



**BESA MRI**  
**User Manual**



# BESA®

## MRI 3.0

# User Manual

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Author(s):	Tobias Boldte, Andre Waelkens, Isabella Paul-Jordanov, Harald Bornfleth, Mateusz Rusiniak, Jae-Hyun Cho, and Abinash Pant
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# 1. Notes

This user manual is a guide to the research product BESA MRI – a stand-alone software program.

The manual introduces the features, workflows, and the main windows and dialogs of the BESA MRI software. A help function is provided within the software. Press **F1** on the keyboard or select the menu item **Help → BESA MRI Help** for help.

Before starting to work with BESA MRI, please read this user manual carefully.

Please report any suggestions and errors found in this manual via email to [feedback@besa.de](mailto:feedback@besa.de)

BESA GmbH provides support to all customers who have purchased BESA MRI directly from our sales office ([sales@besa.de](mailto:sales@besa.de)) or through our distributors.

BESA GmbH  
Freihamer Str. 18  
82166 Graefelfing - Germany

In case of support requests please contact us at <http://www.besa.de/contact/support/>.

Symbols



This symbol indicates potential risks for users of BESA MRI or third parties if the product is not used as intended.

## 2. Start the program

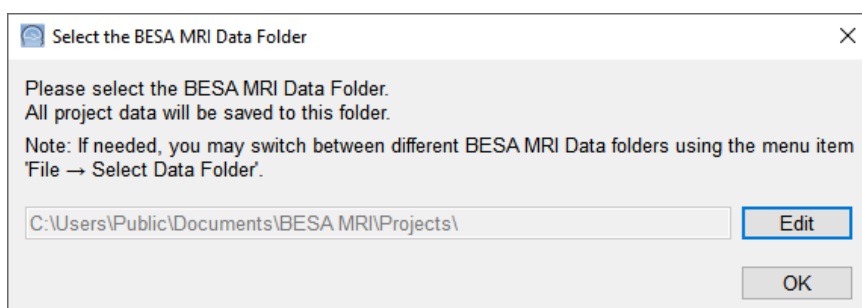


Start BESA MRI using the shortcut created on the desktop or run **BESA MRI** from the **Start → BESA → BESA MRI 3.0** folder in Startup menu. First, the Welcome Screen appears (see chapter 6.1.1). Press **Accept** to start BESA MRI.

### 2.1. Specify the BESA MRI Data Folder

As initial configuration step, the BESA MRI Data Folder must be specified (for details see User manual chapter *How to use BESA MRI*). This is the folder where BESA MRI stores all project and result data to and reads from (typically on the server).

When starting the program for the first time, the following dialog box appears:



The BESA MRI Data Folder is preselected to Public Users on the local PC (shown above for Windows 10). However, it is recommended to create the BESA MRI Data Folder on your server where it is accessible to all BESA MRI users from anywhere in the local network.

**Important note:** For clinical use, it is highly recommended to create the BESA MRI Data Folder on an encrypted medium since the data folder can contain patient information. Furthermore, please ensure that PCs running BESA MRI are password-protected in this case.

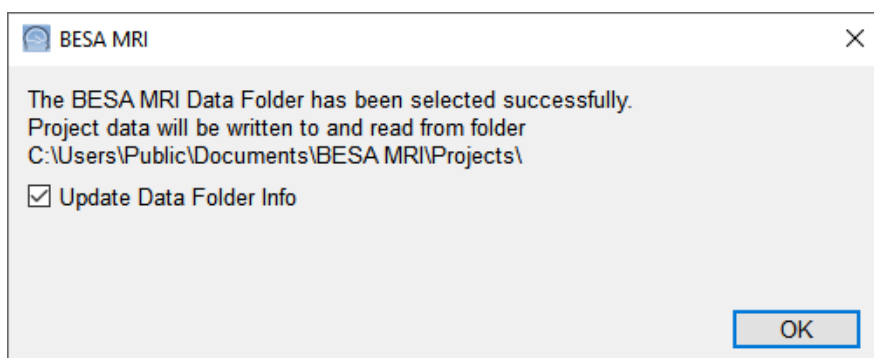


For more details, see User Manual chapters *How to use BESA MRI / Import Dialogs / Select the BESA MRI data folder* (6.4.1) and *Appendix / The BESA MRI data folder* (7.1).

Press the **OK** button if you want to use the preselected local folder in All Users.

Press the **Edit** button to create your BESA MRI Data Folder elsewhere, e.g. on a server.

When the selection is accepted, the following confirmation dialog appears:



2. Start the program



---

Press the **OK** button.

BESA MRI is now configured to start projects.

**Notes:** The procedure to define the shared BESA MRI Data folder on the server needs to be carried out only once at each PC where you install BESA MRI, i.e. when starting the program for the first time.

When switching between BESA MRI Data folders, it is recommended to leave the tick mark on to update all existing projects in the new BESA MRI Data folder (see chapter 2.1).



## 3. Introduction

### 3.1. Features of BESA MRI

The BESA MRI software provides optimized, user-guided workflows to read and transform MRI data to ACPC- and Talairach space, reconstruct the scalp and cortical surfaces, and coregister electrode and MEG sensor coordinates as well as skin markers with the individual scalp.

The key features of the BESA MRI software are:

- Import of MRI data using an automated DICOM, Analyze or NIfTI reader
- Easy definition of ACPC- and Talairach points and other markers
- Automated inhomogeneity correction and reconstruction of individual scalp, skull, CSF and cortical surfaces
- Automatic generation of a 4-layer FEM or a 3-layer BEM model
- Transformation to ACPC- and Talairach space by direct 3D-spline interpolation of the original MRI
- Easy coregistration of digitized electrodes, MEG sensors, and skin markers with individual MRI data
- Morphing of electrodes (e.g. digitized or standard 10-10 system) to the individual scalp
- Creating electrode coordinates automatically on the individual scalp surface by following the 10-10 EEG placement rule
- Computation of leadfield matrix for a given electrode layout (EEG) and/or sensor configuration (MEG)
- Output of coregistration and MRI files (surfaces, meshes and leadfields) for source analysis programs, e.g. BESA Research

The integrated segmentation workflow quickly guides through the necessary initial steps of data preparation from the input of the MRI data to the marking of all reference points. Then, an automatic finalization process performs the preset correction, segmentation, and reconstruction steps and presents the final results for inspection. It is possible to prepare MRI data of several subjects for segmentation and, then, start the automatic finalization of all projects in one step.

The integrated coregistration workflow quickly guides through the loading of a completed segmentation project and of a coregistration file, helps to set fiducial markers, and fits electrodes and/or MEG sensor coordinates as well as skin points to the scalp surface for final inspection.

This workflow concept (see chapter 4) allows for the immediate review of each workstep in the Workflow Window (see chapter 5), and for the modification of specific parameters and the recalculation of the output data if needed.

The segmentation and coregistration worksteps are described in detail in chapter 6, along with more details on how to use BESA MRI.

BESA MRI provides a subject-based data management (see chapter 7.3). All results are stored in subject-related subfolders. Several segmentation and coregistration projects can be managed for each subject.

### 3.2. Why FEM or BEM modeling

**Important note:** FEM or BEM models shall not be calculated and applied in data analysis for patients who have previously undergone a brain resection.



For all source analysis techniques, the forward model describes the relation between the electrical sources in the brain and the measured EEG / MEG. The forward model includes a description of the anatomy of the subject's head. Usually, the exact properties of the individual subject's anatomy are unknown. This is why the forward model is often a spherical or ellipsoidal model, only describing the head anatomy coarsely. In EEG, one-layer models are insufficient, as different head tissues have different conductivities, which influence the current flow greatly. This is why EEG forward models usually consist of 3 (scalp, skull, and brain) or 4 layers (scalp, skull, CSF, and brain) associated with different conductivity values. MEG forward models are usually 1-layer spherical models as magnetic fields are assumed to be less influenced by conducting tissues.

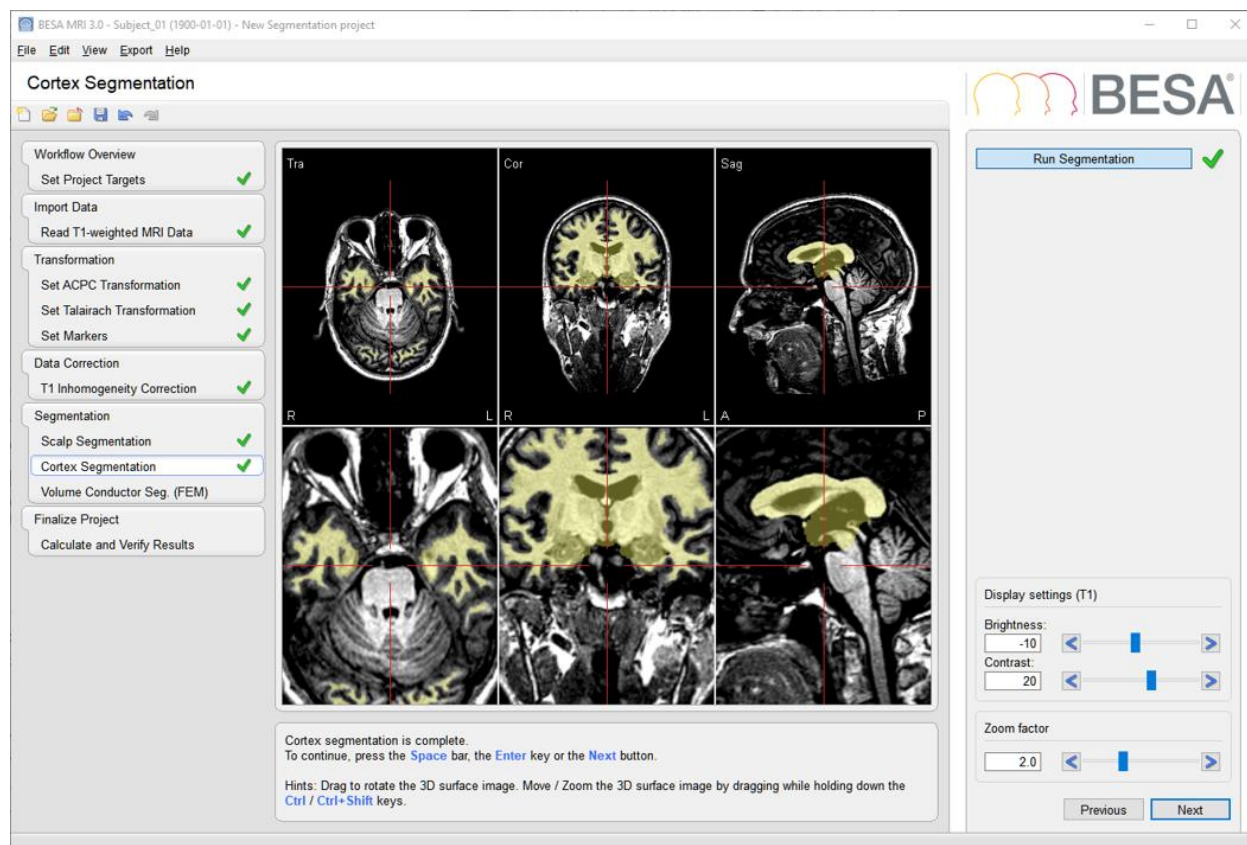
If a subject's MRI is available, it is possible to use individual anatomical information for the generation of the forward model. Thereby, the forward model becomes more tailored to the individual subject and in consequence the inverse solution can become more precise (Vanrumste et al., 2002; Cuffin 1996; Roth et al., 1993). This is especially true (a) for sources in brain regions that are not described well by a spherical head model (e.g. basal temporal lobe); (b) when individual heads show deviations from the norm. Thus, if the research target is to achieve maximal localization precision, an individual realistic head model is strongly recommended.

There are different approaches to realistic head modeling. BESA MRI offers two different head model types: Finite Element Method (FEM) and Boundary Element Method (BEM).

- **FEM modeling:** It allows modeling cerebro-spinal fluid (CSF) and arbitrarily complex geometries. In contrast to 3-layer realistic head models, 4-layer FEM models gain additional precision, as the CSF layer is associated with yet another conductivity value than the other head tissues (Baumann et al., 1997). Neglecting CSF for EEG forward modeling can lead to larger localization errors (Ramon et al., 2003; Wendel et al., 2008).
  - The FEM modeling in BESA MRI was developed in cooperation with the research group around Prof. Carsten Wolters. Detailed literature on the methods can be found in the reference section (see chapter 8).
- **BEM modeling:** The BEM model implemented in BESA MRI uses a 3-layer realistic head model (scalp, skull, and brain). In comparison to FEM, BEM can be applied for a piecewise constant conductivity field, resulting in a simplified description of the head geometry on the boundaries of head tissue. To generate nested closed surface meshes, less detailed volume conductor segmentation is applied for BEM in BESA MRI.
  - To compute the BEM forward solution, BESA MRI uses the OpenMEEG (Kybic et al., 2005; Gramfort et al., 2010) which was developed within the Athena project-team at INRIA Sophia-Antipolis. The OpenMEEG is used solving forward problems in the field of EEG and MEG, and it consists of the symmetric BEM.

## 4. The Workflow Concept

BESA MRI uses a modern workflow concept that guides you through all the worksteps needed to complete a project, suggests and explains necessary inputs and user actions, and performs many worksteps automatically. At any time, you may interrupt and inspect earlier worksteps or redo them with modified input parameters if required.



The workflow window at the left of the BESA MRI screen shown above depicts all the steps of the workflow in a segmentation project – completed up to the segmentation of the cortical surface.

A workflow consists of a series of worksteps that have to be done to finalize a project. Each workstep realizes a set of user interactions needed to achieve the workstep-specific result. Some worksteps can be run in automated processing mode with preset parameters, e.g. inhomogeneity correction and segmentation. Thus, only a few user interactions are needed during the initial worksteps.

When pressing the **Next** button or hitting **Space** a workstep is terminated and the next workstep is loaded. Thus, the workflow of a project proceeds sequentially workstep by workstep.

As described in chapter 5, the layout of the BESA MRI screen is optimized for this workflow concept. The workflow menu - as shown on the left in the **Workflow Window** - gives an overview over all the worksteps to be done in the selected project (see chapter 5). The workflow menu can be used to switch between the worksteps. For example, you may redo an earlier step with different or advanced parameters and continue with automatic processing of all subsequent steps as defined before.

The current results during a workstep are shown in the **Main Window** in the middle (see chapter 5.2). The **Information Window** below (see chapter 5.4) provides advice and help information for the current workstep.

During each workstep a special dialog is shown in the **Interaction Window** on the right to allow for optimized user interaction relevant for the current workstep (see chapter 5.3). The interactions required during a workstep are grouped starting at the top and ending at the bottom of the Interaction Window. After completing all interactions, press the **Next** button at the bottom or hit **Space** to proceed to the next

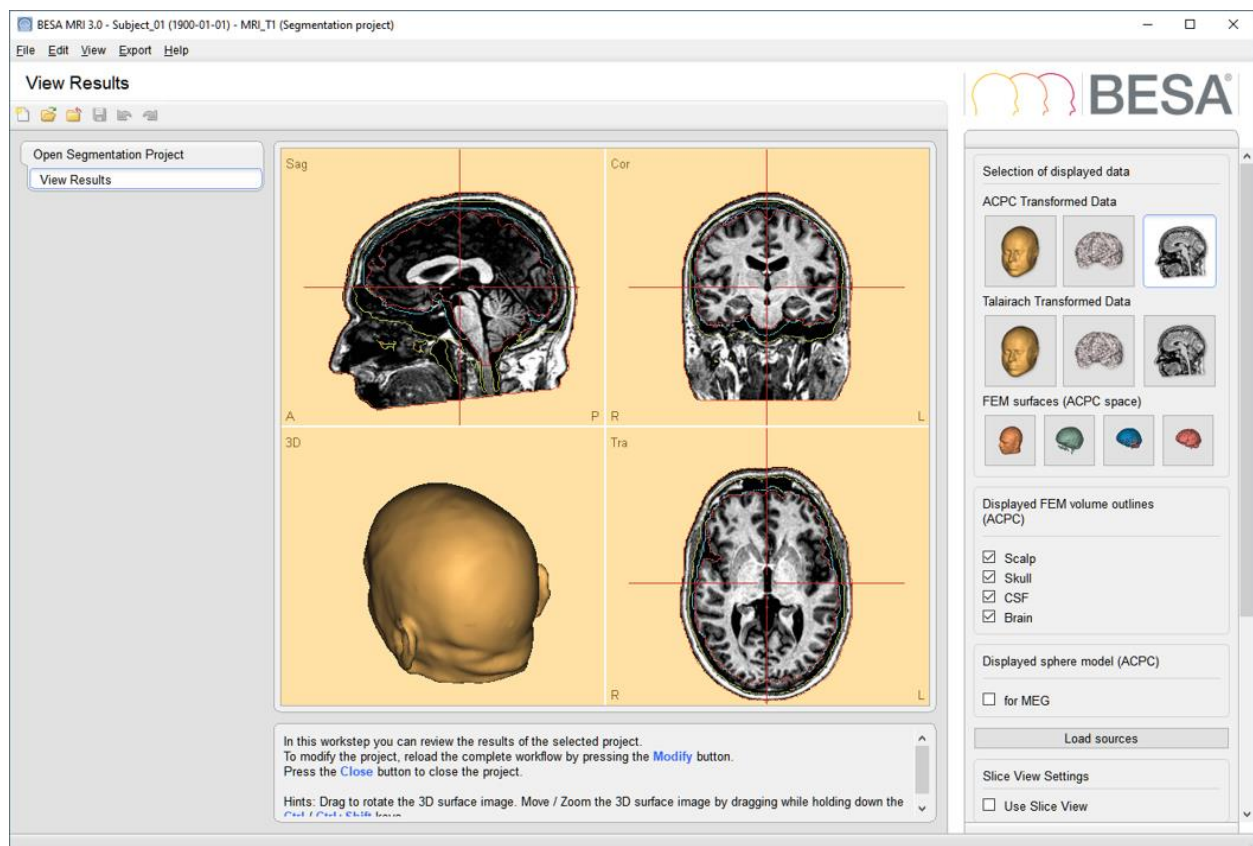
workstep. Press the **Previous** button to go back one workstep. After completing the last workstep of the workflow, press the **Finish** button at the bottom of the Interaction Window to save all data created during the project. This allows reloading the full workflow of a project with all worksteps at any time later.

BESA MRI offers two different workflows associated with the following projects:

- **Segmentation Project:** Initiated by Start New Segmentation Project (see chapter 6.2.1).
- **Coregistration Project:** Initiated by Start New Coregistration Project (see chapter 6.2.2).

A project is defined by a specific workflow together with the stored individual input and output data. Therefore, projects are identified by the name and birth date of an individual subject along with the type of workflow specific for the project, i.e. Segmentation or Coregistration.

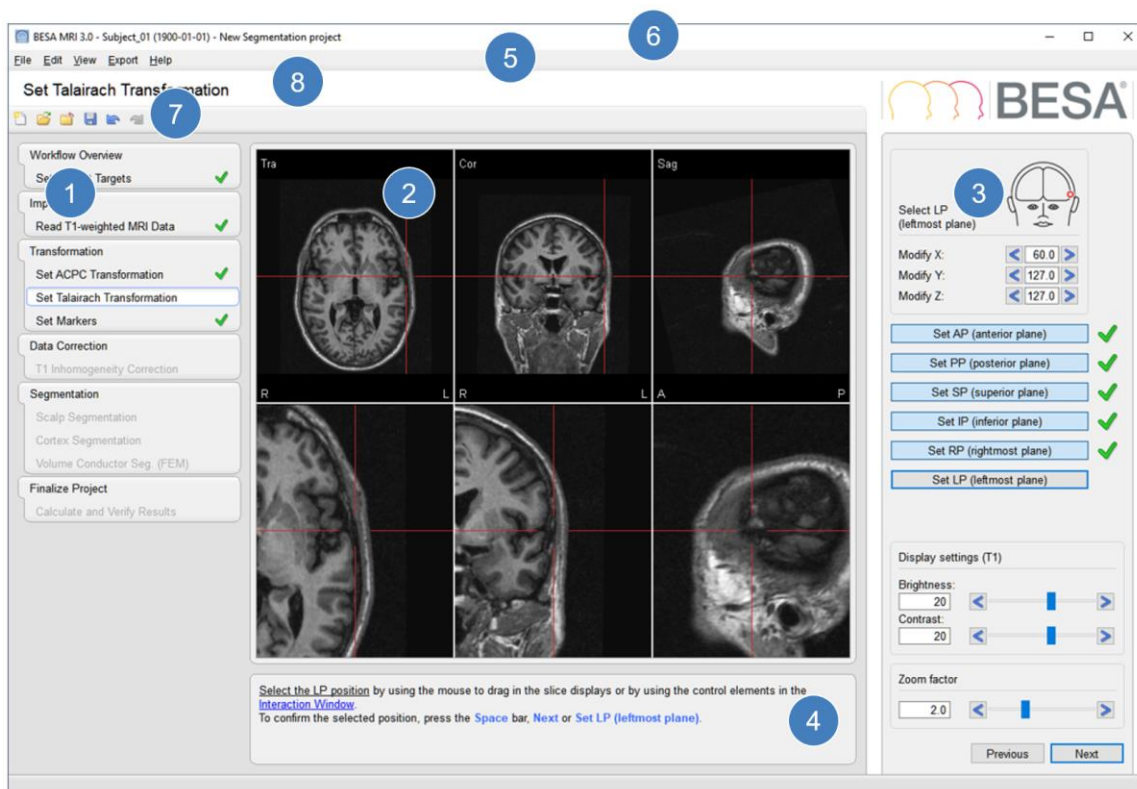
Stored projects can be viewed by selecting the menu item **File → Open Project**, using the open button in the toolbar, or pressing the **Open Segmentation / Coregistration Project** buttons on the start screen. After opening a stored completed project, the final workflow result is displayed in a special viewer workstep (see screen below for a Segmentation project):



To modify the project or to review the completed worksteps, reload the workflow by pressing the **Modify** button.

## 5. Elements of the BESA MRI Screen

The layout of BESA MRI screen is optimized for the workflow concept as described in chapter 4. The figure below shows the BESA MRI screen with all its elements:



- ① Workflow Window (see chapter 5.1)
- ② Main Window (see chapter 5.2)
- ③ Interaction Window (see chapter 5.3)
- ④ Information Window (see chapter 5.4)
- ⑤ Menu Bar (see chapter 5.5)
- ⑥ Title Bar (see chapter 5.6)
- ⑦ Toolbar (see chapter 5.7)
- ⑧ Caption (see chapter 5.8)



## 5.1. Workflow Window

The Workflow Window on the left displays the workflow menu. The workflow menu gives an overview over the sequential steps needed to finish the current project (for details on the steps see chapter 6.2). Steps already completed are marked with a green OK sign ( ✓ )

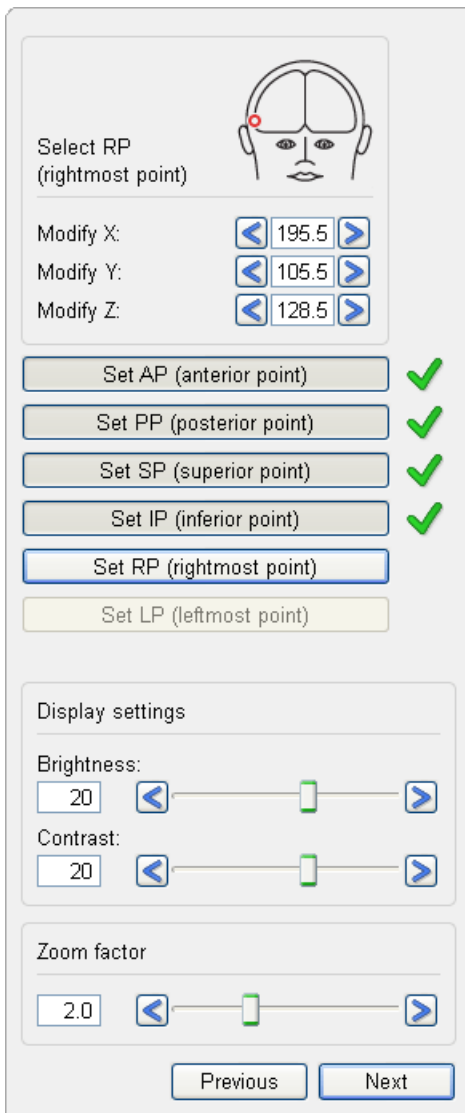
The current workstep is highlighted. This step is also shown in the caption.

The workflow menu can be used like any other menu to jump to another workstep provided that the previous worksteps have already been completed.

## 5.2. Main Window

The Main Window area displays the results of the current workstep. A detailed description how to use the elements shown in this window is given in chapter 6.3.

## 5.3. Interaction Window



The Interaction Window interface includes the following sections:

- Select RP (rightmost point):** A diagram of a head with a red dot on the right side.
- Modify X:** A numeric input field with the value 195.5 and left/right arrow buttons.
- Modify Y:** A numeric input field with the value 105.5 and left/right arrow buttons.
- Modify Z:** A numeric input field with the value 128.5 and left/right arrow buttons.
- Substep buttons:** A vertical list of buttons:
  - Set AP (anterior point) ✓
  - Set PP (posterior point) ✓
  - Set SP (superior point) ✓
  - Set IP (inferior point) ✓
  - Set RP (rightmost point)** (highlighted with a blue border)
  - Set LP (leftmost point)
- Display settings:**
  - Brightness:** A slider with a numeric input field showing 20.
  - Contrast:** A slider with a numeric input field showing 20.
- Zoom factor:** A slider with a numeric input field showing 2.0.
- Navigation buttons:** "Previous" and "Next" buttons at the bottom.

The Interaction Window provides the user interaction for the current workstep. In some worksteps a red marker illustrates the current interaction to be done at the top of the Interaction Window.

The **upper interaction elements** are used to set parameters needed in the workstep by using standard elements like buttons, edit boxes, and sliders. The effect of changing parameters is seen in the Main Window left of the Interaction Window.

The **substep buttons** below describe the substeps to be taken within the workstep. The current substep is highlighted. After a step is completed, a green OK sign appears beside the corresponding substep button.

Current parameters are accepted by hitting **Space**, by pressing the **Next** button at the bottom or the next substep button (in this example the **Set RP (rightmost point)** button).

Thus, the workflow proceeds to the next substep or workstep automatically.

The **Previous** button is used to jump back to the last substep or to the last workstep, respectively.

### Notes:

1. Most parameters are set more conveniently by mouse interactions with the displays in the Main Window (see chapter 6.3).
2. To change parameters of a completed substep, unpress the corresponding interaction button.
3. You can undo or redo a substep or workstep also using the menu items **Edit → Undo** and **Edit → Redo** or by typing **Ctrl-Z** or **Ctrl-Y**.
4. Moving on to the next substep or workstep is fastest by hitting **Space** or **Enter**.

## 5.4. Information Window

The information window displays a comprehensive help text related to the current workstep. The help texts provide additional information, e.g. which file has been loaded. They suggest and explain the next user interaction to be done in the current workstep.

The [Main Window](#) lists the targets to be achieved by the workflow.  
To continue the workflow, you can always type **Space** or **Enter** or press the **Next** button.  
For more information see description of the [Segmentation Workflow](#).

Underlined text in blue provides a hyperlink. Click on such a link to open the BESA MRI help at the indicated topic.

## 5.5. Menu Bar

The Menu Bar provides the menus listed below. Click on a menu to be selected and choose from the menu items that pop up.

### 5.5.1. File Menu

The **File** menu contains functions related to the data management (see chapter 7.3). It contains the following items:

File menu item	Description
<a href="#">Create New Project</a>	Start a new project.
<a href="#">Open Project</a>	Load an existing project (see chapter 6.4.2).
<a href="#">Close Project</a>	Close currently active project. Show the Select Project Page (see chapter 6.1.2).
<a href="#">Save</a>	Save the currently active project.
<a href="#">Save As...</a>	Specify a filename for currently active project and save it (see chapter 6.4.3).
<a href="#">Delete Projects...</a>	Select one or multiple projects that shall be deleted (see chapter 6.4.4).
<a href="#">Select Data Folder</a>	Select the folder to be used as BESA MRI Data Folder (see chapter 7.1).
<a href="#">Update Data Folder Info</a>	Update the information file in the BESA MRI Data Folder (see chapter 7.2).
<a href="#">Exit</a>	Terminate the BESA MRI program.

### 5.5.2. Edit Menu

The **Edit** menu contains the following items:

Edit menu item	Description
<b>Undo</b>	Undo the last step completed in the current workstep.
<b>Redo</b>	Redo the last step that was undone in the current workstep.
<b>Finalize Current Project</b>	Start an automatic finalization of the currently active workflow. This menu item is only enabled, after a workflow state has been reached at which all data are prepared for automatic finalization.
<b>Finalize All Segmentation Projects</b>	Start a finalization of all segmentation projects that are prepared for automatic finalization and defined in the current BESA MRI Data folder.

### 5.5.3. View Menu

The **View** menu can be used to change display settings for BESA MRI. It contains the following entries:

View menu item	Description
<b>Show Workflow Window</b>	By selecting or deselecting this menu item the Workflow Menu is displayed or hidden (see chapter 5).
<b>Show Information Window</b>	By selecting or deselecting this menu item the Information Window is displayed or hidden (see chapter 5.4).
<b>Standard Font Size, Large Font Size, Extra Large Font Size</b>	Select one of these menu items to specify the size of the font to be used in BESA MRI.

### 5.5.4. Export Menu

Use the **Export** menu to export the current main window as an image file format (\*.eps, \*.png, or \*.svg).

Export menu item	Description
<b>Main window</b>	Open the "Save Image As..." dialog.

### 5.5.5. Help Menu

Use the **Help** menu to open the program help or to get information about BESA MRI.

Help menu item	Description
<b>BESA MRI Help</b>	Open the program help.
<b>About...</b>	Get information about the current program version.

## 5.6. Title Bar

The title bar of BESA MRI displays the program name and version number. In addition, it shows the following information on the current project:

- Subject information (subject name and birthday)



- Project name (if specified)
- Project type (segmentation or coregistration project)

## 5.7. Toolbar

The Toolbar provides direct access to the most important menu items:

 **File → Create New Project**

 **File → Open Project**

 **File → Close Project**

 **File → Save Project**

 **Edit → Undo**

 **Edit → Redo**

## 5.8. Caption

The caption is located between the Menu Bar and the Toolbar and specifies the current workstep.

## 6. How to use BESA MRI

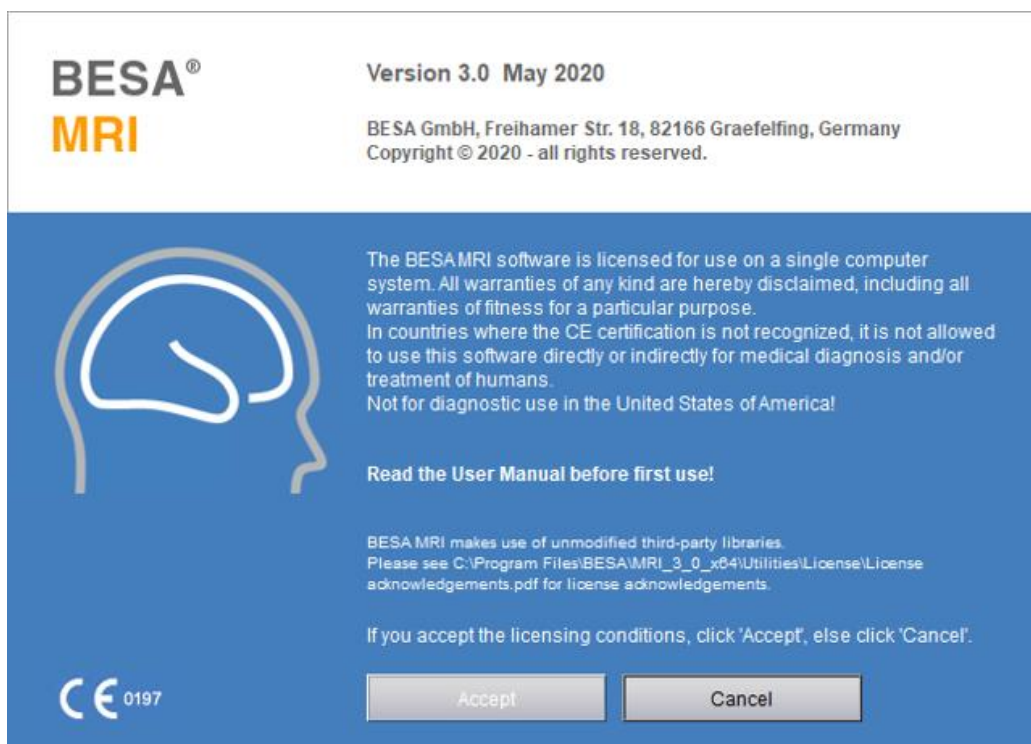
Before working with BESA MRI, please read chapter 4 on the workflow concept. Consult chapter 5 on the elements of the BESA MRI screen while starting to use the program.

### 6.1. Starting BESA MRI

#### 6.1.1. Welcome Screen

Start BESA MRI from its icon on the desktop or from BESA Research during the coregistration process.

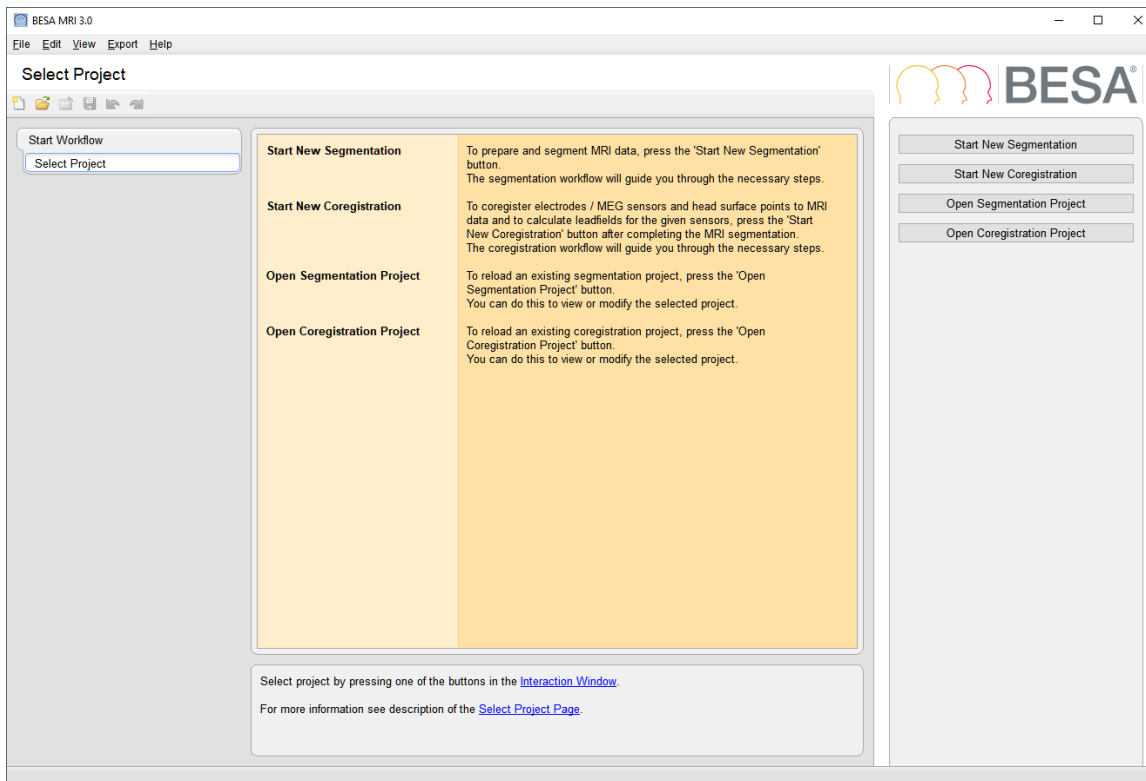
When starting BESA MRI, a welcome screen appears. It provides some information on the BESA MRI program including the current version number and date:



Press **Accept** to start BESA MRI.

## 6.1.2. The Select Project Page

After starting BESA MRI, the page Select Project shows. It allows to select a specific workflow:



Press one of the buttons in the Interaction Window on the right to start the desired project and the related workflow.

Press **Start New Segmentation** to create a new segmentation project. The Segmentation Workflow opens (see chapter 6.2.1).

Press **Start New Coregistration** to create a new coregistration project. The Coregistration Workflow opens (see chapter 6.2.2).

Press **Open Segmentation Project** to load an existing segmentation project. If the selected project has been finished, the View Results screen opens (see chapter 4).

Press **Open Coregistration Project** to load an existing coregistration project. If the selected project has been finished, the View Results screen opens (see chapter 4).

### Notes:

1. Before coregistration can be started for a subject, at least one MRI segmentation project has to be finished for this subject.
2. Projects can also be started or opened at any time by selecting the menu items **File → Create New Project** or **File → Open Project**.

## 6.2. The Workflows of BESA MRI

### 6.2.1. The Segmentation Workflow

In the Segmentation Workflow, individual MRI data are prepared for the segmentation of different head tissues needed for FEM or BEM. Once the head tissues are segmented, a 4-layer FEM model (scalp, skull, CSF and brain) or a 3-layer BEM model (scalp, skull, and brain) is generated based on the segmented volumes. The FEM or BEM model is directly available for source analysis in BESA Research or for exporting to use in third-party software. The Segmentation Workflow consists of the following worksteps:

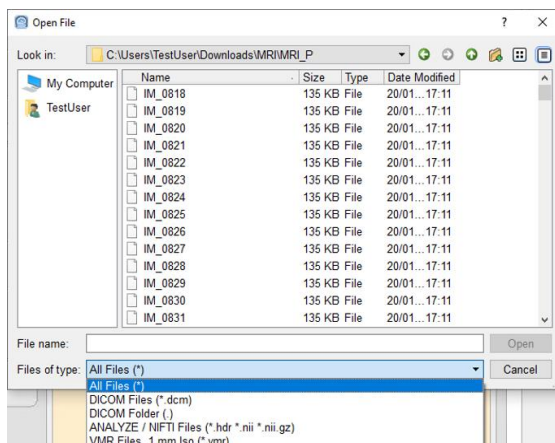
#### 6.2.1.1. Set Project Targets

The first workstep gives an overview over the worksteps that have to be done to complete the loaded workflow. Grayed tick marks indicate obligatory worksteps, empty checkboxes relate to optional worksteps. Please note that if a FEM model or BEM model is to be created, the respective option **Run Volume Conductor Segmentation for FEM** or **Run Volume Conductor Segmentation for BEM** needs to be checked. If an inflated representation of the cortical surface shall be prepared please check the option **Run Cortex Inflation**.

Hit **Space** or press **Next** to continue the workflow.

#### 6.2.1.2. Read T1-weighted MRI Data

In this workstep, MRI data are imported. BESA MRI can read DICOM, ANALYZE and NIfTI format.



### DICOM

Select the subject's MRI folder and one of the files of the DICOM data set to be processed. BESA MRI loads all files of the same imaging sequence stored in the selected folder. Slice data files are read in, sorted, and oriented automatically.

The header information of the DICOM files is evaluated and displayed in the Main Window. Check if subject and sequence are correct and hit **Space** or press **Next** to continue the workflow.

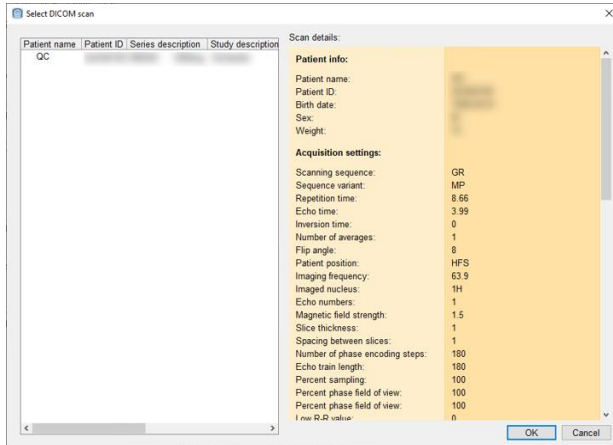
The MRI data are read and oriented automatically based on the official DICOM standards. To avoid left-right permutation, application of a side marker for MRI acquisition is recommended.

Ensure that the acquisition protocol of the DICOM MRI data produces orthogonal slice orientation.



## DICOM Folder

If several DICOM scans (of the same or different subjects) are stored within the same folder, the option **DICOM Folder** should be selected in the drop-down menu **Files of Type**. After selecting the DICOM folder, any of the individual DICOM files within the folder can be selected and BESA MRI will open a dialogue summarizing all the available scans that can then be individually selected. Proceed with **OK**.



## ANALYZE

Select the header (\*.hdr) file of the subject's MRI. The Analyze image is then read in automatically.

## NIfTI

Select the NIfTI (\*.nii) or the compressed NIfTI (\*.nii.gz) file of the subject's MRI. The NIfTI image is then read in automatically.

## Other data formats

BESA MRI can import MRI data in Brain Voyager format (\*.vmr). However, this format is not supported for diagnostic use. **Do not use Brain Voyager Data in a clinical setting.**

## Anonymize data

Optionally, by pressing the **Modify Data Info** button the patients name and date of birth can be changed. Furthermore, one can also remove the file path from the loaded data.

Important note: The patient name and date of birth are important identifiers. Changing the patient name or date of birth is not recommended in diagnostic use.



**Note:** The original MRI data and header information are stored with other project data in an internal format in the BESA MRI Data Folder under the subject name and the project name. This allows reloading the project data later independently of the original MRI data.

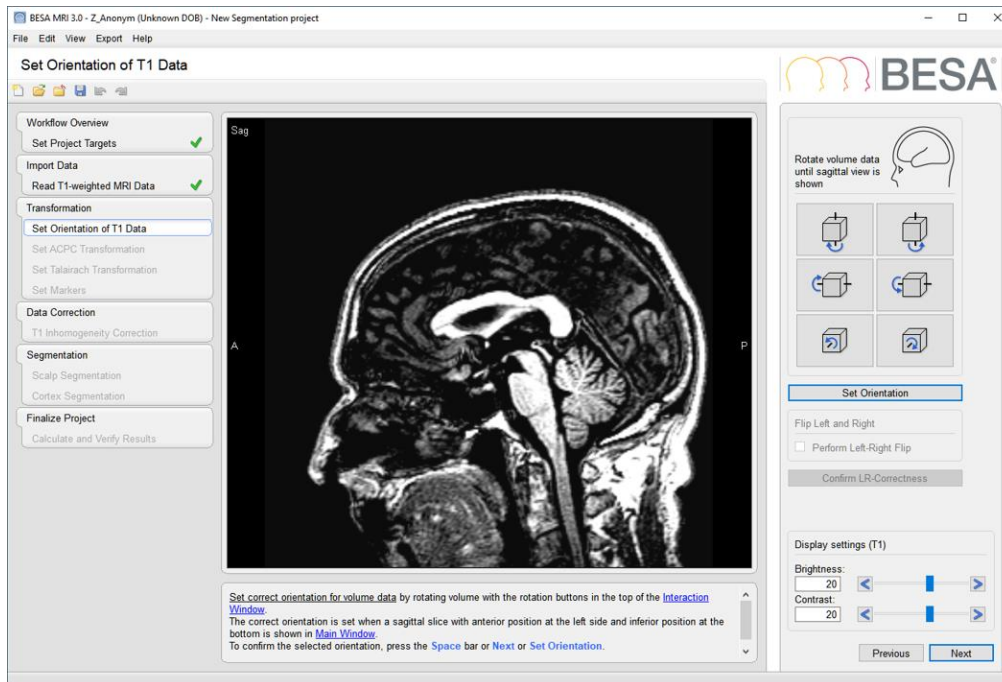
### 6.2.1.3. Read T2-weighted MRI data

Optionally, T2-weighted data can be loaded in this workstep. This is recommended in order to achieve a more precise result for skull labeling, as T1 data alone do not allow a good reconstruction of the skull. BESA MRI does not require T2-weighted data for creating a FEM model. If no T2-data are available, the skull is reconstructed based on the T1 image in combination with internal atlas information.

For BEM, only T1-weighted MRI data is used for generating volume conductor segmentation.

#### 6.2.1.4. Set Orientation of T1 Data

In this workstep, it is possible to re-orient the MRI data to match with BESA MRI standards as indicated by the head schemes in the interaction window.



This should not be necessary for DICOM data but may be required if Analyze or Nifti files are read as they often lack information on image orientation.

Once the orientation is set correctly, it is also possible to flip left and right. This option should only be checked if the user is certain that left and right were wrongly assigned. This is why the LR-Correctness needs to be confirmed explicitly.

Hit **Space** or press **Next** to continue the workflow.

#### 6.2.1.5. Set ACPC Transformation

In this workstep, the transformation of the original data into the ACPC coordinate system is defined by marking the middle of the anterior commissure (AC) and rotating the MRI data set to obtain an optimal view of the ACPC plane (PC: posterior commissure) and the best separation of both hemispheres by the sagittal plane.

In the first substep, the position of the **AC (anterior commissure)** is set by dragging the slices in the lower half of the Main Window such that the AC midpoint meets the crosshair (for dragging slices see chapter 6.3.1). You may also adjust the crosshair in half millimeter steps using the interaction elements in the Interaction Window on the right.

Hit **Space** or press **Next** to set and confirm the AC position and continue with the second step.

In the second substep, **ACPC rotation** is set by rotating the MRI slices such that a) the PC midpoint appears on the crosshair line behind the AC position and b) the sagittal plane separates the two hemispheres optimally. Rotation is most easily done by dragging the lower slices in the Main Window while checking the upper slices for separation of the hemispheres. You may also use the controls in the Interaction Window on the right to set the three rotations, but this is less convenient.

Hit **Space** or press **Next** to confirm the PC position & sagittal plane and continue with the third step.

In the third substep, the position of the **PC (posterior commissure)** is set by dragging the lower left slice in the Main Window such that the PC midpoint meets the horizontal bar of the crosshair.

Hit **Space** or press **Next** to inspect the final ACPC transformation. Readjust if needed by pressing the required substep buttons on the right.

**Note:** The display settings and the zoom factor can be adjusted at any time at the bottom of the Interaction Window for optimal viewing of the MRI data. For example, you may increase the zoom factor to 2.5 or 3.0, unpress the **AC (anterior commissure)** substep button to readjust the AC midpoint and observe that the following rotation and PC setting steps have been preserved. They can be readjusted in the same way to have an optimal definition of the ACPC transformation.

Hit **Space** or press **Next** to continue the workflow and move on to the next workstep.

#### 6.2.1.6. Set Talairach Transformation

In this workstep, the brain boundaries have to be set by the user to enable a Talairach Transformation of the original MRI. This transformation is needed for various masks during segmentation.

During this workstep, one of the six brain boundaries is set in each substep. It is easiest to drag the slice as listed below while observing the cortical gyri disappear and reappear in the cutoff slice to view:

Substep to set	Drag slice	View slice	Check cortical boundary at
AP (anterior plane)	Transversal	Coronal	Frontal brain
PP (posterior plane)	Transversal	Coronal	Occipital brain
SP (superior plane)	Coronal	Transversal	Top gyri
IP (inferior plane)	Coronal	Transversal	Temporal poles
LP (leftmost plane)	Coronal	Sagittal	Lateral temporal cortex
RP (rightmost plane)	Coronal	Sagittal	Lateral temporal cortex

It can be helpful to click into the outermost gyri in the cutoff slice for better viewing in the other slices.

Hit **Space** or press **Next** to proceed step by step. Follow the instructions in the Information Window.

#### 6.2.1.7. Set Markers

In this workstep several markers are set as input for the following automated segmentation worksteps.

In each substep, **Click** onto the requested region as described and illustrated below. A red marker appears. You may drag this marker to adjust. Hit **Space** or press **Next** to confirm the position and conclude the substep. The accepted marker is now shown in blue.

Alternatively, you may **Double Click** onto the requested region. The marker will appear in blue immediately and the workflow proceeds to the next substep.

Corrections can be made by unpressing any substep button in the Interaction Window on the right and hitting **Space** or pressing **Next** to continue. For more details on setting or modifying markers see chapter 6.3.2.

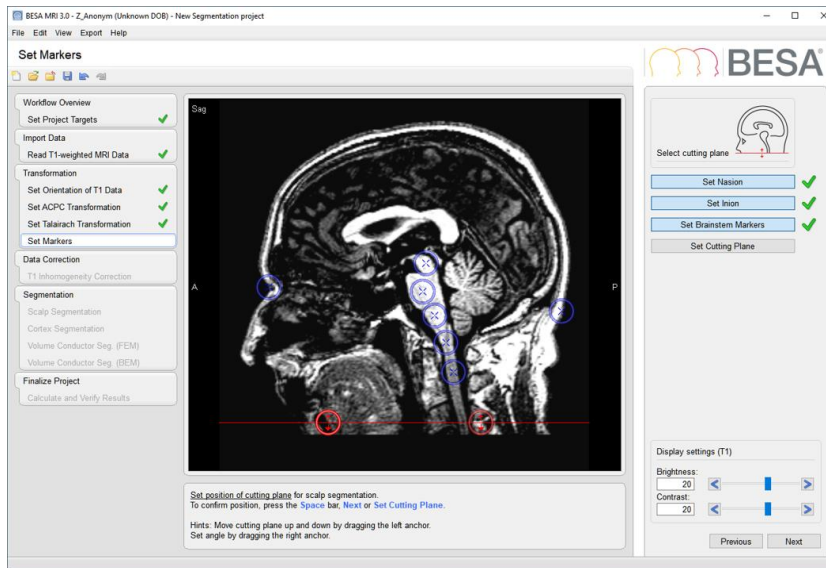
In the **first two substeps**, the positions of the nasion and the inion are set. These positions are needed for the segmentation of the skull.

In the **third substep** white matter is marked in the brainstem and medulla oblongata by three to five markers. Set the markers equally spaced from top to bottom. The markers identify the gray values of the white matter at the lower portion of the head and are needed as input for the automated inhomogeneity correction. Make sure you mark only white matter portions.

In the last and **fourth substep** a cutting plane is specified by two markers. All parts below this cutting plane will be cut off during Scalp Segmentation. The cutting plane can be moved up and down by dragging the left marker. By dragging the right marker, a different cutting angle can be set.



In the figure below, the Set Markers workstep is illustrated at its end before confirming the Cutting Plane.



#### 6.2.1.8. Register T2 Image

In the registration workstep of BESA MRI, a T2-weighted image is registered to the T1-weighted image using an affine registration approach. Registration is performed on multiple coarse to fine resolution levels to improve convergence and robustness (Maes et al., 1999). Mutual information (Wells et al., 1996) is used as a registration measure as it allows the registrations of different image modalities (e.g. T2-weighted MRI to T1-weighted MRI).

The automatic registration is run by pressing the **Run Registration** button. If required one can perform manual corrections to the nine transformation parameters describing the translation, rotation, and scaling, using the interaction elements right below the **Run Registration** button. The optional **Run Registration Step** button will perform a very similar procedure to **Run Registration**, alas with the initial state given by the currently set transformation parameters and using a smaller "search radius". I.e. it assumes the currently set transformation parameters to be already rather close to the optimal solution.

The quality of the registration can be evaluated by the user by toggling between the T1 and T2 data sets by pressing the **Toggle Data Selection** button.

Select the **Prepare Volume Data** button to confirm the registration parameters and prepare the data for the next working steps.

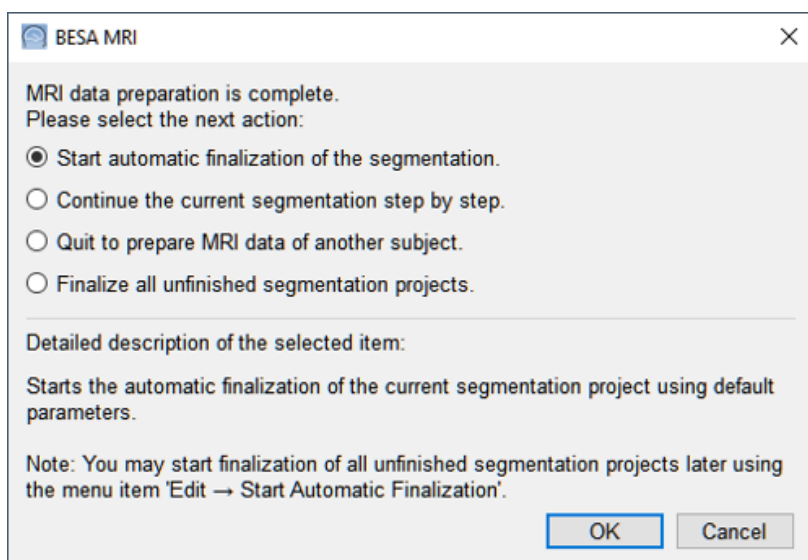
Hit **Space** or click **Next** to continue.

#### 6.2.1.9. Automatic Finalization

With the completion of this and the previous worksteps, all steps needing your input have been done and the MRI data preparation is complete.

Therefore, BESA MRI offers the option to continue with the Automatic Finalization of the segmentation project or to follow and adjust the segmentation process step by step. For most data sets, adequate segmentation output is generated using the default parameters of the Automatic Finalization.





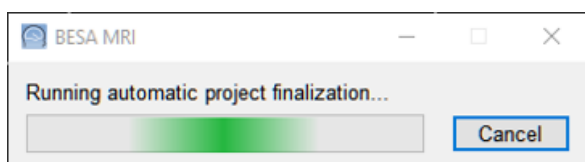
Thus, at the beginning of the correction and segmentation worksteps, you have the following options:

Since the correction and segmentation worksteps take about 20-30 minutes per MRI data set, it is recommended to use Automatic Finalization and inspect the results before deciding whether parameter adjustment is needed.

If the default segmentation results are inadequate, you may return to the segmentation worksteps using the Workflow Window or by pressing the [Previous](#) button. Then, modify the required segmentation parameter(s) and continue the segmentation step by step.

Another advantage of Automatic Finalization is that you can prepare several individual MRI data sets for finalization and work on other tasks while all prepared projects are being finalized automatically. It takes only about 5 minutes to prepare one MRI data set.

When automatic finalization is running, it may be interrupted at any time by pressing the [Cancel](#) button in the progress bar:



The current workstep will be completed automatically, but it can also be canceled at the lower right of the Information Window, e.g. to change the number of iterations during inhomogeneity correction.

When doing correction and/or segmentation step by step, automatic finalization can be restarted at any time pressing the [F9](#) key, or by selecting the menu item [Edit → Finalize Current Project](#) (or All Segmentation Projects).



#### 6.2.1.10. Inhomogeneity Correction

The gray values of the white matter are not homogeneous throughout the brain in typical MRI data. Therefore, inhomogeneity correction is needed as a major workstep prior to the segmentation of the different brain tissues. In BESA MRI, this correction is done by an automated workstep realized as an iterative procedure based on the AFCM (Adaptive Fuzzy C-Means) algorithm enhanced by incorporating anatomical template masks. For more details on the AFCM algorithm see Pham et al. (1999).

For adequate results at least 5 to 10 iterations are needed. By incrementing the number of iterations above the default of 10 iterations the correction can sometimes be improved.

Hit **Space** or press **Next** to continue.

#### 6.2.1.11. Scalp Segmentation

The reconstruction of the scalp surface is done by segmenting the subject's head from the background using a level set algorithm. For more details on this algorithm see (Chan et al., 2001). First, a rough start mask is constructed by thresholding the image and using subsequent morphological operations. Based on this start mask, level set segmentation on a coarse computational grid is performed. The result of this segmentation is then refined using a higher resolution grid.

For the creation of the initial rough start mask, a gray value threshold is used to select all voxels inside the head with higher gray values and to exclude all outside voxels with lower gray values. As default **threshold for start mask** a gray value of 30 is used during automated segmentation. Increase this threshold to remove artifacts that might be present outside of the head in the segmented scalp. Decrease the threshold if some parts of the subject's head are not adequately reconstructed in the segmented scalp.

The **default number of iterations** is set to 3 for automated segmentation. Scalp segmentation results may be improved by increasing the number of iterations.

**Set smoothness parameter** allows handling MRI scanner artifacts. If a lot of unwanted noise is present in the background of the MRI images, it can be helpful to increase the smoothness parameter in order to prevent the segmentation algorithm from categorizing artifacts as scalp tissue. The default setting is 5.0.

Both processes, scalp segmentation and refinement have been automated in one segmentation workstep combining these two substeps. If you want to improve scalp segmentation after inspecting the automatically obtained results, unpress the **Run Segmentation** button in the Interaction Window, adjust the threshold and/or the number of iterations, and press the **Run Segmentation** button again or hit **Space** to recalculate this segmentation workstep.

Hit **Space** or press **Next** to continue.

#### 6.2.1.12. Cortex Segmentation

In this workstep the cortical surface is reconstructed. Optionally, an inflated representation of the cortical surface can be generated for visualization purposes.

The cortical surface is reconstructed in an automatic process consisting of several steps. First, a voxel-based classification of the white matter is performed. Then, using the level set algorithm, the surface of the classified white matter is reconstructed, carefully smoothed and inflated to generate the cortical surface. This surface can be used as an approximate source space for cortical source imaging, e.g. in BESA Research.

The inflated representation of the cortex is generated by smoothing out the cortical foldings while minimizing metric distortions. The inflation algorithm is based on the work by Fischl et al. (1999). The original location of gyri and sulci is indicated by a lighter, respectively, darker gray color.

Currently, cortical surface reconstruction and inflation are done by fully automated procedures not requiring the user to define specific parameters.

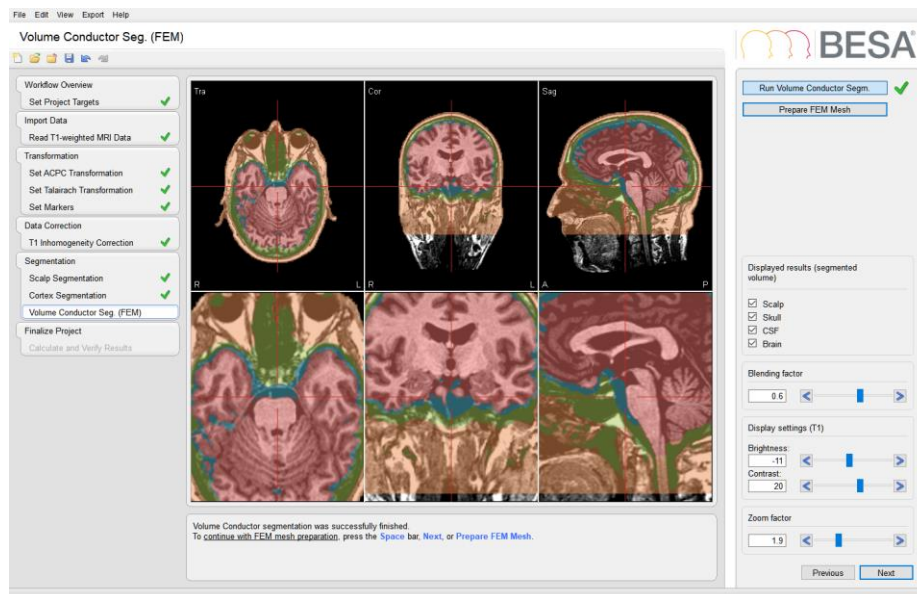
Hit **Space** or press **Next** to continue.

**Note:** Cortex segmentation and inflation were tested and optimized for a large number of data sets acquired on current MRI systems. You are invited to submit any questions or feedback here:

<https://www.besa.de/support/support-page/>, if you are not getting sufficient results with older MRI data sets.

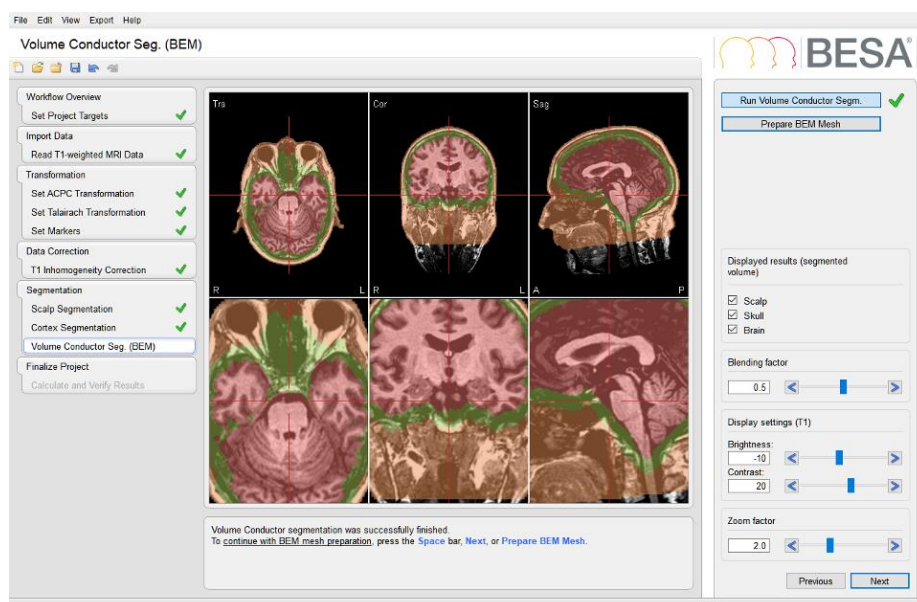
### 6.2.1.13. Volume Conductor Segmentation

This optional workstep consists of two sub-steps. First, all four layers (Scalp, Skull, CSF, Brain) are labeled. To run this sub-step, press **Run Volume Conductor Segmentation**.



It is possible to review the segmentation results by changing the **Blending factor** so that more or less of the underlying MRI is displayed. Second, the FEM model is generated based on the segmentation results (Wolters et al., 2007) and surface meshes of the 4 tissue layers are extracted. Press **Prepare FEM meshes** to run the algorithm. The meshes are displayed as colored lines.

The workstep of the volume conductor segmentation for BEM also consists of similar steps. First, all three-layers (scalp, skull, and brain) are labeled after pressing **Run Volume Conductor Segmentation** button. Then, the nested closed surface meshes for the three-layers are generated after pressing **Prepare BEM meshes** button.



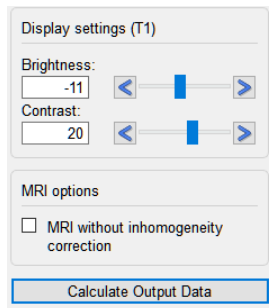
Hit **Space** or press **Next** to continue.

### 6.2.1.14. Calculate and Verify Results

During this workstep, the final segmentation results are calculated and displayed for inspection.

Before finalizing the output, you may adjust the display settings, i.e. the brightness and contrast values, of the generated MRI volume data sets if needed. These values have been set to a preset standard during the segmentation project. If you need to adjust these values, use the controls at the upper right in the **Adjust gray scale** section of the Interaction Window. While adjusting, inspect the MRI slices in the Main Window carefully.

To use the original MRI volumes instead of the inhomogeneity-corrected MRI volumes, you should check the check box **MRI without inhomogeneity correction** in the MRI options section.



Hit **Space** or press **Next** or **Calculate Output Data** in the Interaction Window to continue.

The calculation creates the output MRI volumes in ACPC and Talairach spaces using one direct 3D spline interpolation of the original MRI data (this way we reduce interpolation errors to a minimum). Surfaces are also calculated for both the ACPC and Talairach spaces.

You may inspect the results in more detail by selecting one of the ACPC, Talairach, or FEM (scalp, skull, CSF, or brain) / BEM (scalp, skull, or brain) **Head symbol buttons** in the **Set main window display** section at the lower right of the Interaction Window. The FEM / BEM results can also be displayed as slices overlaying the ACPC MRI. If results are not satisfactory, you may select any previous workstep in the Workflow Window, modify specific parameters in the workstep that generated insufficient output, and redo the following worksteps manually or using automatic finalization. Use the workflow menu on the left to select the workstep to be modified.

Hit **Space** or press **Finish** to complete the segmentation workflow and create the output data. Follow the dialogs to save all data of the segmentation project (see chapter 6.4.3).

This ends the segmentation workflow and the Select Project page appears offering to start a new project or open a saved project.

### 6.2.2. The Coregistration Workflow

The coregistration workflow provides the coregistration of digitized surface points (electrodes and/or MEG sensors, fiducials, and skin points) or standard EEG electrodes with an individual MRI data set. Coregistration is done by marking the 3 standard fiducials (nasion, left and right preauricular points) on the reconstructed individual scalp surface and fitting the fiducials and selected sensors & skin points to this surface.

Standard electrodes can be also matched approximately with an individual MRI. They need to be labeled according to the 10-20 or 10-10 international system.

The coregistration workflow consists of the following worksteps:

#### 6.2.2.1. Set Project Targets

The first workstep gives an overview over the worksteps that have to be done to complete the loaded workflow. Grayed tick marks indicate obligatory worksteps, empty checkboxes relate to optional worksteps.

To skip electrode and fiducial fit, the check box **Skip electrode and fiducial fit** needs to be checked.

When the check box **10-10 electrode placement** is checked, electrode coordinates can be automatically generated on the subject's scalp surface following 10-10 placement rules in the Fit Surface Points workstep.

Please note that in case a FEM / BEM model was created that is to be used in BESA Research or for exporting, the option **Generate FEM EEG Leadfield**, **Generate FEM MEG Leadfield**, **Generate BEM EEG Leadfield**, or **Generate BEM MEG Leadfield** needs to be checked.

Hit **Space** or press **Next** to continue the workflow.

#### 6.2.2.2. Set Fiducials

In this workstep, select an individual subject for coregistration and mark the three fiducials on the scalp surface.

First, choose an individual subject for coregistration by selecting the related segmentation project. At least one segmentation project must have been completed for a subject prior to coregistration with MRI.

To select a project, hit **Space** or press **Next** or **Select Input Project** in the Interaction Window.

The **Select Input Project** box opens. Select the subject and one of the projects if several exist. Press **OK** to load the selected segmentation data of this subject as input for coregistration.

Next, set the Nasion position. Click onto the surface to set the nasion marker. You may adjust by dragging the marker with the mouse.

To confirm the position, hit **Space** or click **Next** or **Set Nasion**. You can also double click.

The head now turns to show the left side for marking the next fiducial. Click onto the surface to mark the left preauricular point. You may adjust by dragging the marker with the mouse.

To confirm the position, hit **Space** or press **Next** or **Set Left Preauricular Point**.

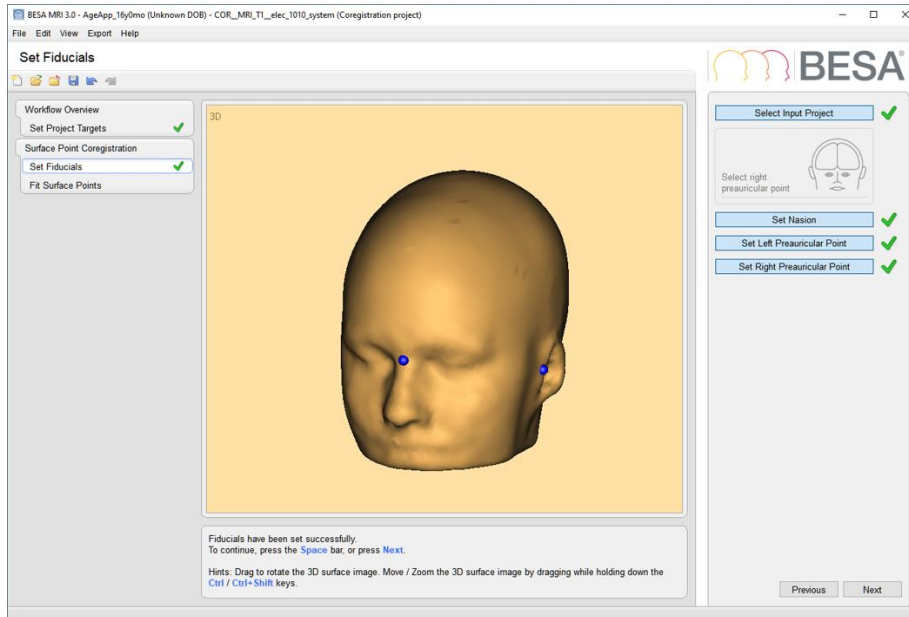
The head now turns to show the right side for marking the next fiducial. Click onto the surface to mark the right preauricular point. You may adjust by dragging the marker with the mouse.

To confirm the position, hit **Space** or press **Next** or **Set Right Preauricular Point**.

Rotate the head to reinspect the positions of the 3 markers (see chapter 6.3.3). Modify, if needed, by unpressing the required **Set ...** button in the Interaction Window.



The figure below displays the completed workstep. The head is rotated to show both the nasion and the left preauricular markers:



Hit **Space** or press **Next** to continue the workflow.

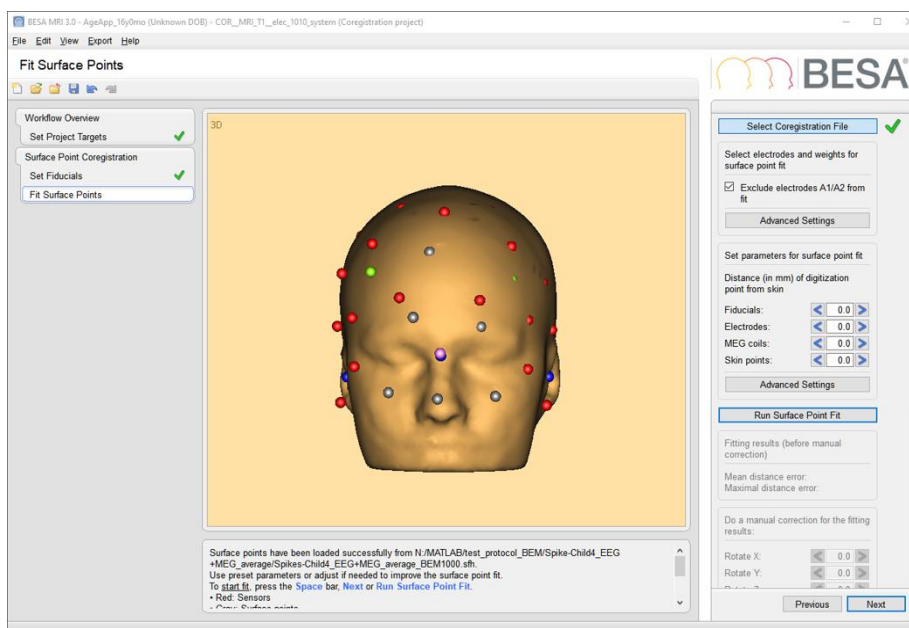
### 6.2.2.3. Fit Surface Points

In this workstep, fiducials, electrode / MEG sensor positions, and skin points are loaded from a surface head point file (\*.sfh), aligned, and optimally fitted to the loaded individual MRI scalp surface.

Hit **Space** or press **Next** to load a coregistration file (\*.sfh) of the selected subject created when initiating the coregistration process with a selected EEG or MEG data set (e.g. in BESA Research).

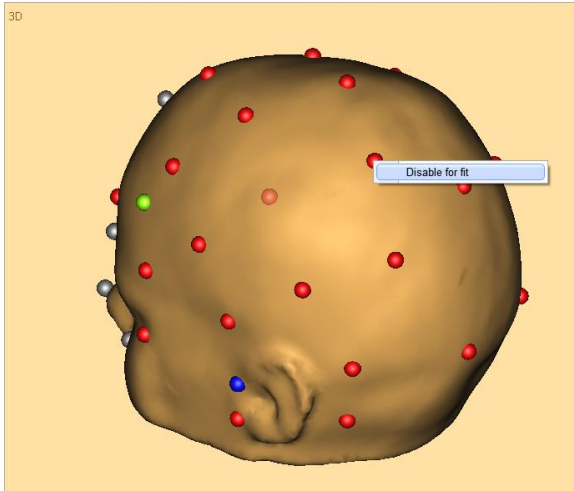
The **Open File** box comes up. Select the appropriate coregistration file (\*.sfh) and open.

After loading the .sfh file, an initial coordinate transformation is calculated to match and align the three fiducials marked on the MRI scalp surface with the fiducial positions stored in the .sfh file. The loaded surface positions are displayed taking into account this transformation.

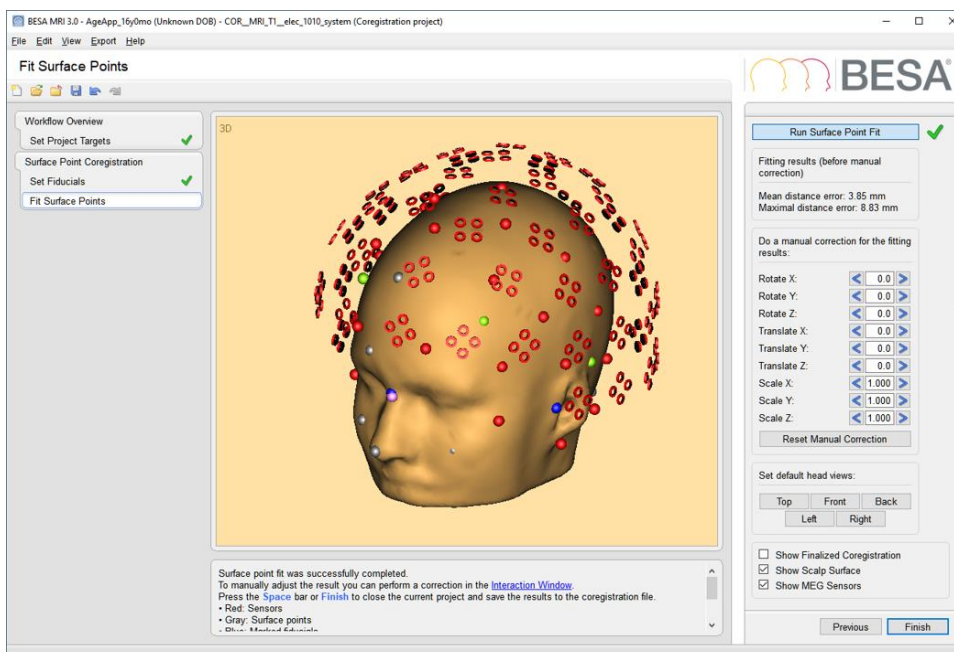


In the next step, the loaded coordinates are transformed again using shift, rotation and linear 3D shrinking operations to fit electrodes and surface points optimally to the skin surface. For this fitting process, **only electrodes and surface points higher than A1/A2 ( $z \geq -30$  mm in the head coordinate system) are used** while a variable elastic bound is attached to the fiducials to preserve their closeness.

You can also manually exclude or include electrodes or surface points from the fitting. To do that, right click on an electrode and then select **Disable for fit** / **Enable for fit** in the popup menu. The shading of the point is changed to show that it is excluded from the fitting.



To start the fitting process, hit **Space** or press **Next** or **Run Surface Point Fit**.



Inspect the results by rotating the head, and inspect the positions of the fitted (pink) vs. marked (blue) fiducials as well as the right/left symmetry of the electrodes when fitting standard electrodes. The head views can be toggled using the button in the section Set default head views.

If the surface point fit is not adequate, one can manually correct the electrode cap position directly using the rotation, translation, and scaling elements in the interaction window. The button **Reset Manual Correction** moves the manual correction back to the defaults.

Alternatively, one can also tune the automatic surface point by unpressing the button **Run Surface Point Fit** and changing the parameters in **Advanced Settings**. This can be done either in the upper section of the Interaction Window (e.g. to change weights of fiducials vs. electrodes and skin points) or in the lower

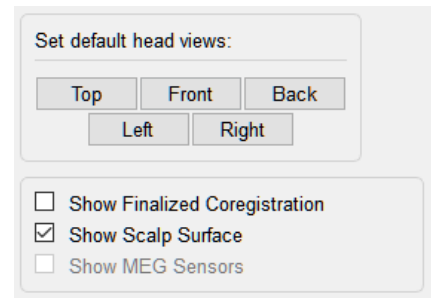
section (e.g. to modify the strength of the fiducials bound by restraining to a distance smaller than the default of 2 mm).

You might also want to modify the marked fiducials for better matching. To return to the previous workstep, press the **Previous** button or select the **Set Fiducials** workstep in the Workflow Window on the left. For example, if standard electrodes appear asymmetric, it may be helpful to modify the position of the preauricular fiducials to improve the symmetry along with increasing the weight of the fiducials (e.g. to 10) and decreasing the distance restraint (e.g. to 0.5 mm) in the **Advanced Settings** of the **Fit Surface Points** workstep.

After finishing the fitting, you can display final coregistration results (the one that are used i.e. in BESA Research) by checking the check box **Show Finalized Coregistration**. In this view, electrodes (and only electrodes) are orthogonally projected to the skin surface. This option has no effect for MEG sensors, fiducials and other surface points. When button is checked all the computation relevant buttons are disabled.

Scalp surface can be toggled using the check box **Show Scalp Surface**

MEG sensors can be visualized using the check box **Show MEG sensors** after finishing the fitting.

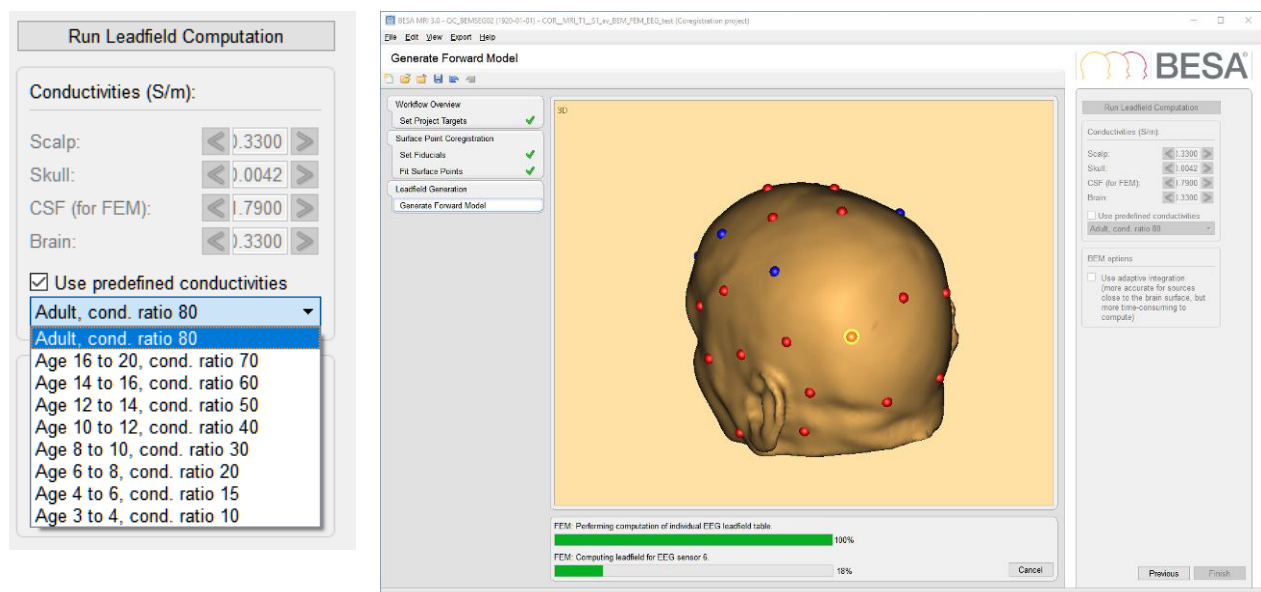


#### 6.2.2.4. Generate Forward Model

If the option **Generate FEM EEG Leadfields**, **Generate FEM MEG Leadfield**, **Generate BEM EEG Leadfields**, or **Generate BEM MEG Leadfield** is checked under **Set Project Targets**, BESA MRI will calculate leadfields for the given electrode / sensor layout in this workstep. The leadfield information can then be used directly in BESA Research for source localization.

It is possible to use default conductivity values for different age groups (available from the drop-down menu **Select pre-defined conductivities** after checking the check box **Use predefined conductivities**) or to manually adjust conductivity settings for scalp, skull, CSF, and brain. The conductivity value for CSF is used for FEM.

When the checkbox **Use adaptive integration** in the BEM options section is checked, adaptive integration is applied in BEM leadfield computation. The leadfield vectors for a source close to a brain surface can be estimated more accurate when adaptive integration is applied, but the computation time is increased.





**BEM options**

- ☒ Use adaptive integration  
(more accurate for sources  
close to the brain surface, but  
more time-consuming to  
compute)

Please note that this step can take a while to compute, depending on the number of electrodes / sensors in the channel layout. For FEM, the electrode / sensor, for which the leadfield is currently computed is highlighted in orange, and the electrodes / sensors that are already finished are displayed in blue.

Hit **Space** or press **Finish** to complete the coregistration workflow. Follow the dialogs to save all data of the coregistration project (see chapter 6.4.3).

**Notes:**

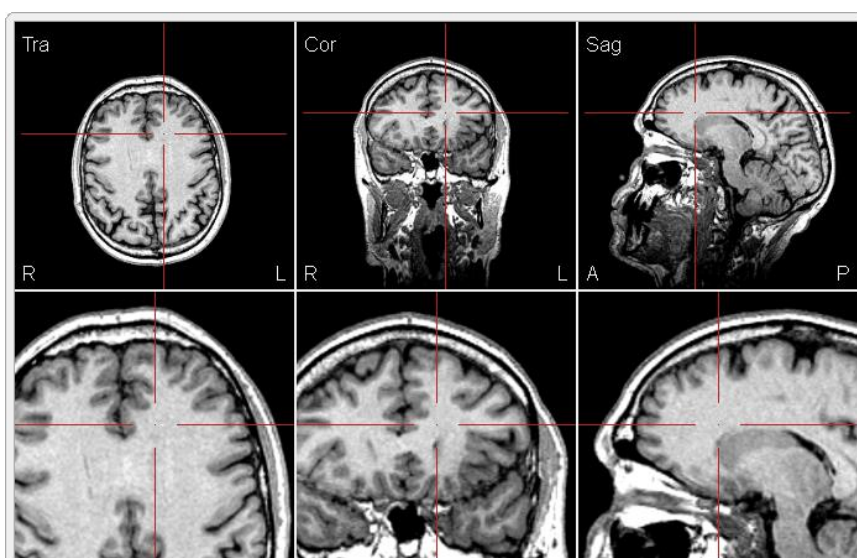
- The loaded coregistration file will be modified, i.e. the current coordinate transformations and MRI output file information are added to the end of the file when saving the project. When refitting with modified parameters, and saving, it is modified again.

## 6.3. User Interaction in Main Window

The Main Window is used to display the results of the current workstep. In addition, it may be used for user interactions like setting positions in volume data or markers onto surface data. These user interactions are described in detail in this section.

### 6.3.1. How to use the Slice Displays

Slice displays are used for depicting MRI volume data. These displays show three orthogonal cross-sections of the MRI data set, i.e. the transversal (Tra), coronal (Cor), and sagittal (Sag) slices. A red crosshair line marks the plane where two slices intersect. The slice center is the 3D position where the three slices – and the three crosshairs - intersect. In the upper row, the three slices are shown fully, centered relative to the midpoint of the MRI data set. In the lower row, zoomed slices are shown, centered at the slice center.











Thus, in the upper row, the slice center and the crosshair can be moved by clicking onto the slice or dragging the crosshair. In the lower row, the crosshair (and slice center) is fixed relative to the display frame and the slices move when clicking or dragging.

In BESA MRI, several 3D positions need to be set in the volume data (e.g. the AC & PC positions). You may approximate such positions by clicking on the slice displays in the upper row and do fine adjustments by dragging the lower slices to the desired position.

The mouse wheel can be used to move to the next/previous slice.

Some positions require adjustment only in one dimension, e.g. the setting of the PC position below AC in the transverse slice or the Rotation of a selected slice. Therefore, the effects of clicking or dragging will be limited to the allowed dimensions.

When moving the mouse over a slice display, the mouse cursor symbol signals the available interaction associated with clicking or dragging:

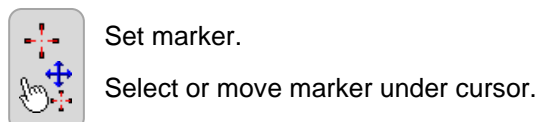
	dragging possible.		Rotate the slice (around fixed mid-position).
	Click to set slice center (anywhere in slice).		Move the slice.
	Click to move slice center (only up-down).		Move the slice (only left-right).
	Click to move slice center (only right-left).		Move the slice (only up-down).

### 6.3.2. Setting Markers in Slice Displays

Slice displays can also be used for setting markers at specific positions.

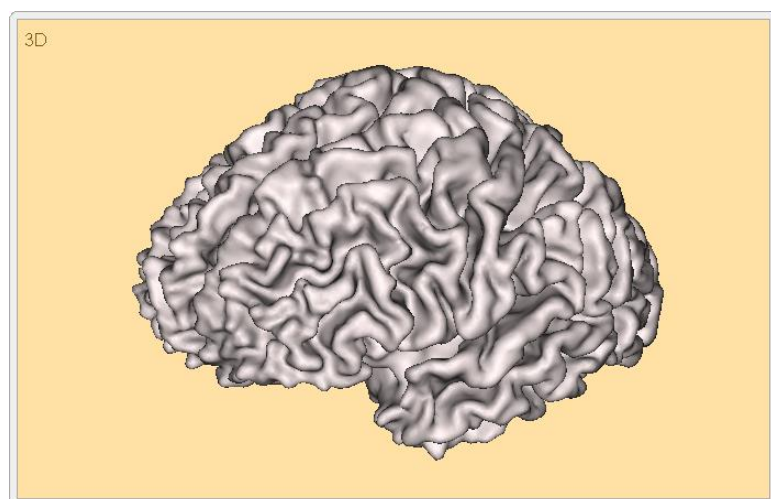
A marker is set in a slice display by a single click onto the desired position in the slice. A marker can be selected by clicking onto it and it can be moved within a slice by dragging the mouse. Selected markers can be removed by pressing the **Del** key.

The mouse cursor symbol specifies which marker interactions can be done at a specific position:



### 6.3.3. How to use 3D Surface Displays

The 3D surface displays are used to show the surfaces reconstructed by BESA MRI.



The 3D surface images can be rotated by dragging the mouse. They can be moved / zoomed by dragging the mouse while holding down the **Ctrl** / **Ctrl+Shift** key.

A marker is set on a 3D surface by a single click on the desired position on the surface (e.g. to specify fiducials for coregistration). A marker can be selected by clicking onto it and moved along the surface by dragging the mouse. Selected markers can be removed by pressing the **Del** key.

The mouse cursor symbol signals the available interaction associated with clicking and/or dragging:

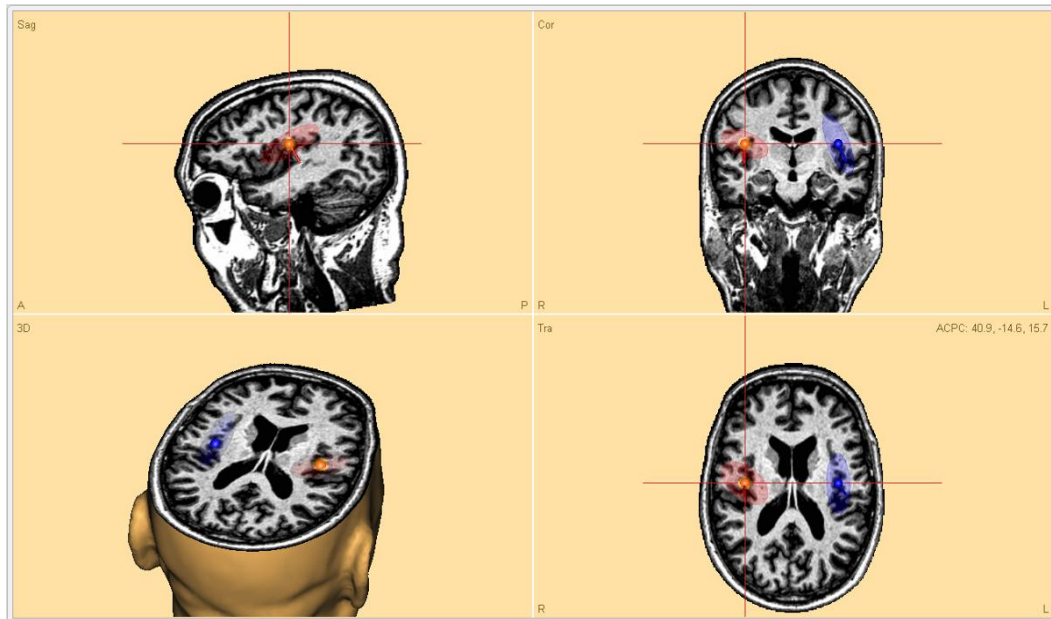


### 6.3.4. BESA Research Solution Display




#### Loading a solution file

Press the **Load sources** button to open a dialog that allows selecting a discrete source solution exported from BESA Research. When the solution file is loaded the sources will automatically be displayed; if the solution was saved by BESA Research 7.1 or higher in Talairach coordinates, then sources are displayed together with confidence ellipsoid and error rim, provided that this information was calculated and saved

by BESA Research – see the note below for restrictions. Source positions are automatically adjusted to the displayed transformation of MRI data (ACPC or Talairach).



Source type is indicated by symbols:

-  single dipole
-  regional source
-  spatial component

**Note:** Sources are not displayed for surface views.

### Additional controls

When sources are displayed, additional controls are available. It is possible to independently disable or enable display of **Sources**, **Confidence area** and **Error rim**. The source size can also be adjusted by the **Sources scale** slider.

**Note:** Confidence ellipsoid and error rim is only visible for single dipole sources, and requires solutions created with BESA Research 7.1 or higher.

### Source file format and sources preparation

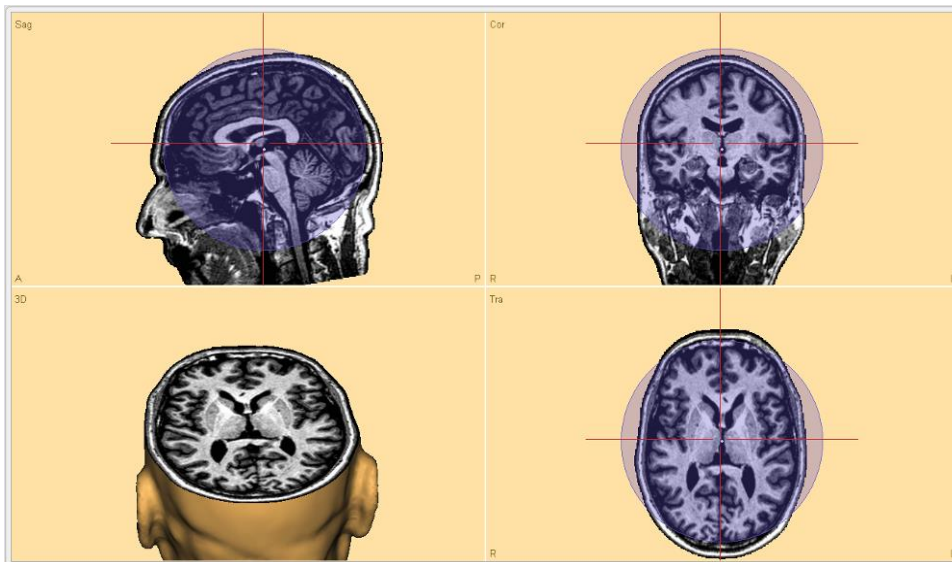
Any solution obtained in BESA Research can be exported from there, and displayed in BESA MRI. To export a solution from BESA Research use menu **File / Save Solution As...** in the Source Analysis window of BESA Research. When the *Save file* dialog is open make sure to select **BESA Solutions - Talairach (\*.bsa)** file type in the **Save as Type** drop down menu. From BESA Research 7.1, the source confidence will be automatically computed and added to the solution file. For older BESA Research versions radii for confidence ellipsoid and error rim are set to default values.

## CFG file

The default values for confidence ellipsoid and error rim can be defined in the BESA MRI configuration file. Please see the appendix for more details (section 7.4).

## Head sphere

It is also possible to display the spherical model of the MEG for ACPC transformation. If the check box **for MEG** is checked in the section Displayed sphere model (ACPC), the spherical model is displayed as transparent overlay. The center of the sphere is indicated by a small circle.



## 6.3.5. Brain Atlases

### 6.3.5.1. Introduction

A brain atlas is a priori data that can be applied after successfully finishing the segmentation workflow. It is a reference value that strongly depends on the selected brain atlas and should not be used as medical reference since individual brains may differ from the brain atlas.



**Note:** Brain Atlases display is only available for Talairach transformation views.



In BESA MRI, the atlases listed below are provided. BESA is not the author of the atlases; please cite the appropriate publications if you use any of the atlases in your publication.

**Brainnetome** This is one of the most modern brain probabilistic atlas where structural, functional, and connectivity information was used to perform cortical parcellation. It was introduced by Fan and colleagues (2016), and is still work in progress. The atlas was created using data from 40 healthy adults taking part in the Human Connectome Project. In March 2018, the atlas consists of 246 structures labeled independently for each hemisphere. In BESA we provide the max probability map with labeling. Please visit the Brainnetome webpage to see more details related to the indicated brain regions (i.e. behavioral domains, paradigm classes and regions connectivity).

**AAL** The Automated Anatomical Labeling atlas was created in 2002 by Tzourio-Mazoyer and colleagues (2002). It is the mostly used atlas nowadays. The atlas is based on the averaged brain of one subject (young male) who was scanned 27 times. The atlas resolution is 1mm isometric. The brain sulci were drawn manually on every 2mm slice and then brain regions were automatically assigned. The atlas consists of 116 regions which are asymmetrical between hemispheres. The atlas is implemented as in the SPM12 toolbox.

**Brodmann.** The Brodmann map was created by Brodmann (1909). The brain regions were differentiated by cytoarchitecture of each cortical area using the Nissi method of cell staining. The digitization of the original Brodmann map was performed by Damasio and Damasio (1989). The digitized atlas consists of 44 fields that are symmetric between hemispheres. BESA used the atlas implementation as in Chris Roden's **MRICro** software.

**AAL2015** Automated Anatomical Labeling revision 2015. This is the updated AAL atlas. In comparison to the previous version (AAL) mainly the frontal lobe shows a higher degree of parcellation (Rolls et al., 2015). The atlas is implemented as in the SPM12 toolbox.

**Talairach** The Talairach atlas was created in 1988 by Talairach and Tournoux (1988) and it is based on the post mortem brain slices of a 60-year old right-handed European female. It was created by drawing and matching regions with the Brodmann map. The atlas is available at 5 tissue levels, however we used only the volumetric gyrus level as it is the most known in neuroscience and is the most appropriate for EEG. The atlas consists of 55 regions that are symmetric between hemispheres. The native resolution of the atlas was 0.43x0.43x2-5 mm. Please note that the poor resolution in Z direction is a direct consequence of the atlas definition, and since it is a post-mortem atlas it will not correctly match the brain template (noticeable mainly on brain edges). The atlas digitization was performed by Lancaster and colleagues (2000) resulting in a "golden standard" for neuroscience. The atlas was first implemented in a software called *Talairach Daemon*.

### 6.3.5.2. Visualization modes

When an atlas is shown, the following information is provided in the top right corner of the Transverse view:

- the current cursor position in Talairach Coordinates
- brain atlas
- brain region name

Atlas overlay can be displayed as:

**brainCOLOR.** The atlas is visible as an overlay over the MRI. The coloring is performed using the algorithm introduced by Klein and colleagues (Klein et al. 2010). With this method of coloring the regions which are part of the same lobe are colored in a similar color but with different color shades. The shade is computed by the algorithm to make these regions visually differentiable from each other as much as possible.

**Individual Color.** In this mode the native brain atlas color is used if provided by the authors of the brain atlas (i.e. Brainnetome). Where this is not available BESA auto-generates colors for the atlas using an approach similar to political map coloring. This approach aims to differentiate most regions that are adjacent to each other and no presumptions on lobes is applied.

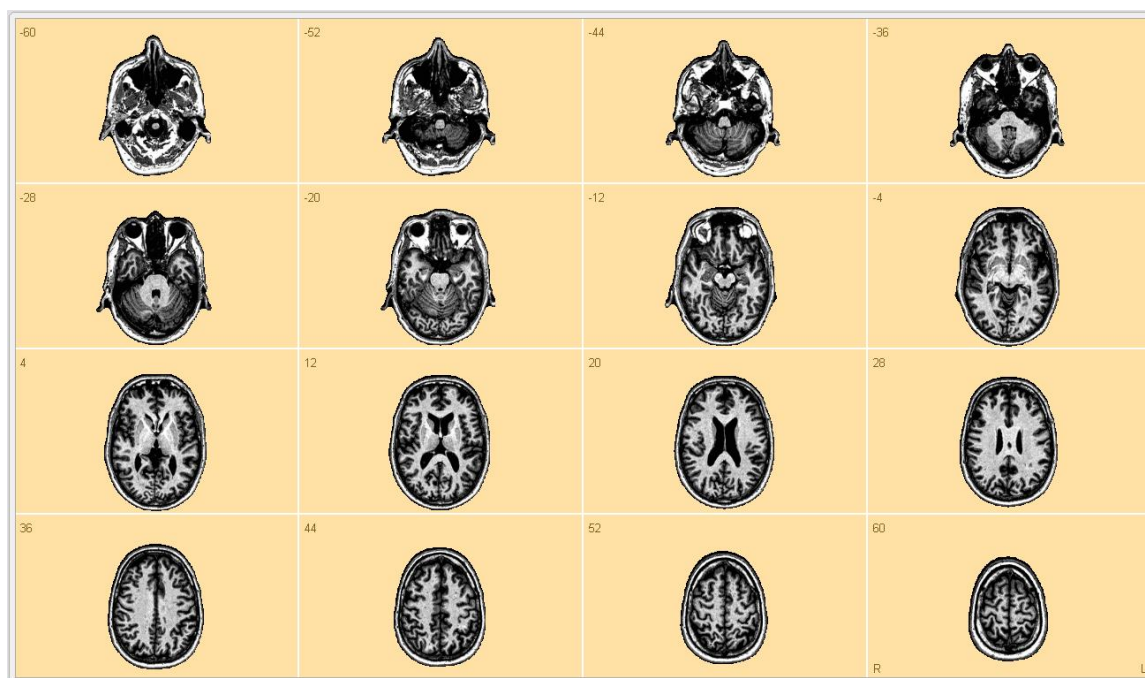
**Contour.** Only region contours (borders between atlas regions) are drawn with blue color.

### 6.3.5.3. References

- Brodmann, Korbinian. 1909. Vergleichende Lokalisationslehre Der Großhirnrinde. Leipzig: Barth. <https://www.livivo.de/doc/437605>.
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- Fan, Lingzhong, Hai Li, Junjie Zhuo, Yu Zhang, Jiaojian Wang, Liangfu Chen, Zhengyi Yang, et al. 2016. "The Human Brainnetome Atlas: A New Brain Atlas Based on Connectional Architecture." Cerebral Cortex 26 (8): 3508–26. <https://doi.org/10.1093/cercor/bhw157>.
- Klein, Arno, Andrew Worth, Jason Tourville, Bennett Landman, Tito Dal Canton, Satrajit S. Ghosh, and David Shattuck. 2010. "An Interactive Tool for Constructing Optimal Brain Colormaps." 40th Annual Meeting for the Society for Neuroscience <https://osf.io/h7rpk/>.
- Lancaster, Jack L., Marty G. Woldorff, Lawrence M. Parsons, Mario Liotti, Catarina S. Freitas, Lacy Rainey, Peter V. Kochunov, Dan Nickerson, Shawn A. Mikiten, and Peter T. Fox. 2000. "Automated Talairach Atlas Labels for Functional Brain Mapping." Human Brain Mapping 10 (3): 120–131.
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- Thomas Yeo, B. T., F. M. Krienen, J. Sepulcre, M. R. Sabuncu, D. Lashkari, M. Hollinshead, J. L. Roffman, et al. 2011. "The Organization of the Human Cerebral Cortex Estimated by Intrinsic Functional Connectivity." Journal of Neurophysiology 106 (3): 1125–65. <https://doi.org/10.1152/jn.00338.2011>.
- Tzourio-Mazoyer, N., B. Landeau, D. Papathanassiou, F. Crivello, O. Etard, N. Delcroix, B. Mazoyer, and M. Joliot. 2002. "Automated Anatomical Labeling of Activations in SPM Using a Macroscopic Anatomical Parcellation of the MNI MRI Single-Subject Brain." NeuroImage 15 (1): 273–89. <https://doi.org/10.1006/nimg.2001.0978>.

### 6.3.6. Multi-slice View

A convenient way to review MRI data and export it in graphical form is a multi-slice view. To enable multi-slice view check the **Use Slice View** button.



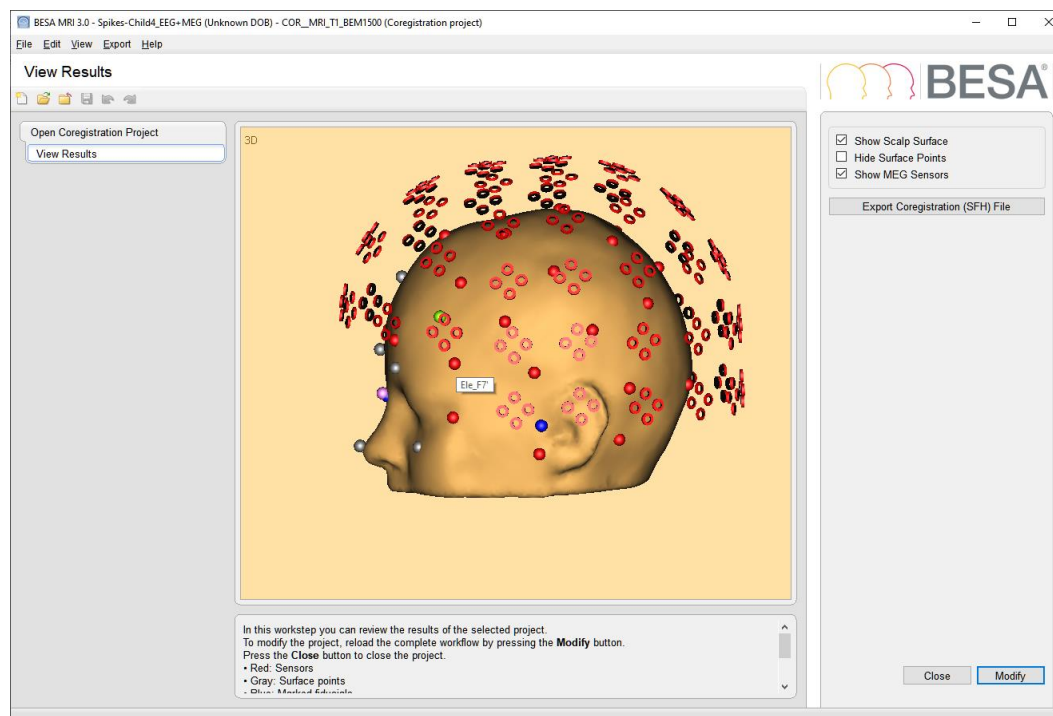
In this view all additional information can also be displayed (i.e. sources, brain atlas). The display matrix can be adjusted by additional controls that are shown after enabling slice view. One of these slicing directions can be selected: **Transverse**, **Coronal**, **Sagittal**. By adjusting **First slice** and **Last slice** sliders, the span of the volume that will be displayed can be adjusted. The interval between slices can be adjusted by changing the **Spacing** slider value. The layout of slices will be automatically adjusted to fill the full space of the main window. All values in the sliders are given in mm.

**Note:** The last slice value will be adjusted to the closest possible number matching the given first slice and spacing value. During multi-slice view the cursor is disabled and no atlas information is provided.



### 6.3.7. View results for a coregistration project

After opening a finalized project, the project is locked and the View Results work step is shown as the screen shot below.



The color of the spheres indicates:

- Red: sensors
- Gray: surface points
- Blue: marked fiducials
- Pink: fitted fiducials
- Green: MEG HPI coils

When you place the mouse pointer over a sphere, the label for the sphere is displayed in the tooltip.

Scalp surface display can be toggled using the check box **Show Scalp Surface**.

When the checkbox **Hide Surface Points** is checked, only EEG or MEG sensors are shown in the main window.

When the checkbox **Show MEG Sensors** is checked, MEG sensors are displayed in the main window as red circles

The co-registration file can be exported to a new location using the button **Export Coregistration (SFH) File**.

At the bottom of the Interaction Window, it is possible to modify the project using the button **Modify**. This will unlock the project and run through the worksteps automatically.

### 6.3.8. Save the main window as an image file

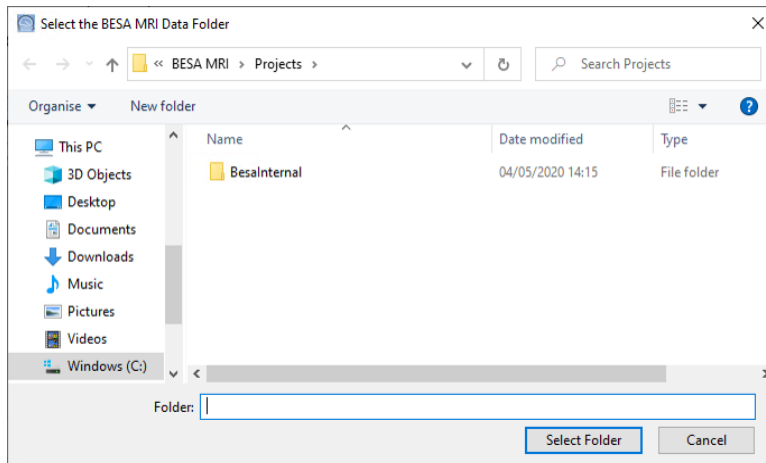
On right-click in the main window, a popup menu appears with **Export** option. After selecting the “Export” option, the “Save Image As...” dialog is shown as the Export Menu (see the chapter 5.5.4). The main window can be saved as \*.eps, \*.png, or \*.svg image file format.

## 6.4. Important Dialogs

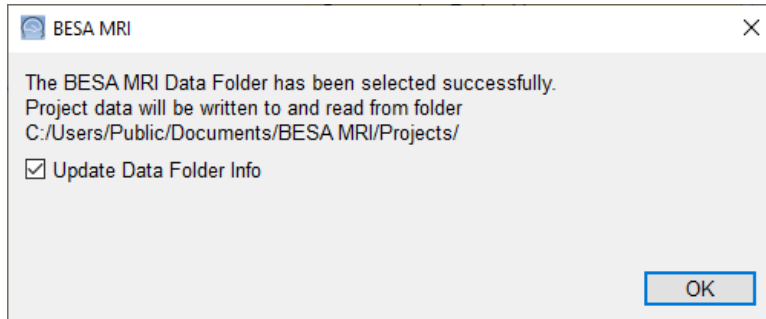
This section describes important user interactions realized by dialogs.

### 6.4.1. Select the BESA MRI Data Folder

If required, you may switch to different or create a new BESA MRI Data Folder by selecting the menu item **File → Select Data Folder**. In the dialog box below, select an existing folder to store all result data of BESA MRI or create a new folder accessible to all users in your workgroup (see chapter 7.1):



Select a folder in this dialog and press **Select Folder** to set this folder as the current BESA MRI Data Folder. After selecting a new BESA MRI Data Folder, the following confirmation dialog appears:



Press **OK** to activate the new BESA MRI data folder.

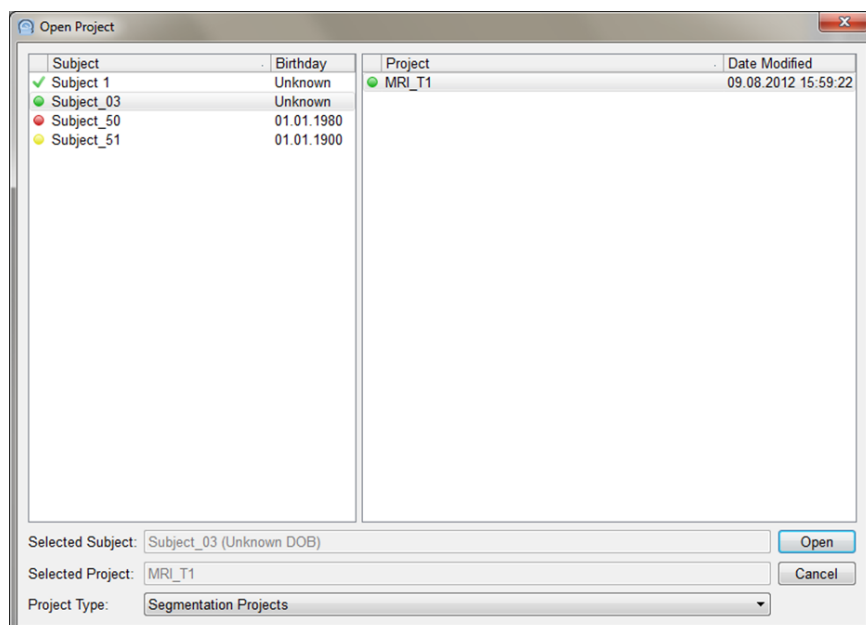
It is recommended to leave the tick mark on to update all existing projects in the new BESA MRI Data folder, if you switch between folders (see chapter 2.1).

**Note:** When switching between different BESA MRI Data folders, the project data are preserved in each folder and are not copied to the new folder.

### 6.4.2. Open Projects

Projects can be opened by pressing **Open Segmentation Project** or **Open Coregistration Project** in the Select Project Page (see chapter 6.1.2) or by selecting the menu item **File → Open Project**.

The project type to be opened is displayed at the bottom of the Open Project dialog box shown below and may be modified using the **Project Type** dropdown list:



Icons in the list of subjects:

- Green tick mark: All projects of this subject have been finalized.
- Green circle: All steps have been completed for all projects of this subject, but at least one project has not yet been finalized.
- Yellow circle: All manual steps have been completed, but at least one project is still in progress.
- Red circle: For at least one project, some manual steps have not yet been completed

Icons in the list of projects:

- Green tick mark: The project has been finalized.
- Green circle: All steps have been computed, but the project has not yet been finalized.
- Yellow circle: All manual steps have been completed, but the project is still in progress.
- Red circle: Some manual steps have not yet been completed.

Projects are stored under subject name and birth date. First, select the desired subject clicking on the left. If different projects exist for this subject, select the desired project by clicking on the right.

Press **Open**.

### 6.4.3. Finish, Save and Close Projects

#### 6.4.3.1. Finish a project

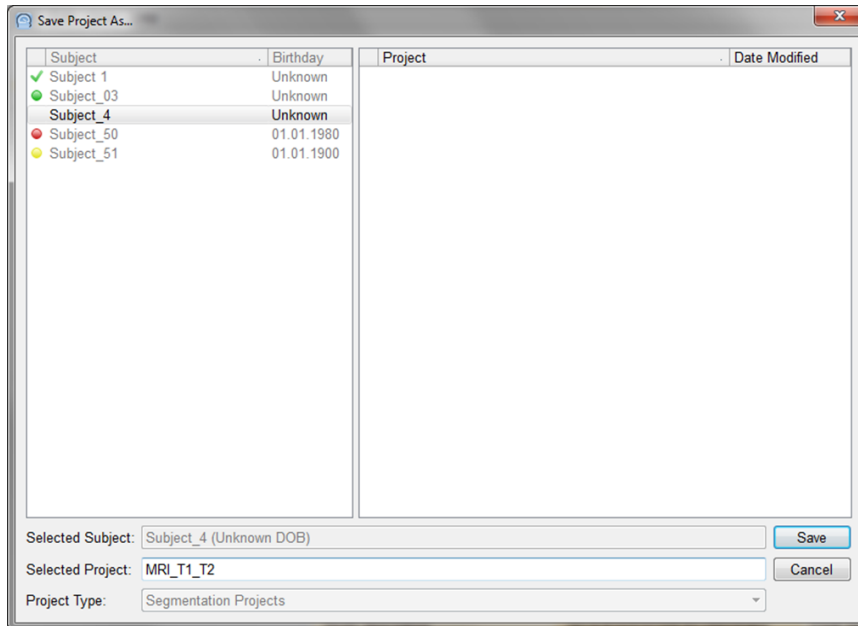
The last step in any workflow is finishing the project by typing **Space** or pressing **Finish**. This last action ensures that the project data with all result files are stored in the BESA MRI Data Folder.

The "Save Project As..." dialog box comes up proposing a project name if the project is new (see figure below). If a previous project has been opened and modified, the previous name is proposed.

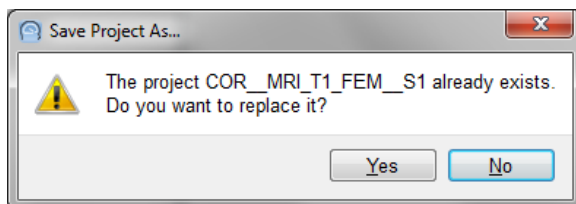
The selected subject and proposed project names are highlighted automatically. To save under a different project name, enter a new project name in the **Selected Project** edit field.

Press **Save** to store the project data including all volume and surface data sets.

If the selected project name does not yet exist, the project is saved with all result files automatically.



If you keep the highlighted project name of a previous project or select another previous project name of the current subject in the **Projects** selection box on the right, you will be asked whether to replace the previous project by the new project data:



Press **Yes**, if you want to discard the previous project data and store the new data under the previous project name.

Press **No**, if you prefer to save under a different project name. The Save Project As... dialog box comes up again.

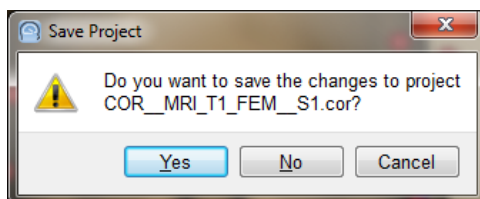
This workstep is complete when the Select Projects page comes up again offering to select another project or exit the BESA MRI program.

**Note:** You may get to the Save Project As... dialog box at any time during the workflow using the menu item **File → Save As**, e.g. if you want to store the current data preparation under a specific project name to be completed later by Automatic Finalization.

#### 6.4.3.2. Close a project

At any time during the workflow, you may close the current project using the **Close button** in the toolbar or the menu item **File → Close**.

When closing a project, the following dialog box comes up:



Press **Yes** to save the changed project data. Previously stored data will be overwritten.

Press **No** if you want to discard all changes, e.g. when accidentally modifying user defined parameters during reinspection after opening an existing project. In this case, the stored data of the current, previously saved project will not be overwritten and changes to the project will not be stored.

Press **Cancel** to return to the project workflow, e.g. if you want to save the current changes under a new project name using the menu item **File → Save As**.

### 6.4.3.3. Save a project

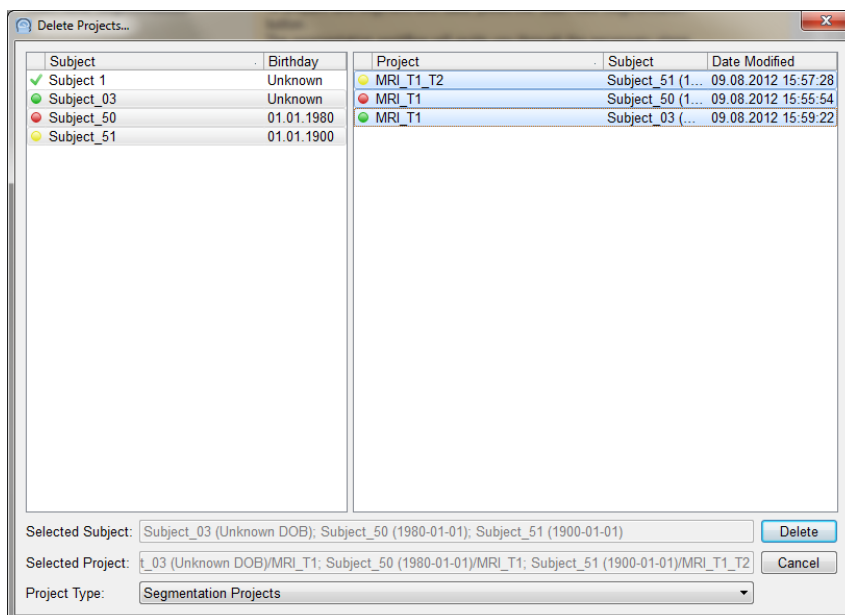
At any time during the workflow, data can be saved by selecting the menu item **File → Save** or typing **Ctrl+S**. However, previously stored data will be overwritten automatically.

#### Notes on closing and saving:

1. Closing and saving can be done at any time during the preparation of a project to preserve the user input up to the completed workstep.
2. If a previously completed project has been opened, previous project data will be overwritten and replaced by the current state of the project. Therefore, do not use the save function when opening a previous project simply for inspection. In this case, use the menu item **File → Save As**.
3. Select the menu item **File → Save As** to store a modified project under a new project name.
4. The current project state and name can always be seen in title bar.

### 6.4.4. Delete Projects

Stored BESA MRI projects can be deleted if no longer needed, e.g. if an improved coregistration project has made a previous project obsolete. To delete, select the menu item **File → Delete Projects...**. The Delete Projects dialog box appears:



In the **Project Type** drop down selection box at the bottom, select the type(s) of projects to be deleted. Select **Segmentation Projects** to delete segmentation projects, **Coregistration Projects** to delete coregistration projects, or **All Projects** to delete segmentation and coregistration projects.

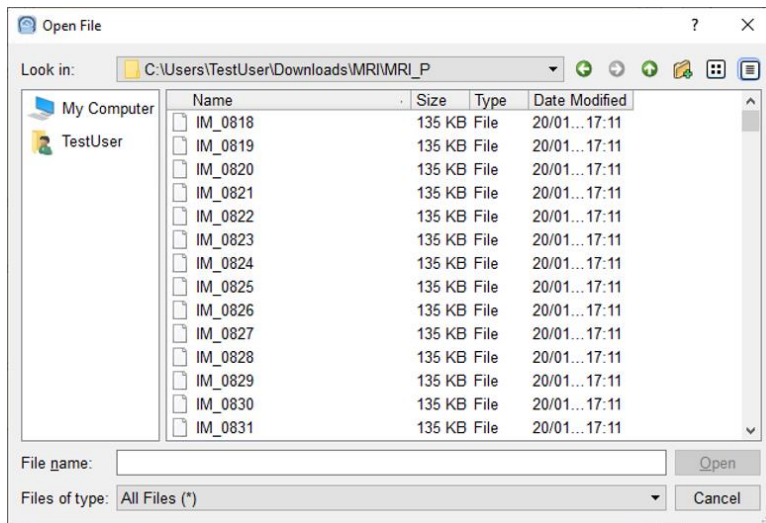
Mark all subjects for whom project data shall be deleted in the **Subjects** selection box. Then select the projects to be deleted in the **Projects** selection box (multiple subjects or projects can be selected by holding the **Ctrl** or **Shift** key while selecting).

A confirmation box is displayed, after selecting and pressing **Delete**.

Press **Yes** only, if you do not need the listed project data any more. Restoring is no longer possible after deleting. Press **No** to prevent deleting.

### 6.4.5. Select Files

When selecting input data, the following dialog appears:



The drop-down menu **Files of type** allows choosing between DICOM files, DICOM Folder, ANALYZE/NIFTI Files, and VMR Files (see also 6.2.1.2). DICOM Folder should be selected if multiple scans of the same or different subjects are stored within one folder.

Use the drop-down folder list at the top to navigate to the desired input folder. Then, select a file in the current folder and press **Open**.

## 7. Appendix

For an easy data management, the data generated by BESA MRI are stored in one folder. In this folder, the so-called BESA MRI Data Folder, the data are organized in subject-based subfolders.

### 7.1. The BESA MRI Data Folder

The BESA MRI Data Folder is the folder or path where BESA MRI stores all project data to and reads completed or prepared projects from. This folder should exclusively be used for storing BESA MRI data.

When starting BESA MRI for the first time (see chapter 2), a local folder accessible to all users is suggested as the **default folder**. Depending on the operating system, this folder is located as follows:

- Windows 10: **C:\Users\Public\Public Documents\BESA MRI\Projects\**
- Windows 7: **C:\Users\Public\Public Documents\BESA MRI\Projects\**

In most cases, however, it might be more useful to create a shared folder on a **server drive**, e.g. **E:\Server\BESA MRI Data** that is accessible to all users from anywhere in the local network. This is more convenient, since BESA MRI uses a network dongle allowing the software to be run from any computer in the local network where BESA MRI has been installed and configured with the shared BESA MRI Data folder.

**Important note:** In clinical use, it is highly recommended using an **encrypted drive** to store the data folder, since it can contain patient information, unless the option to anonymize patient data is used in the workflow step of MRI data reading. Furthermore, please ensure that PCs running BESA MRI are password-protected such that only eligible users have access to BESA MRI.

**Note:** If you have a multi-license installation, make sure that two users do not work on the same subject and project at the same time. Currently, BESA MRI does not lock projects within the network.

If there are several major research studies with different subjects, you might want to create separate folders to store the data of the different studies separately. BESA MRI offers the choice to switch between different BESA MRI Data folders (see chapter 6.4.1) by selecting the menu item **File → Select Data Folder**.

**Note:** When switching between different BESA MRI Data folders, the project data are preserved in each folder and are not copied to the new folder. Thus, you may have to segment a subject's MRI twice unless you copy the subject's subfolder to the new BESA MRI Data folder using, e.g. Windows Explorer, and update the Data Folder Information as described below.

### 7.2. The BESA MRI Data Folder Information File

For faster access on the different projects in the BESA MRI Data folder, an information file called Data Folder Info is created in the subfolder **BesaInternal** within each BESA MRI Data folder. The Data Folder information stores the subject and project file names of all projects in the BESA MRI Data folder.

After copying or moving subject data folders from a previous to a new BESA MRI Data folder using, e.g. Windows Explorer, update the Data Folder information by selecting the menu item **File → Update Data Folder Info**. When switching between folders, make sure that the tick mark of the update option stays on in the confirmation dialog box (see chapter 6.4.1).



## 7.3. Subject-based Data Management

Project data are stored on a subject name basis. Subjects are identified by family name, first name, and birth date as read from the input files (DICOM). If a subject name is not known, e.g. if the MRI data have been anonymized, the default subject name **Z\_Anonym** is used. If the birthday is not specified, the default birthday **1901-01-01 (Unknown DOB = unknown date of birth)** is set.

All project data of a subject are stored in one subfolder of the BESA MRI Data folder having the composed folder name **<SubjectName>\_<Birthday>**.

Project data are managed by BESA MRI using special dialogs for opening, saving or closing, and deleting projects (see chapter 6.4.4). These dialogs provide a subject-and project based selection of completed or prepared project data.

## 7.4. The configuration file

Some settings can be adjusted in the **BESA MRI.cfg** file, located in:

**C:\Users\<USER>\Documents\BESA MRI\Settings\BESA MRI.cfg**

**Default error ellipsoid radius:** A new group can be added to the config file (the values provided in the example below show the default values):

```
[SphereAndError]
1st=20.000000
2nd=20.000000
3rd=20.000000
ErrorMax=60
ErrorMin=5
UseDipoleColorAsDefault=0
OverrideBSA=0
```

The values for radii are expressed in mm. The first three values define the radii of ellipsoid and rim. The first value (**1st**) is the primary radius, oriented radially from the source to the head center. The second value (**2nd**) is the secondary radius, whose orientation is a projection of dipole orientation onto the plane perpendicular to radial direction. In case that the dipole orientation is also radial, the direction is the x direction of the unit sphere coordinate system. However, if the source location lies in x direction, then the direction is the z direction of unit sphere coordinate system. The third value (**3rd**) is the tertiary radius, oriented orthogonally to the previous two.

Maximum and minimum values of the error radii can be set using **ErrorMax** and **ErrorMin**, respectively.

When **UseDipoleColorAsDefault** is set to 1, ellipsoids will be colored using the dipole color instead of gray even for cases when default sizes are used.

If the **OverrideBSA** is set to 1, the error radii information of the BESA Research solution will be discarded and default values will be used instead.

**Inhomogeneity correction for displayed MRI:** If the setting

[Settings]

InhomogeneityCorrectionDisplay=0

is set, then the inhomogeneity correction will not be applied for visualization. The default is 1 (it will be applied).

## 7.5. List of error and warning messages

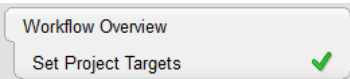

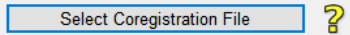
### 7.5.1. Error messages

Workflow Workstep	Message Text / Symbol	Description
<b>BESA MRI</b>	<b>Sentinel LDK Protection System</b> No valid license detected. Please attach a BESA license key in your local network. Make sure that the HASP driver is installed. Also ensure that your HASP is up-to-date and that you own a license for this version of BESA MRI (contact sales@besa.de). (H0007)	This message shows up when a dongle with a valid license is not found or the license driver is not correctly installed.
<b>BESA MRI</b>	BESA MRI is already running. A second instance cannot be run on this PC.	When you run BESA MRI while BESA MRI is already running, BESA MRI displays this error message.
<b>BESA MRI</b>	The internal error MF_211 occurred. Please contact <a href="http://www.besa.de/contact/support/">www.besa.de/contact/support/</a>	The error MF_211 means that something unexpected happened (e.g., there is not enough space available on the disk or you do not have permission to write files on the disk) and the program noticed that. You can request support using our support form.
<b>Start Workflow</b> Select Project	<b>Select the BESA MRI Data Folder</b> You don't have write privileges for the selected folder. Please select a valid BESA MRI Data Folder.	This message appears when you select a folder where you do not have permission to write as the BESA MRI Data Folder.
<b>Start Workflow</b> Select Project	Your current BESA MRI Data Folder does not contain any segmentation projects.	When there are no saved segmentation projects, this message shows up after clicking the <a href="#">Open Segmentation Project</a> button.
<b>Start Workflow</b> Select Project	Your current BESA MRI Data Folder does not contain any coregistration projects.	When there are no saved coregistration projects, this message shows up after clicking the <a href="#">Open Coregistration Project</a> button.
<b>Start Workflow</b> Select Project	The following projects could not be finalized due to an error: ***.seg; ***.seg	This message appears when the automatic finalization for segmentation projects (Edit   Finalize All Segmentation Projects) is interrupted during the process.
<b>Segmentation</b> Read T1-weighted MRI Data Read T2-weighted MRI Data	The selected file could not be read. Please check if the correct file type is selected. In case file type and file format match and this problem still prevails, please	This message occurs when the selected MRI file is empty or corrupted.

	contact <a href="http://www.besa.de/contact/support/">www.besa.de/contact/support/</a> .	
<b>Segmentation</b> <i>Read T1-weighted MRI Data</i> <i>Read T2-weighted MRI Data</i>	<b>No scans found</b> No DICOM scans were found in the selected folder. Please select another folder.	This message occurs when the selected folder does not have DICOM scans.
<b>Segmentation</b> <i>Read T1-weighted MRI Data</i> <i>Read T2-weighted MRI Data</i>	<b>Subject Mismatch</b> The patient info of the loaded data set for image registration does not match the patient info of the current MRI data set. Please make sure that this is the correct data set for registration. If this is not the correct data set, load another data set by pressing the Load Data button.	This message appears when the subject of the selected image data for image registration is different from the subject of the loaded main image data.
<b>Coregistration</b> <i>Set Fiducials</i>	The segmentation project you have specified as input for this project does not exist any more. Do you wish to select a new input project?	This message appears when specified input project (segmentation project) does not exist.
<b>Coregistration</b> <i>Set Fiducials</i>	The segmentation project you have specified as input for this project has not been completed. Do you wish to finalize the input project? <div style="text-align: right;">[Yes] [No] [Cancel]</div>	This message appears when specified input project (segmentation project) has not reached finished state. <ul style="list-style-type: none"> <li>• Yes: The current workflow is closed; instead, the segmentation workflow is resumed.</li> <li>• No: The dialog box closes.</li> <li>• Cancel: Same as No.</li> </ul>
<b>Coregistration</b> <i>Fit Surface Points</i>	The selected coregistration file does not contain any EEG electrode information (needed as input for FEM/BEM leadfield generation). If you want to select this coregistration file for a coregistration, please uncheck the option "Generate FEM EEG leadfield" and "Generate BEM EEG leadfield" in "Set Project Targets" workstep.	This message shows up when an EEG FEM/BEM calculation is part of the project targets but the selected co-registration file (.sfh) does not contain electrodes.
<b>Coregistration</b> <i>Fit Surface Points</i>	No POS file exists for the selected coregistration file (*.sfh). If you want to generate a FEM/BEM MEG leadfield, a POS file containing information on the MEG sensors must exist with the same basename as the coregistration file. If you want to select this coregistration file for a coregistration, please uncheck the option "Generate FEM MEG leadfield" and "Generate BEM MEG leadfield" in "Set Project Targets" workstep.	This message shows up when an MEG FEM/BEM calculation is part of the project targets but no MEG sensor coordinate file (*.pos) exists for the selected co-registration file (.sfh).

<b>Coregistration</b> <i>Fit Surface Points</i>	The update information could not be written to the coregistration file <b>***.sfh</b> .	This message shows up when the selected coregistration file (.sfh) cannot be modified.
<b>Open Segmentation Project</b> <i>View Results</i>	Solution files need to be saved in Talairach coordinates in order to be opened in BESA MRI	This message shows up when you select a solution file (*.bsa) saved not in Talairach coordinates from BESA Research after clicking the <b>Load sources</b> button.
<b>Open Segmentation Project</b> <i>View Results</i>	<b>Information window</b> Error: At least one of Brain Atlas data files is missing. Choose a different Brain Atlas and contact BESA team for support Press the Close button to close the project.	This message appears in the Information window when the data file of the selected brain atlas is missing or corrupted. To resolve this issue, you should reinstall BESA MRI.

## 7.5.2. Warning messages and symbols

<b>Workflow</b> <i>Workstep</i>	<b>Message Text / Symbol</b>	<b>Description</b>
<b>BESA MRI</b>		A green check mark shows up next to the finished worksteps in the Workflow window.
<b>BESA MRI</b>		A green check mark shows up next to a button in order to indicate that the related process is successfully finished.
<b>BESA MRI</b>		A yellow question mark shows up next to a button in order to indicate that the related process is not successfully finished.
<b>BESA MRI</b>	Another program has requested to start a coregistration. Do you wish to close the current project and start coregistration? [Yes] [No]	This dialog box appears when BESA Research requests a new MRI coregistration project while a project is opened or processed in BESA MRI. <ul style="list-style-type: none"><li>• Yes: The left and right sides of the MRI image are flipped.</li><li>• No: The dialog box closes.</li></ul>
<b>Start Workflow</b> <i>Select Project</i>	The last BESA MRI session was not closed properly. Do you wish to restore the previous session? [Yes] [No]	This message appears when you run BESA MRI again after abrupt termination during running a project. <ul style="list-style-type: none"><li>• Yes: You can restore the previous project.</li><li>• No: The dialog box closes.</li></ul>
<b>Segmentation</b> <i>Set Orientation of T1 Data</i> <i>Set Orientation of T2 Data</i>	You have selected to flip the left and right side of your volume data. For correct data sets this inversion will lead to incorrect results. Are you sure that the flip of the left and right side is correct for your data and shall be performed?" [Yes] [No] <input type="checkbox"/> Do not show this message again	This message shows up after checking the check box "Perform Left-Right Flip". <ul style="list-style-type: none"><li>• Yes: The left and right sides of the MRI image are flipped.</li><li>• No: The dialog box closes.</li></ul>

<b>Segmentation</b> Read T1-weighted MRI Data	Data info for the primary volume data (T1) has been changed. Do you want to change the info of the currently read secondary volume data (T2) accordingly?	This message shows up when you modify the data information of the main image after finishing the worksteps for reading T1 and T1 MRI data.
<b>Segmentation</b> <i>T1 Inhomogeneity Correction</i> <i>T2 Inhomogeneity Correction</i>	<b>Run Inhomogeneity Correction</b> You have reduced the number of iterations. All iterations have to be recalculated. Do you wish to continue?	This message appears when you reduce the number of iterations and run inhomogeneity correction again.
<b>Coregistration</b> <i>Set Fiducials</i>	The segmentation project you have specified as input for this project has not prepared a volume conductor segmentation yet (needed as input for the generation of a FEM or BEM forward model).  Note: To perform a volume conductor segmentation, check the option "Run Volume Conductor Segmentation" in the "Set Project Targets" workstep of your input project and finalize it. Do you wish to open the input project to perform a volume conductor segmentation? [Yes] [No] [Cancel]	If a FEM or BEM forward model was requested in the project targets, but no volume conductor segmentation was performed in the segmentation workflow, the dialog box appears.  <ul style="list-style-type: none"> <li>• Yes: The workflow is closed; instead, the segmentation workflow is resumed with the existing project, and the user can change the project targets to indicate the volume conductor segmentation.</li> <li>• No: The dialog box closes, and then you can navigate back to the Set Project Targets workstep to change the project targets or choose another segmentation project.</li> <li>• Cancel: Same as No.</li> </ul>
<b>Coregistration</b> <i>Fit Surface Points</i>	The result of surface point fit has changed since the last calculation. Do you wish to reset manual correction parameters?	This message appears when surface point fit results have changed and you had already done manual corrections before.
<b>Coregistration</b> <i>Fit Surface Points</i>	<b>Info</b> Scaling on *-axis is already at ###.##. Please check scaling of MRI.	This message appears after running surface point fit when scale values exceed the limit range of scaling.  When you use an individual MRI with the coregistration file where the electrode locations are defined on a sphere, scale values might exceed the limit range.

## 7.6. Range, accuracy and precision of displayed values

The following table lists measured quantities that are displayed to the user during certain work steps in clinical usage of BESA MRI. The range, accuracy and precision are also listed.

<b>Workflow</b> <i>Workstep</i>	<b>Measured quantity</b>	<b>Range</b>	<b>Accuracy</b>	<b>Precision</b>
<b>Segmentation</b> <i>View segmentation results</i>	Source position or position of anatomical structure in the brain, in AC-PC coordinate system	The permitted range lies within -127.5 mm to +127.5 mm, measured from the AC point.	Accuracy of this value depends on the accuracy with which the definition of the anatomical landmarks and the rotation can be carried out during segmentation. Typical MRI quality enables an accuracy of $\pm 1.5$ mm.	Precision of this value was established by an internal test. It depends on precision of transformation (definition of AC coordinate and rotation of brain).  Mean precision is $\pm 2$ mm.

<b>Segmentation</b> <i>View segmentation results</i>	Source position or position of anatomical structure in the brain, in Talairach coordinate system	The permitted range lies within -127.5 mm to +127.5 mm, measured from the AC point.	Accuracy of this value depends on the accuracy with which the definition of the anatomical landmarks and the rotation can be carried out during segmentation. Typical MRI quality enables an accuracy of $\pm 2$ mm.	Precision of this value was established by an internal test. It depends on precision of transformation (definition of AC coordinate and rotation of brain). Mean precision is $\pm 2.5$ mm.
<b>Coregistration</b> <i>Fit surface points</i>	Mean distance error of the fit (digitized surface points to reconstructed head surface)	The range starts at 0.0 mm and has no fixed upper limit.	$\pm 0.5$ mm	$\pm 0.5$ mm
<b>Coregistration</b> <i>Fit surface points</i>	Maximal distance error of the fit (digitized surface points to reconstructed head surface)	The range starts at 0.0 mm and has no fixed upper limit.	$\pm 0.5$ mm	$\pm 0.5$ mm





## 8. References

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BESA GmbH  
Freihamer Str. 18  
82166 Gräfelfing – Germany

Phone + 49.89.89 80 99 66  
Email [info@besa.de](mailto:info@besa.de)  
Web [www.besa.de](http://www.besa.de)



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