



PHILIPS

Customer Services
Clinical Education

MR IViewBOLD

[IntelliSpace Portal](#)

[MR Applications](#)

[Quick Step Guides](#)

Application

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 IViewBOLD indicates those pixels with a significantly increased signal intensity.

Before you begin

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.

Background

Task guidance depends on the computation method that you want to use. The following methods are available.

The 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.

The 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.

The Resting State Paradigm

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.

Preparation: Create and Manage Paradigms

Manage Paradigms

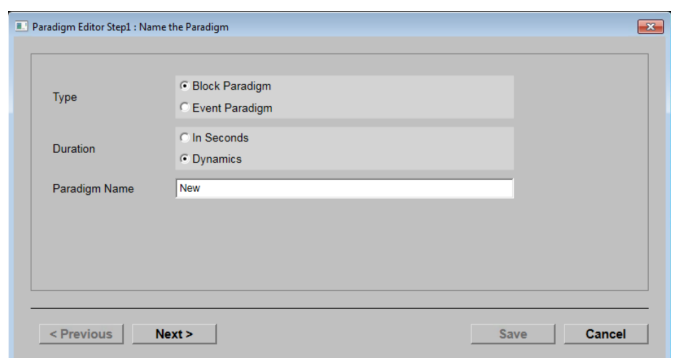
A paradigm is a set of instructions that are given to the patient during acquisition. These instructions are focused on delineating a certain area of brain function.

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

1. To add a new paradigm, click on the **More** dropdown menu from the task guidance and select **Manage Paradigms**. Click on **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.



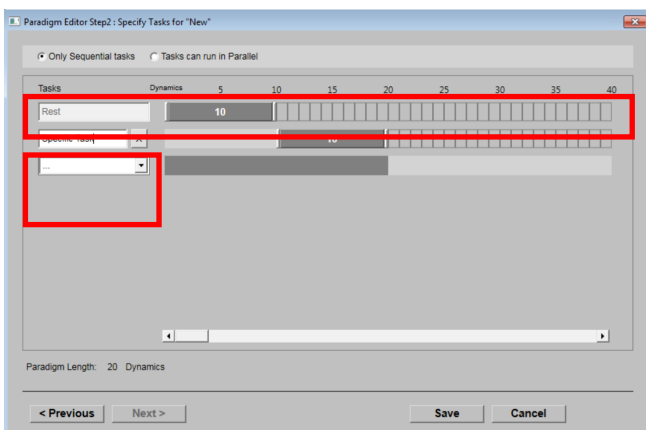
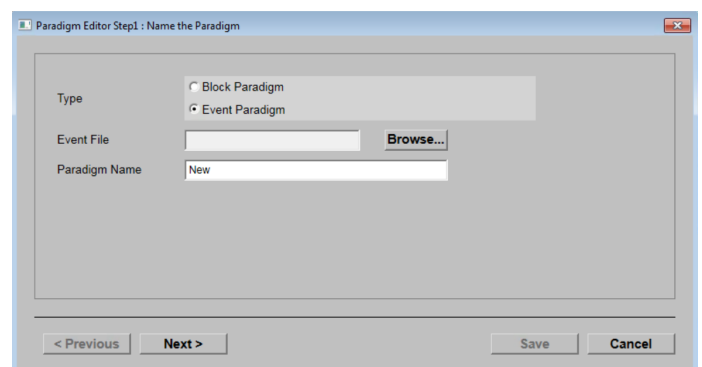
How to create a Block Paradigm

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.
 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. Continue adding tasks or rest periods until the block paradigm is configured.
 8. To change the duration of a task or rest period, drag the end sliders to the corresponding block.
 9. To remove a block, click **Delete** next to the block.
 10. Click **Save** to save the block paradigm.
 11. To create an event paradigm, do the following in Step 1 of the Paradigm Editor:

How to create an Event Paradigm

- 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.
1. 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.
2. Click **Save** to save the event paradigm.
 3. To modify an existing paradigm, select the paradigm in the **Manage Paradigms** dialog box and click **Modify**.



Workflow

Launch the MR IViewBOLD package

In the 'Directory' tab of the activity bar:

1. Select a suitable fMRI series.
2. Click 'MR IViewBOLD'.

The MR IViewBOLD 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 chapter "Anatomical Reference Preferences" on page 12.

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 **Inspect/Correct Data Alignment** step.

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.

This step is optional, but it is enabled by default when you start IViewBOLD. If desired, you can hide this function by clearing the check mark in the **More** menu.

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.

Select Paradigm

NOTICE

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

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** box, select the statistical parameter maps that you want to calculate.

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. 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.

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

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.

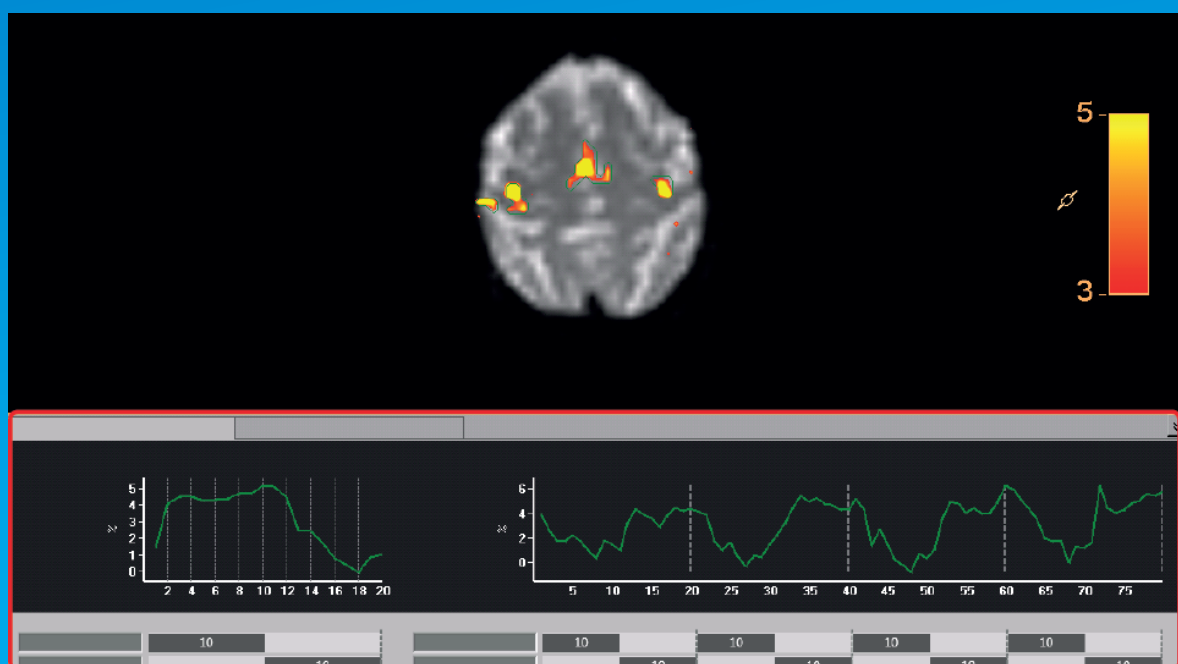
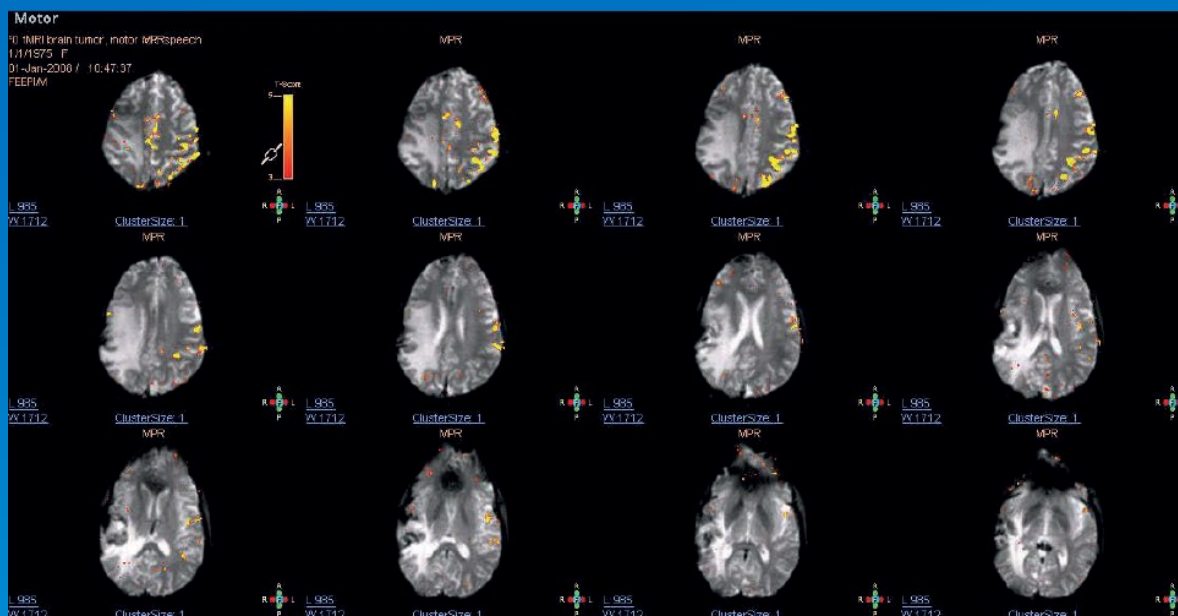


The T-score range is indicated in the colormap legend in the viewport. Changing the T-score allows you to increase or decrease the range of pixels included in the color overlay.



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.



Time-Intensity-Curve for a specific Area of Interest

Double-click a viewport to view a single slice in detail. To view the Time Intensity Display (TID) for an activation area, right-click the activation area and click **Show TID**.

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

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

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

Alignment between functional and anatomical series should be inspected and corrected using the registration inspection step!

Select Anatomical Underlay

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.

➔ The **Select Anatomical Series** dialog box is displayed.

➔ 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. The name of the series used is displayed in the task guidance panel.

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 **Select** again and choose an alternative series, if available.

Save SPMs



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.



