3 MR T2* Neuro Perfusion

This postprocessing package is meant to evaluate T2* perfusion studies and generate numerical and graphical results and maps.

Paramagnetic contrast agents influence the local magnetic field and reduce the T2* relaxation time of surrounding tissue.

If a valid Diffusion input series is available with the loaded study, Diffusion-Perfusion Mismatch can be performed.

Valid imaging series

A valid imaging series for the Neuro Perfusion package is a series which is sensitive to T2* changes over time. In other words a series where a stack of slices is repeatedly acquired over time (dynamics). The MR Neuro Perfusion package requires at least 5 dynamics.

Indications for Use

The Philips Medical Systems' MR T2* Neuro Perfusion application is a post processing software application supporting the analysis of Dynamic Susceptibility Contrast (DSC) T2* perfusion studies to generate numerical and graphical results The Philips Medical Systems' MR T2* Neuro Perfusion application is a post processing software application supporting the analysis of Dynamic Susceptibility Contrast (DSC) T2* perfusion studies to generate numerical and graphical results of TTP, T0, MTT, rCBV, corrected rCBV, rCBF, Tmax and K2 (leakage). Four methods are available for analysis, including Gamma Variate, Model Free, Leakage Correction and manual Arterial Input Function (AIF). AIF also enables Perfusion-Diffusion Mismatch analysis if a Diffusion input dataset is available in addition to the Perfusion series.

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User Interface

Screen layout

The MR Neuro Perfusion package has a default layout of task guidance panel and toolbars, and four viewports. The viewports contain the following views:

- Source image in the middle of the imaging volume.
- In real-time calculated parametric perfusion maps.
- Table Viewer (numerical results) and Anatomical Viewer
- Graph Viewer (graphical results) and Anatomical Viewer

Switch between Graph Viewer, Table Viewer and Anatomical Viewer

1. Click the 'Graph Viewer' tab to switch to the Graph Viewer.
2. Click the 'Anatomical Viewer' tab to switch to the Anatomical Viewer.

3. Click the 'Table Viewer' tab to switch to the Table Viewer.

More information on the Graph Viewer and the Table Viewer can be found in the Results section.

More information on the Anatomical Viewer can be found in the Workflow section.

Task Guidance

Similar to all packages on the IntelliSpace portal, also the MR Neuro Perfusion package provides a Task Guidance panel in the left part of the screen. The task guidance panel provides the following steps:

- Select the Desired Maps
- Select Underlay
- Analysis
- Generate Maps
- Optional step: Diffusion-Perfusion Mismatch - this step can be performed if a valid Diffusion input series is available.

Follow the steps of the Task Guidance to make optimal use of the package.

The following workflow description is based on this Task Guidance.

Toolbar

Color LUT (Look-Up Table)

- To select the color look-up table for the maps.

  Possible settings are: 'Blue to Red', 'ASIST' and 'Gray'.

Color LUT	Minimum value				Maximum value
Blue to Red	Blue	Green	Yellow	Orange	Red
ASIST	Black	Light blue	Green	Yellow/ Orange	Red
Gray	Black		Gray		White

The ASIST LUT is a LUT specifically designed for acute stroke imaging. The Acute Stroke Imaging Standardization Group - Japan (ASIST-Japan) is a group that conducts medical research projects dedicated to the standardization of brain computed tomography (CT) and magnetic resonance imaging (MRI) in the clinical setting of acute cerebral stroke.

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Layout

To select another screen layout, click  **Layout** and select a layout option. You can also edit the current layout and save it as a preset using the **More** menu. Custom layouts that you have saved as presets are also available in the **Layout** list.

Follow Mouse

Select this option to display real-time results for the current voxel (indicated by the current position of the cursor).

More Menu

Show Skip Dynamics Step

Select this option to display an additional step in the **Analysis** task guidance panel. If desired, you can skip the first dynamics in a study to ignore the initial dynamics in which the steady state has not yet been reached. To skip dynamics, enter the number of dynamics that you want to skip in the box in the Skip Dynamics step.

Save Layout Preset

Select this option if you want to save a custom layout that you have created. Enter a name in the **Create New Preset** dialog box that is displayed when you select this option, and then click **Save**. Your layout is now available in the drop down list of the **Layout** button in the toolbar.

Delete Layout Presets

Select this option if you want to delete one or more custom layouts that you have previously saved. Select the layouts to be deleted in the **Layout** dialog box that is displayed when you select this option, and the click **Delete**.

Tip

You can only delete custom layouts. You cannot delete system layouts. Additionally, you cannot delete a custom layout if it is currently selected. First select a different layout, and then delete it.

Viewing Tools

 **Mirror**

This function mirrors the image(s) (Right <-> Left)

Flip

This function flips the image(s) (Up <-> Down)

Rotate Clockwise

This function rotates the image(s) clockwise

Rotate Counter-Clockwise

This function rotates the image(s) counter-clockwise

More Functions within the Perfusion packages

In IntelliSpace Portal MR packages, the most important functions can be performed via the Task Guidance and the toolbar. However there are more functions which you can access via the right mouse menus.

For more information, see section “Right mouse menus” on page 12.

Workflow - MR Neuro Perfusion

MR Neuro Perfusion supports analysis workflows with and without using AIF (Arterial Input Function). The following analysis techniques can be used:

- **Gamma Variate**: This workflow is based on the assumption that the ideal shape of a passing contrast bolus as acquired in a T2* perfusion series is highly comparable to the gamma variate function.
- **Model Free**: This workflow does note require a specific shape or model. The analysis detects the start and the end of the bolus passage by determining a baseline at the front and at the end.
- **Manual AIF** (Deconvolution): The AIF analysis workflow uses a deconvolution algorithm based on the knowledge of the Arterial Input Function to calculate the perfusion values. The AIF describes the input of contrast agent into the tissue of interest. When using this workflow, you define the AIF by selecting voxels (typically in or around an artery) that show the T2* effect as induced by the passage of the contrast agent bolus. The average of the selected voxels represents the shape of the arterial input function. This arterial input function is used to calculate the parametric maps.
- **Leakage Correction**: This workflow allows you to assess brain perfusion curves that have been corrected for leakage of contrast agent into the brain tissue. Leakage Correction in MR Neuro Perfusion uses the Boxerman – Weisskoff approach.

You can choose between these techniques in the **Analysis** task guidance step (instructions are provided in the procedural steps later in the this section). The other task guidance steps are the same for all techniques.

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Launch the MR Neuro Perfusion package

▷ In the 'Directory' tab of the activity bar:

1. Select a suitable perfusion series.
2. 

Click ’MR NeuroPerfusion’.

   The MR Neuro Perfusion package opens.

Scroll through images

1. 
To scroll through dynamics, drag to the left or to the right in the image viewport.
2. 
To scroll through slices, drag upward or downward in the image viewport.
3. 
To scroll through maps, drag to the left or to the right in the map viewport.

Analysis

1. In the **Analysis** list in the task guidance panel, select one of the following methods:
   - **Gamma Variate** (non-AIF workflow)
   - **Model Free** (non-AIF workflow)
   - **Manual AIF**
   - **Leakage Correction** (non-AIF workflow)
2. Set the mask by dragging with the right mouse button in the source data. For details, see section “Define the mask” on page 38.
3. If you selected a non-AIF workflow, continue to the section "Creating a ROI".
4. If you selected **Manual AIF** analysis, you should first define the AIF. The **Define AIF** window is displayed automatically when you select **Manual AIF** analysis. The **Define AIF** window displays the middle slice.

⇨ A red square is displayed in the image viewport. The red square spans the size of 7x7 voxels. In the right viewport the dynamic curves of these 7x7 voxels are shown.

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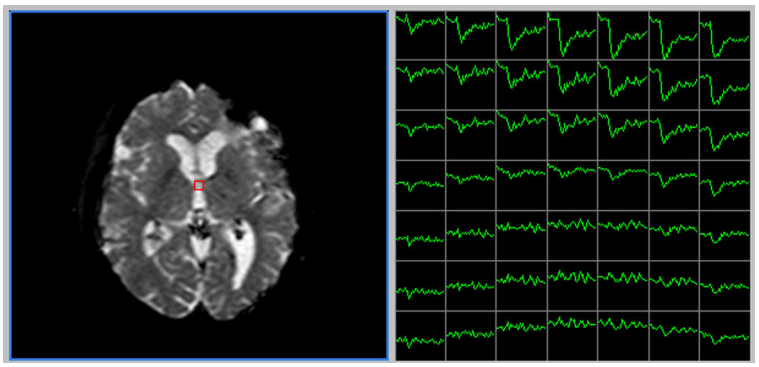

Fig. 13: Define AIF window. Left: Middle image with rectangular ROI of 7x7 voxels. Right: Time-Intensity curves of these voxels.

5. Navigate to the slice with the vessel relevant for Manual AIF definition.
6. Zoom, pan and window the slices so that this vessel is clearly visible.
7. Drag the red box over this vessel.

   The display of the curves will automatically be updated.
8. Click on individual graphs to include them in the definition of the AIF.

   The selected graphs are yellow. For best results, the selected voxels should show an AIF curve with a narrow and high peak.

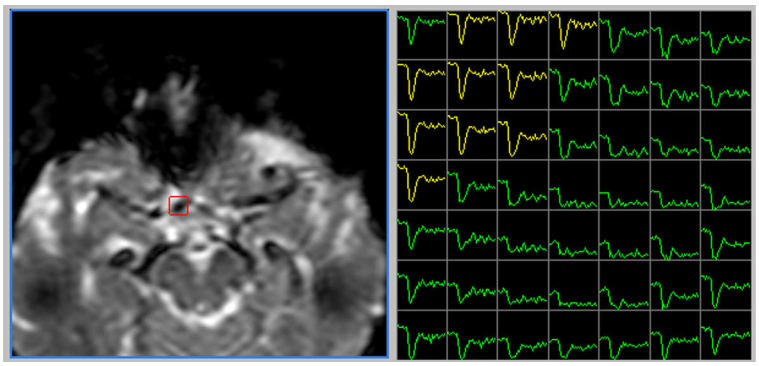

Fig. 14: The AIF is defined

⇨ To exclude a voxel that you previously included, click the graph again.

9. Click OK to confirm.

   The AIF is identified and the resulting maps are displayed.

Tip

To open the Define AIF window again and adjust the AIF definition, click Define AIF in the task guidance panel.

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Manual AIF Results

NOTICE

Using the AIF function, the relCBF and the relCBV are also displayed with units: relCBF [ml/100g/min] and relCBV [ml/100g].

The calculation is based on known delay-insensitive deconvolution techniques and results may be influenced by incorrect assumptions in such a model.

Manual AIF analysis measures relCBF (relative Cerebral Blood Flow) and relCBV (relative Cerebral Blood Volume) using a deconvolution between the time courses of tissue signal and an Arterial-Input-Function (AIF).

The results of deconvolution perfusion analysis may under- or overestimate the true perfusion depending on various factors:

WARNING

Inaccurate definition of the AIF: The AIF may suffer from partial-volume effects. Due to the limited temporal resolution, the AIF is not very accurately sampled. A very sharp high peak is in general not well represented by the user-defined AIF. For this reason the AIF time course will not correctly represent a 100% blood signal.

WARNING

Patient motion: Patient motion during the scan may introduce irregularities in the definition of the AIF and individual tissue signal time courses, causing deviations from the correct relCBF and relCBV.

NOTICE

Temporal resolution: The temporal resolution of the measurement may be too low, causing difficulty to identify the bolus curve giving poor results.

NOTICE

Poor bolus injection: If the contrast bolus is too slow, the relCBF and relCBV may be incorrectly calculated. Results may be influenced by the assumptions in such a model.

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Delay maps with AIF algorithm

If the AIF algorithm has been chosen for processing, the Generate Series window provides the possibility of enabling the calculation of a Delay map. For each pixel, the delay map shows the time between the AIF peak concentration, and the tissue peak concentration. The time is measured in seconds, with accuracy defined by the dynamic scan time of the acquisition sequence. The delay time is often referred to as Tmax.

Apply Spatial Smoothing

- To spatially smooth the resulting maps.

Possible settings are: None (no smoothing), Weak, Medium or Strong.

The strength of the smoothing setting determines the size of the kernel used to average neighboring voxels. Respective kernel sizes are 1, 3x3, 5x5, and 7x7.

Spatial smoothing smooths the maps and the original images. In such a way, spatial smoothing has an effect on the numerical results.

Apply Temporal Smoothing

- To temporally smooth the resulting maps.

Possible settings are: None (no smoothing), Weak, Medium or Strong.

The temporal smoothing makes use of a uniform filter with user-adjustable width. The width describes the total number of dynamics contributing to the filter; the applicable sizes are 1, 3, 5, and 7.

Define the mask

This optional workflow step serves to adjust the mask and to enable the display of the mask while adjusting.

Drag with the right mouse button on the source image to adjust the mask.

Leakage Correction

When you adjust the mask, the reference voxels are affected. If you are using **Leakage Correction** analysis, this may have some effect on the results.

Select the Desired Maps

You can select the maps in the task guidance panel for real-time calculation and display, and for the generation of new imaging series.

1. Click the checkbox of a map to select/deselect this map.

   The display of the real-time calculated maps will be updated accordingly.

Leakage Correction

If you are using the **Leakage Correction** analysis method, you can enable advanced maps in the **More** menu in the toolbar. This option adds the following additional information:

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- **Goodness of Fit** is added to the parametric maps and the results page.
- **Ref Voxels** are added to the parametric maps.

Select Series for Anatomical Viewer

Upon startup of the package, the Anatomical Viewer is empty. However an additional imaging series in the Anatomical Viewer might help during navigation through the data set and in order to draw ROIs.

Any type of imaging series can be loaded into the anatomical viewer. The orientation of the series in the Anatomical Viewer is always identical to the orientation of the source image and the map. This might require the calculation of real-time Multiple Planar Reformats.

NOTICE

When you load an imaging series with an orientation different to the source image into the Anatomical Viewer, the series in the Anatomical Viewer will be a real-time Multiple Planar Reformat (MPR).

Always be aware that the imaging parameter of this series determine the image quality of the resulting MPR. Low resolution imaging series will result in blurry MPRs and might hamper the workflow.

To load an imaging series into the Anatomical Viewer

1. Click the **Anatomical Viewer** tab to switch to the **Anatomical Viewer**.
2. Right-click the **Anatomical Viewer** and click **Select Series** from the right mouse menu.
3. Click on a series in the **Select Series** window and click **OK** to confirm the selection.
4. You can also load a series by dragging and dropping a series.

Tip

When you save a layout, the series displayed in the viewer at that time is saved with the layout. When you reload the layout for another case, the same series is also reloaded in the viewer. You can save a layout using the More menu in the task guidance panel.

Creating a ROI

1. You can draw a ROI to focus on a specific area, for example, a lesion.

   For information on how to draw, modify, and rename a ROI, see section “Draw ROI” on page 15.

2. To display a mirror line, select **Show Mirror Line**.

   A vertical mirror line will show up in the middle of the image. If desired, drag the line to move it to another position.

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3. To create a contra-lateral ROI when you draw the first ROI, select **Create contra-lateral ROI automatically**.
4. Draw a ROI.

   When finished, the drawn ROI will be mirrored and the contra-lateral ROI will be created automatically.
5. Drag the mirror line to change the position of the contra-lateral ROI.

NOTICE

You should manually align the brain center-line to get exact mirroring between both sides.

⇨ Lesion/reference ratio values are displayed in the results panel.

6. If desired, you can remove the last drawn ROI. Do one of the following:
   - Press Ctrl+Z.
   - Right-click the ROI and then click **Delete Last Drawn ROI** in the shortcut menu.

Setting a Reference ROI

As an alternative, you can mark a single ROI as a reference ROI, and view the ratios of all other ROIs in relation to the selected reference ROI.

1. Right click the ROI that you want to set as the reference ROI and click **Declare as reference ROI** in the shortcut menu.

⇨ The label "-ref" is added to the name of the ROI to indicate that it is currently selected as the reference ROI.

⇨ The ratio table in the table viewer displays the ratio of all other ROIs in relation to the reference ROI.

⇨ If you create a bookmark, the selection of the reference ROI is maintained in the bookmark.

2. You can change the reference ROI at any time.

⇨ All ratio results are updated automatically when you change the reference ROI.

NOTICE

Mirrored ROIs are not included in the ratio results for a reference ROI. Results for a mirrored ROI only show the ratio in relation to the ROI that it is mirrored from. However, if you break the link for a mirrored ROI, then both ROIs are included in ratio results for a reference ROI. Note that there can only be one reference ROI.

Displaying Curves in the Graph Viewer

You can enable/disable the display of curves in the Graph Viewer.

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1. Check the checkbox 'Roi1', 'Roi2' or any 'Roi' in the Graph Viewer to enable the display of the related graph.
2. Uncheck the checkbox 'Roi1', 'Roi2' or any 'Roi' in the Graph Viewer to disable the display of the related graph.

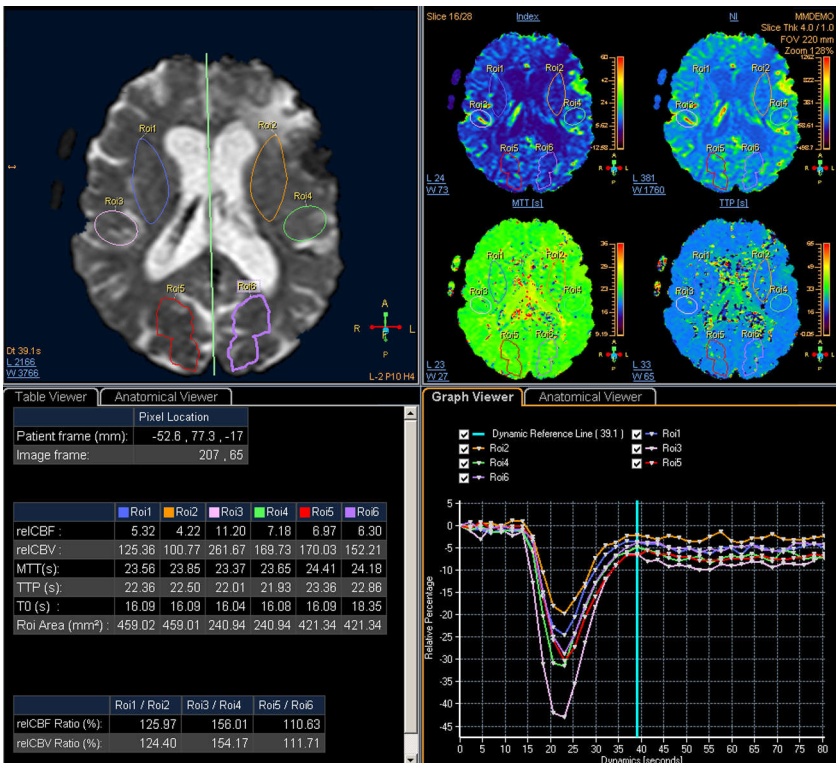

Fig. 15: Three different ROI types mirrored from left to right hemisphere with graphical and numerical results.

Select Underlay

You can select an MR series as underlay of the parametric maps allowing for better allocation.

In order to optimize the display you can also adjust the opacity of the overlaying parametric maps.

NOTICE

MR series are suitable source images. Secondary captures are not suitable because they are lacking in general geometry information.

The underlay is automatically reformatted to the geometry of the overlay. The resolution is determined by the resolution of the overlay in the preview viewer.

Select Underlay

1. Select an option:
   - **None**

The parametric maps will be displayed without underlay.

- **Source as Underlay**

  The source series will be displayed as underlay.

- **Select Other Underlay**

  Browse to the series you would like to use as underlay and click **OK** to confirm. You can also load a series by dragging and dropping a series.

Tip

When you save a layout, the series displayed in the viewer at that time is saved with the layout. When you reload the layout for another case, the same series is also reloaded in the viewer. You can save a layout using the More menu in the task guidance panel.

NOTICE

There can be a mismatch between underlay and overlay also in the Anatomical viewer if there was any patient motion between the acquisitions of these series.

Adjust the opacity of the overlay

1. Drag the slider to adjust the opacity of the parametric maps.

You may also drag the right mouse button in the color maps to change the opacity of the overlay.

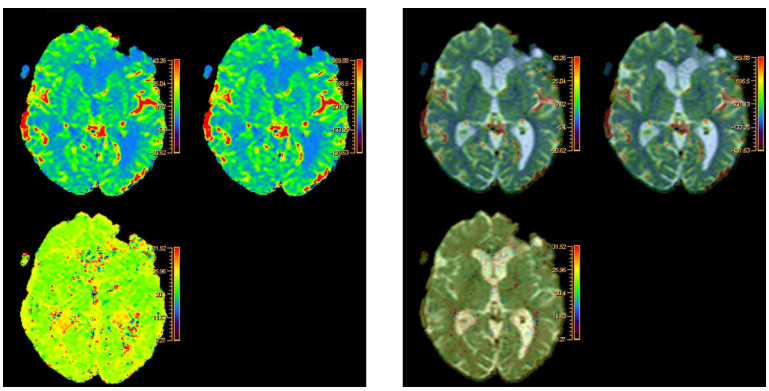

Fig. 16: Left: 100% opacity of the parametric maps. Right: 20% opacity of the parametric maps

Generate Series

You can generate a new imaging series containing the parametric maps and results as defined in the previously described workflow.

1. To generate a standard DICOM-compatible series, select **Generate Series** using the Secondary Capture option from the drop-down list, and then click the button.
2. Enter the name of the new imaging series in the **Name** box.

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3. To generate a series as RGB images (high resolution color maps), select **Generate Series** using the Secondary Capture RGB option.

Register Data While Saving

Once enabled, this function performs registration when generating actual maps. In such a way image quality will most likely improve in the maps.

NOTICE

If the input data is unregistered, there can be a mismatch between the previewed and generated maps as the generated maps are calculated after registering the input.

Results

The package calculates the following results:

Graphical and numerical results

- The graphical results present a **Time-Intensity Diagram** (intensity versus time).

  In 'Follow Mouse' mode, the graph correlates to a specific pixel and shows the intensity value (intensity) over the time for this pixel.
- The results will be provided as **parametric maps** and in a **table of numerical results**.

  Scrolling through the maps, the type of the map is indicated in the map's series type field.

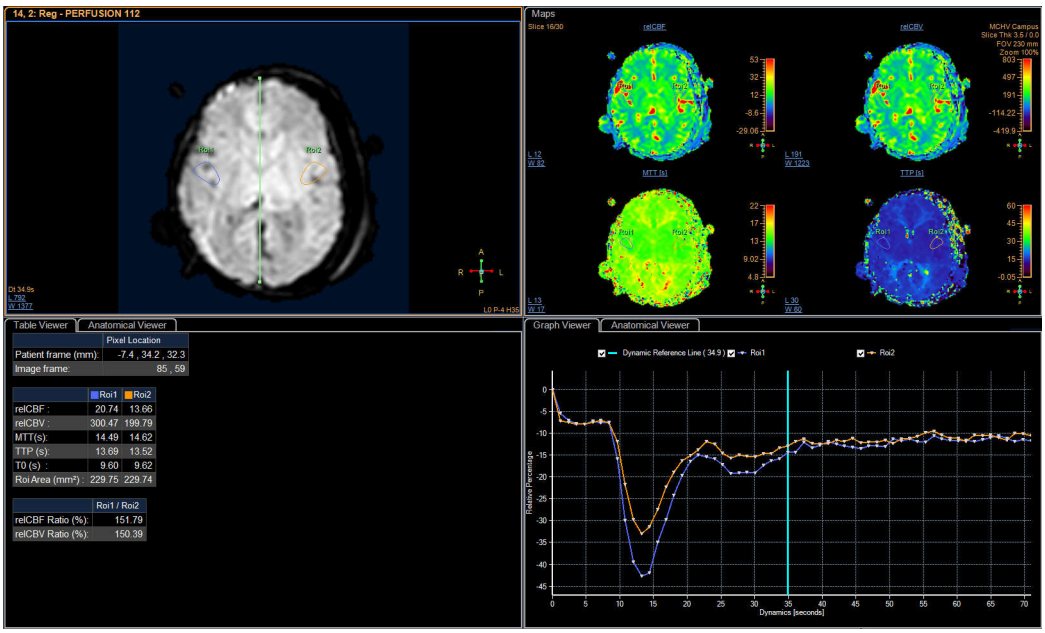

Fig. 17: Results screen: source image and maps with ROIs, Table Viewer and Graph Viewer. The dynamic reference line indicates the currently shown dynamic.

Measurement Type Selection

To change the type of measurement for all parametric maps, right-click the results summary table and select an option.

- **Region Parameters (Factory default)**: The application calculates T2 parameters using the time intensity curve for the drawn ROI and displays the values in the table viewer.
- **Mean Voxel Parameters**: The application calculates the mean of all the voxels inside the ROI of the output parameters and displays the values in the Table Viewer.

The table heading is updated based on the selected type.

Show ROI Statistics

You can right-click the results summary table and choose to show ROI voxel statistics (or) select from More menu.

An additional numerical results table is displayed as floating window and display Maximum, Minimum, Median, Average and Standard deviation of the quantitative parameters for the ROI voxels with in the parametric maps.

When the number of columns in the table viewer exceeds default width or number of rows exceeds default height, the auto scroll is visible to allow the user to scroll to see all the columns and rows

To export table results:

1. Select **Copy to Clipboard**, open either Microsoft Word or Excel and paste the contents from your clipboard into the application.
2. Select secondary capture. A dialog box is displayed allowing you to select a file name, file format, and destination. You can save the series in DICOM format, or in non-DICOM format. If you select a non-DICOM format, you should additionally select a file system destination for exporting the table results.

To draw a windowing ROI, right-click a map and then click **Draw Windowing ROI**. The color scale of the map is recalculated to display maximum color heterogeneity inside the ROI. You can draw windowing ROIs on each map independently.

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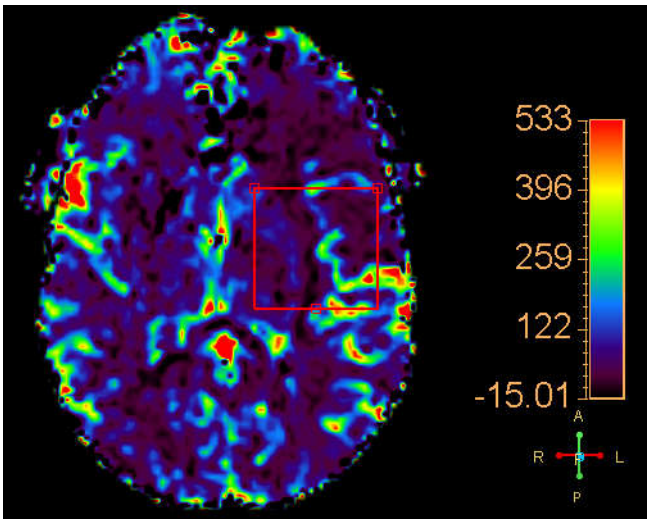

Fig. 18: Drawing a windowing ROI

Gamma Variate Results

The figure below gives an overview of the Neuro Perfusion results when using gamma variate analysis.

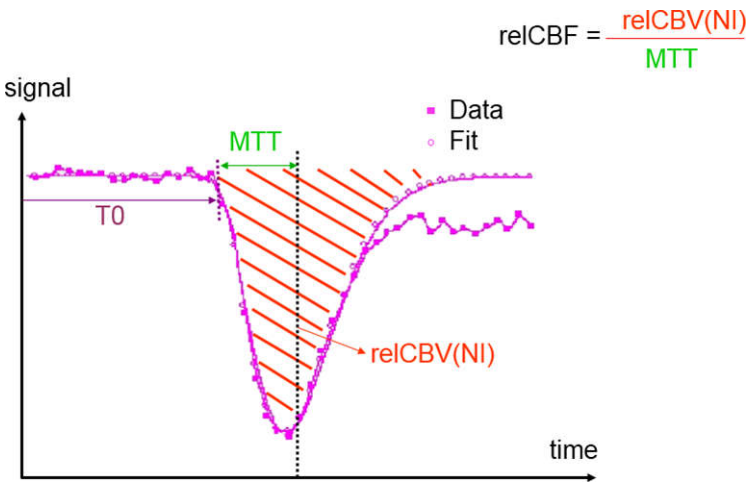

Fig. 19: Time Intensity Diagram for Gamma Variate Analysis

The relCBV is determined by calculation of the area under the curve.

The Mean transit time is derived as MTT = Σ (Si * ti)/ Σ Si.

The CBF is calculated based on central volume principle CBF = CBV / MTT.

Model Free Results

The figure below gives an overview of the Neuro Perfusion results when using model-free analysis.

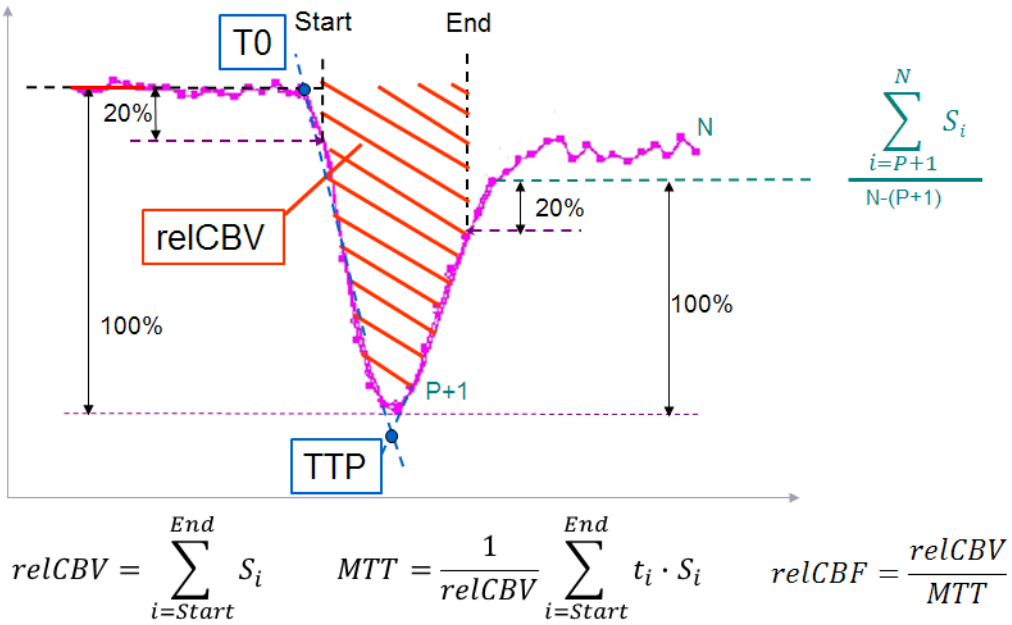

Fig. 20: Time Intensity Diagram with definitions of relCBV, T0, TTP, MTT.

Mean Transit Time [s] (MTT)

- MTT = Area (S*t) / Area (S)
- The time the bolus spends in the region of interest before leaving.

T0 - Time of Arrival [s] (T0)

- Arrival of the contrast agent, i.e. begin of the enhancement curve.

Time to Peak [s] (TTP)

- Time till contrast agent bolus reaches peak intensity.

relCBV (relCBV)

- The calculated area under the curve.

relCBF (relCBF)

- relCBV divided by the MTT.

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Leakage Correction Results

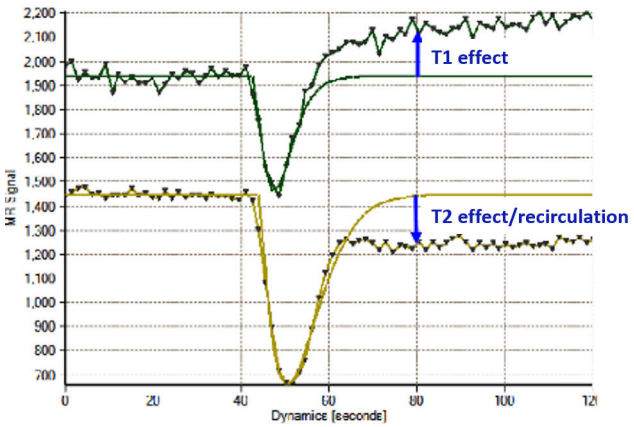

Fig. 21: Time Intensity diagram, showing T1 and T2 effects, and the effect of recirculation

Graphical results provide a best-fit curve for the time signal.

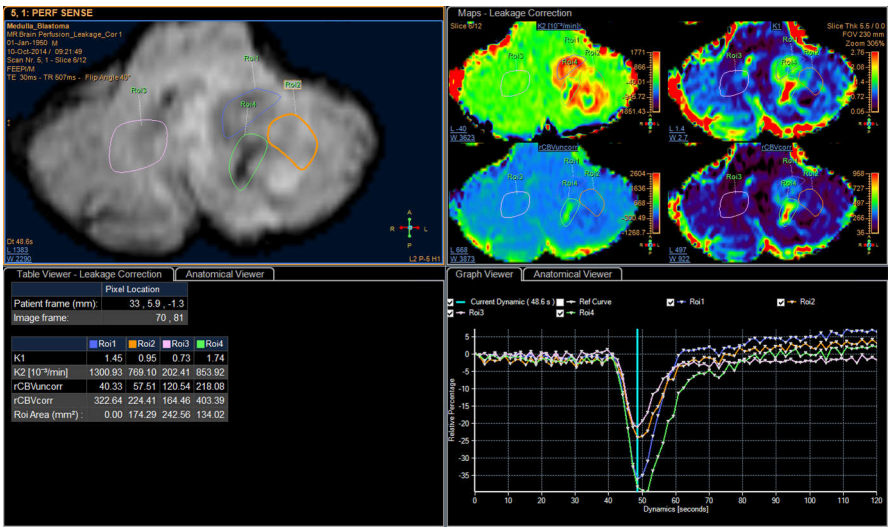

Fig. 22: Leakage Correction graphical results and results table

Leakage Correction analysis provides the following results for all defined ROIs:

- relCBV$_{uncor}$: Uncorrected relative cerebral blood volume.
- relCBV$_{corr}$: Corrected relative cerebral blood volume.
- K1: This is the scaling factor to fit the contrast passage signal of the reference voxels to the bolus passage of a voxel.
- K2: This is the scaling factor needed for an optimal fit of the leakage term. The leakage term is derived from the reference curve. The reference curve is the average of all non-enhancing or reference voxels. The leakage term is the time integral of the reference curve. It is specified in [1/min] and is a measure for the leakage.

- Reference curve: This is the reference signal used to fit with the help of linear regression K1 and K2 to match the acquired signal: K1 scales to bolus passage peak (typical range [0 -2]), K2 scales the leakage tail, K2 is positive in case of T1 dominance (the tail of the actual curve is higher than the tail of the reference curve), K2 can be negative in case of T2/T2* dominance (the tail of the actual TID is lower than the tail of the reference curve).
- R^2: (Advanced map, available from the **More** menu in the toolbar.) This represents the goodness of the fit.
- Ref Mask: (Advanced map, available from the **More** menu in the toolbar.)The reference mask show all pixels that have been used to determine the reference signal, which is assumed to be the signals from the voxels that don't show leakage/signal enhancement.

If **Follow Mouse** mode is enabled in the **More** menu, you can view real-time results for the voxel at the current pointer position.

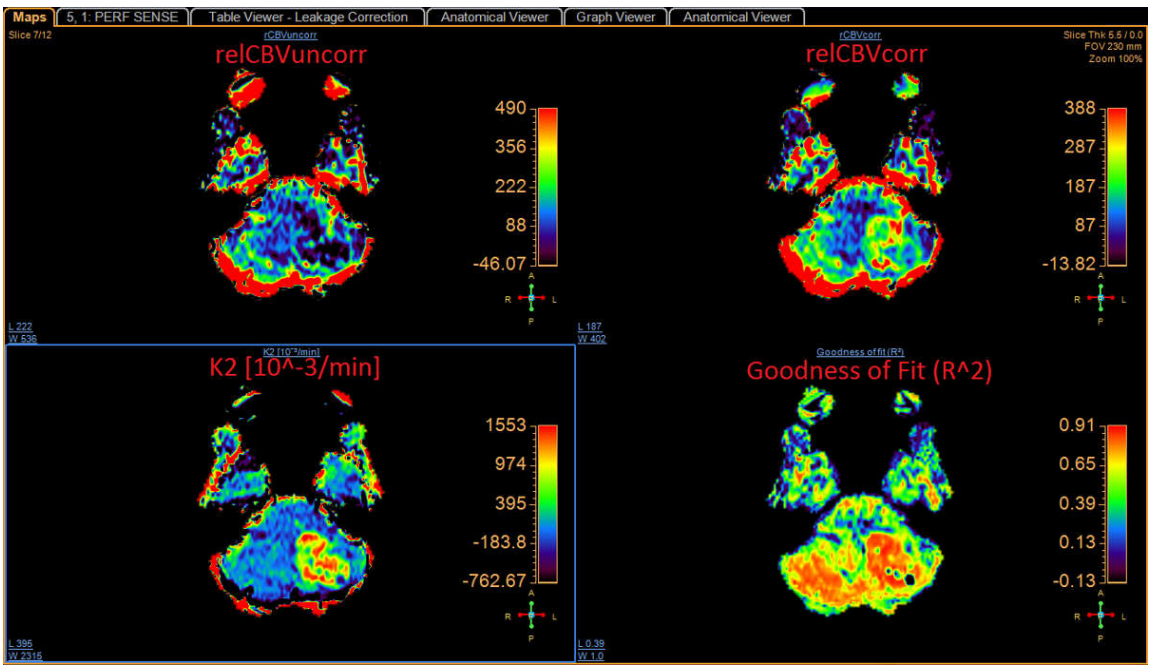

Fig. 23: Leakage Correction maps

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Gamma Variate Analysis

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Model-Free Analysis

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MR Diffusion-Perfusion Mismatch

The Diffusion-Perfusion Mismatch stage of the MR Neuro Perfusion application helps to distinguish potentially reversible from irreversible ischemia, which in turn aids in the decision to undertake intravenous or intra-arterial thrombolysis.

Performing Diffusion-Perfusion Mismatch

WARNING

If the anatomical data sets are not in the same frame of reference, the anatomical image might be mispositioned.

WARNING

Volume construction may require interpolation.

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NOTICE

For DTI/DWI series or if only multivendor maps are available, ADC iso and/or EADC iso maps are automatically generated when you launch the Diffusion-Perfusion Mismatch stage. This allows you to analyze mismatch without having to perform MR Diffusion analysis first.

NOTICE

In the Diffusion-Perfusion Mismatch application, the first volume of the perfusion series is automatically registered to the b0 volume of the diffusion series. Since the contrast of the b0-volume and the first dynamic of the T2* series are very similar, the co-registration makes use of the local correlation algorithm by default.

1. Click **MR Diffusion-Perfusion Mismatch**.

⇨ A 2x2 layout is displayed:

- The upper-left viewport contains the latest diffusion maps and series in tabbed viewports.
- The upper-right viewport contains perfusion maps and series that you created in the perfusion workflow.
- The table and graph viewports are empty.

⇨ The diffusion viewports and the perfusion viewports are registered and linked for position, zoom, and pan interactions. If desired, you can edit the registration using any diffusion series with the perfusion series as a reference.

⇨ If desired you can select a 2x3 layout using the **Layout** tool  in the toolbar. You can also edit the current layout and save it as a preset.

2. To perform mismatch analysis, you can choose between Manual analysis and Automatic analysis. Both options are described below.

Co-Registration Inspection

When co-registration is performed, you should verify the accuracy of the registration. You can inspect and edit the registration using the **Review & edit co-registration** step.

NOTICE

If you edit and accept the registration, the results are updated accordingly in the mismatch stage of the application.

1. Click **Manual Alignment** in the toolbar to open the **Review & edit co-registration** step.

⇨ The input series and the reference series are displayed as fusion views in three orthogonal orientations. You can change the orientation of the view, if desired.

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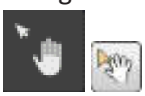
⇨ The initial alignment is calculated using the **Normalized Mutual Information** algorithm.

2. To change the alignment algorithm, select an option from the drop-down list in the task guidance panel.
3. You can make the following manual adjustments to the registration using tools in the task guidance panel:
   - **Translation Tools**: Click an arrow to nudge the registration in the corresponding direction, or use the **Translate** tool  to move the registration manually.
   - **Rotation Tools**: Click an arrow to rotate the registration clockwise or counter-clockwise, or use the **Rotate** tool  to rotate the registration manually.
4.  To undo an adjustment, click **Undo**.
5.  To reapply an adjustment that you have undone, click **Redo**.
6.  To reset the registration to the original position, click **Reset All Alignment**.
7. To save the registration and continue with the analysis, click **Save co-registration**.
8. To ignore the changes, go back to analysis.

Manual Mismatch Analysis

1. Click **Manual** in the task guidance panel if it is not already selected.
2. Select a **Diffusion ROI** type and draw an ROI on the diffusion series.

⇨ The ROI is propagated to the other diffusion series and maps, and to the perfusion series and maps.

3. Select a **Perfusion ROI** type and draw an ROI on the perfusion series.

⇨ The ROI is propagated to the other perfusion series and maps, and to the diffusion series and maps.

Automatic Mismatch Analysis

1. Click **Automatic** in the task guidance panel if it is not already selected.

2. In **Apply segmentation** click to mark a seed point on the ADC or Delay map.

⇨ After you mark a seed point, segmentation is calculated according to the threshold ranges indicated in the task guidance panel.

⇨ The threshold deficit mismatch is displayed as an overlay in the anatomical viewer.

⇨ The corresponding volume measurements are displayed in the tables.

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⇨ Signal intensity plots corresponding to the perfusion and diffusion deficits are displayed in the graph.

3. To adjust the default threshold values, enter new values in the task guidance panel and click **Apply Resegment**.

4. To segment additional regions, add additional seed points from the task guidance panel on the map.
5. To edit the segmented regions, draw an ROI to exclude the area in the segmentation that you want to erase.

⇨ After you edit the segmentation, the results viewers are automatically updated.

Adjust Segmentation Color Opacity

From the right click context menu, select **Segmentation Opacity** and adjust Segmentation color opacity independently in different view ports (ADC map, Delay map and Anatomical view-ports).

Results

The type of results generated depends on the type of analysis that your performed:

- Manual analysis mode generates area results (ROIs).
- Automatic analysis mode generates volume results (segmentation).

When you have created diffusion ROIs/segmentation and perfusion ROIs/segmentation, mismatches are calculated. The results are displayed as penumbra in the anatomical views, and numerical results are displayed in the table viewport and graph viewport.

Anatomical Viewers

Penumbra is displayed in the anatomical viewers with details of the ROIs, the amount of mismatch, and the mismatch ratio.

1. Click the **Anatomical Viewer** tab in one of the lower viewports.
2. Drag a series from the **Series** panel to the anatomical viewer.

⇨ The series in the anatomical viewer is displayed as MPR images and is automatically co-registered with the perfusion input series. ROIs in the diffusion and perfusion viewers are propagated to the anatomical viewer.

⇨ You can scroll over dimensions in the anatomical viewer (up to a maximum of three dimensions). Scrolling is linked to the diffusion and perfusion viewers.

3. To view penumbra as a color overlay in the anatomical viewers in manual segmentation, select **Fill Color Overlay** in the task guidance panel.

Tables

The table viewport displays the following tables:

- Table 1 displays details about each ROI/segmentation and ADC for each item. Clicking a column in the table displays the corresponding slice.

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- Table 2 displays mismatch information and mismatch ratio (%) for each pair of analyzed diffusion/perfusion results. The mismatch ratio is calculated as (Perfusion-Diffusion)/ Perfusion.

Graph

The graph viewport displays a signal intensity graph corresponding to the perfusion ROIs/ segmentation. You can select or deselect results as desired using check boxes.

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