CT Viewer Slab Mode

The CT Viewer - Slab mode allows you to view and manipulate slab images. You can perform some tissue definition functions. You can also create Curved Planar Reformat (cMPR) images and Paddle Wheel rotations in the x- or y-axis.

Slab is the default view mode when you open the CT Viewer.

WARNING

Verify correct semi-automatic volume segmentation for bed and head holder removal operations.

WARNING

When thick-slice Brain images are viewed in the slab mode some partial volume artifacts might occur.

Cross sectional images might rotate around the centerline. Please note orientation annotations on images.

In cases where the orientation annotations are not displayed on the image - you must not assume any specific orientation. For correct orientation information - use only the images which display such information.

One or more of the following image types may appear in this application: curved MPR, straightened MPR, volume images, and thick slab images. Measurements you make on such processed images can sometimes be misleading. When saving such images, make sure they are labeled properly.

Objects in thick curved MPR images may appear distorted. Use caution when making measurements on MPR images.

NOTICE

When loading data into an application, ensure the orientation shown on the images is consistent with the images' appearance. This precaution is required for data that contains wrong orientation information because the data will be incorrectly presented within the application.

Slab Mode

The Slab mode window consists of a slab image and two orthogonal reference images. You can view the slab image by rotating it and changing its thickness. You can set the slab’s rotation center by moving the cross hairs in the reference images.

NOTICE

The layout of the display may appear differently on your IntelliSpace Portal. The opening window shows the Slab mode. An alternate viewing mode is the Planar mode.

The two reference images show orthogonal axis orientations (regardless of slab rotation in the main image). Color-coded cross hairs in the reference images indicate the orthogonal axes: axial (red), coronal (green), and sagittal (blue). Only the axial (red) crosshair can be rotated.

2x2 Layout

The CT Viewer Slab mode 2x2 layout includes a volume image. To display segmented tissues on the volume image: Accept the tissue; go to Tissue Management tab; click on the volume image. Within the Tissues list un-check the “Volume” option and check the newly created tissue.

Planar Mode

The planar mode displays the three orthogonal views in three viewports. There is no “main” or Slab image. See section “Planar Mode” on page 26.

Paddle Wheel

A paddle wheel function allows viewing images radially around a horizontal or vertical axis. See section “Paddle Wheel” on page 31.

Load Multiple Studies in Application

To load multiple studies in the application:

1. Use the **Ctrl** key when selecting studies from the Directory list.
2. Select the application from the Applications menu.
3. Confirm the studies are from the same patient.

Slab Viewer Tool Panel

The tool panel of the Slab mode consists of a variety of buttons, boxes, and tabs that allow you to access the available functions.

The upper third of the panel provides functions for selecting and manipulating images.

The middle third of the panel provides functions affecting scenes: Series, Curve, Clip & 3D Segmentation, Batch, Tissue Management and Fusion functions.

The lower third of the panel consists of the Common Tools. Common tools provide many basic functions, including saving, filming, reporting, scrolling, measurements, annotations, panning, zooming, rotating, and windowing.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Improved Brain Contrast

WARNING

In the CT Viewer - Slab mode application, when you use the Improved Brain Contrast feature on Brain images, the resulting images should not be used as the SOLE basis for clinical diagnosis.

The CT Viewer - Slab mode application allows you to enhance the contrast of brain images with the Improved Brain Contrast button, which appears in the upper part of the viewing tools section of the tool panel.

A drop-down menu allows you to select one of three brain Contrast Settings: Soft, Medium, and Strong. The settings change the extent of the enhancement applied on the image. The last setting used before exiting CT Viewer will be the default setting the next time you activate the Improve Brain Contrast feature.

- To activate the function, click the **Improved Brain Contrast** button. The brain image in the active viewport is processed at the current enhancement setting, and the message “Processed - Enhanced Brain Contrast” appears near the bottom of the viewport.
- To deactivate the Improved Brain Contrast function, click the button again.

Dynamic Viewer

Dynamic Viewer changes image characteristics (slice width and enhancement parameters) according to the window width you set while viewing the study. This helps to assure a consistent and optimal ratio between noise and window width.

- Click the **Dynamic Viewer** button to activate its function.
- Change the window width using the middle mouse wheel or use the relevant predefined windowing presets in the toolbox (Brain, Abdomen, Bone, or Lungs, for example.)

  Based on the window width value, the dynamic viewer applies changes to the slice width and enhancement parameters to create the displayed image.

The dynamic viewer allows using one single reconstruction for reviewing any window.

Use thin and sharp images to achieve the optimal image quality. Try several reconstruction filters each time you use a new protocol with the dynamic viewer. (It is recommended to use the Y filter.) The filter that delivers the best results should then be used in the Scan Protocol on the scanner.

NOTICE

When reconstructing the images do not use smoothing / enhancement. The dynamic viewer does not take into account any smoothing / enhancement performed on the images before the images are loaded into the CT Viewer.

When to Use Dynamic Viewer

The dynamic viewer works only with CT images. It does not work with mixed modalities (CT, PET, SPECT).

The dynamic viewer works only with Average, MinIP and MIP renderings.

The dynamic viewer is disabled if Magic Glass is active.

If the active series cannot be assigned to one of the available dynamic viewer protocol groups in the system (for example non-Philips scans or non-CT images), the dynamic viewer button is grayed out and cannot be activated.

Dynamic Viewer Protocol Groups

When you load any series into the CT Viewer application, the series is classified as belonging to a predefined group according to the parameters of the scan: filter group (same extent of sharpness), rendering and scan type (if one exists). Each acceptable group has a corresponding dynamic viewer protocol. (For example, all scans with filter B, “Body” scan type, standard resolution, and MIP rendering mode belong to the same group.)

NOTICE

The keyboard shortcut key “P” allows you to switch between all protocol presets available in the current study’s group.

If such additional presets are available, pressing P repeatedly scrolls through the presets.

If the Compare mode in ON, and the Dynamic Viewer is open on several volumes, the shortcut works on the active volume only.

Create Dynamic Viewer Protocol

If you have modified a dynamic viewer protocol at a certain window width level by changing the thickness and/or enhancement parameters, you can save it as a new protocol using the Settings function.

The Settings function is accessed from the drop down menu of the dynamic viewer.

From the Settings dialog, you can select a protocol from a list of all dynamic viewer protocols that are available for the group that your current series is part of.

NOTICE

When adjusting the dynamic viewer protocol, you should change both the enhancement and the thickness at the same window width rather than at different window widths.

Save Dynamic Viewer Protocol

It is possible to save, rename, delete and set as default a user defined protocol by clicking on the relevant button.

Save Protocol as ...

Save the active protocol by a new name. A dialog opens for typing the new name. Saving a protocol preset saves it to the current protocol group.

Save Protocol as Default

The active protocol is saved as the default for the current protocol group.

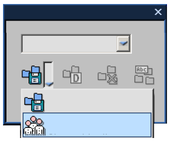
Delete Protocol

Delete the active protocol.

Rename Protocol

Rename the active preset.

More about Dynamic Viewer Protocols



Factory protocols cannot be overwritten or renamed.

A dynamic viewer protocol is retained for specific series during the same application run. If, during an ongoing application run, you activate dynamic viewer, perform changes to the default protocol, and then deactivate and activate dynamic viewer again, the last used protocol for this series is retrieved. When you open the CT Viewer again and activate the dynamic viewer, the default protocol will be used.

If you are a Clinical Administrator and are saving a new Dynamic Viewer protocol, the Share with all users function is available.

When a Clinical Administrator shares a protocol, it becomes available to all existing and new users of the originating IntelliSpace Portal system. (Non-administrative users cannot delete, rename, overwrite, or modify shared presets).

Slab Viewer Tools

Use the Slab Viewer Tools to review images.

Orientation

Use these buttons to select the viewing orientation of the main viewport: axial, coronal, or sagittal.

Flip

Use this function to flip the image in the main viewport. A selection arrow allow you to flip: Rotate 180 horizontal (right to left); Rotate 180 vertical (top to bottom).

Planar Mode

Use this mode to view the three orthogonal plane images. The planar mode is activated by the Planar button which displays the three orthogonal views in three viewports. There is no “main” or Slab image.

Each image can be manipulated independently, while the axes remain oriented at 90 degrees to each other.

Crosshairs appear on all 3 planar viewports. They can be moved and rotated.

The crosshairs mark rotation center in the Planar mode, around which the views can be rotated.

Changing the rendering and thickness in one Planar viewport affects all viewports.

Slab Viewer Layout

There are 2 layouts:

The 1+2 layout consists of one main image and 2 reference images.

The 2X2 layout shows equal size viewports in 4 quadrants.

In these two layouts there is the option to display the surview image (if it was loaded with the study) or MPR images.

To switch an image to another viewport, hold down the right mouse button and drag the image to the desired position.

To view surview images in the reference viewport, right click over the reference image and select Frontal or Lateral localizer. (These options only appear if the surview has been loaded)

1+3 Curve-mode

When you activate the Curve mode, a third reference viewport replaces the 1+2 viewport in the layout. This displays the 3 orthogonal views, with the results of the drawn path in the upper right viewport.

Compare

The Compare function allows you to perform a side-by-side review of selected images.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Automatic Registration and Alignment

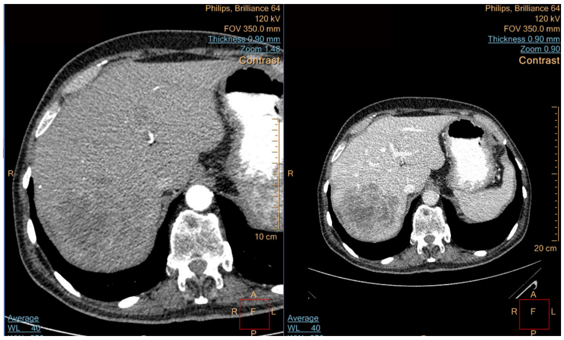
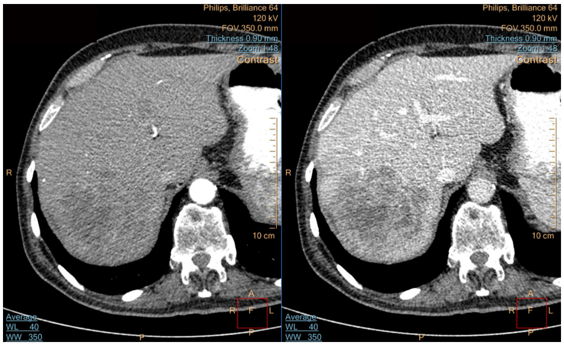
Automatic Registration automatically aligns the display of the compared series in order to display the same anatomical region with the same zoom for all of the compared volumes.

The Automatic Registration algorithm improves the speed and efficiency of the workflow for comparing different series. Automatic Registration between the various series automatically runs when the application is loaded.

To apply registration between the series, activate the **Compare** mode button followed by the **Auto-register compared volumes** button (located in the upper toolbox).

The following anatomical alignment occurs when **Auto-register compared volumes** is activated after selecting a series with the same orientation:

- Compared series (with the same orientation) scroll to the same slice.
- The rotation center is aligned to the same anatomical location on all of the compared series using the automatic registration algorithm.
- All of the compared series are panned and zoomed to align the display, such that all the compared series will display the same anatomical area within the viewport.
- The **Link** button is activated automatically (if it was not activated already).

Status	Example
Not Aligned	
Aligned (after selecting **Auto-register compared volumes**)	

Tab. 1: Pan and Zoom Alignment Examples

NOTICE

When automatic registration is applied between the compared series, it is necessary to verify that the compared series are correctly aligned. Edit alignment as required.

Correcting Registration

If automatic registration results are inaccurate and corrections are required:

1. De-select the **Link** button.
2. Scroll, pan or zoom the compared series to correct alignment.
3. Select the **Link** button again.

NOTICE

After de-selecting the **Link** button, the **Auto-register compared volumes** button is also de-selected.

If the Apply Registration button is not activated and the link button is activated, in **Compare** mode, the alignment between compared volumes is relative to the location/zoom/pan of the compared volumes when first clicking the **Link** button.

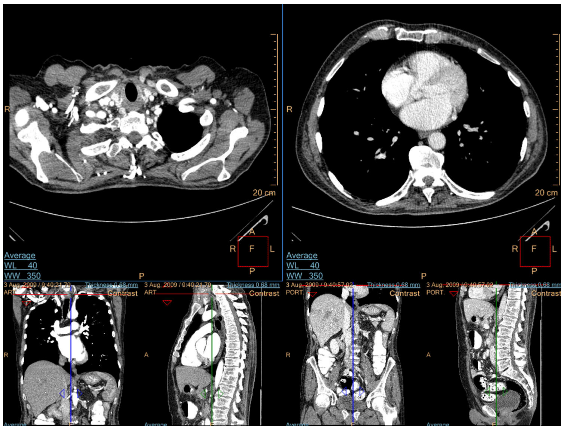
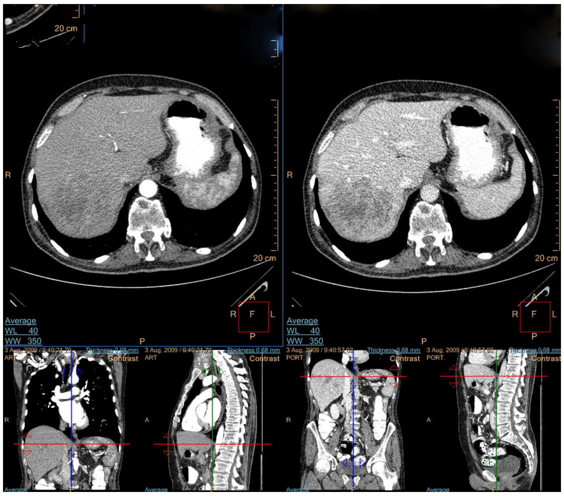
Registration by Frame of Reference for Series from the Same Acquisition

1. Select several series with the *same* orientation that was reconstructed from the *same* acquisition (for example, different reconstructions that were reconstructed from the same scan).
2. Activate the **Compare** mode button followed by the **Auto-register compared volumes** button.

   Anatomical alignment is performed using the frame of reference and *not* any automatic algorithm.

Different Z-coverage

If the compared series do not completely overlap in the z-direction (for example, one series is Chest + Abdomen and another series is only abdomen), when scrolling the longer series to a location that has no matching location on the other series, the other series will stop at the last slice. When scrolling the first series back, the other series will become aligned again and will start scrolling together once they reach the overlapping area. An example is provided below.

Status	Example
The series are not aligned as long as the slice displayed on the Chest +Abdomen series is *not* overlapping with the Abdomen + Pelvis series.	
The series are aligned when the slice displayed on the Chest +Abdomen series overlaps with the Abdomen + Pelvis series (for example, liver area).	

Relate Button Behavior

It is possible to use the Relate tool in **Compare** mode when comparing between different volumes, as long as the **Auto-register compared volumes** button is activated.

When de-activating the **Auto-register compared volumes** button, the Relate tool will only be available between different images of the same volume.

Supported Spectral Results

The following results are supported by the automatic registration algorithm:

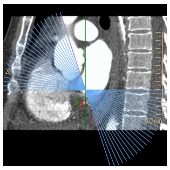
- Conventional [HU]
- MonoE XX keV [HU]
- MonoE XX keV (Equiv. to conventional CT [HU]

- VNC [HU*]
- Calcium Suppression XXX Index [HU*]

The automatic registration algorithm is applied on the remaining spectral results only if one of the following conditions is met:

- The corresponding SBI series is available in the application.
- A supported series that was reconstructed from the same scan is available in the application.

Paddle Wheel



The Slab viewer offers both the normal viewing mode and the paddlewheel mode. The normal mode allows you to scroll and view images that are parallel to each other (that is, in parallel slices).

The paddle wheel mode allows you to scroll and view images radially around the x-axis or y-axis. (The image from the Paddlewheel Batch function demonstrates the x-axis paddle wheel effect.)

The location of the line in the volume is determined by the cross hair on the reference images.

Use Paddle Wheel

1. Click the **Paddle wheel** button.
2. Select X-Axis or Y-Axis from the viewport controls.
3. Scroll the main viewport to navigate through the generated paddle wheel MPRs.

   The image rotates around the axis that is set by the crosshair in the reference images. The reference images remain constant.

Crosshair and Rotation-center

These tools allow you to:

- **Show Crosshair (default).** Shows the crosshairs on reference images.
- **Rotation Center.** Show the center point around which the volume can be rotated.
- **Center Cursor.** This function moves the middle of the image to the rotation center.

Layout Manager

The Layout Manager allows you to perform various layout (display) management functions.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Slab Viewer Functions

To access additional Slab Viewer functions, click the down arrow in the tab window, or hover the mouse over the tab window. The list of available functions displays.

See the **Report**, **Film**, **Common Processes** and **Common Tools** sections (in the "Instructions for Use" volume) for information on using common options, tools, functions, and processes.

Curve

The Curve function allows you to draw a curve (or load an existing curve to produce a curved path to produce a Curved Planar Reformat (cMPR) image, or a curved path for the Endo viewer’s fly through function.

Batch

The Batch function allows you to create a series of sequential slab images for viewing, saving, reporting and filming purposes.

Tissue Management

The Tissue Management function allows you to control the viewing of the active tissue, based on the tissue definitions for the current study that have been created in the current work session, or that were previously saved for this study, from this and other applications.

Fusion

The Fusion Viewer employs standard CT Viewer functions, allowing you to view PET and SPECT images, and to fuse NM images with CT images.

Slab Viewer Common Tools

The common tools area provides many basic functions, including measuring, saving, panning, zooming, rotating, and windowing. Common tools are, in general, common to all the CT Viewers, and are shared with many other applications of IntelliSpace Portal. If a common tool has a special function in the Slab mode, that function is described in this section.

See **Report**, **Film**, **CT Common Processes** and **CT Common Tools** for information on using common options, tools, functions, and processes.

Relate

In the Slab viewer the relate point is positioned in the middle of the slice thickness. As a consequence, if a relate point is created on a vessel when the slab thickness is set to 10 mm (for example), the vessel might not appear in the reference ports because the vessel may not pass through the middle of the slab.

To prevent this, you can set the slab to the minimum thickness so that when you create a relate point over the vessel, the desired vessel appears in the reference images.

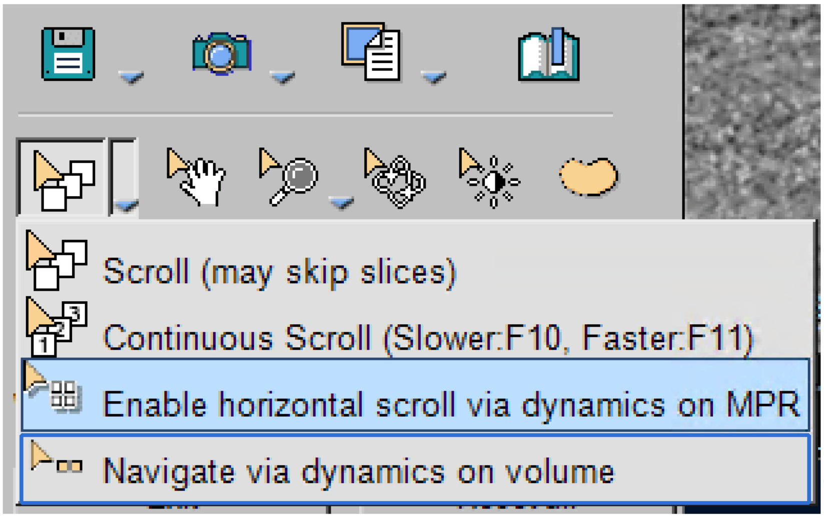
Slab Mode 4D Visualization

Slab mode provides viewing, scrolling and navigation capabilities of 4D datasets/ multi-dimensional data.

The 4D visualization feature in CT Viewer Slab mode supports multidimensional and multimodality data (MR support in CT Viewer is limited for this functionality)”.

Enable horizontal Scroll through the dynamics on MPR images

1. To activate dynamic scrolling, select **Enable horizontal Scroll through the dynamics on MPR** (#1) from the Scroll tools menu in Common tools (or via the right click context menu).



2. Drag the left mouse horizontally in left/right on MPR image to navigate through dynamics.
3. Horizontal scroll can be stopped at a specific temporal phase for other interactions such as zoom.
4. Scroll through the images in a vertical direction, stop at any point and scroll in a horizontal direction.
5. The Series number and Slice number are dynamically updated on Scroll along with the fourth dimension (Phase/ time).

6. According to the scroll performed on volume image, the MPR images are updated accordingly and display the updated dynamic image synchronized.

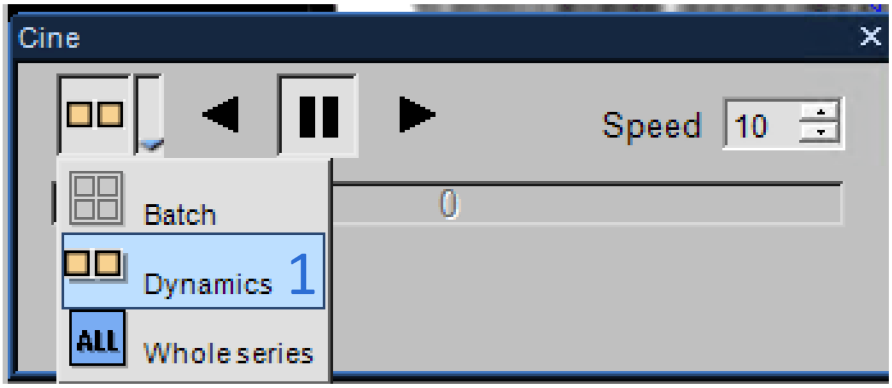
Enable 4D Scroll on Volume Viewport Image in Slab Mode

You can select option **Navigate via dynamics on volume** (#2 above) from the Scroll tools menu in Common tools (or via the right click context menu).

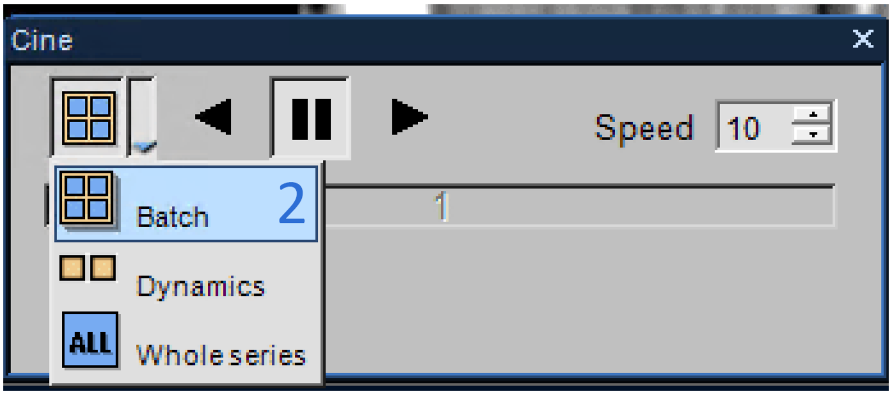
1. To activate dynamic scrolling, select **Navigate via dynamic on volume** (#2 above) from the Scroll tools menu in Common tools (or via the right click context menu).
2. Drag the left mouse horizontally in left/right on Volume image to navigate through dynamics.
3. Horizontal scroll can be stopped at a specific temporal phase for other interactions such as zoom.
4. The Series number and Slice number are dynamically updated on Scroll along with the fourth dimension (Phase/ time).
5. According to the scroll performed on volume image, the MPR images are updated accordingly and display the updated dynamic image.

Cine Functions for 4D datasets in Slab

- The application support seamless cine play across different dimensional volumes /Temporal phases. The Dynamics option (#1 below) in Cine Dialog is automatically selected for 4D/ Dynamic datasets. The **Dynamics** option appears active only if data is multi- dimensional and plays cine along the dimensions. If data is not multi-dimensional, the option is disabled.

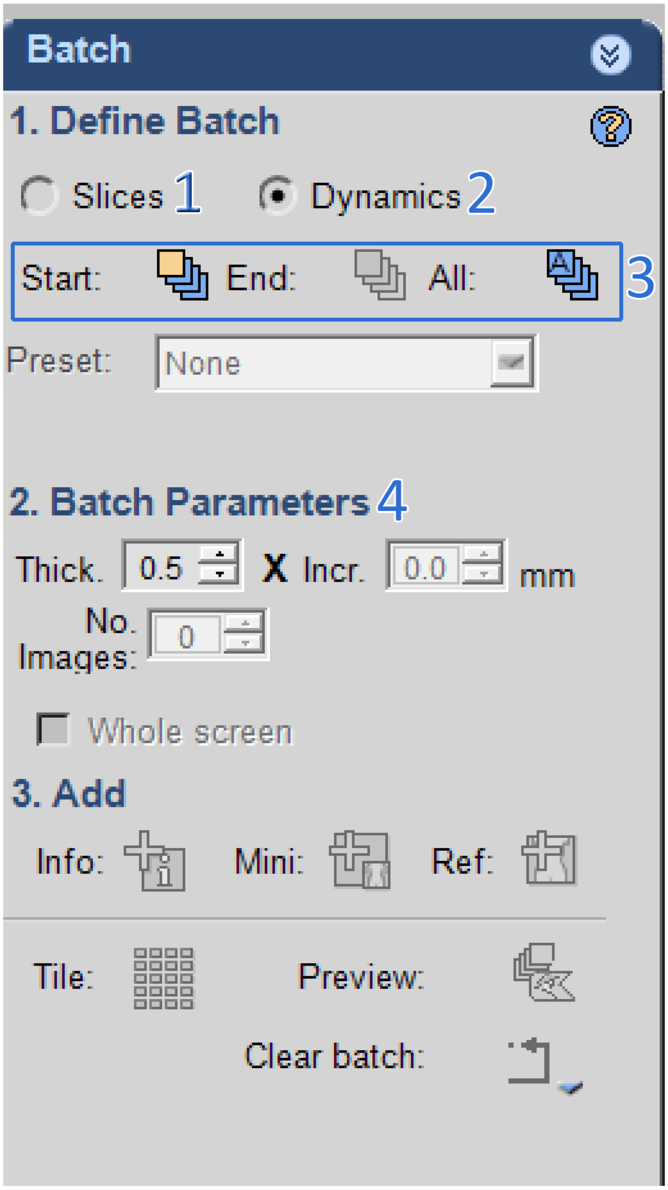


- In Dynamics cine mode, cine plays through all phases/time point for selected slice from phase 1 to “n” continuously.
- While cine is playing, use the available interactive tools to scroll through the slices and volumes.
- While cine is playing, all the view ports are synchronized.
- Control the Cine Speed by adjusting the speed control.
- Cine Batch – plays cine of the created Batch, displayed using the Batch option (#2 below) in the Cine Dialog.



Batch functionality –Create Dynamic Batches for MPR Images

When multi-dimensional data is selected for Batch creation on an MPR image, Define Batch section shows Slices (#1) and Dynamics (#2) .



○ Slices ● Dynamics

Preset: None

Thick. 0.5 X Incr. 0.0 mm

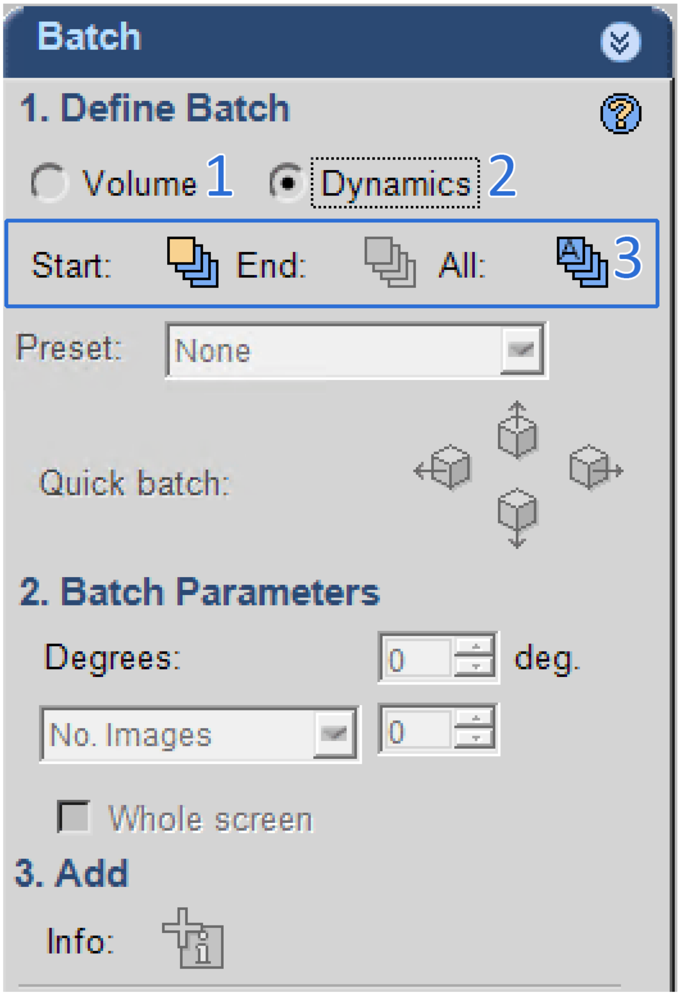
No. Images: 0

☐ Whole screen

- **Slices** is the default selection for creating batches through the slices.
- For Dynamic datasets, select the **Dynamics** option, activate dynamic scroll, mark the **Start/End** or **All** buttons (#3) and create a batch of dynamics for the currently shown location.
- Specify Slice thickness, number of images and define other batch parameters (#4). Increment selection is not applicable for Dynamics.

Dynamic Batches for Volume images

When multi-dimensional data is selected for Batch creation on Volume image, Define Batch section shows (#1) Volume and (#2) Dynamics.



Preset: None

Degrees: 0 deg.

No. Images 0

☐ Whole screen

- **Volume** is the default selection for creating batches of the Volume.
- For Dynamic datasets, select the **Dynamics** option, activate dynamic scroll, mark the **Start**/**End** or **All** buttons (#3) and create a batch of dynamics volume.
- To create dynamic batches in a freestyle, select a Batch start location, navigate through the phases, rotate the volume, modify parameters such as zoom, windowing and then choose batch end location. Click on Batch end location each time you perform the above actions.

Key Board Shortcut for Dynamic Scrolling

For multi-dimensional datasets, use the keyboard shortcut key **Ctrl+right/left arrow** to navigate between dynamics.