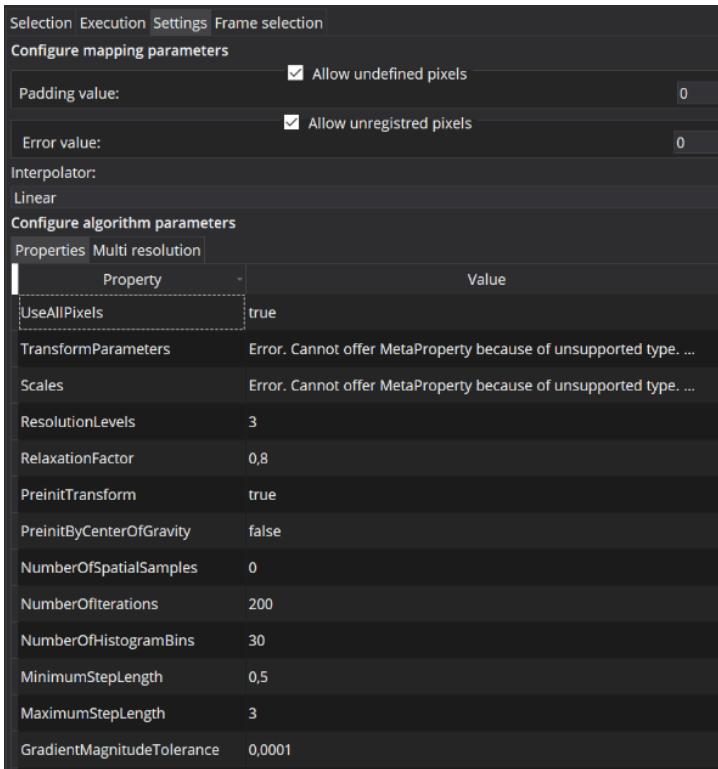
Clear log on algorithm start      Save log to file

Details of the execution tab.

In this tab you can specify a name for the correction job (this will determine the names of the result nodes in the data manager).

Clicking the *Start* button will trigger the correction process.

## Settings tab



Details of the settings tab.

In this tab, you can configure the [Mapping settings](#) which are used for the corrected frames, or parameterize the loaded algorithm (before it starts), if it offers any possibility to do so.

### Mapping settings

For the mapping of corrected images, you have several settings available:

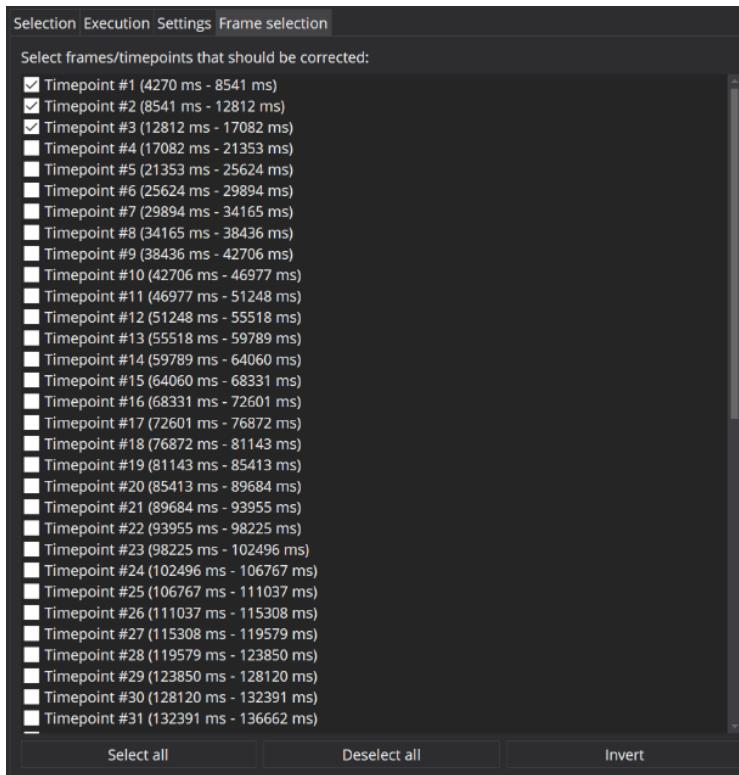
- Allow undefined pixels: Activate to handle pixels of the result image that are not in the field of view of the input image. These pixels will get the *padding value*.
- Allow error pixels: Activate to handle pixels of the result image that can not be mapped because the registration does not support this part of the output image. These pixels will get the *error value*.
- Interpolator: Set to choose the interpolation strategy that should be used for mapping. See details at [Interpolation](#) .

### Interpolation

You can choose from the following interpolation strategies:

- Nearest Neighbour: Use the value of the nearest pixel. Fastest, but high interpolation errors for gray value images. Right choice for label images or masks.
- Linear: Fast linear interpolation with often sufficient quality. Tends to blur edges.
- BSpline (3rd order): Good trade off between time and quality.
- Windowed Sinc (Hamming): Good interpolation quality but very time consuming.
- Windowed Sinc (Welch): Good interpolation quality but very time consuming.

## Frame selection tab



Details of the frame selection tab.

In this tab you can specify the frames of the currently selected image that should be corrected. As default all frames of an image will be selected. If you only select specific frames, these frames will be corrected whilst all other frames will be just copied unchanged.

# The MatchPoint Image Mapper View

Icon of the MatchPoint Image Mapper

## Introduction

This view offers the possibility to map any loaded image or point set using a user selected registration object. When mapping images the user can control the field of view (image geometry) the image should be mapped into, as well as the interpolation strategy and padding values that should be used.

It is one of several MatchPoint registration plugins.

### Typical usage scenarios

You have registered image I1 onto image I2. Now you want to

(Most obvious) map I1 onto I2 with the registration, e.g. to make a joint statistical analysis.

map image I3 (e.g. an other MRI sequence of the same session) also onto I2 with the same registration.

map a segmentation created on I1 also onto I2 with the same registration.

map a point set of image I1 also onto I2 with the same registration.

## Usage

To use the mapper at least the input (image or point set) must be selected. Additionally, you may select a registration object and, in case the input is an image, an optional reference image.

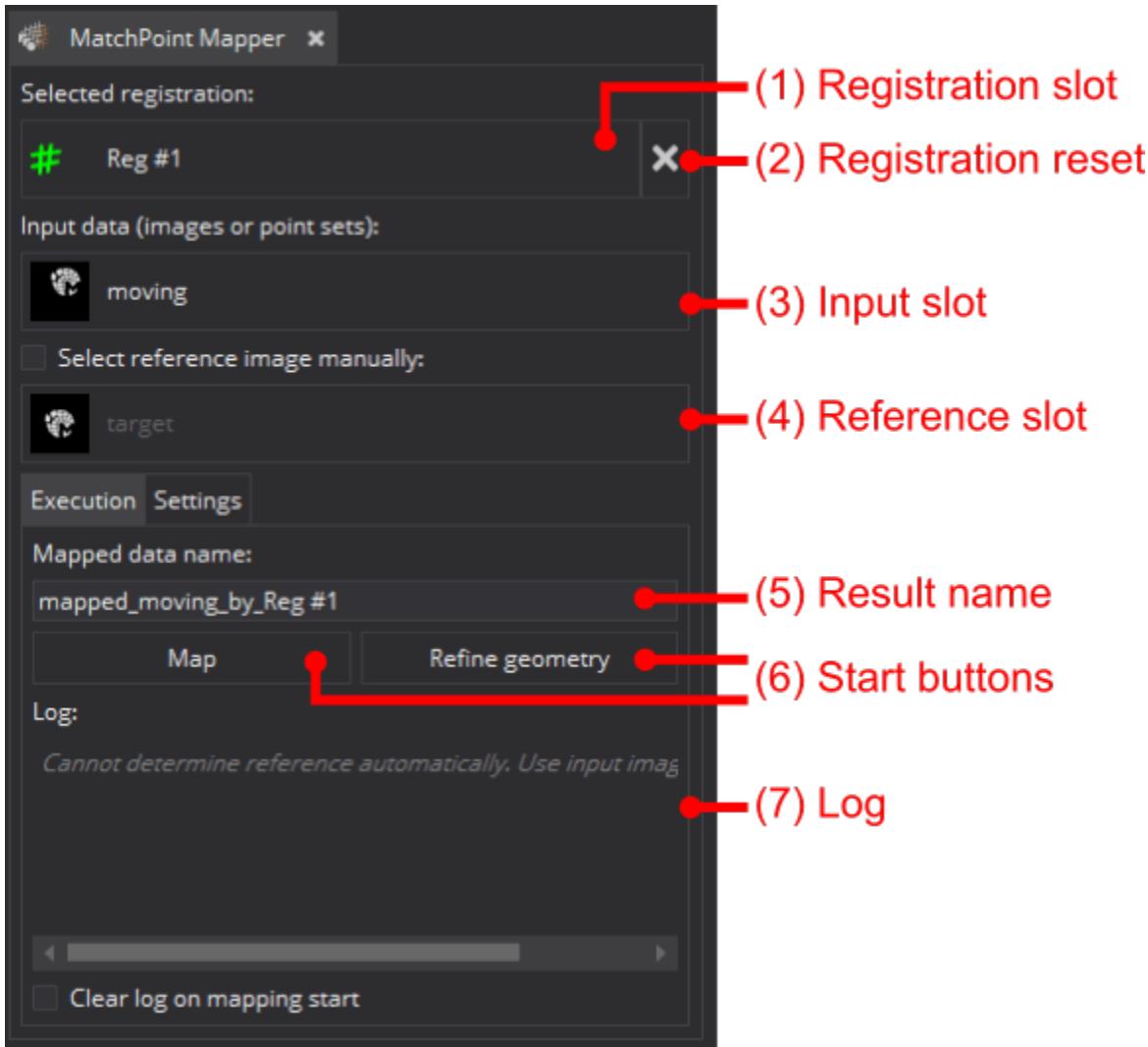
The reference image defines the geometry (field of view, orientation, spacing) that should be used for the result image. The view will try to automatically determine the reference image. By default it is the target image that was used to determine the selected registration. If auto selection cannot determine the reference (e.g. because it was not specified or it is currently not loaded), the input image will be selected as reference. The reference image can be also defined by the user explicitly by activating manual selection.

REMARK: If you map point sets you can ignore the reference image slot. It has no effect.

REMARK: The mapping results will be added as child nodes to the used input node.

REMARK: If you do not select an registration the view will assume that you make an identity transform. This is a convenient way if you just want to resample an image into the geometry of an other image (when no registration is needed). Also in this use case you can take advantage of the

different interpolation and sub/super sampling strategies.



Main elements of the mapper view.

- (1) The currently selected registration that will be used for mapping. Click to change.
- (2) Reset button that will remove the current selected registration and switch back to an identity transform.
- (3) The currently selected input data, that will be mapped. Click to change.
- (4) The currently (automatically or by user) selected reference image, that defines the geometry of the result. Click to change.
- (5) The name of the result data in the data manager.
- (6) The start button(s) to commence the mapping process. For details regarding the two options see [Mapping or geometry refinement](#).
- (7) Log windows with messages regarding the mapping process.

## Mapping or geometry refinement

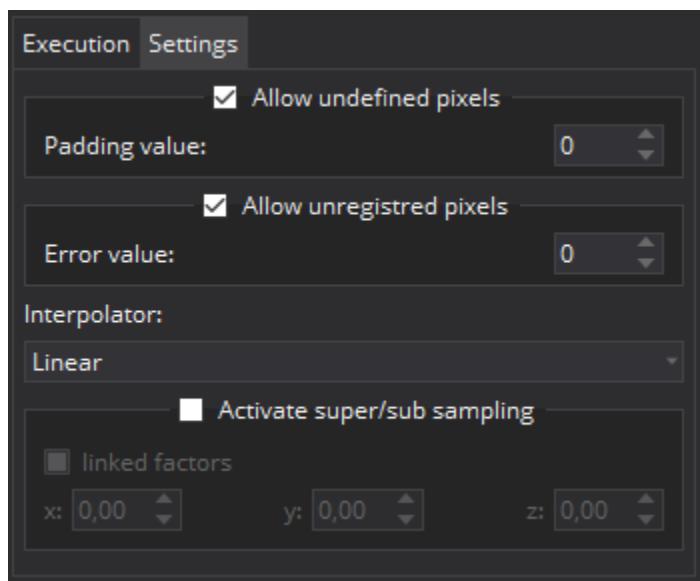
The mapper view offers two options to map images:

"Map" (default)

"Refine geometry" For images "Map" fills the pixels of the output image by interpolating input image pixels using the registration object. This option always works, but may take longer and introduces interpolation errors, because a new image is resampled.

The second option "Refine geometry" is only offered, if the registration (more precisely its inverse kernel) is matrix based and the selected data is an image. In this case it just clones the image and refines its image geometry (origin and orientation) to project it to the position indicated by the registration; thus no interpolation artefacts are introduced.

## Settings



Available settings for mapping images.

If you map the image (and not just refine the geometry), you have several settings available:

"Allow undefined pixels": Activate to handle pixels of the result image that are not in the field of view of the input image. These pixels will get the "padding value".

"Allow unregistered pixels": Activate to handle pixels of the result image that can not be mapped because the registration does not support this part of the output image. These pixels will get the "error value".

"Interpolator": Set to choose the interpolation strategy that should be used for mapping.

"Activate super/sub sampling": Activate if you want to use origin and orientation of the reference image but want to alter the spacing.

## **Interpolation**

You can choose from the following interpolation strategies:

"Nearest Neighbor": Use the value of the nearest pixel. Fastest, but high interpolation errors for gray value images. Right choice for label images or masks.

"Linear": Fast linear interpolation with often sufficient quality. Tends to blur edges.

"BSpline (3rd order)": Good trade off between time and quality.

"Windowed Sinc (Hamming)": Good interpolation quality but very time consuming.

"Windowed Sinc (Welch)": Good interpolation quality but very time consuming.

## **Handling of masks/segmentations**

If you select an mask as input image, the plugin will be automatically reconfigured to settings that are suitable for the task of mapping masks. Most importantly the interpolator will be set to "Nearest Neighbor".

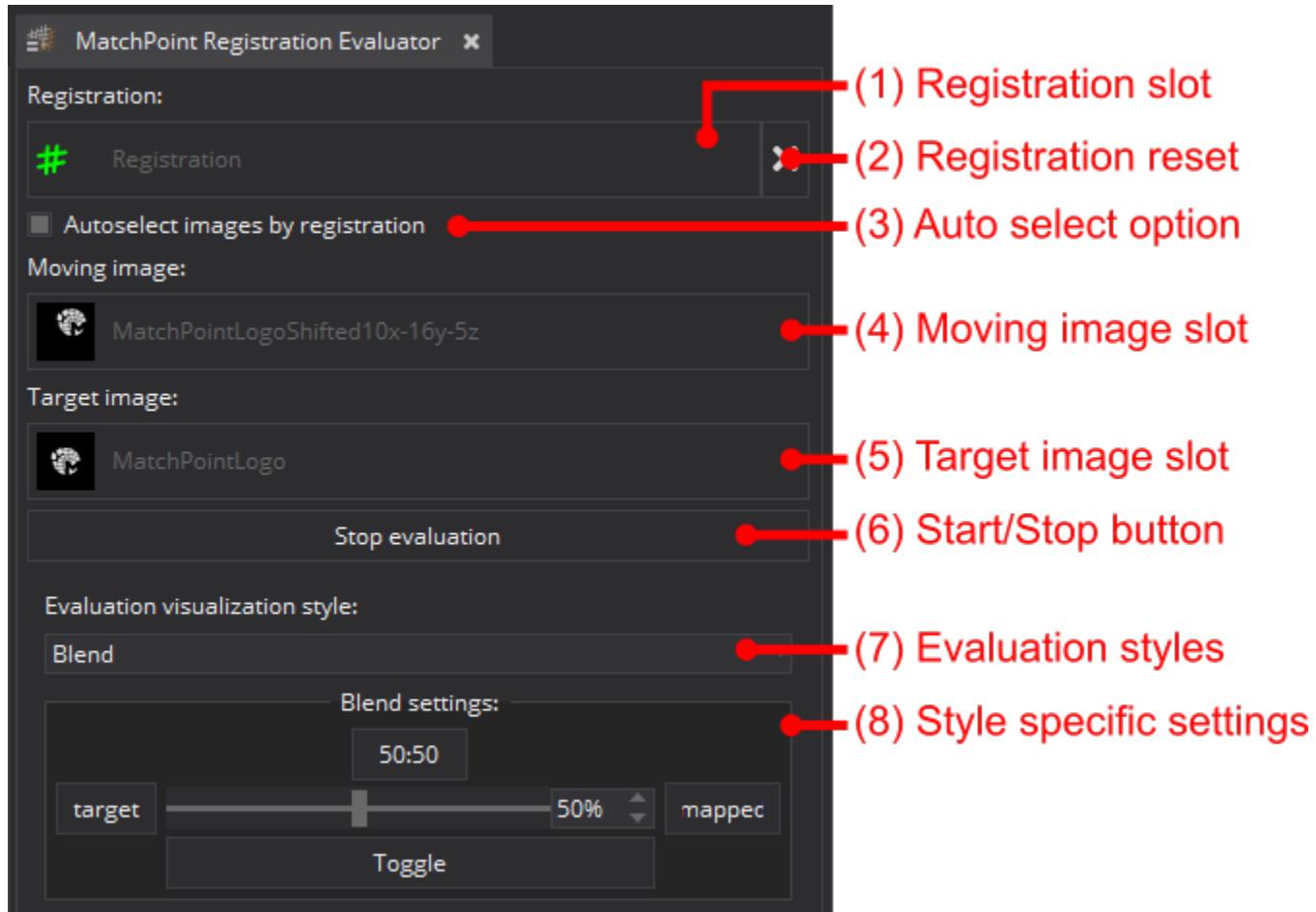
# The MatchPoint Registration Evaluation View

Icon of the MatchPoint Registration Evaluator

## Introduction

This view offers the possibility to evaluate the quality of the registration/mapping of two given images by visual inspection. This can either be used to assess the visual quality of a registration or to assess how well the image contents are already aligned by default. To achieve the latter, one may select no registration. Then the images will be displayed in evaluation mode assuming an identity transform (so no mapping). It is one of several MatchPoint registration plug-ins.

## Usage



Example screenshot showing the main elements of the view.

(1) The currently selected registration that should be used to map the moving image for evaluation.

Click to change. If no registration is selected, a direct evaluation will be performed.

(2) Reset button will remove the currently selected registration.

(3) Auto select option. If active the view will try to deduce and automatically select (if loaded in the application) the moving and target image when the registration changes. The view assumes that the moving and target images used to determine the registration should be used.

(4) The currently selected moving data. Click to change.

(5) The currently selected target data. Click to change.

(6) Start/Stop button used to activate/deactivate the evaluation. This button become active when at least the moving and the target image are selected.

(7) Selection of the visualization style. (only visible if evaluation is active)

(8) Style specific settings. (only visible if evaluation is active)

If the evaluation view is active you can choose between different modes of visualization. For more details see [Visualization styles](#).

To stop the evaluation mode, you may use the "Stop evaluation" button or just close the evaluation view.

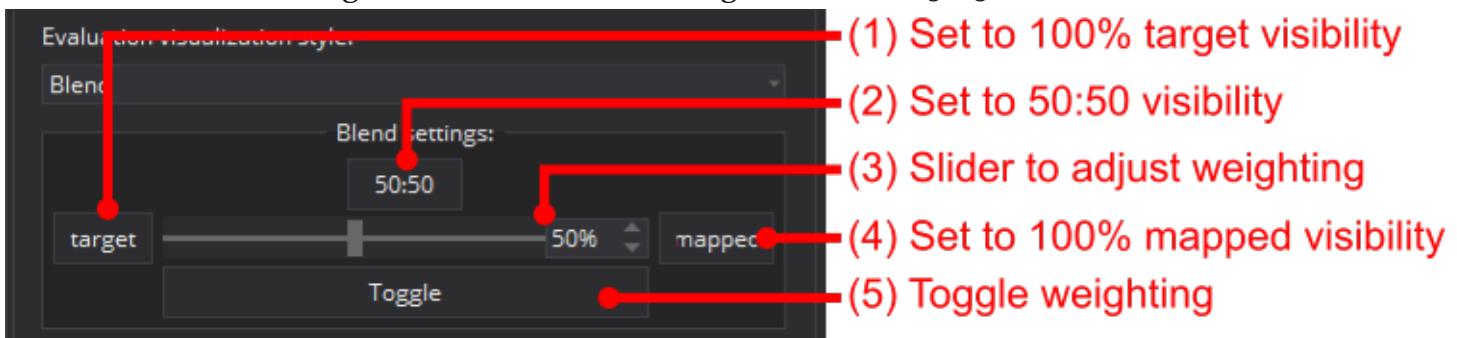
## Evaluating accuracy

**Important note:** Please be aware, that a visual inspection of registration quality is only a weak surrogate for a thorough accuracy analysis based on representative and suitable ground truth data. From a visually good mapping you can not deduce a correct registration. This is especially true if the degrees of freedom of the registration increases. For a rigid registration it might be feasible to discern correct and incorrect registration. But for non rigid registrations you definitely should use this view only for first visual inspection (to check if it SEEMS to do the right thing and is worth further exploration) or illustrating the registration effect for registration you have assessed in a sound way.

## Visualization styles

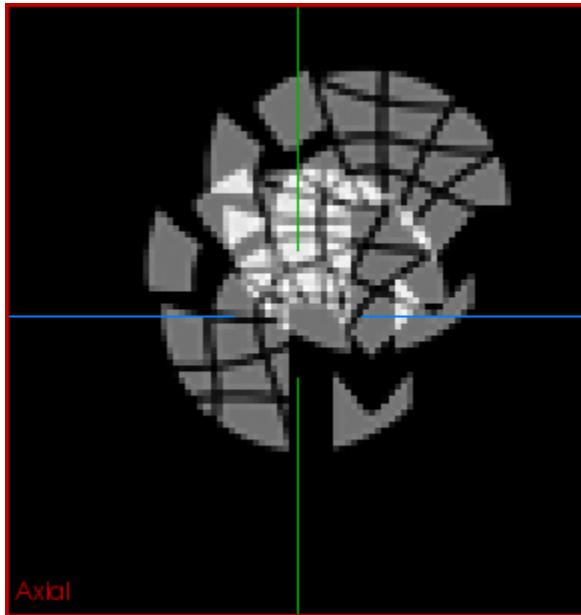
You can choose from the following visualization styles to evaluate the registration/mapping quality:

"Blend": Blends the images with a user defined weight. Default is 50:50.



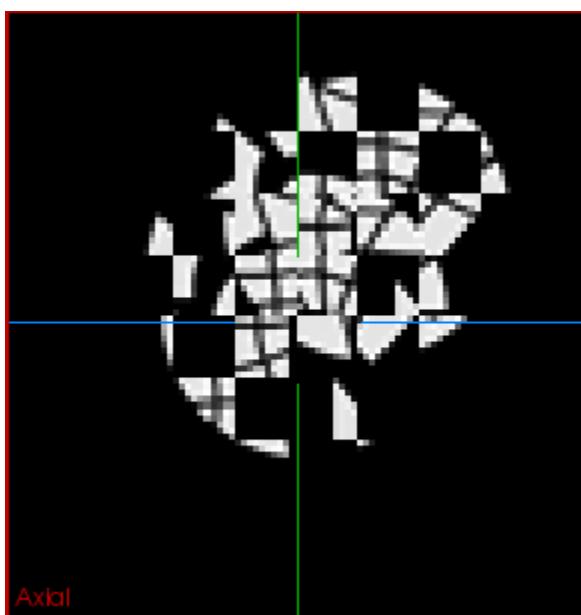
Settings of the Blend style

- (1) Click to set the weights to 100% target image.
- (2) Click to set the weights to 50:50 (equal blend).
- (3) Slider to adjust the weights between target image and the mapped input image. The spin box shows the weight of the mapped input image.
- (4) Click to set the weights to 100% mapped input image.
- (5) Click to toggle the weight between both images.



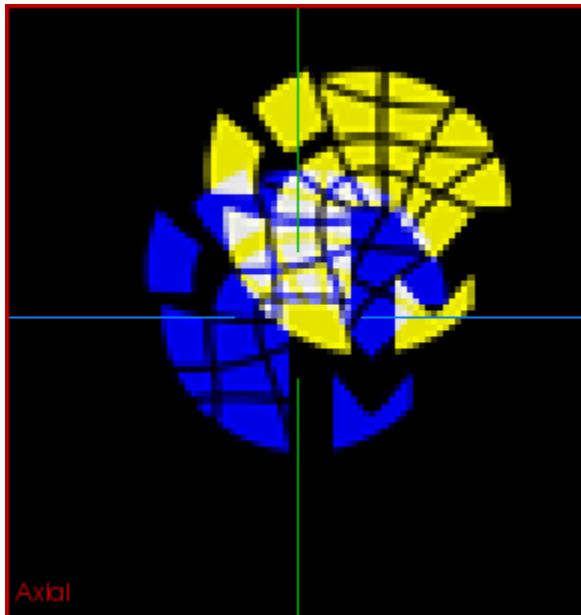
Example for mode: Blend (50:50)

"Checkerboard": Checkerboard style that composes both images by showing image 1 in all light squares and image 2 in all dark squares. You can define the resolution/number of squares of the checkerboard.



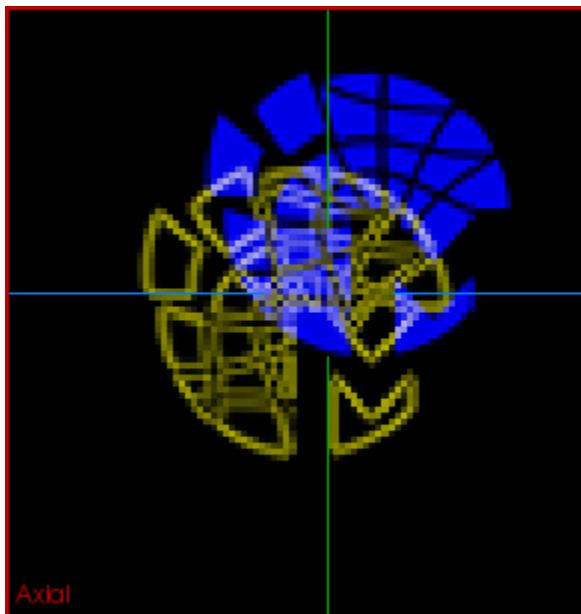
## Example for mode: Checkerboard

"Color blend": Color blend of the images (blue: target image; yellow: moving). Areas where you see no color implies good intensity matchings.



## Example for mode: Color blend

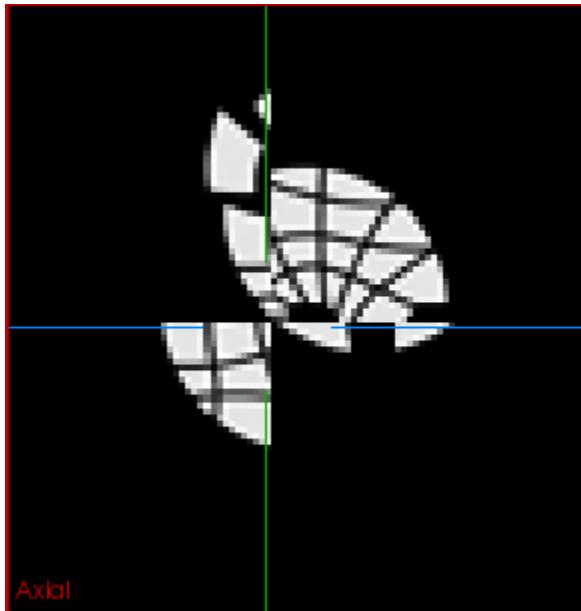
"Contour": Blend mode that displays one image as blue "background" and the other image in yellow contours. You can choose the role of the images.



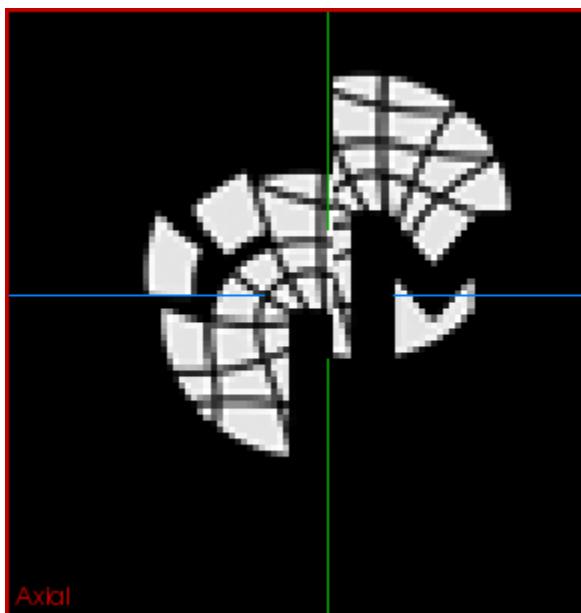
## Example for mode: Contour

"Difference": Displays the absolute difference of both images.

"Wipe": Blend mode that makes a rectilinear combination of the images. You can choose the mode how the images are split. The split is synchronized with the current selection. So you may interact with the split border to position it on interesting areas.



Example for mode: Wipe cross



Example for mode: Wipe horizontal

# **The MatchPoint Registration Manipulator View**

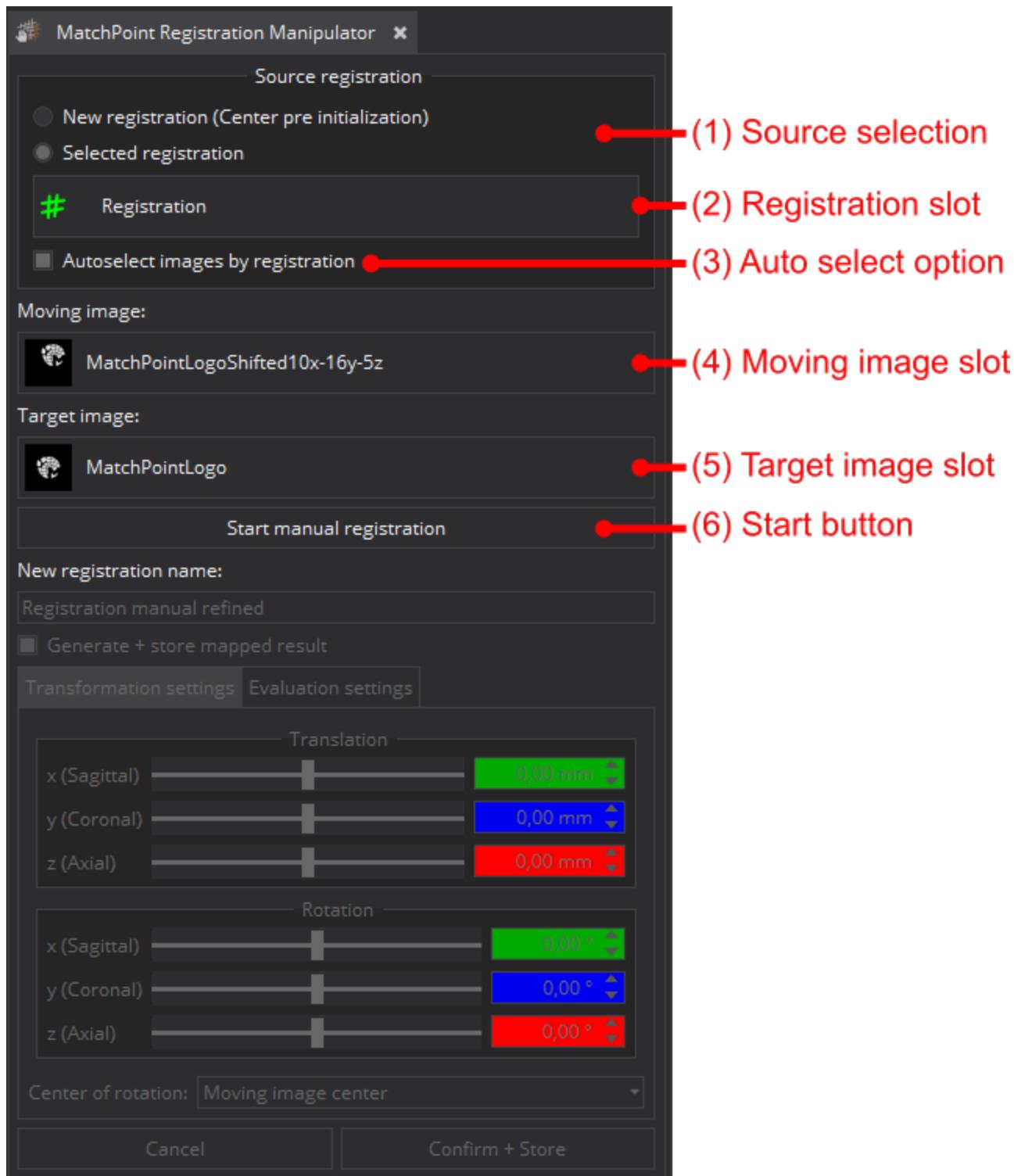
Icon of the MatchPoint Registration Manipulator

## **Introduction**

This view offers the possibility to manually manipulate a registration to establish a good mapping between data. The effect of manipulation is visualized with two user defined images to allow for visual inspection.

It is one of several MatchPoint registration plug-ins.

## **Usage**



Example screenshot showing the main elements of the view used to start a manipulation.

The typical workflow with the manipulator has following steps/sections:

**(1) Source selection:** You can choose between starting a new registration and using a selected registration. For latter option, the registration must be selected (see (2)).

**(2) Registration slot:** Shows the currently selected registration that serves as baseline. Only active if (1) is selected appropriately. Click to change.

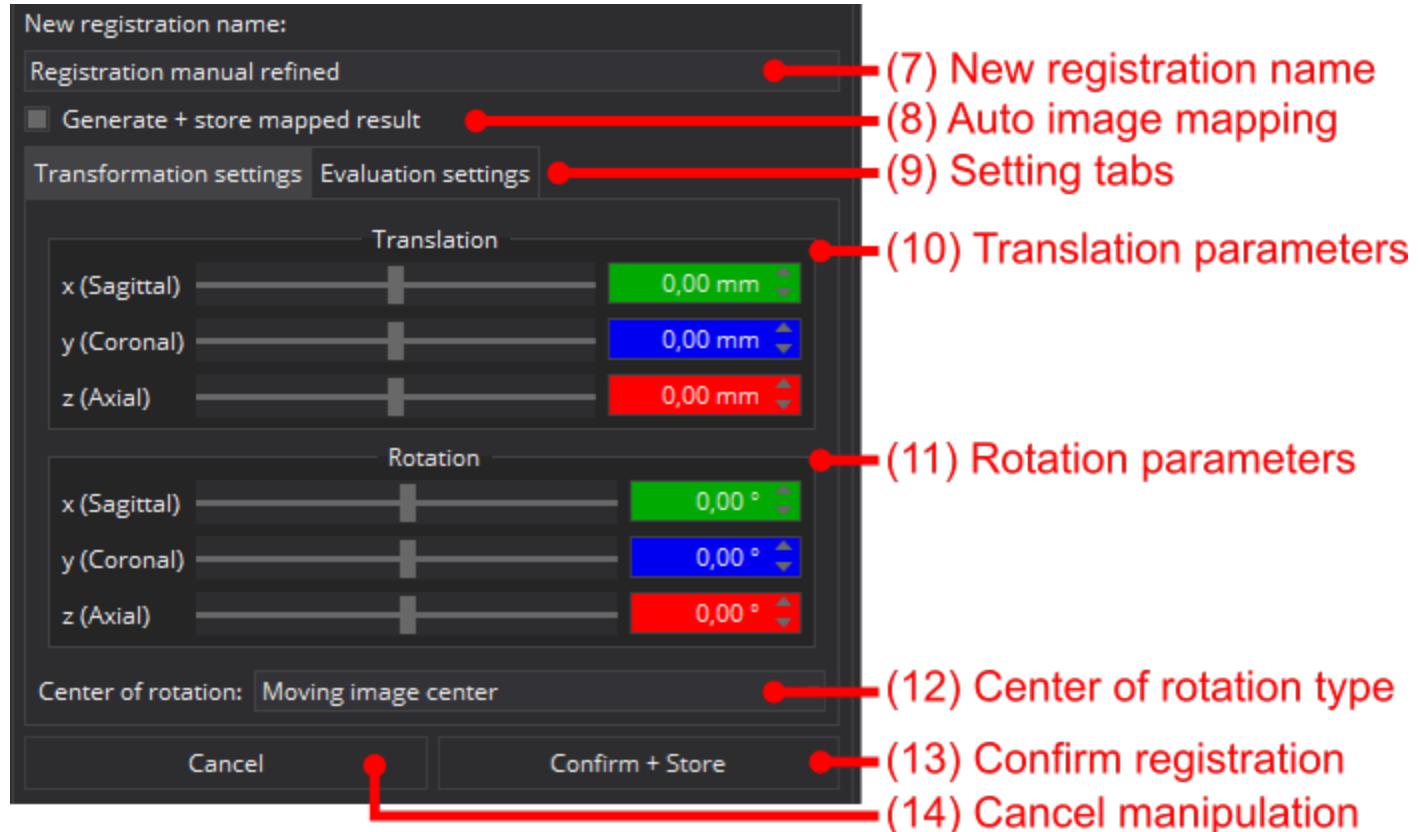
**(3) Auto select option:** If active the view will try to deduce and automatically select (if loaded in

the application) the moving and target image when the baseline registration changes. The view assumes that the moving and target images used to determine the registration should be used to illustrate the effects of the manipulation.

(4) **Moving image slot:** To allow for visual inspection of the manipulation a moving image must be specified. This image is mapped by the manipulated registration to illustrate the effects of the manipulation. Click to change the image.

(5) **Target image slot:** To allow for visual inspection of the manipulation a target image must be specified. This image is used to compare against the mapped moving image to illustrate the effects of the manipulation. Click to change the image.

(6) **Start manual registration:** If all settings are valid, you can start the manipulation. The render windows will automatically switch to the visual inspection mode. The views will be reinitialized to the field of view of the target image.



Controls after the manipulation session is started.

(7) **New registration name:** You may choose to give the resulting registration a special name.

(8) Additionally you can choose the convenience option to map the moving image with the confirmed registration automatically and also store the mapped image.

(9) **Settings:** You can alter the settings of the transform ([Transformation settings](#)) and the rendering settings ([Evaluation settings](#)) for the visual inspection.

(10) **Translation parameters:** You can alter the translation parameter of the transform by using the sliders or the spinboxes. For more details see transform settings section ([Transformation settings](#)).

(11) **Rotation parameters:** You can alter the rotation parameter of the transform by using the sliders or the spinboxes. For more details see transform settings section ([Transformation settings](#)).

(12) **Center of rotation:** You may choose the center of rotation for your manipulation. For more details see transform settings section ([Transformation settings](#)).

(13) **Confirmation:** You may confirm the determined registration and store it in the data storage with the given name. The manipulation session will be automatically closed.

(14) **Cancel:** You may cancel the session any time. No changes will be stored and the manipulation session will be automatically closed.

## Transformation settings

You can alter the translation and the rotation of the transform. In addition you may choose the center of rotation type. You have the following options:

- **Moving image center:** Rotate around the center of the moving image.
- **World origin:** Rotate around (0.0,0.0,0.0), the world origin.
- **Current navigator position:** Rotate around the current navigator position in the render views.

### Note

To ease the orientation, the edit fields have background colors which resemble the colors of the plane the changes will "happen".

For translation, the translation vector will be perpendicular to the indicated plane (The image moves "through" the plane). For rotation, the rotation axis will be perpendicular to the indicated plane.

## Evaluation settings

The settings you can choose are equal to the settings of the evaluation view ([The MatchPoint Registration Evaluation View](#)). Please see the documentation of the MatchPoint Registration Evaluator view for more details.

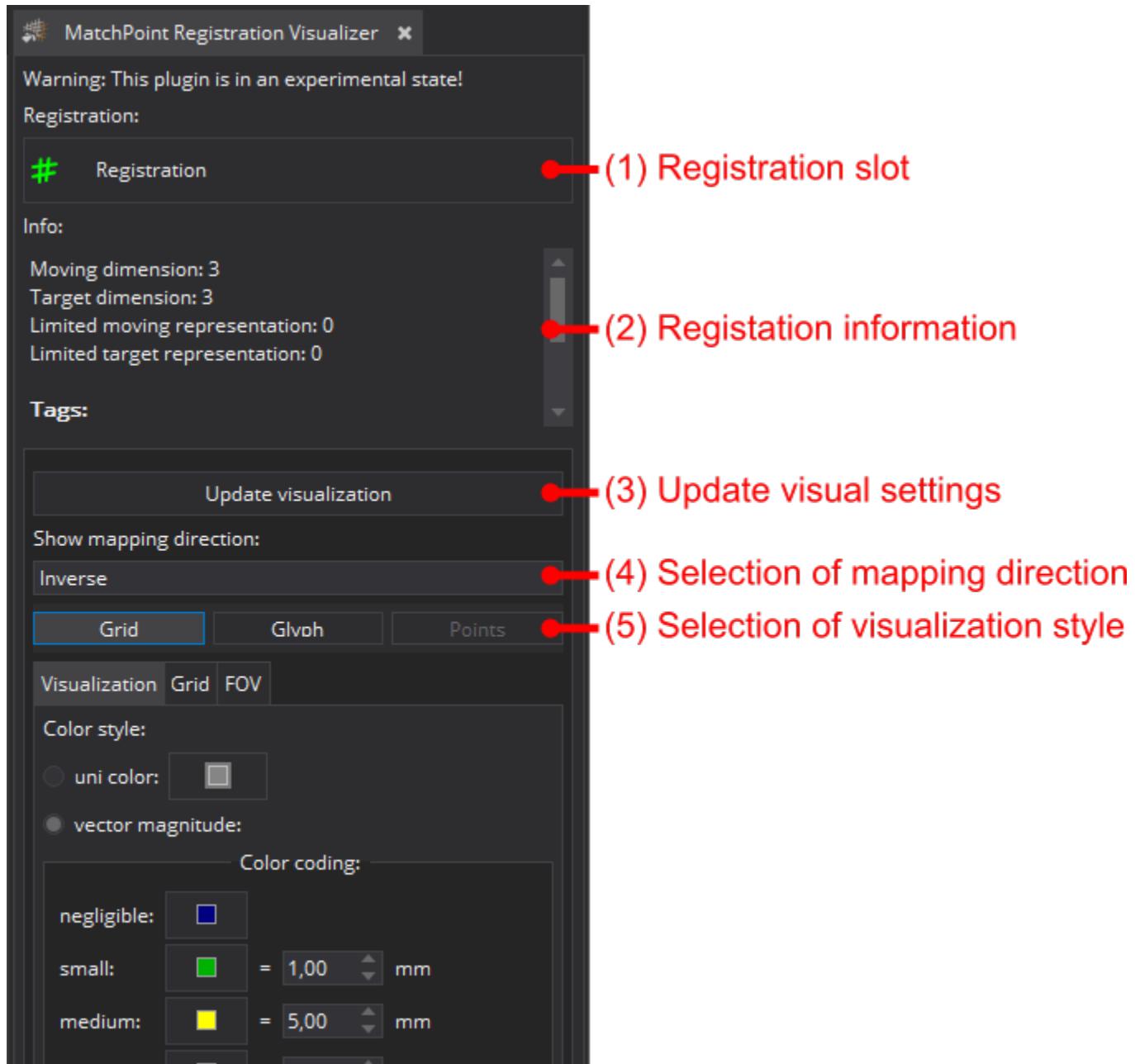
# The MatchPoint Registration Visualizer View

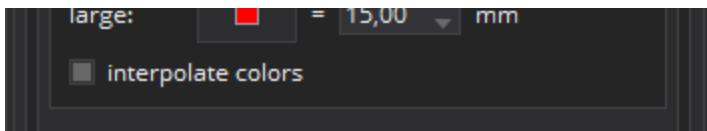
Icon of the Registration Visualizer

## Introduction

This view is in development to offer the user a way to visualize MatchPoint registrations (so the transformation/deformation field they represent) in a MITK scene. Currently, a simple grid visualization and glyph visualization is implemented.

## Usage





Example screenshot showing the main elements of the view used to visualize a registration.

The view has following steps/sections:

(1) **Registration slot:** Shows the currently selected registration which is visualized and whose visualization settings should be altered. Click to change.

(2) **Registration information:** General information on the selected registration.

(3) **Update visual settings:** By clicking the button the current settings will be accepted and the visualization of the registration will be updated accordingly.

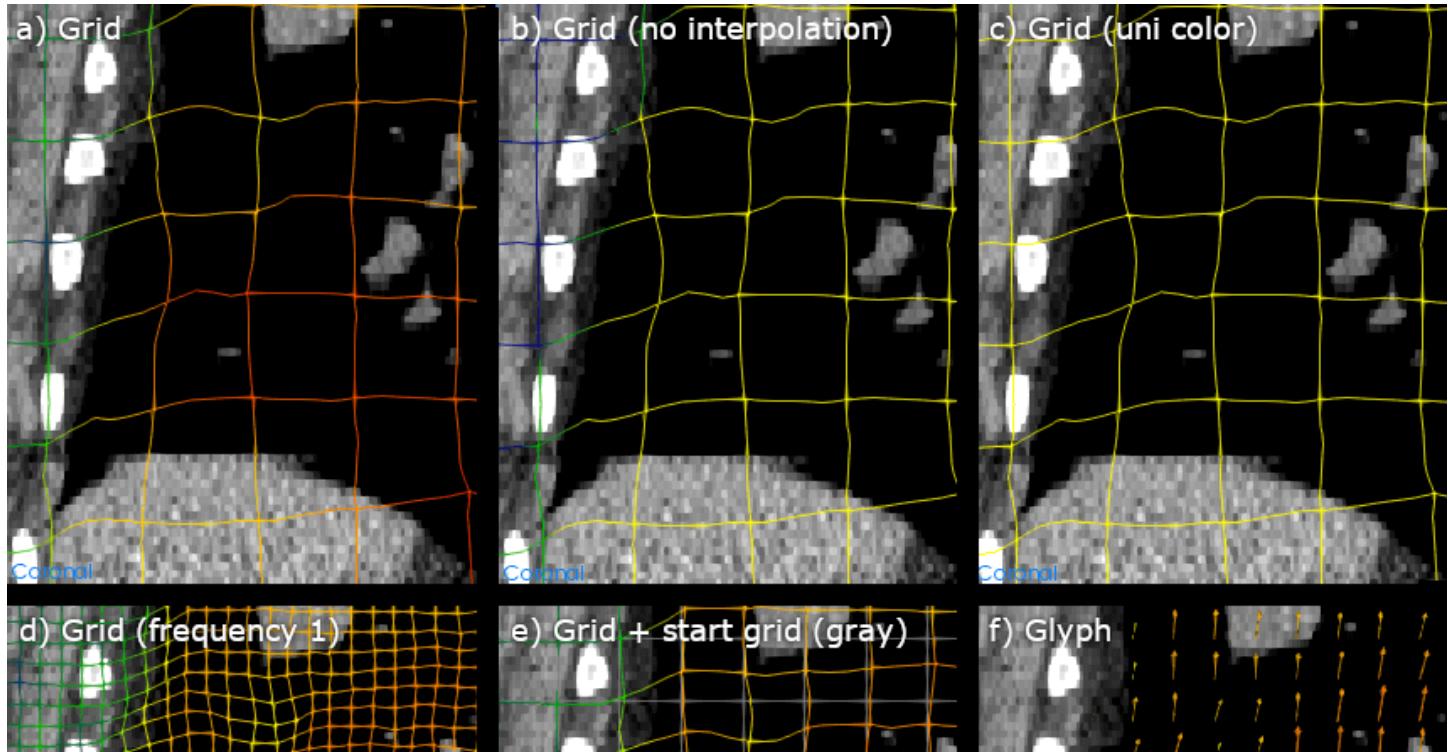
(4) **Mapping direction:** Allows to select the mapping direction that should be visualized (more details see below [Information regarding the directions](#)).

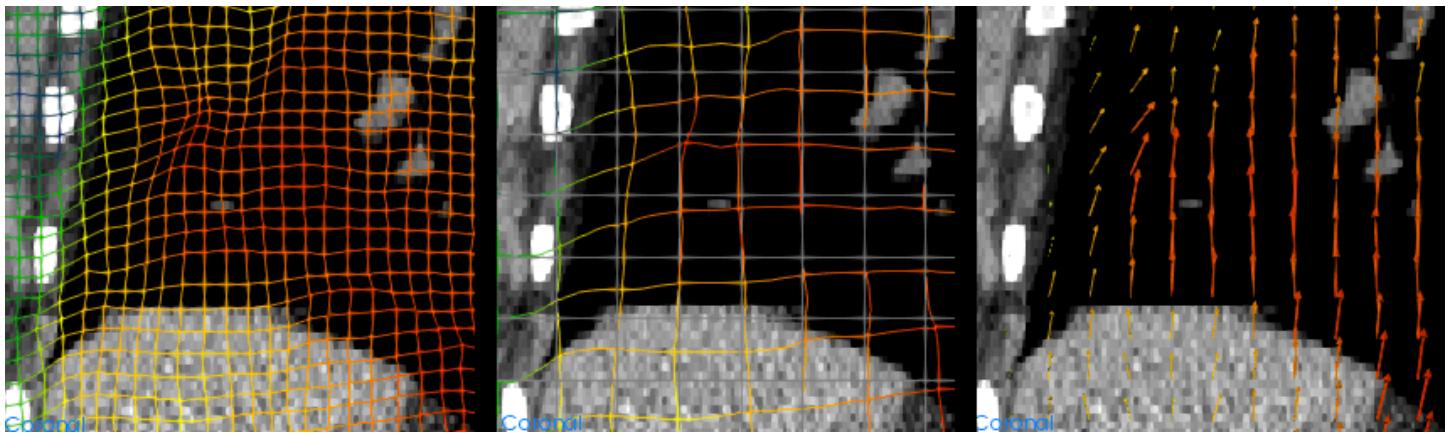
(5) **Visualization style:** Select how the registration should be visualized. Currently two options are available.:

Grid: Visualize as a wire frame grid that is deformed by the registration. The magnitude of deformation can be encoded in the grid color (cf style example "a)" below).

Glyph: Visualize as a cloud of arrows that follow the deformation vectors of the registrations. The magnitude of deformation can be encoded in the glyph color (cf style example "f)" below).

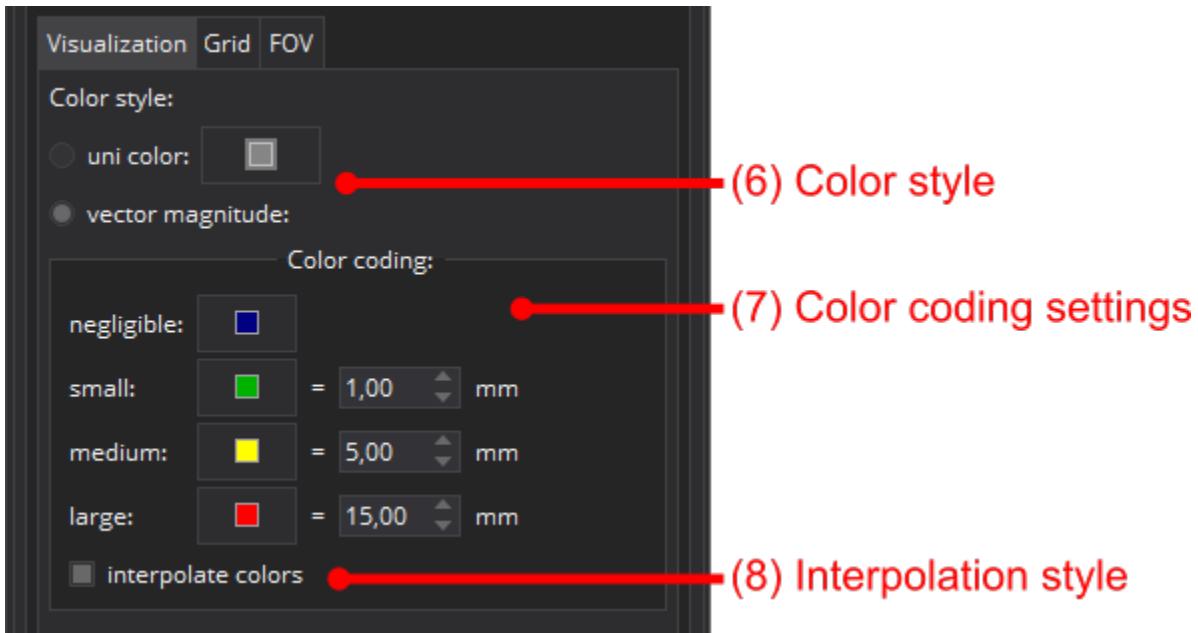
More details can be found in the settings and style section below.





Example of the appearance of different style settings: a) grid style; b) grid with no color interpolation; c) grid in unicolor; d) grid with different grid frequency (frequency=1); e) grid also showing start grid (in gray); f) glyph style.

## Visualization settings



Visualization settings offered by view.

**(6) Color style:** The following color styles are available:

uni color: everything painted in the selected color (cf style example "c)"). Click on the color button to change the used color.

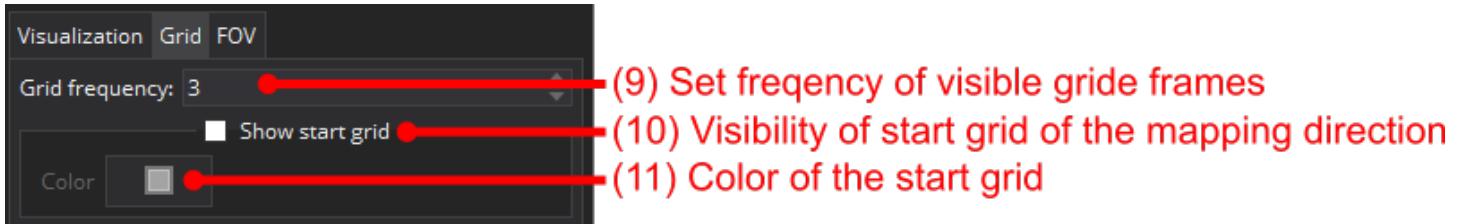
vector magnitude: the color is depending on the respective vector magnitude of the deformation field (cf style example "a)" and "b)"). See (7) for instructions to change the used color encoding for the magnitude.

**(7) Color coding settings:** One can change the color and associated vector length (in mm) for 4

classes of magnitude (negligible, small, medium and large). The color is encoded accordingly.

(8) **Interpolate colors**: By default activated, the colors between magnitude classes (see (7)) will be linear interpolated (e.g. with the settings given in the example shifts of 5 mm will be yellow, 10 mm will be orange and  $>=15$  mm will be red). If interpolation is deactivated the color of one class is used till a next higher class is reached. Cf style example "a)" and "b)", in "b)" no red color can be seen because no shift was 15 mm or greater (magnitude class "large").

## Grid settings



Grid settings offered by view.

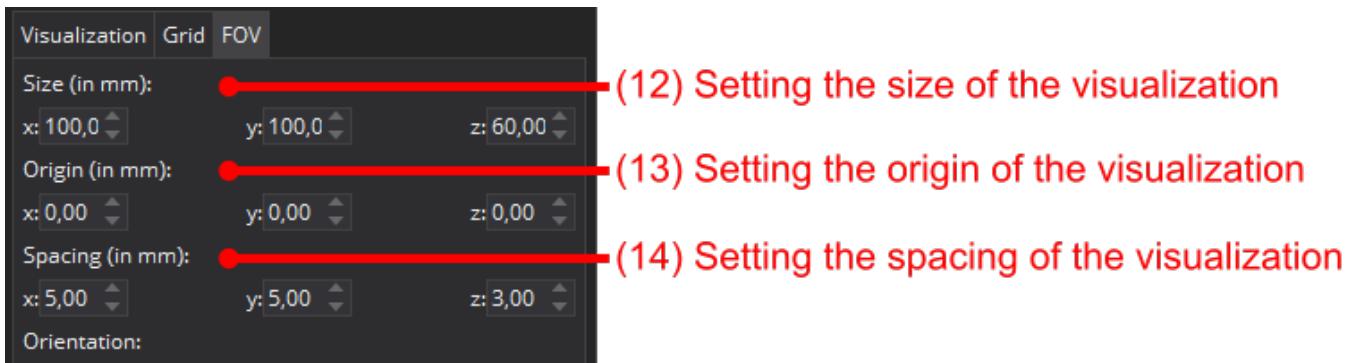
These are only available for style "grid".

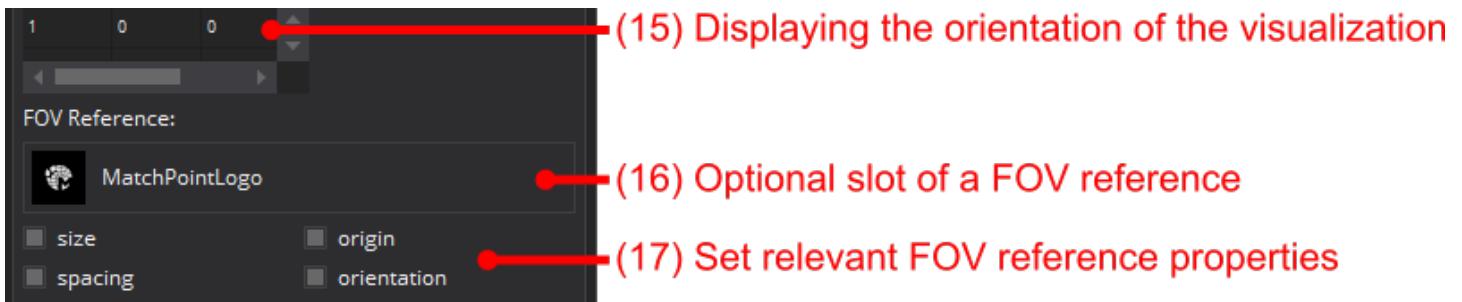
(9) **Grid frequency**: Allows to control how sparses the grid frame should be. With a frequency  $n$  only each  $n$ -th element of the frame will be visualized, so the visual grid has  $n$ -times the spacing of the FOV. One can also achieve something similar with just changing the FOV spacing (see below), but using the frequency allows for a sparse frame and still having a high resolution in the frame deformation. The latter one would loose if just using a low FOV spacing. Style example "a)" and "d)" illustrate different frequency settings and there effect.

(10) **Start grid**: If activated also the start grid of the registration will (for the chosen direction) will be visible. This is another grid specific possibility to illustrate the amount of deformation (cf style example "e)").

(11) **Start grid color**: Select the color that should be used for the start grid. Click on the color button to change the used color.

## Field of view (FOV) settings





FOV settings offered by view.

The field of view defines the area of space (grid) that should be used for the visualization of the registration.

(12) **Size**: Size of the FOV in mm.

(13) **Origin**: Origin of the FOV in mm.

(14) **Spacing**: Spacing of the FOV in mm. This directly impact the visualization's level of detail.

**IMPORTANT:** Please be careful with setting small spacings, as it can lead to computational very expensive visualizations.

(15) **Orientation**: Orientation matrix of the FOV (only readable).

(16) **FOV Reference slot**: Select an image that should be used to define the geometric properties of the FOV. By default (and available) the target image used to determine the registration will be used. Click slot to change the FOV reference.

(17) **Relevant FOV reference properties**: One can select which properties of the reference image will be used to specify the FOV.

## Information regarding the directions

Registrations can have two supported directions (direct and inverse). The direct kernel maps from the moving space into the target space, so this is the direction that "naively" people assume when they think about registrations. But practically it is only used to map continuous data like point sets. The inverse kernel maps from the target space into the moving space and is used to map images by so called inverse mapping. The effect is most obvious in the glyph style, where the glyphs points from the mapped space to the point in the moving space.

## Data reference

The data visible in the visualization styles images is part of the Patient 1 of the DIR\_validation\_data data set. For further information: [https://www.creatis.insa-lyon.fr/rio/dir\\_validation\\_data](https://www.creatis.insa-lyon.fr/rio/dir_validation_data)

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By downloading this data, you agreeing to follow these guidelines. When using any of the data

provided for publications, please make reference to:

The institution from which they were obtained: the Léon Bérard Cancer Center & CREATIS lab, Lyon, France.

The article containing the description of this data:

J. Vandemeulebroucke, S. Rit, J. Kybic, P. Clarysse, and D. Sarrut. Spatiotemporal motion estimation for respiratory-correlated imaging of the lungs. In Med Phys, 2011, 38(1), 166-178. pdf

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# Medical Imaging Interaction Toolkit: The Measurement View

Icon of the Measurement View

## Overview

The Measurement view allows you to measure distances, angles, paths and several geometric figures on 2D images or image slices of 3D and 4D images. The measurement view is repeatedly usable with the same or different measurement figures that are related to the chosen image and can be saved together with it for future use.

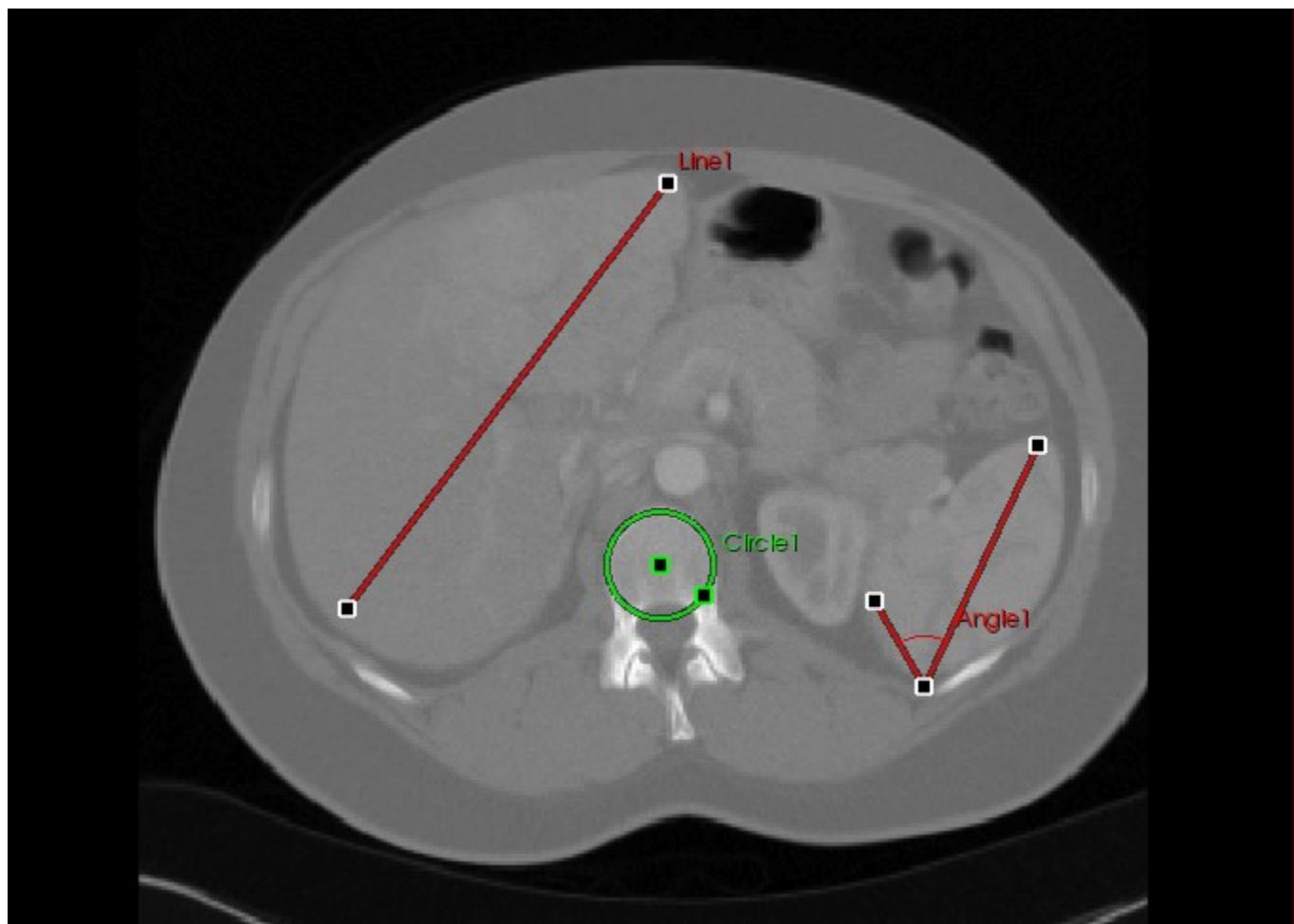
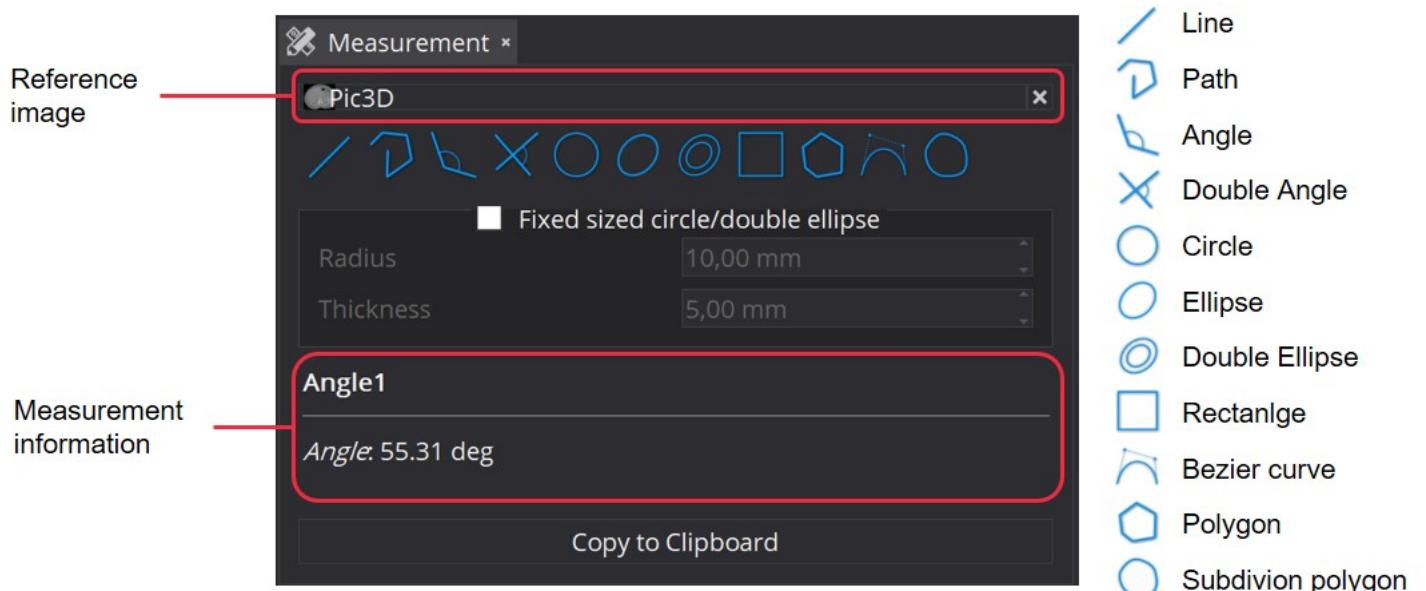


Image with measurements

## Usage

The first step to perform measurements is to select a reference image on top of the view. All resulting measurements will be assigned as child nodes of the image in the data manager. The standard

working plane is 'Axial' but the other standard view planes ('Sagittal' and 'Coronal') are also valid for measurements.



## Measurement View

After selecting an image, you can click on any of the geometrical symbols. The respective measurement will appear as soon as you click on the image location you want to measure.

The view offers a variety of measurement options that are introduced in the following:

### **Line:**

Draws a line between two set points and returns the distance between these points.

### **Path:**

Draws a line between several set points (two and more) and calculates the overall length, which is all lines length summed up. Add the final point by double left-click.

### **Angle:**

Draws two lines from three set points connected in the second set point and return the inner angle at the second point.

### **Four Point / Double Angle:**

Draws two lines that may but do not have to intersect from four set points. The returned angle is the one depicted in the icon.

### **Circle:**

Draws a circle by setting two points, whereas the first set point is the center and the second the radius

of the circle. The measured values are the radius and the included area.

### **Ellipse:**

Draws an ellipse that can be modified by three points. The middle point can be used to move the whole measurement. The lower point modifies the ellipse axes. The right point can be used to modify the radius of the ellipse. The measured values are the major and minor axes and the area.

### **Double Ellipse:**

Draws two ellipses by adjusting four points. The middle point can be used to move the whole measurement. The left point is used to adjust the distance between the two ellipses. The lower point modifies the ellipse axes. The right point can be used to modify the radius of the ellipse. Can be used for measuring e.g. the wall thickness of a vessel. The measured values are the major and minor axes and the thickness.

### **Rectangle:**

Draws a rectangle by setting two points at the opposing edges of the rectangle starting with the upper left corner. The measured values are the circumference and the included area.

### **Polygon:**

Draws a closed polygon that can have an arbitrary number of points. New points are added by left mouse-click. To finish the drawing the user can double click on the last control point. The measured values are circumference and area.

### **Bezier curve:**

Draws a bezier curve by adding some control points with left mouse-click. To finish the drawing the user can double-click on the last control point. The measured value is the length of the bezier curve.

### **Subdivision Polygon:**

Draws a closed subdivision polygon by adding some control points with left mouse-click. To finish the drawing the user can double-click on the last control point. The measured value is the circumference of the polygon.

## **Fixed sizes of measurement figures**

The measurement view offers a fixed size for circle and double ellipses to preset a radius and a thickness. This is useful e.g. for diagnostic studies where you want to derive gray value statistics from a well defined region.

## **Modify measurements**

All measurements can be modified later on by moving the respective control points. Note that they can only be modified if the view is open.

## **Multiple measurement figures**

When applying more than one measurement figure to the image the actual measurement figure is depicted in red and the displayed values belong to this measurement figure. All other measurement figures appear white. They can be selected by a left-mouse click on the respective node.

## **Save the measurement information**

The entire scene containing the image and the measurement figures can be saved for future use. Scenes are saved with a '.mitk' extension by pressing 'Save Project' and contain all nodes and relevant information. Alternatively, you can just save the measurement solely (with file extension '.pf') by right-click on the node in the data manager.

The content of the measurement widget can be copied to the clipboard with the corresponding button for further use in a table calculation program (e.g. Open Office Calc etc.).

## **Remove measurement figures or image**

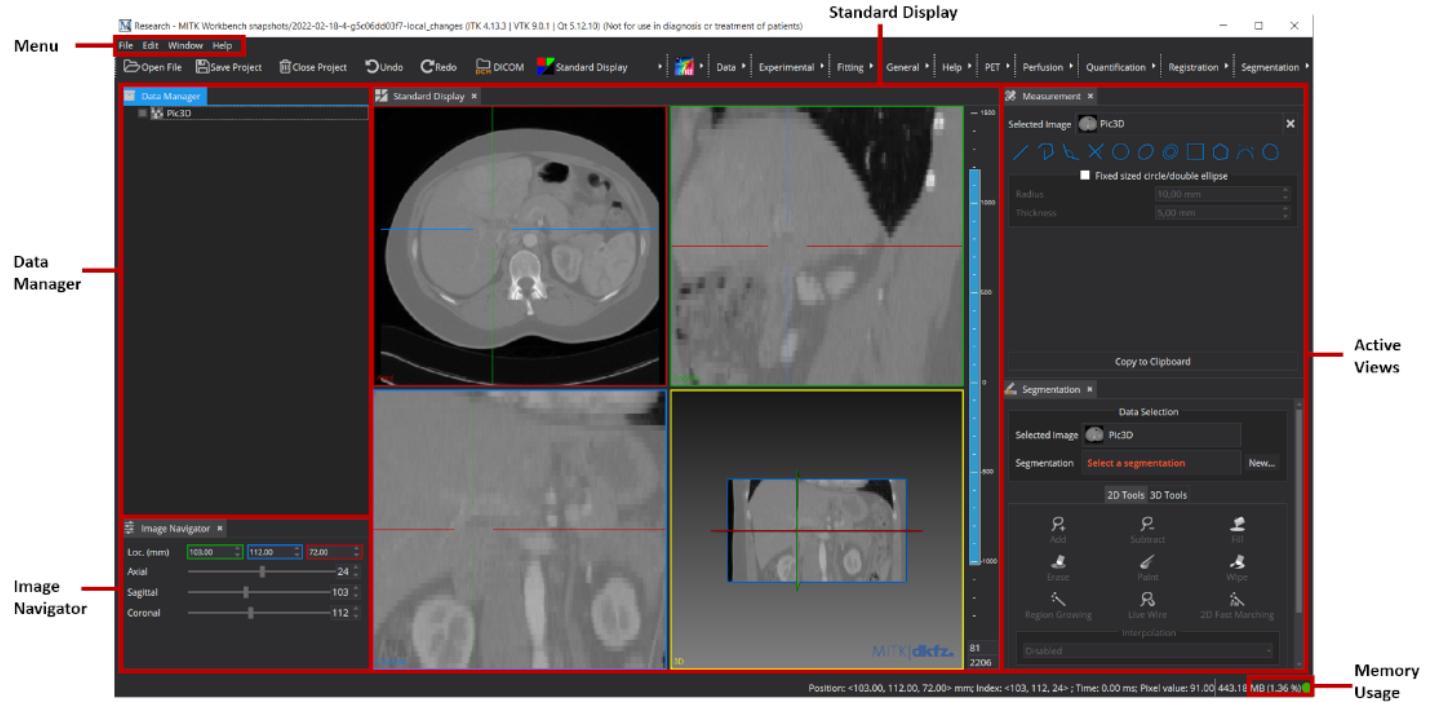
If the single measurement figures or the image is not needed any longer, it can be removed solely or as an entire group. The image can't be removed without simultaneously removing all the dependent measurement figures that belong to the image tree in the data manager. To remove, just select the wanted items in the data manager list by right-clicking on the respective node or, if several items wanted to be removed, right-click on all wanted by simultaneously holding the ctrl-button pressed.

# Medical Imaging Interaction Toolkit: The MITK Workbench

Welcome to the basic MITK user manual. This document gives a concise overview of the basic functions of MITK and instructions how to use them.

## The User Interface

The layout of the MITK applications is designed to give a clear distinction between the different work areas. The following figure gives an overview of the main sections of the user interface.



The Common MITK Application Graphical User Interface

## Menu

### File

This dialogue allows you to save, load and clear entire projects. This includes any nodes in the data manager.

### Edit

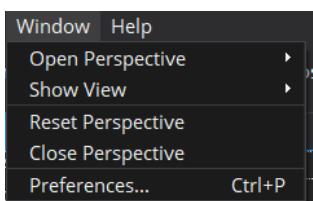
This dialogue supports undo and redo operations.

### Window

This dialogue allows you to change between the [Perspectives](#) and reset your current ones to default settings.

If you want to use certain [Views](#) within a perspective the "Show View" menu allows to select a specific function that is opened and can be moved within the working areas according to your wishes. Be aware that not every view works with every perspective in a meaningful way.

The Preferences dialogue allows you to adjust and save your general and view-specific custom settings.



Window dropdown menu

## Help

This dialogue contains the help perspective containing the view-specific documentation, the welcome screen and information about MITK.

## Perspectives

The different tasks that arise in medical imaging need very different approaches. To acknowledge this circumstance MITK supplies a framework that can be build upon by very different solutions to those tasks. These solutions are called perspectives, each of them works independently of others although they might be used in sequence to achieve the solution of more difficult problems.

It is possible to switch between the perspectives using the "Window"->"Open Perspective" dialogue. Available default perspective are "Research", "Viewer" and "Visualization". Various views can be added to each perspective to tailor the chosen perspective to your specific requirements.

## Views

Each solution for a specific problem is realized as a self contained view. Thus you can create a workflow for your problem by combining the capabilities of different views to suit your needs within a perspective.

By pressing and holding the left mouse button on a view tab you can move it around to suit your needs, even out of the application window.

## System Load Indicator/Memory Usage

The System Load Indicator in the lower right hand corner of the screen gives information about the memory currently required by the MITK application. Keep in mind that image processing is a highly memory intensive task and monitor the indicator to avoid your system freezing while constantly swapping to the hard drive.

## Data Manager

The Data Manager is the central component of MITK to manage medical data like images, segmentation masks, registrations, surfaces, point sets, annotations and measurements. For a detailed description of the Data Manager please be referred to the view documentation: [The Data Manager View](#).

## Image Navigator

Fast movement through the available data can be achieved by using the Image Navigator. By moving the sliders around you can scroll through the slides and timesteps. For a detailed description of the Image Navigator please be referred to the Image Navigator view documentation: [The Image Navigator](#).

## Standard Display

The four window view of the standard display is the heart of the MITK image viewing. For a detailed description of the four window view and the levelwindow please be referred to the standard display view documentation: [The Standard Display](#).