7 MR Brain Function Analysis (Brain Function)

This processing package helps to identify active regions of the brain, relying on local metabolic and hemodynamic changes that occur in activated cortical brain. MR Brain Function Analysis indicates those pixels with a significantly increased signal intensity.

Contrast mechanisms

- **BOLD** (Blood Oxygen Level Dependent): During brain activation (increase of metabolism), the oxygen consumption of local tissue increases by approximately 5%.
- **Vasodilatation**: Vasodilatation occurs resulting in a local increase of blood volume and flow by 20% to 40%.

The above hemodynamic response to brain activation leads to an increased local oxygen level resulting in a signal increase in T2*W sequences.

Valid imaging series

- Heavily T2*weighted sequence. With matrices of around 64 - 96, this will yield a TR of 2 s to 4 s depending on the number of slices used.
- Dynamic study, e.g. 80 dynamics or more: Acquisition of 10 dynamics in rest, 10 dynamics during activation until a minimum number of dynamics (e.g. 80 is obtained).
- Basic fMRI BOLD scans typically take 4 min. to 5 min with typically 25 slices, 80 dynamics of 3 s each.
- Also the 3D PRESTO is often used for BOLD imaging (utilizing phase navigation). With this type of acquisition high temporal resolution can be produced by applying SENSE-factors in both phase and slice encoding directions.

Indications for Use

The MR Brain Function Analysis application assists users in the processing, viewing and analysis of fMRI Data. The application is designed to support the user to identify and visualize functional regions of the brain, relying on local metabolic and hemodynamic changes that occur in activated brain areas.

Intended Users

Advanced Visualization Workspace MR Brain Function Analysis application is intended to be used by adequately trained and qualified medical professionals, including but not limited to physicians and medical technicians. The main clinicians or medical and para-medical professionals who use the Philips Advanced Visualization Workspace MR Brain Function Analysis application are listed below:

- Radiologists in the radiology department/clinic
- 3D technologists in the radiology department

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Other clinicians/roles using the Philips Advanced Visualization Workspace are listed below:

- Oncologists and oncology technologists
- Neurologists
- Referring Physicians

Intended Patient Population

The intended patient population covers all patients with functional MRI scans as part of their brain imaging examinations.

Benefits

When used as specified in the Intended Use, under the circumstances and conditions as specified in the Indications for Use, the application assists the user with the processing, viewing and analysis of fMRI Data on par with the state of the art, thus realizing a positive impact on diagnosis or patient management.

Contraindications

None.

User Interface

Screen layout

The MR Brain Function Analysis package has a default layout of viewport displaying source images and panels to the left.

Task Guidance

The MR Brain Function Analysis package provides a Task Guidance panel in the left part of the screen.

The Workflow section later in these Instructions for Use is based on this Task Guidance. For details, see section “Workflow” on page 116.

NOTICE

Follow the steps of the Task Guidance to make optimal use of the MR Brain Function Analysis function.

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Task guidance depends on the computation method that you want to use from Analyze SPMs in the left task guidance.. The available methods are described below.

Compute Using "Block" Paradigm

The block paradigm is typically used to detect correlations between brain activation and a task that the subject performs during the scan. A block paradigm requires that the subject perform a certain task in time blocks that are interleaved with time blocks of rest.

- Set Smoothing Width
- Select Anatomical Underlay
- Select Paradigm
- Compute SPMs
- Save SPMs

A block paradigm calculates statistical parameter maps based on activation and control tasks performed for a duration of at least a few dynamics.

Compute Using "Event" Paradigm

The event paradigm is used to discover correlations with specific cognitive states that are induced in the subject, such as memory and recognition. Typically this is done by randomly offering the subject a known visual stimulus, such as a picture.

- Set Smoothing Width
- Select Anatomical Underlay
- Select Paradigm
- Compute SPMs
- Save SPMs

An event paradigm calculates statistical parameter maps using randomized stimuli (not task based, as with the block paradigm).

Compute Using "Resting State" Data

Brain activity is present even in the absence of an external task, and the resting state paradigm evaluates such interactions that occur in the brain when the subject is resting. This activity represents the functional connectivity of a number of networks which are consistently found in healthy subjects, and which represent specific patterns of synchronous activity. The resting state paradigm is useful for exploring whether the functional organization of the brain is altered in neurological or psychiatric diseases.

- Set Smoothing Width
- Select Anatomical Underlay
- Draw a ROI to automatically generate a paradigm
- Save SPMs

Compute using resting state data allows you to draw a contour on the anatomy to set the reference area for SPM calculation. Fluctuations in the BOLD signal during resting state (as a result of tissue vascularization, for example) can be indicators for disease.

Toolbar

NOTICE

MR Brain Function Analysis does not provide a toolbar. All functions are selected from the task guidance panel or from the right mouse menu.

More Functions within the MR Brain Function Analysis package

In the 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 14.

The following functions are available:

- Manage Paradigms
- Use Smoothing Step
- Show Skip Dummy Dynamics Step
- Series selection for multi sessions

Manage Paradigms

A paradigm is a set of instructions that are given to the patient during acquisition. These instructions are focused on delineating a certain area of brain function.

The **Manage Paradigms** function allows you to add, edit, or delete paradigms using the **Manage Paradigms** dialog box.

1. To add a new paradigm, click **New** in the **Manage Paradigms** dialog box.

⇨ The **Paradigm Editor** is displayed. The Paradigm Editor consists of the following two steps:

- Step 1: Select the paradigm type and provide a name for the new paradigm.
- Step 2: Configure the paradigm tasks.

2. To create a block paradigm, do the following in Step 1 of the Paradigm Editor:
   - Select **Block Paradigm**.
   - Select whether to measure the duration in **Seconds** or **Dynamics**.
   - Enter a unique name for the paradigm.
3. Click **Next** to move to Step 2 of the block paradigm process in the Paradigm Editor.
4. At the top of Step 2 of the Paradigm Editor, select whether blocks will run sequentially or whether they can run in parallel.

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5. Click the down arrow in the first task box, and select a rest period.
6. Continue to add tasks and rest periods as desired.
7. To assign or change color overlay, click on the color legend next to the added task and select from the predefined color presets.
8. Continue adding tasks or rest periods until the block paradigm is configured.
9. To change the duration of a task or rest period, drag the end sliders to the corresponding block.

10. To remove a block, click **Delete** next to the block.
11. Click **Save** to save the block paradigm.
12. To create an event paradigm, do the following in Step 1 of the Paradigm Editor:
    - Select **Event Paradigm**.
    - Click **Browse** and select the event file that you want to use.

      Presentation files can be selected for analysis of events created with Presentation software.
    - Enter a unique name for the paradigm.
13. Click **Next** to move to Step 2 of the event paradigm process in the Paradigm Editor.

⇨ Tasks for the event paradigm are configured according to the events file specified in Step 1.

14. Click **Save** to save the event paradigm.
15. To modify an existing paradigm, select the paradigm in the **Manage Paradigms** dialog box and click **Edit**.

    Modify the settings of the paradigm using the Paradigm Editor (you can't change the type of paradigm).
16. To create a copy of an existing paradigm, select the paradigm in the **Manage Paradigms** dialog box, click the down arrow next to the **New** button and then click **Copy**.

⇨ A copy of the selected paradigm is added to the paradigm list as a new paradigm. You can then modify the new paradigm using the Paradigm Editor.

17. To delete an existing paradigm, select the paradigm in the **Manage Paradigms** dialog box and click **Delete**.

Show Smoothing Step

This function is enabled by default and is available in the task guidance panel when you start MR Brain Function Analysis. If desired, you can hide this function. For details, see section “Set Smoothing Width” on page 117.

Show Skip Dummy Dynamics

Selecting the **Show Skip Dummy Dynamics** option in the **More** menu adds an optional step to the task guidance panel called **Skip Dummy Dynamics**.

Skipping dynamics allows you to ignore a number of the initial dynamics, in which the steady state may not have been reached. This may be apparent as "dummy scans" in the Time Intensity Display. Skipping these dynamics improves the analysis. After skipping dynamics, you need to compute the SPMs again.

This optional step is available for all computational methods.

Series selection for multi-sessions

Use this function to add series to the selection when you are performing a multi-session analysis. When you select this item, the **Select Series** dialog box is displayed, allowing you to select additional series.

Workflow

Launch the MR Brain Function Analysis package

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

1. Select a suitable fMRI series.

2. Click ’MR Brain Function Analysis’.

   The MR Brain Function Analysis package opens.

⇨ Co-registration is performed automatically as the package opens, according to the reference series settings in the MR preferences. For more information, see Anatomical Reference Preferences.

Review and Edit Co-registration

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

NOTICE

If you edit the registration and save your adjustments, all computed results are deleted.

1. Click **Review co-registration** in the toolbar to open the **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.

⇨ 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.

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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 to default registration**.
7. To save the registration and continue with the analysis, click **Save**.
8. To ignore the changes, click **Cancel**.

Set Smoothing Width

Selecting the **Show Smoothing Step** option in the **More** menu adds an optional step to the task guidance panel called **Set Smoothing Width**. Smoothing reduces noise level while retaining the underlying signal.

NOTICE

If very small activation regions are expected, smoothing should not be performed to avoid signal reduction.

This step is optional, but it is enabled by default when you start Brain Function Analysis. If desired, you can hide this function.

This step is available for all computational methods.

1. To adjust the smoothing width, drag the slider in the task guidance panel.

⇨ An appropriate setting for the smoothing width is twice the in-plane resolution (voxel size) of the images.

⇨ To fine-tune the smoothing width by small increments, click the slider control and then use the left and right arrow keys on the keyboard.

⇨ Increasing the smoothing width smooths the boundaries of calculated areas. This reduces noise in the image, but also reduces spatial resolution.

WARNING

Software does not recognize wrong correlation between tasks specified by input paradigm and acquired data. Correlation can be manually checked by users using time intensity display.

Anatomical Series

If desired you can select an underlay to provide additional anatomical information in the image.

1. To display an anatomical underlay, select **Use anatomical series as underlay** in the task guidance panel.

⇨ Select a different anatomical series from the drop down list using select anatomical series dialog box.

⇨ Alternatively, a message is displayed if an anatomical series is not available.

2. Select a series from the dialog box and click **OK**.

⇨ The anatomical series is loaded as an underlay in the main viewport with co-registration. The name of the series used is displayed in the task guidance panel.

NOTICE

When changing an anatomical underlay with results, all computed results are deleted. A message appears. Select **Continue** or **Cancel**.

If **Continue** is selected, all results are deleted. The new underlay is applied and is automatically registered with the overlay.

3. To hide the underlay, clear the **Use anatomical series as underlay** check box in the task guidance panel.

⇨ The underlay remains available in the task guidance panel. To display it, select the check box again.

4. To use a different series as the underlay, click the **Select** dropdown list and choose an alternative series, if available.

Analyze SPMs

NOTICE

This task is applicable to block and event paradigms only. For Resting State Data, continue to the "Compute SPMs" task.

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1. Click the down arrow in the **Select Paradigm** box in the task guidance panel and select the paradigm that you want to use for the analysis.
2. Optional step for Event paradigms: you can override the configured event file for the paradigm and use a file with different timepoints. Select **Change the Event File** and click **Browse**  to select an alternative file.
3. In the **Select SPMs** tasks for display box, select the statistical parameter maps that you want to calculate.
4. To assign or change color overlay, click on the color legend next to the added task and select from the predefined color presets.

Compute SPMs

1.  Additional step for Resting State Data only: Select an ROI tool in task guidance panel and draw a contour on the anatomy to set the reference area for SPM calculation.

   Click the arrow next to the ROI tool to access the following options:

   -  Smoothed Polygon
   -  Ellipse
   -  Freehand Contour
2. 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** in the shortcut menu.
   - Right-click the image and then click **Delete Last Drawn ROI** in the shortcut menu.
3. For all paradigms or Resting State Data: In the Compute SPMs section of the task guidance panel, select the masks to be used for the computation. The following masks can be used separately or together:
   - Select **Apply Default Mask** to use the default correction algorithm. This mask suppresses calculation and display of activation areas outside the brain. It also provides faster calculation.
   - Select **Suppress Motion Related Artifacts** to use the motion correction algorithm. However, if the motion has a similar pattern to the stimulus, it may also reduce interesting activation.

NOTICE

When analyzing series that have been registered on the MR console, the option to suppress motion-related artifacts option is not available. This option is only available for series that have been registered on the Advanced Visualization Workspace.

4. Click **Compute SPMs** to start the analysis and display the statistical parameter maps in the main viewport.

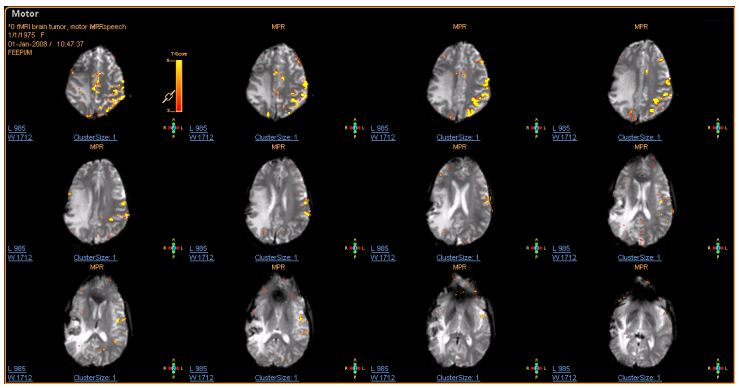

Fig. 36: Statistical parameter maps after computation

5. To change the layout of the tiled viewports, right-click a viewport and select a new layout in the right mouse menu.
6. To change SPM (Statistical Parameter Map) color overlay, right click on the image, select **Color** and select from the predefined color presets.

7. To change the T-score of the colormap, move the pointer over the upper threshold or the lower threshold, and drag up or down to change that threshold.

⇨ The T-score range is indicated in the colormap legend in the viewport. Changing the T-score allows you to increase or decrease the range of pixels included in the color overlay.

8. To change the blending (transparency) of the SPMs, right-click the image and click **Alpha Blending** in the right mouse menu.
   - Drag up or down to adjust the blending. The level of blending is displayed as a percentage at the top of the viewport.
9. Double-click a viewport to view a single slice in detail.
10. To view the Time Intensity Display (TID) for an activation area, right-click the activation area and click **Show TID** or select Mark activation area for TID and place the seed point on the image at the center of the activation area.
11. **Limit TID Computation to Marked Slice Only**: By default the Time Intensity Display shows the average value of the total 3D activation volume. Set this option to limit the computation to the 2D area in the selected plane.

⇨ The TID is displayed below the viewport, with the average TID displayed in the graph on the left.

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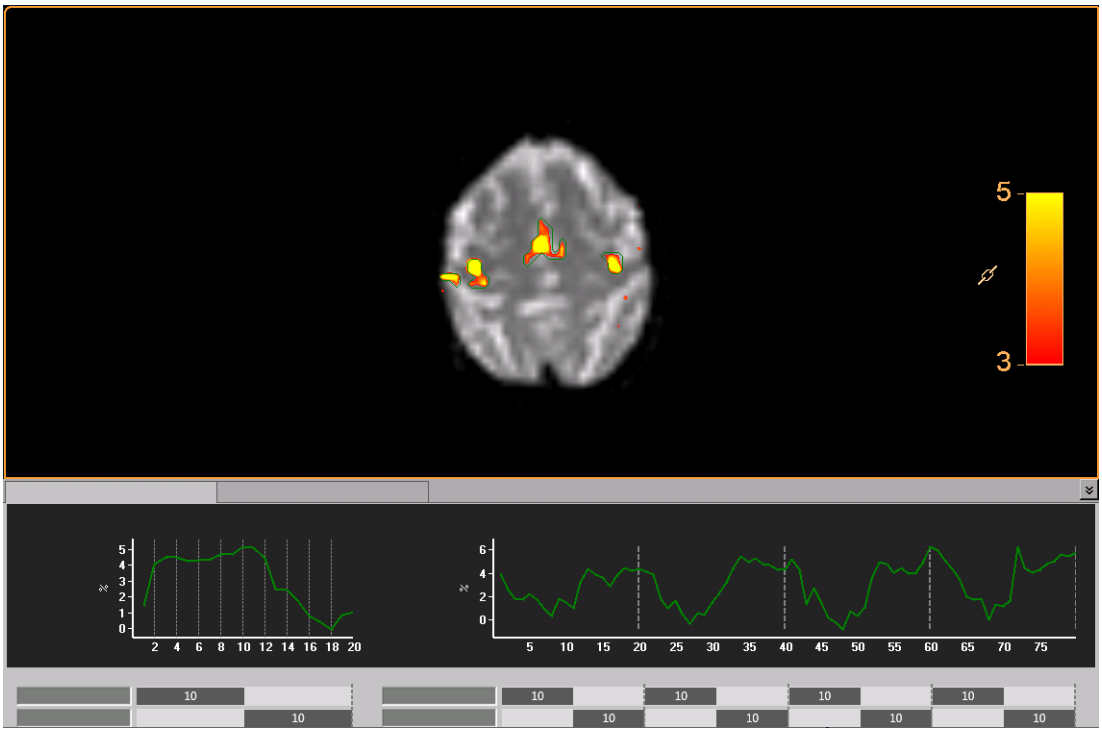

Fig. 37: Time Intensity Display for a picked activation area

⇨ If the signal response was taken from a region of interest with a high statistical value, the response should closely follow the applied paradigm.

⇨ You can hide or show the TID by clicking the double arrow in the upper-right corner of the TID.

⇨ The colormap scale is displayed on the right side of the viewport. By default, only positive values are displayed.

12. To view negative values, right-click the viewport and click **Also Show Negative T-Scores**.

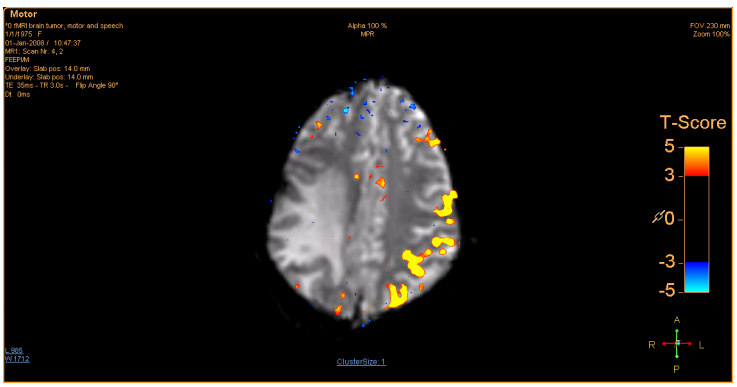

Fig. 38: Displaying negative T-Scores

13. To view the Quality Check graph, click the **fMRI Quality Check Graph** tab above the TID display.

⇨ The Quality Check graph is displayed below the viewport.

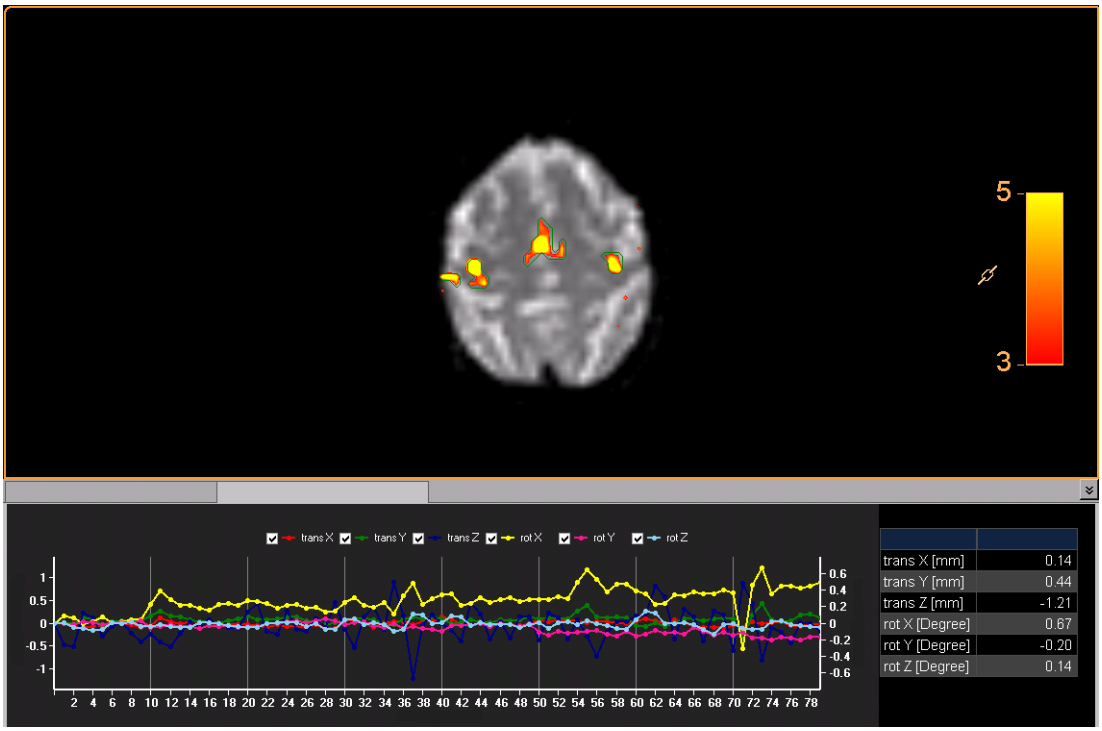

Fig. 39: fMRI Quality Check Graph

⇨ The left axis of the Quality Check graph displays the translation in mm symmetric around zero, and the right axis displays the rotation in degrees symmetric around zero. The graph uses the following colors:

⇨ You can show or hide individual plots using the check boxes above the graph.

- Red: **trans x** (representing the shift in the x direction)
- Green: **trans y** (representing the shift in the y direction)
- Dark blue: **trans z** (representing the shift in the z direction)
- Yellow: **rot x** (representing the rotation around the x-axis)
- Pink: **rot y** (representing the rotation around the y-axis)
- Light blue: **rot z** (representing the rotation around the z-axis)

14. To change the cluster size, click the **ClusterSize** viewport control and enter a value.

⇨ Changing the cluster size allows you to filter out smaller activation areas or "false positives".

WARNING

Before Analysis Alignment between functional and anatomical series, series should be inspected and corrected using the registration inspection step in MR Brain Function Analysis and FiberTrack. When saving changes performed in registration, all earlier computed results are deleted.

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Save SPMs

1. To save the statistical parameter maps, enter a name in the **Save SPMs** section of the task guidance panel and click **Save**.

⇨ The saved SPMs are saved with the series and are available from the **Series** panel.

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