16 MR Liver Health

The MR Liver health application provides volumetric or ROI analysis for Liver and Liver segments for muti-parametric maps on MR data sets in order to assist the user with evaluation of liver diseases. For liver VOI measurements, the application allows to define a range of fat fraction respectively T2* values to be included into the calculation. It also provides longitudinal analysis by comparing results for liver quantification values of more than one time point.

CAUTION

Volumes (e.g., lobes and liver) obtained with MR Liver Health should not be used as the sole basis for procedure planning.

CAUTION

Do not use liver health application for evaluation of volume and fat accumulation in other organs such as spleen or kidneys.

Indications for Use

MR Liver Health is a post-processing application providing tools to assess liver characteristics from MRI biomarkers such as Fat Fraction or T2*/R2* for the whole liver, its segments, and user-defined ROIs.

Key Features

The MR Liver Health application performs automatic liver segmentation and allows landmark based lobe segmentation.

It performs MR-MR inter-series and inter-study registration for providing per-lobe multi-parametric quantification and aligned visualization.

- MR Liver Health supports multi-vendor data.
- MR Liver Health supports Longitudinal follow-up assessment of the liver.
- MR Liver Health provides tabular/graphical representation for multi-parametric results and relative results for longitudinal follow up.
- MR Liver Health provides 3D visualization of the liver and its lobes.

Starting MR Liver Health

1. In the **Patient Directory**, select one or two studies with **mDIXON Quant** data.

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NOTICE

The Liver Health application supports Philips data and multivendor data. For additional information, contact your Philips representative.

NOTICE

If you select two studies, you can compare them side by side in the **Liver Health** application.

⇨ The **Liver Health** application automatically identifies the following data types:

- mDIXON
- mDIXON Quant with Fat Fraction and T2*/R2* maps
- T1W Dynamics
- Water Dynamic image
- Echo with T2*/R2* maps

2. Start the **Liver Health** application.

⇨ The application loads all series from the selected studies that have a valid, parallel stack of images. If none of the series contains valid images, the application cannot be started.

⇨ During loading, the application creates a volume/MPR from the valid series and generates parametric maps. When appropriate data is available in the series, the following maps are created:

- T2*(ms)
- R2*(1/s)
- Fat Fraction (%)
- ADC (10-3 mm2/s)
- EADC
- ISP generated ADA Maps: Diffusion coefficient D (10-3 mm2/s), Perfusion Fraction f, Kurtosis K, Pseudo diffusion (10-3 mm2/s)
- ISP generated T1 Perfusion maps: Max Rel Enhancement (%), T0 (s), Time to Peak (s), Wash out Rate (1/s), Wash in Rate (1/s)

⇨ If the series contains a T2* map and the R2* map is missing, the R2* map is created from the T2* map and is saved with the study (the R2* map is calculated as 1000/T2*, with a unit of 1/sec).

⇨ If the loaded data contains R2* map and T2* map is missing, then the T2* map is created by the application. The T2* map is calculated as 1000/R2* and the unit is ms. The R2* map or T2* map contains the series description of the original series as prefix, from which it was created.

⇨ When the selected studies are loaded, the first study is displayed as a slab in the volume.

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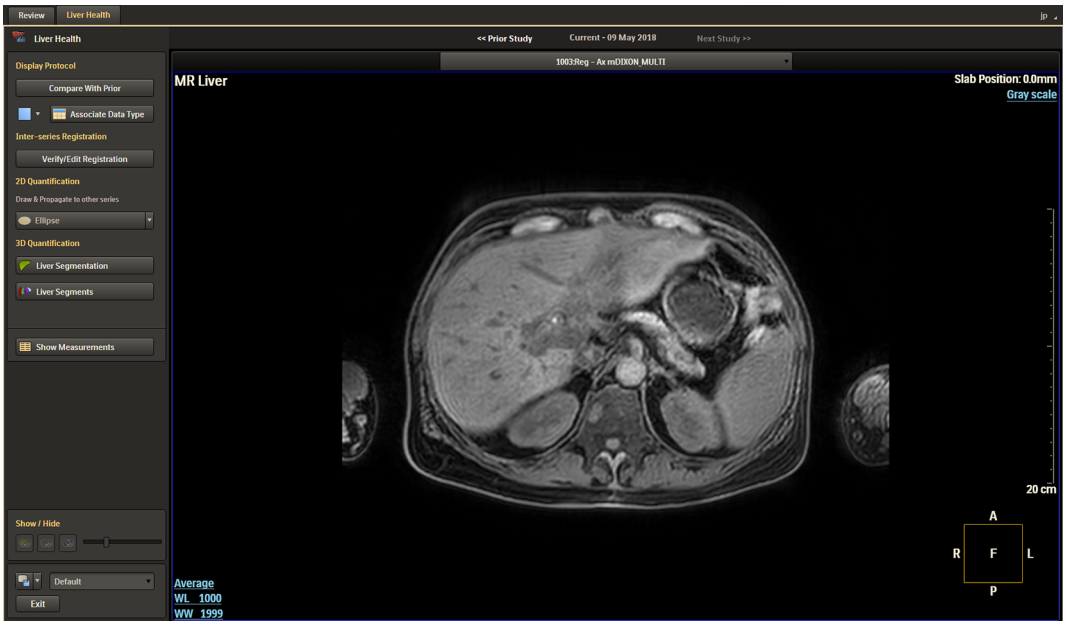

Fig. 140: MR Liver Health - Review screen

NOTICE

The studies and series are registered automatically when they are loaded and liver segmentation starts automatically in the background. If you decide that the segmentation is not accurate after reviewing the series, you can re-register the series manually and restart segmentation.

Using Multivendor Data

If you load multivendor data, the Liver Health application identifies Fat Fraction, T2* and R2* map data. If the application is unable to identify the data, a system message is displayed with the option to associate these data types, if available, in the loaded data.

1. To associate multivendor data, click **Associate Data Type** when the system message.

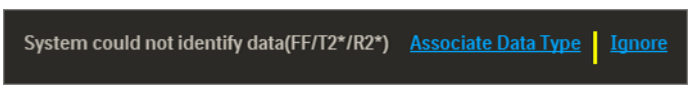

Fig. 141: System message when unidentified data is found

⇨ The **Associate Data Type** task guidance panel is displayed.

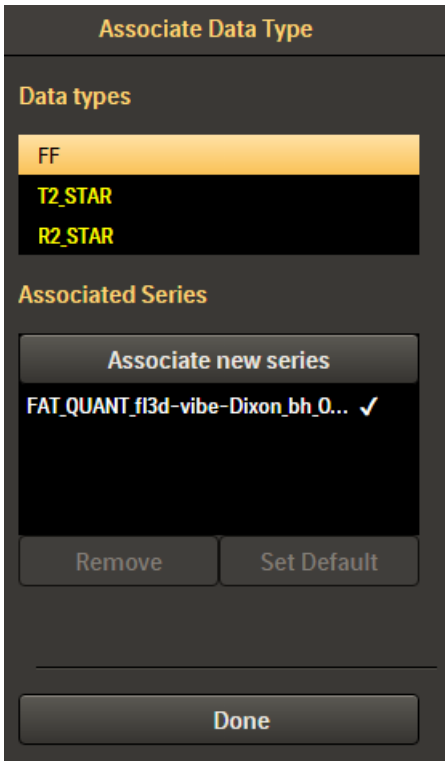

Fig. 142: Associate Data Type task guidance panel

2. Select a data type in the **Data Types** list, then click the drop-down menu above the viewport and select the series that you want to associate with the data type.

⇨ A system message is displayed.

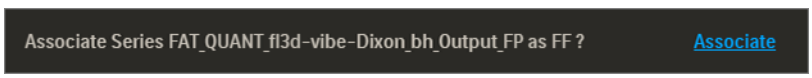

Fig. 143: System message to associate a series with the selected data type

3. Click **Associate** to associate the series with the selected data type.

⇨ The associated series name is shown in the **Associated Series** section in the task guidance.

4. If you want to use this data type as the default data type for additional series, if available, click **Set Default**.
5. To associate another series with a data type, click **Associate New Series** and repeat this task.
6. To remove an association, select the series in the **Associated Series** section and click **Remove**.

Reviewing the Liver Segmentation

When liver segmentation is complete, the segmentation is visualized on the displayed slab. You should review the segmentation by scrolling through the slabs. There are multiple viewing options for visualizing the segmentation.

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1. To configure the liver segmentation visualization, use the following **Show / Hide** functions at the bottom of the task panel:

    **Show/Hide Liver Segmentation**

    **Show/Hide Liver Contour**

    **Show/Hide Liver Segments**

   When you select **Show/Hide Liver Segments**, **Show/Hide Liver Contour** is hidden.

2. Drag the opacity slider in the **Show / Hide** section of the task panel to adjust the opacity of the segmentation.

⇨ Reducing the opacity may help you determine whether the segmentation accurately matches the anatomy in the series.

3. To change the layout (to view multiple viewports, for example), click **Layout** in the **Display Protocol** section of the task panel and select a layout.

⇨ When viewing multiple viewports, you can double-click a viewport to maximize it. Double-click again to return to the selected layout.

4. To change to a different series loaded in the in the study, click the series name in the title bar of the viewport and select a series.

⇨ If you change the volume, a system message is displayed allowing you to set the new volume as the default volume (optional).

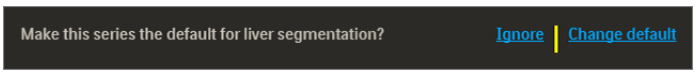

Fig. 144: System message for setting the default volume (optional)

NOTICE

Changing liver segmentation volume deletes any created 2D and 3D measurements.

5. Review the study by scrolling through the slabs.
6. To scroll through the second dimension (such as dynamics), use the Left arrow and Right arrow keys.
7. To change the render mode of a viewport, click the render mode viewport control in the lower-left corner of the viewport and select a render mode.
8. To change the color mode of a viewport, click the color mode viewport control in the upper-right corner of the viewport and select a color mode.

⇨ The color bar is displayed by default. You can show or hide the color bar using the **Image Information** item group in the shortcut menu when you right-click the viewport.

9. If multiple studies were selected when the application started, you can change to the other study by clicking **Prior Study** or **Next Study** in the title bar of the application.

⇨ The date of the currently displayed study is also displayed in the title bar.

Comparing Studies

If you selected two studies in the **Patient Directory** before starting the **Liver Health** application, you can compare the two studies side by side.

NOTICE

It is not possible to compare two studies with different magnetic field strength or two studies from different vendors. In this case, the **Compare With Prior** function is not available.

1. Click **Compare With Prior** in the task panel.

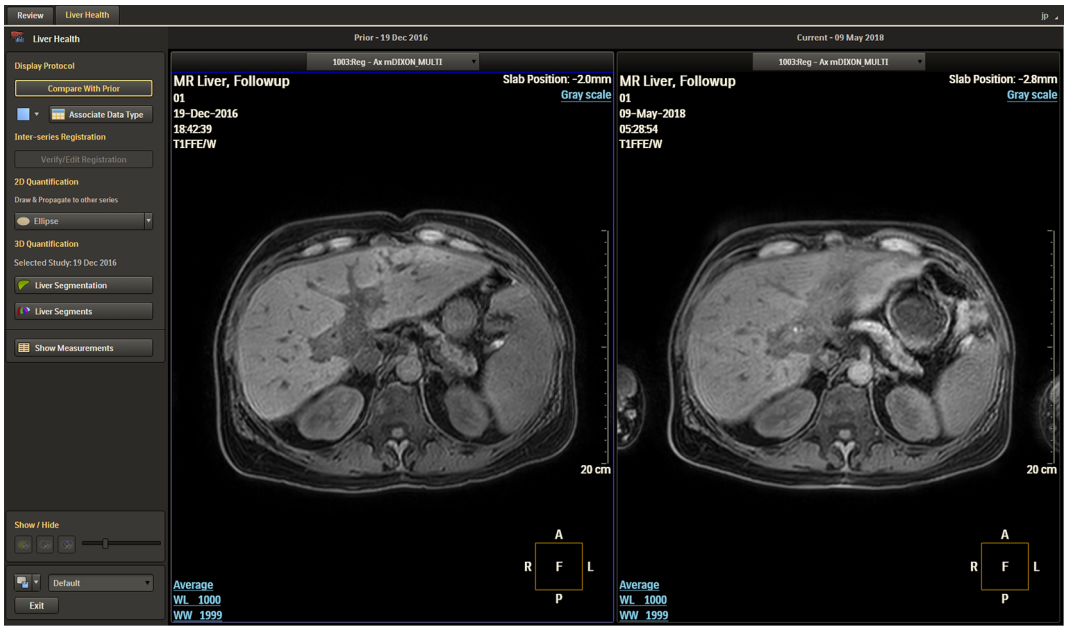

Fig. 145: Viewing studies side by side using the **Compare With Prior** function

⇨ The **Compare With Prior** function displays the studies as follows:

- The studies are registered using MR-MR rigid registration.
- The older study is displayed on the left and the newer study is displayed on the right.
- Scroll, zoom, pan, and orientation functions are linked.
- 1x1 and 2x1 layouts are available.

2. You can select other series for comparison using the drop-down lists above each viewport.

⇨ When you select a series from the drop-down list above a viewport, the same series from the other study is selected, in the same row, based on the series description.

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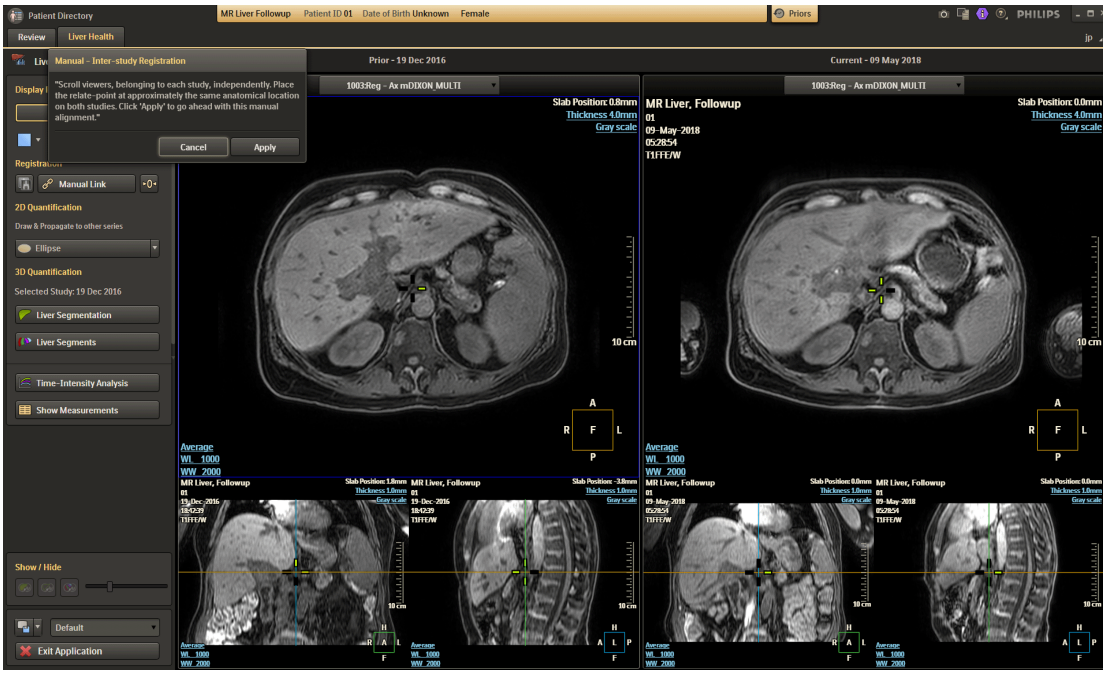
Adjusting the Registration Link

If desired, you can unlink the automatic inter-study registration and adjust the link manually.

1. In the task panel, select **Manual Inter-Study Registration**.



2. Scroll each study to a slice image so that each slice shows the same anatomical landmark.
3. In each study, click on the same anatomical landmark.
4. If needed, drag the registration points to a better location (or just click on a new location).
5. When all points show the same anatomy, select **Apply** in the task panel.

⇨ The registration of the series is now based on the selected points.

6. If you want to return to automatic inter-series registration, select **Reset Inter-Study Registration** in the task panel.

Editing the Registration

When the **Liver Health** application starts and studies are loaded, MR-MR inter-series rigid registration is performed. The registration reference series is the volume on which the liver is segmented. All subsequent registrations use the source series as reference, to maintain the quality of the registered images.

However, if the registration of a particular series does not seem accurate, you can edit the registration.

1. Display the series for which you want to modify the registration.
2. Click **Verify/Edit Registration**.

⇨ The reference series and the viewport series are displayed in a fusion view with reference views.

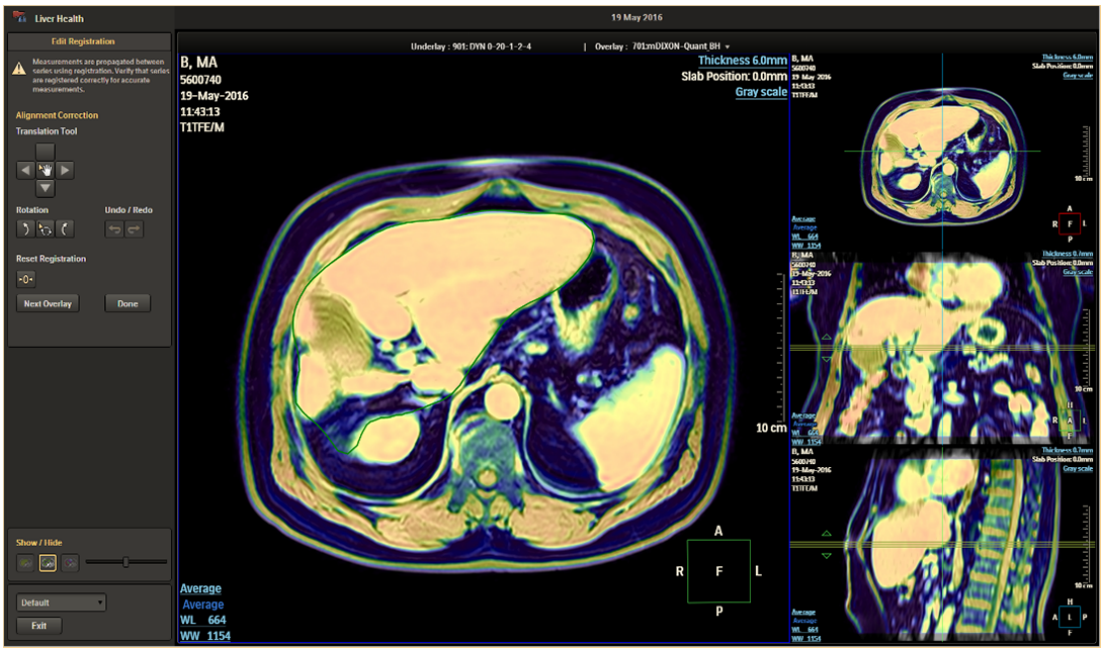


Fig. 146: Editing the registration

3. To pan the series in relation to the reference series, click in the **Translation Tool** section of the task panel and drag the series in the desired direction.
4. To nudge the series, use the arrow buttons in the **Translation Tool** section of the task panel.

5. To rotate the series in relation to the reference series, click **Rotate** in the **Rotation** section of the task panel and drag the series in the desired direction.
6. To nudge the rotation of the series, use the clockwise/counterclockwise arrow button in the **Rotation** section of the task panel.

7. To undo or redo an action, use the **Undo/Redo** tools in the task panel.

8. To reset all your modifications to the initial state, click **Reset Registration** in the task panel.
9. To display the next series in the fusion view and edit its registration with the reference series, click **Next Overlay** in the task panel (optional).

⇨ You can also change the series by clicking the series name in the title bar of the viewport and selecting a different series.

NOTICE

An option to disable the registration is provided in the task guidance panel to disable the applied registration between the fused underlay and overlay. If you select this option, the application removes the registration applied between the fused series, and removes measurements propagation with results from the table for the overlay series.

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10. When you have completed all desired registration actions, click **Done**.

Creating an ROI

You can create a total of 9 ROIs on any series. An ROI is a 2D measurement; all data from ROIs can be viewed in the histogram and data tables.

If the **Verify/Edit Registration** step has not been accessed when you create a measurement, a message reminds you to verify the registration.

1. Display the series to which you want to add and ROI.
2. In the task panel, click the ROI button in the **2D Quantification** section.

⇨ You create the following types of ROI:

- **Ellipse**
- **Freehand**
- **Spline**

⇨ If the type of ROI that you want to create is not displayed on the ROI button, click the arrow on the right side of the button and select the desired ROI type.

3. Drag to create an ROI.

⇨ When you create an ROI, the measurement is automatically propagated to the following maps using registration:

- Fat Fraction
- T2*
- R2*
- ADC

⇨ On other types of maps, you can propagate the measurement manually; right-click the map and click **Enable Measurements**.

⇨ If you change the render mode or slice thickness after an ROI has been created, the ROI is displayed as a dotted line.

⇨ Functions for editing or deleting an ROI are available in the shortcut menu.

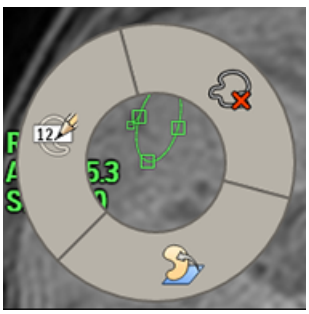

Fig. 147: Editing for deleting an ROI

4. To rename an ROI, right-click the ROI, click **Rename** in the shortcut menu, and enter a new name.

5. To align the current view to the ROI, right-click the ROI and click **Align View To Measurement** in the shortcut menu.

6. To delete an ROI, right-click the ROI and click **Delete** in the shortcut menu.

⇨ You can also delete an ROI by selecting it and pressing Delete on the keyboard.

Editing and Approving the Liver Segmentation

The application performs liver segmentation automatically when series are loaded. The segmentation is performed on one of the following types of series, when available (in descending order of priority):

- Contrast-enhanced dynamic T1W - Portal phase
- Water image from contrast-enhanced dynamic – Portal phase
- 3D T1W or highest resolution T1W (resolution higher than water image, if available)
- Water image from mDIXON or mDIXON Quant (volume with highest resolution)

1. To start reviewing the liver segmentation, click **Liver Segmentation** in the **3D Quantification** section of the task panel.

⇨ The **Liver Segmentation** screen is displayed, containing three orthogonal slab views and 3D view of the liver segmentation.

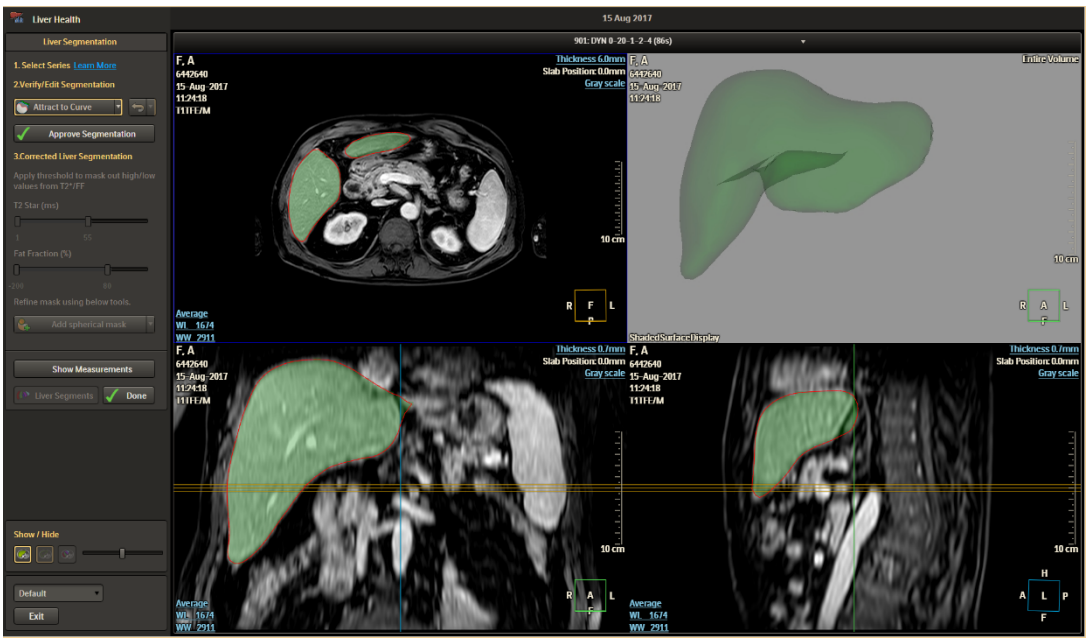

Fig. 148: Liver Segmentation screen

2. To change the layout of the viewports, right-click the main display area and select a new layout from the **Layout** options in the shortcut menu.

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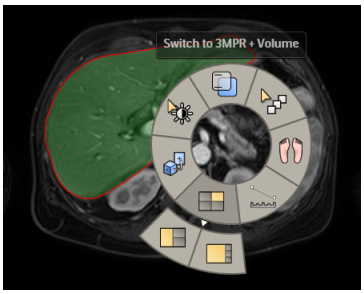

Fig. 149: Viewport layout options in the shortcut menu

3. To select a different series on which to perform liver segmentation, click the series name at the top of the screen and select a series from the list.

⇨ Only series that are suitable for liver segmentation are displayed in the series list.

NOTICE

For the best results when placing landmarks in the segmentation, select a series that uses Portal phase data.

4. Review the liver segmentation by scrolling through the orthogonal views.
   - To adjust the opacity of the liver segmentation in the orthogonal views, drag the slider in the **Show/Hide** section at the bottom of the task panel.
   - To roll or rotate the 3D liver segmentation view, drag the segmentation model in the viewport.
5. To edit the liver segmentation, select a tool in the **Verify/Edit Segmentation** section of the task panel.

   The following tools are available:

    **Attract to Curve** (selected by default): This tool allows you to draw a line along the edge of the tissue to define a section of the contour.

    **Drag to Point**: This tool allows you to drag the existing contour to fit the edge of the tissue.

    **Add Smart ROI**: This tool allows you to click an area and grow the contour based on the contrast of the image in the volume.

    **Remove Smart ROI** This tool allows you to click an area and reduce the contour based on the contrast of the image in the volume.

   You can make edits on any slice, orientation, and reference images. Your edits are automatically updated in the 3D liver segmentation view.

6. To undo or redo an action, use the **Undo/Redo** tools in the undo/redo drop-down button group in the task panel.

7. To undo all your edits and reset the liver segmentation, click **Reset Segmentation** in the undo/redo drop-down button group in the task panel.

8. When the liver segmentation is correct and complete, click **Approve Segmentation** in the task panel.

⇨ After approving the liver segmentation, the data table and histogram are populated with results.

⇨ You can now view the corrected liver segmentation and apply thresholds to investigate the segmentation further.

NOTICE

If desired, you can make further edits to the liver segmentation after approving it, but you must approve it again before viewing the corrected liver segmentation again.

Viewing the Corrected Liver Segmentation

NOTICE

The **Corrected Liver Segmentation** step is only available after you have approved the liver segmentation.

The **Corrected Liver Segmentation** step displays the liver segmentation corrected with a threshold setting to mask particular values that are not of clinical interest. The main display area displays the T2* map and the Fat Fraction map. Default high/low thresholds are applied as follows:

- T2* map
  - Lower threshold: 1 ms
  - Upper threshold: 55 ms
- Fat Fraction map
  - Lower threshold: 200%
  - Upper threshold: 55%

Tissue outside these thresholds is masked and displayed in orange in grayscale images and in black in color images.

The data table and histogram are populated with results from the corrected liver segmentation. Masked tissue is excluded from the results.

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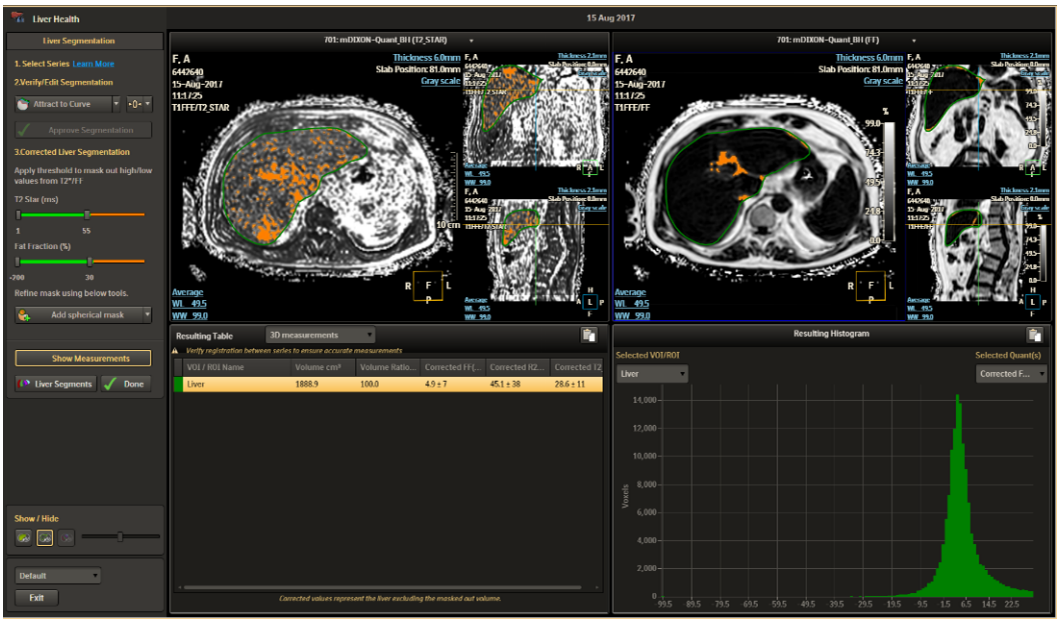

Fig. 150: Corrected Liver Segmentation step

1. To edit the mask, adjust the threshold by dragging the sliders in the **Corrected Liver Segmentation** section of the task panel.

⇨ The data table and histogram are updated automatically. The data table displays results for the total liver, the corrected liver, and any ROIs.

2. To refine the mask in the **T2 Star** map or the **Fat Fraction** map, do the following:
   - Select **Add Spherical Mask** in the task panel.
   - Move the pointer over the area to be edited.
   - Define the size of the mask by holding Ctrl and rotating the wheel button on the mouse.

NOTICE

The mask applied to the T2* map is also shown on R2* map, but it is not possible to edit the mask on the R2* map. Make your edits on the T2* map or the Fat Fraction map.

3. You can also unmask areas that have been incorrectly masked using the **Remove Spherical Mask** tool in the drop-down list in the task panel.
4. To change the opacity of the masked tissue in the images, drag the opacity slider in the task guidance panel.
5. To show or hide the masked tissue in the images, click **Show/Hide Masked Tissue** in the task guidance panel.

Creating Liver Segments

When viewing the corrected liver segmentation, you can also create liver segments within the segmentation, if desired. You create segments by placing landmarks in the segmentation. You can select from the following liver segment options:

Segments	Landmarks
2 Segments Left/Right Lobe	• Inferior Vena Cava • Umbilical Fissure • Left portal Bifurcation • Superficial Ligamentum Venosum • Deep Ligamentum Venosum • Superior Deep Ligamentum Venosum
2 Segments Left/Right Liver	• Inferior Vena Cava • Mid Hepatic Vein
4 Segments L/R Medial and Lateral	• Inferior Vena Cava • Right Hepatic Vein • Mid Hepatic Vein • Umbilical Fissure • Left Portal Bifurcation • Superficial Ligamentum Venosum • Deep Ligamentum Venosum • Superior Deep Ligamentum Venosum
7 Segments	• Inferior Vena Cava • Right Portal Bifurcation • Right Hepatic Vein • Mid Hepatic Vein • Umbilical Fissure • Left Portal Bifurcation • Superficial Ligamentum Venosum • Deep Ligamentum Venosum • Superior Deep Ligamentum Venosum

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Segments	Landmarks
8 Segments Couinaud *(Default option)*	• Inferior Vena Cava • Right Portal Bifurcation • Right Hepatic Vein • Mid Hepatic Vein • Umbilical Fissure • Left Portal Bifurcation • Tip Left Liver • Superficial Ligamentum Venosum • Deep Ligamentum Venosum • Superior Deep Ligamentum Venosum
9 Segments Bismuth	• Inferior Vena Cava • Right Portal Bifurcation • Right Hepatic Vein • Mid Hepatic Vein • Umbilical Fissure • Left Portal Bifurcation • Tip Left Liver • Superficial Ligamentum Venosum • Deep Ligamentum Venosum • Superior Deep Ligamentum Venosum

NOTICE

Before starting **Liver Segments** mode, ensure that the liver segmentation volume is selected. It is not possible to change the volume after starting **Liver Segments** mode.

1. In the task panel, click **Liver Segments** to display the **Liver Segment** step.

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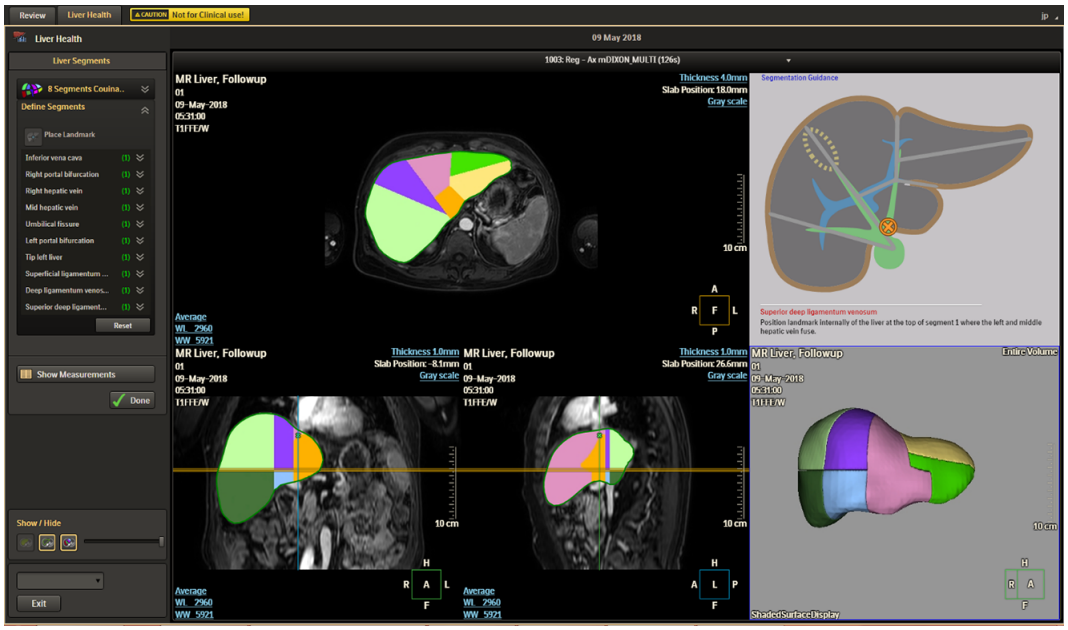

Fig. 151: Liver Segment step

2. To change the layout of the viewports, right-click the main display area and select a new layout from the **Layout** options in the shortcut menu.

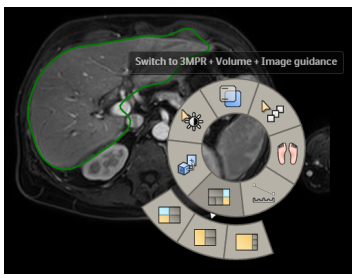

Fig. 152: Viewport layout options in the shortcut menu

3. In the task panel, select the number of segments that you want to define.

   For details, refer to the table at the start of this section.

4. Based on the landmarks that you need to create, scroll to the location of the first landmark in the orthogonal views.

5. In the task panel, click **Place Landmark**.

⇨ The first landmark that has no seed points is automatically selected in the **Define Segments** list in the task panel.

NOTICE

While the **Place Landmark** tool is active, you can scroll through the volume by dragging with the middle mouse button.

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⇨ Use the guidance in the **Segmentation Guidance** view in the upper-right corner to find the appropriate location for the landmark. Any existing landmarks are indicated by an orange marker in this view.

6. Click in the volume to place a landmark.

⇨ When a landmark is placed, the next segment in the **Define Segments** list is selected.

7. Continue placing landmarks for segments until all segments are marked.

⇨ You can add and remove landmark seeds using the available options for each landmark in the **Define Segments** list.

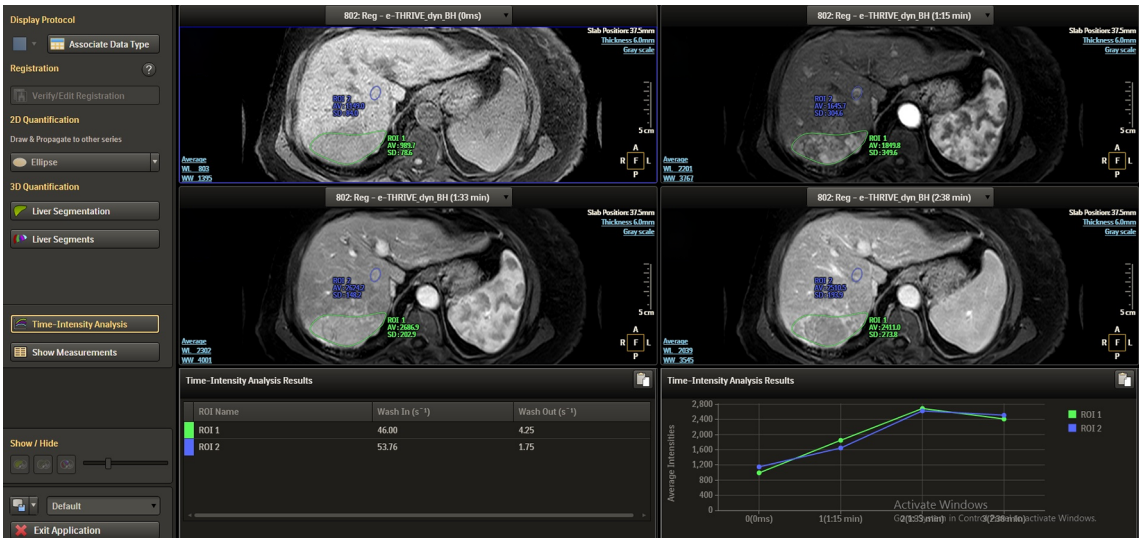
⇨ When there are enough landmarks to create a segment, the segment is displayed in the orthogonal images and in the 3D view. Segments are included in the results views.

8. If desired, you can remove all landmarks and start again by clicking **Reset** in the task panel.

Viewing and Saving Results

Time-Intensity Analysis

When selecting **Time-Intensity Analysis** from the left task guidance in overview mode, the application displays the dynamic series split in 2x2 layout. Each viewport shows different dynamic time data with the header showing the time as a suffix after the series description.



The drop down provides only the different dynamic volumes present in the dynamic series for selection to view. The bottom viewports show **Time-Intensity Analysis Results** with a table and graph.

Time-Intensity Analysis Results are available for all 2D measurements.

The table provides the following parametric values with ROI Name:

- Wash In (S^-1)
- Wash Out (S^-1)

The graph provides the graphical representation of the change in the average intensity under the region of interest over dynamics. It is possible to export the results from copy to clipboard option.

In compare mode, the application shows dynamic data of both studies side by side, with first two dynamics by default in 2x1 layout, for prior and current respectively.

The Time-Intensity Analysis Results shows only the graphical results for prior and current respectively, side by side.

Show Measurements

1. To view the measurement results, click **Show Measurements** in the task guidance panel.

⇨ The layout displays viewports containing series on which measurements were automatically propagated for the loaded data either, in 1x2 or 2x2 layout. If measurements are not automatically propagated to any data, the layout is 1x1. The table is shown maximized by default. The first row in the table provides the series number from which the parametric measurements are computed.

Fig. 153: Show Measurements screen

⇨ Results are automatically updated and displayed in the data table and histogram. The table and graph can be displayed by moving the viewports on top in 2x1 layout with the second row viewport showing the selected parameter map from the table.

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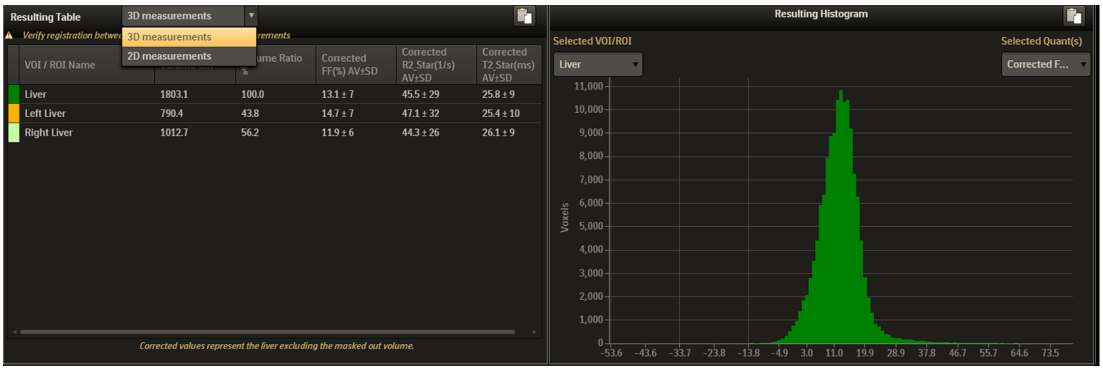

Fig. 154: Results views: data table and histogram

2. To change the image type displayed in a viewport, click the image type drop-down list at the top of the image and select an image type.

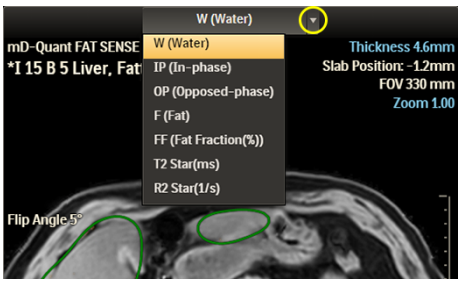

Fig. 155: Changing the image type

3. To change the color mapping of the image displayed in a viewport, click the color mapping information item in the upper-right corner of the image.

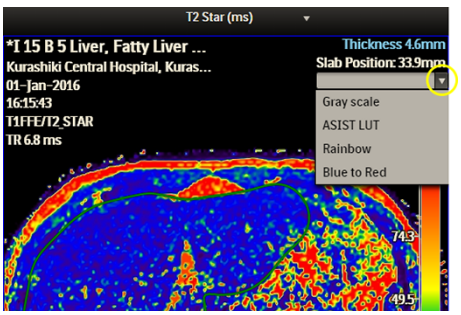

Fig. 156: Changing the color mapping

4. To switch between 2D measurements (ROIs) and 3D measurements (segments), click the drop-down menu at the top of the data table viewport and select an option.

⇨ Each measurement is displayed on a line in the data table.

⇨ You can view results for the total liver, the corrected liver, or any ROI or segment. You can choose to display any of the following parameters:

- ROI or segment
- Fat fraction (FF) as a percentage
- T2* in ms
- R2* in 1/s

- ADC (10^{-3} mm^2/s)
- Volume (for 3D measurements)
- Volume Ratio % (for 3D measurements)
- Area (cm^2, for 2D measurements)

⇨ In the data table, the selected parameter results are shown with absolute values with relative changes in the table. The resulting graph for the selected parameter and ROI or segment is shown on the right side.

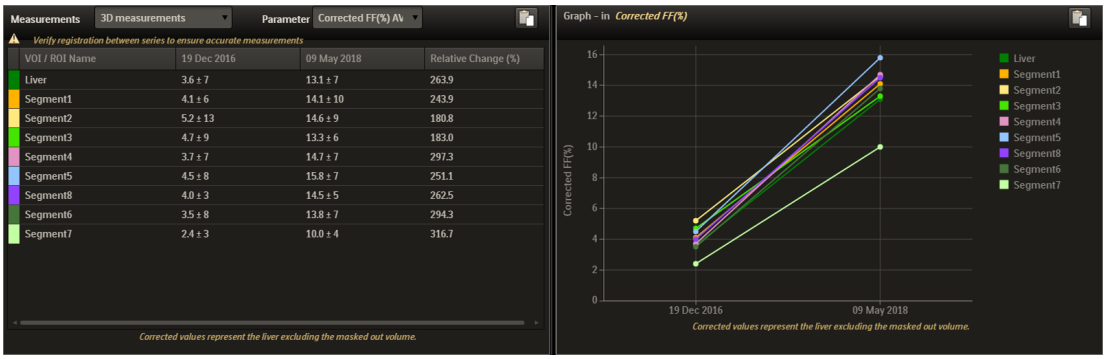

Fig. 157: Data table and graph

5. To match two ROIs from different studies for comparison, select the ROIs in the table while pressing Ctrl.

⇨ On selection of two ROIs, the shortcut menu is displayed. Click **Match** to compare the ROIs. The comparison is displayed in a graph.

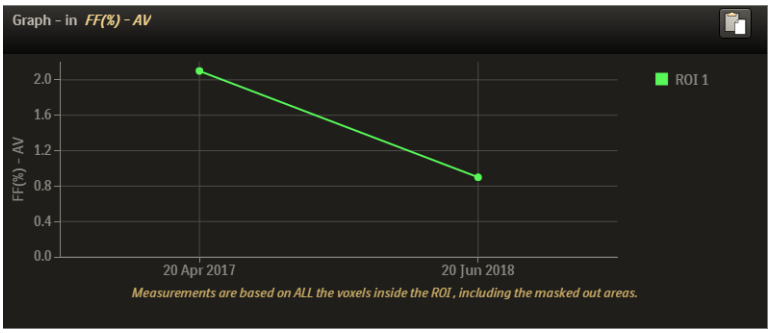

Fig. 158: Comparing two ROIs

6. To focus the histogram viewport on a specific set of results or parameters, use the drop-down lists at the top of the viewport.

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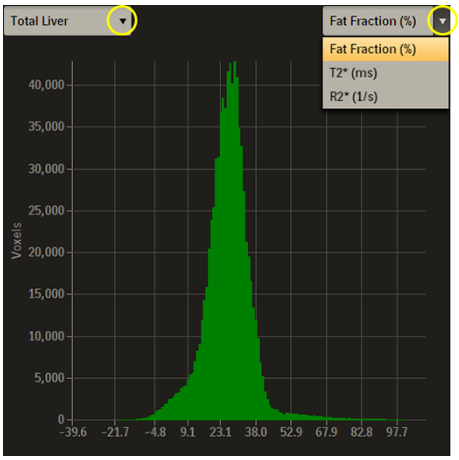

Fig. 159: Configuring the histogram

⇨ In the histogram viewport, the value of the selected parameter is displayed on the x-axis, and the number of voxels is displayed on the y-axis (the histogram is only displayed for segments).

7. To copy the results in the table, the histogram, or the graph, click **Copy To Clipboard** in the upper-right corner of the corresponding viewport.

   You can then paste the copied data into another application.

8. To save the results, select one of the save options from the drop-down list in the lower-left corner of the task guidance panel:
   - Select one of the save options from the drop-down list in the lower-left corner of the task guidance panel:
     - **Save Selected Image As**
     - **Save Display As**
     - **Save Results As**
     - **Save Batch** (refer to the following step for details)
   - Configure the desired **Format**, **File Name**, and **Destination** in the dialog box and click **Save**.

   ⇨ On saving the results, the segmentation status and results are saved with the study and are reloaded in the current state if you close and reopen the study in the **Liver Health** application.

9. To save the results as a batch, select **Save As Batch**.

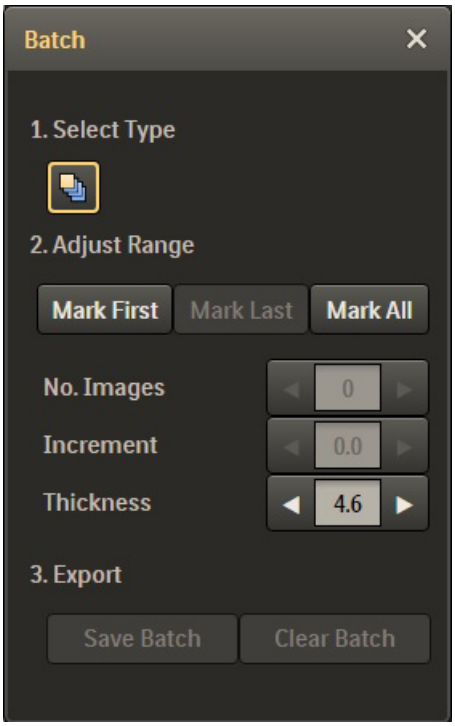

Fig. 160: Batch dialog box

10. To configure the batch, do the following:
    - Select a viewport.
    - Do one of the following:
        - Select the first image and click **Mark First**, and then select the last image and click **Mark Last**.
        - Select **Mark All**.
    - Configure the number of images, increment, and thickness.
    - Click **Save Batch** to open the **Save Batch As** dialog box.
11. In the **Save Batch As** dialog box, do the following:
    - Enter a name for the batch.
    - Select a destination folder.
    - Click **Save**.

NOTICE

When saving a batch, you can only save as DICOM Secondary Capture.

⇨ On saving the results, the segmentation status and results are saved with the study and are reloaded in the current state if you close and reopen the study in the **Liver Health** application.

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Using the Shortcut Menu

The shortcut menu is displayed when you right-click in an image, and it provides quick access to many functions.

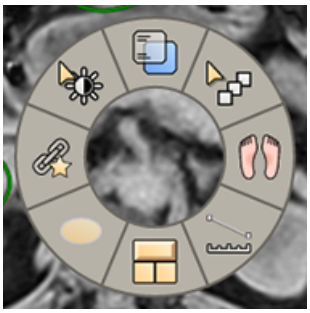

Fig. 161: Shortcut menu

Click a function to select it.

Some functions have a submenu containing further functions.

Image Information Submenu

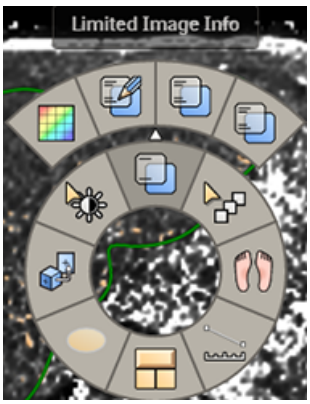

Fig. 162: Image Information submenu

The Image Information submenu provides access to the following functions:

- **Show/Hide Color Scale**
- **Interactive Image Information**
- **Full Image Information**
- **Intermediate Image Information**
- **Limited Image Information**

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Interactor Submenu

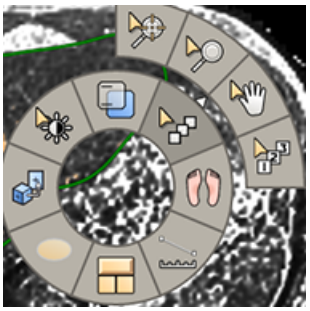

Fig. 163: Interactor submenu

The Interactor submenu provides access to the following functions:

- **Zoom to Point**
- **Zoom**
- **Pan**
- **Continuous Scroll**
- **Scroll**

Orientation Submenu

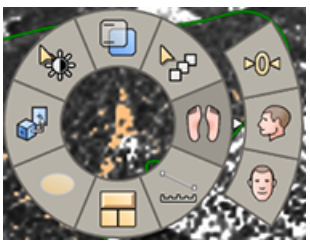

Fig. 164: Orientation submenu

The Orientation submenu provides access to the following functions:

- **Reset Orientation**
- **Sagittal**
- **Coronal**
- **Axial**

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ROI Submenu

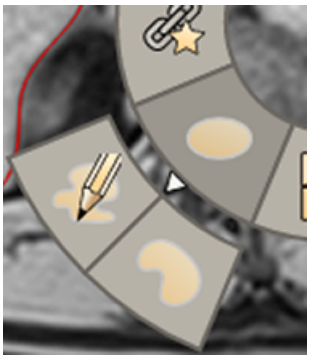

Fig. 165: ROI submenu

The ROI submenu provides access to the following functions:

- **Freehand ROI**
- **Spline ROI**
- **Ellipse**

Annotation Submenu

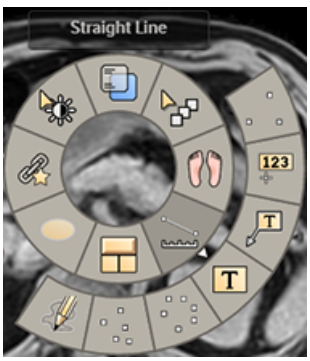

Fig. 166: Annotation submenu

The Annotation submenu provides access to the following functions:

- **Freehand Line**
- **Spline Line**
- **Polyline**
- **Angle**
- **Text with Arrow**
- **Text**
- **Pixel Value**
- **Line**

Link Options Submenu

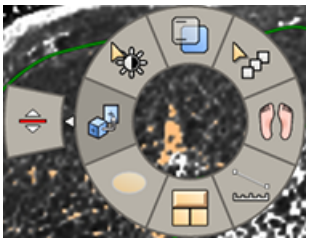

Fig. 167: Link Options submenu

The Link Options submenu provides access to the following functions:

- **Show Crosshair**
- **Relate Viewports**

Windowing Submenu

Fig. 168: Windowing submenu

The Windowing submenu provides access to the following functions:

- **Invert**
- **Change Window Level**

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