



BESA MRI
User Manual

BESA®

MRI 2.0

User Manual

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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

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

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

Symbols



Follow the instructions in this manual to prevent damage resulting from misuse of the program. In addition, this symbol marks important sections that shall be read before starting to work with BESA MRI.



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



1. Intended Use

- BESA MRI is intended for the Use (MDD 93/42/EEC)
 - For Human Beings
 - But NOT for Animal Beings
- BESA MRI is a software-only product compatible with personal computers running under a Windows operating system.
- BESA MRI alone does not provide any diagnostic conclusion about the subject's condition. The analysis results of BESA MRI can be used for diagnosis only when combined with the application BESA Research.
- The segmentation component of BESA MRI imports digital MRI data, segments and labels different brain and head tissues, transforms the MRI data into ACPC- and Talairach spaces, and renders the scalp and cortical surfaces.
- BESA MRI segmentation requires a patient age of at least 10 years.
- The coregistration component of BESA MRI imports EEG electrode and/or MEG sensor coordinates and fits these to the scalp surface provided by the segmentation component. Optionally, it computes an EEG and/or MEG lead field table for the head tissue segmentation provided by the segmentation component.

BESA GmbH is not liable for the use of the software beyond the intended purpose.

1.1. Intended User

- The intended user is a neuroscience professional who is trained in the review of MRI images. He or she is expected to be literate in the usage of computer programs in the Windows environment.
- BESA MRI is only to be used by appropriate trained specialist personnel who also have an understanding of English sufficient to enable them to read the User Manual and operate the software.
- Users who use BESA MRI in combination with BESA Research must consider the national requirements for EEG and MEG evaluation independently of the manufacturer's liability.
- The BESA GmbH assumes no liability for unauthorized access to this product or unauthorized use. Children, laymen and patients shall not use the product.



2. Introduction

2.1. 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 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 10-20 system) to the individual scalp
- 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.

2.2. Why FEM modeling

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, Brain) or 4 layers (Scalp, Skull, CSF, 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; Cuffin; Roth). 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 FEM modeling, as it also 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). Neglecting CSF for EEG forward modeling can lead to larger localization errors (Ramon; Wendel)

The FEM modeling in BESA MRI was developed in cooperation with the research group around Dr. Carsten Wolters. Detailed literature on the methods can be found in the reference section (see chapter 8).

2.3. Product Classification

BESA MRI 2.0 is a medical product intended for the use for human beings for the medical purpose of the investigation of a physiological process.

According to **MDD 93/42/EEC**, Annex IX, rule 10, BESA MRI is a **Class IIa** software product for the preprocessing and segmentation of human scalp MRI data stored on computer disk with the following properties:

- 1.1. Duration of application: short term
- 1.2. Non-invasive (stand-alone software not controlling any equipment physically connected to the patient)
- 1.4. Active medical device since the PC needs electrical supply
- 1.6 Used to supply information for detecting and diagnosing physiological conditions

BESA MRI is analysis software that may be used in the field of scientific research, and for providing assisting information supporting the diagnosing of disorders in neural processes by analyzing neuroanatomical data.

BESA GmbH is not liable for the use of the software beyond the intended purpose.

According to safety classifications in **DIN/EN IEC 62304**, BESA MRI is a **Class A** product (class A: no injury or damage to health is possible):

It is designed purely for data analysis. No physical devices are controlled or driven by BESA MRI, nor is any active feedback provided to the patient. Any direct physical damage to the subject can therefore be excluded.

BESA MRI is classified as “**Analysis unit for long-term EEG data**”

UMDNS code: 16-307

GMDN: 35163

GMDN collective term: CT112 (Software, application program)

2.4. Certification



The CE marking certifies that this product fulfills the basic requirements of the Medical Devices Directive **MDD 93/42/EEC**.

The number represents the identification number of the Notified Body that carried out testing and certification.

2.5. System Requirements

- Operating system: Windows® 10
Windows® 8.1
Windows® 7 (32bit and 64bit versions)
- CPU: Minimum 2 GHz
- RAM: Minimum 4 GB
- Display resolution: Minimum 1280x800 pixels
- Graphics card: OpenGL 1.1 with 16 MB RAM or more

2.6. Application Environment

According to **DIN EN IEC 60601-1:2005**, BESA MRI does not affect the possibility of using any computer within the patient environment. Other programs or hardware connected to the computer (third party equipment) may not be suitable for use within the patient environment.

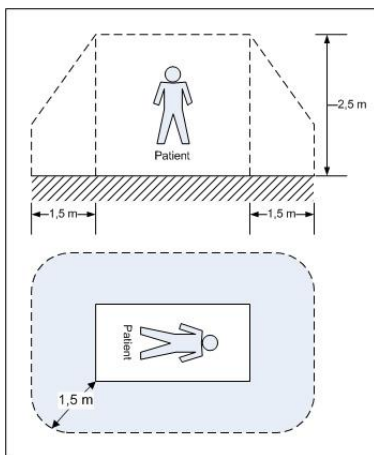
If the product is installed on a PC or Notebook within the patient environment, the PC/Notebook must conform either

(a) to DIN EN IEC 60601-1 medical PC

or

(b) must be isolated from the patient by means of protection (IEC 60601-1 3rd Edition) e.g. by an isolating transformer fixed at the PC, or mobile isolating devices for Notebooks.

The patient environment is defined as follows:



Please note: It is User's responsibility to ensure the safety of combined medical-non-medical-devices (whether in institutes, clinics or practitioners' location).

2.7. Disposal Information

The BESA dongle and the BESA USB stick must be disposed of according to the national guidelines on environmental protection.

2.8. License Information

The HASP SRM dongle System

BESA MRI is protected with a network Sentinel HASP protection key ("dongle"). BESA MRI will not run unless a HASP dongle with valid license information is connected to a USB port of a computer in your local area network. The license management in your network is handled by the Sentinel HASP Run-time Environment.

The Sentinel HASP run-time environment is installed automatically with the BESA MRI installation (a manual installation of the Environment can be started by the program

HASPUserSetup.exe located in subfolder Utilities\License\System of your BESA MRI installation directory).

After installing BESA MRI, your system is ready for use. Optional specific settings can be performed as described below. For example, by default every computer in your local network can access the license on the HASP dongle that is attached to your local computer. To change that, please see the Configuration section below.

Individual license settings: The Sentinel HASP Admin Control Center (ACC)

The Sentinel HASP Run-time Environment includes the HASP device drivers and the Sentinel Admin Control Center (ACC). ACC is a customizable, web-based, end-user utility that enables centralized administration of HASP license managers and Sentinel HASP protection keys. ACC can be used to monitor licenses and sessions when a protected application is operating, and to manage detachable licenses. To run the ACC please type the following address in your internet browser (internet connection is not required): <http://localhost:1947>.

The following Administration Options are available:

The Sentinel Keys page shows which HASP dongles are currently present in the network, including locally connected HASP dongles.

The Products page lists all BESA products available on all accessible HASP dongles in the network (this includes not only BESA MRI, but e.g. also possibly licenses for BESA Research, BESA Statistics and BESA Epilepsy).

The Features page lists all BESA program components (called Features in the Sentinel HASP system) that are licensed in each of the HASP dongles that are currently present in the network, including locally connected HASP dongles. In addition you can see the conditions of the license, and the current activity related to each Feature.

The Sessions page lists all sessions of clients on the local machine, and of clients remotely logged in to the local machine. This page enables you to view session data and to delete sessions.

The Configuration page enables you to specify basic settings. On this page you can also configure access to or from other computers. For example, to specify that the license on the local HASP dongle can be used only locally on that computer, switch to tab Access from Remote Clients and remove the checkmark at Allow Access from Remote Clients.

License Update

To download license updates for your HASP dongles, please visit <http://www.besa.de/updates/license/>.

3. Installation and Initial Setup

The installation and initial setup of BESA MRI must be carried out by an administrator or an experienced technician. Chapter 3.1 illustrates the installation process, and chapter 3.2 introduces the initial setup of BESA MRI.

- The installation of the product must be carried out by the system administrator or an authorized person.
- Product updates must also be carried out by the system administrator or an authorized person.
- After installation and setup are complete, please submit this user manual to all users of the program.
- If the product is installed on a PC or Notebook within the patient environment, the PC/Notebook must conform either to DIN EN IEC 60601-1 medical PC or must be isolated from the patient by means of protection (IEC 60601-1 3rd Edition) e.g. by an isolating transformer fixed at the PC, or mobile isolating devices for Notebooks.



3.1. Installation and Uninstallation

3.1.1. Installation

If you are installing from the USB stick:

1. Start Windows and insert the USB stick.
2. Browse to the **Setups** folder. Start the setup that is suitable for your environment (64 bit or 32 bit - 64 bit recommended). Continue with step 3.

If you used the setup download option from the BESA website (<https://www.besa.de/downloads/besa-mri/>):

1. Download the setup that is suitable for your environment (64 bit or 32 bit).
2. Browse to the download folder and start the setup executable.
3. Please follow the on-screen instructions.
4. Once the installation is complete, proceed with the initial setup as explained in the following chapter.

3.1.2. Uninstallation

Uninstallation of BESA MRI is done following the standard protocol for uninstalling Windows programs. To un-install BESA MRI, start the System Control Panel (in Windows 8.1, this is found under PC Settings). Then click on "Programs and Features" and select BESA MRI in the list of programs. There is an Uninstall button available after the selection.

3.2. Initial Setup

This section explains the steps to be performed for an initial setup of BESA MRI.

3.2.1. Before Setup

BESA MRI is available as a 32 bit or a 64 bit program. The latter version prevents memory problems caused by a 32 bit restriction. Therefore, **we recommend using the 64 bit version** if your Windows system supports it. Please make sure to check this before the installation.

3.2.2. Connect the BESA Dongle

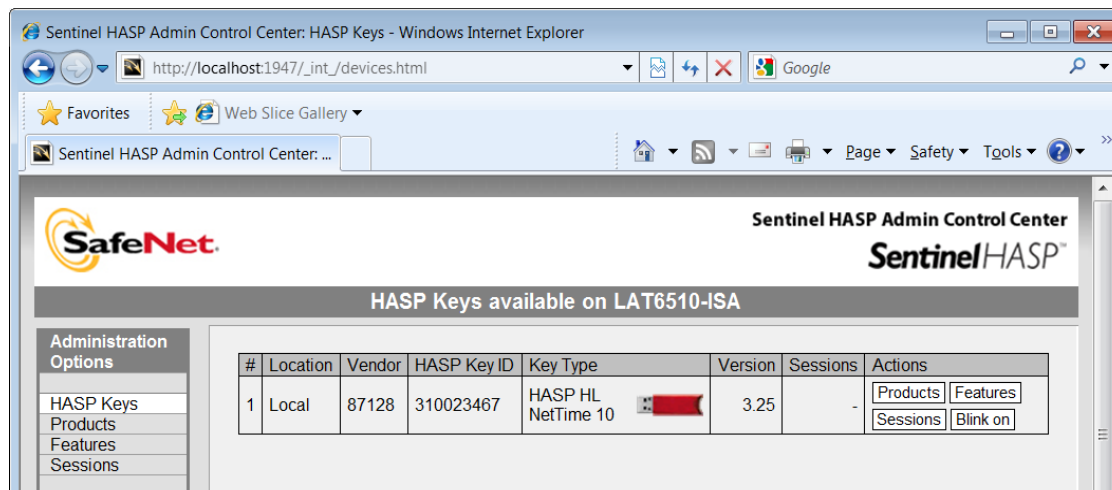
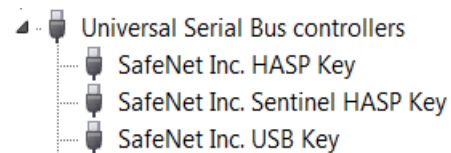
BESA MRI is protected by a licensing scheme developed by SafeNet Inc. During the installation as explained in chapter 3.1 the device drivers for the BESA dongles will be installed automatically.

Connect the BESA dongle to your personal computer or a server machine and proceed with the next step. If required, check for correct installation as described below.

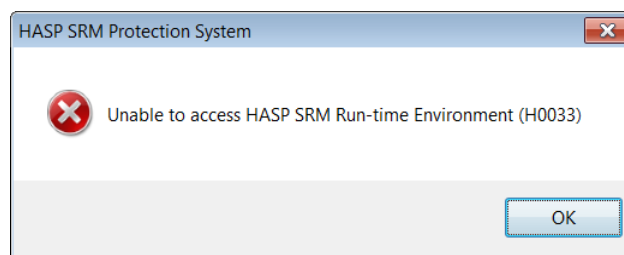
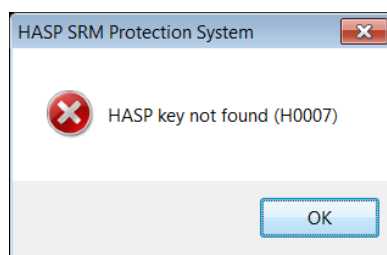
If the dongle is installed correctly, the Windows Device Manager reports three items in the "Universal Serial Bus controllers" section: SafeNet Inc. HASP Key, SafeNet Inc. Sentinel HL Key, SafeNet Inc. USB Key. The SafeNet Inc. HASP key installer includes the HASP License Manager application:

C:\Windows\system32\hasplms.exe

When this application is running, you should be able to load the HASP License Manager Admin Control Center by typing <http://localhost:1947> in your internet browser. The connected dongle should be displayed there. If you do not see the dongle, please wait a few seconds.



If the dongle is not installed correctly, one of the following message boxes is displayed when the program is started.



The message box on the left appears for one of the following reasons:

- The BESA dongle is not connected.

Solution: Ensure that the key is accessible in order to run the program.

- USB port is defective.

Solution: Check if the LED is lit on the HASP Protection Key. If not, remove and re-insert. Wait for the operating system to detect the device. If it still does not light up, try another USB port.

- Faulty dongle.

Solution: On rare occasions, the HASP Protection Keys may be faulty. The dongle does not light up in this case and is not detected in the Device Manager. Request a replacement dongle.

The above right message box comes up for one of the following reasons:

- **C:\Windows\system32\hasplms.exe** is blocked by a firewall or an anti-virus application.

Solution: Add **C:\Windows\system32\hasplms.exe** in the exception list of the anti-virus and firewall applications.

- Port 1947 is blocked by a firewall application.

Solution: Add port 1947 to the exception list of the firewall application.

- HASP License Manager Service is stopped.

Solution: Restart the HASP License Manager Service ([Control Panel](#) → [Administrative Tools](#) → [Services](#))

3.2.3. Start the Program

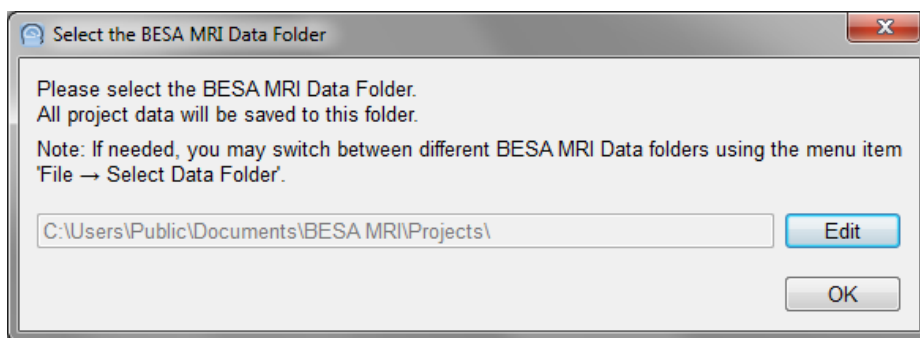


Start BESA MRI using the shortcut created on the desktop or run **BESA MRI.exe** from the **All Programs → BESA → MRI 2.0** folder in Startup menu. First, the Welcome Screen appears (see chapter 6.1.1). Press **Accept** to start BESA MRI.

3.2.4. Specify the BESA MRI Data Folder

As initial configuration step, the BESA MRI Data Folder must be specified (for details see chapter 7.1). This is the folder where BESA MRI stores all project and result data to and reads from (typically on the server).

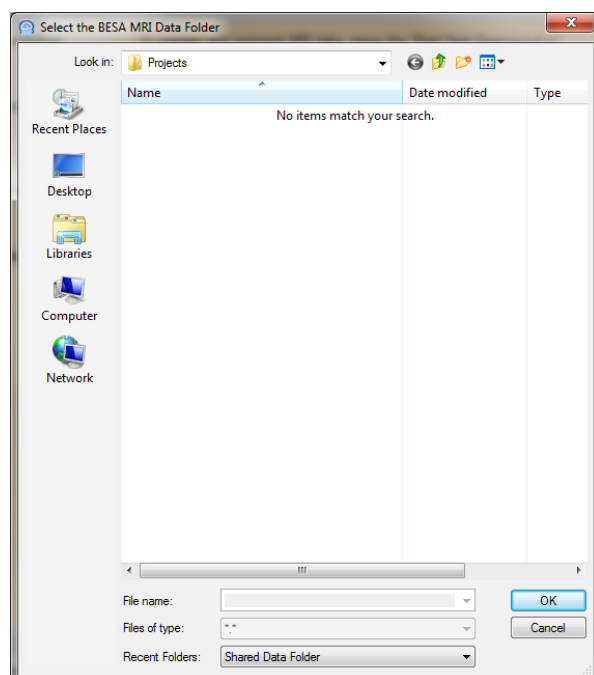
When starting the program for the first time, the following dialog box appears:



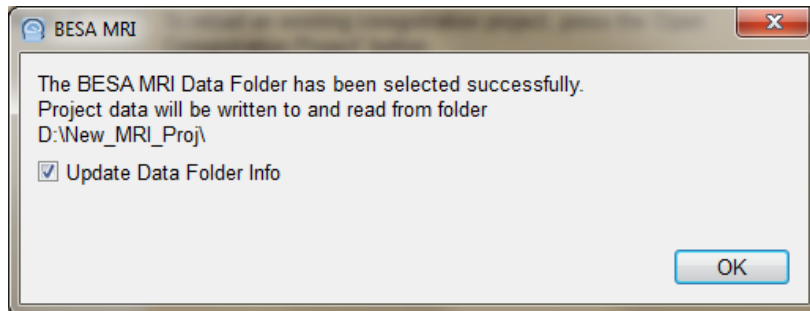
The BESA MRI Data Folder is preselected to All Users on the local PC (shown above for Windows 7). However, it is recommended to create the BESA MRI Data Folder on your server where it is accessible to all users from anywhere in the local network. For more details, see chapters 6.4.1 and 7.1.

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:



Press the **OK** button.

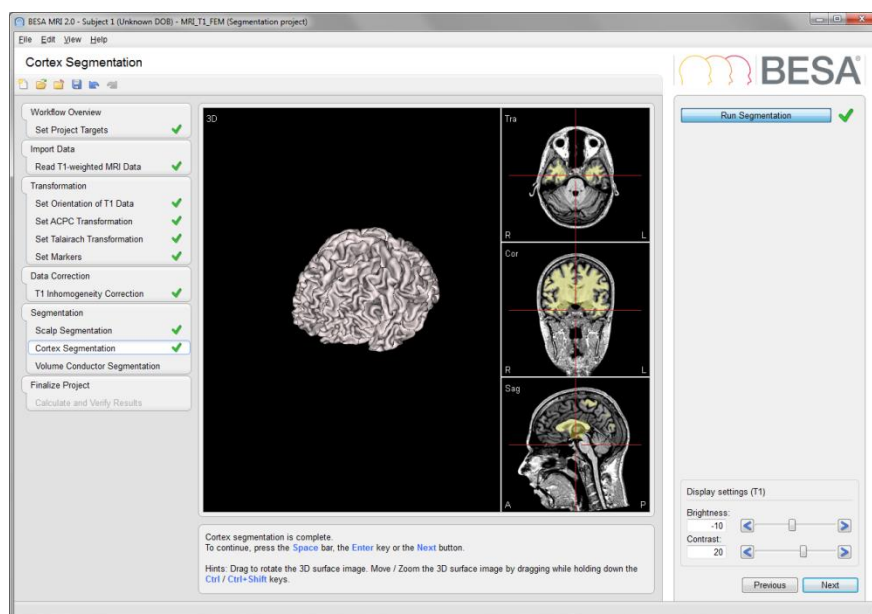
BESA MRI is now configured to start projects.

Notes:

1. 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.
2. 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 7.1).

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.

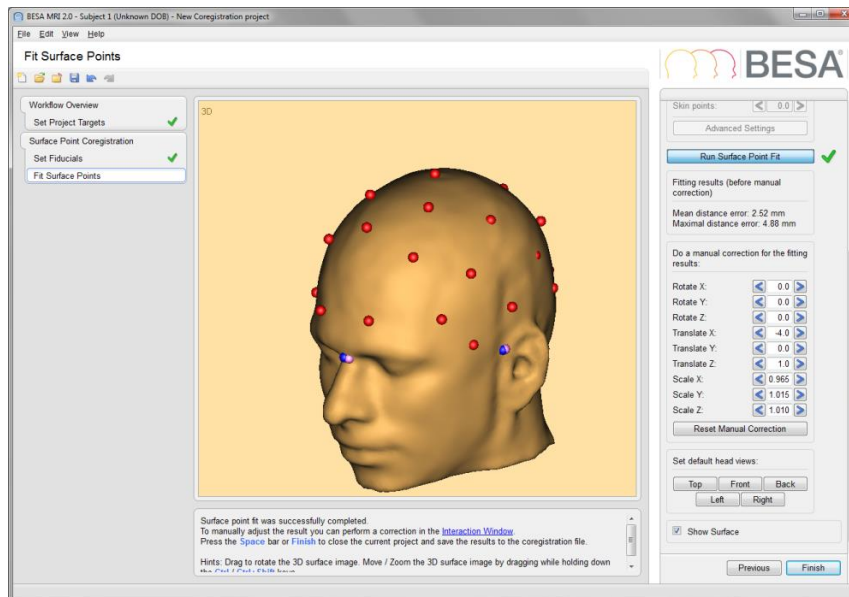
When pressing the **Next** button or hitting **Space** a workstep is terminated and the next workstep is loaded. Thus, the workflow of a project proceeds sequentially workstep by workstep.

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 5.1). 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:

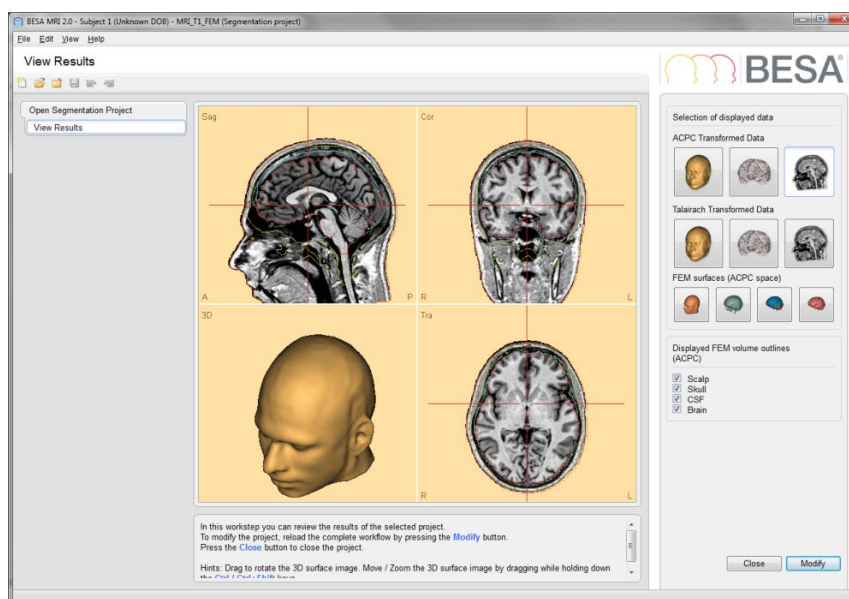


Segmentation Project: Initiated by Start New Segmentation Project (figure on previous page, see chapter 6.2.1).

Coregistration Project: Initiated by Start New Coregistration Project (figure above, 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.

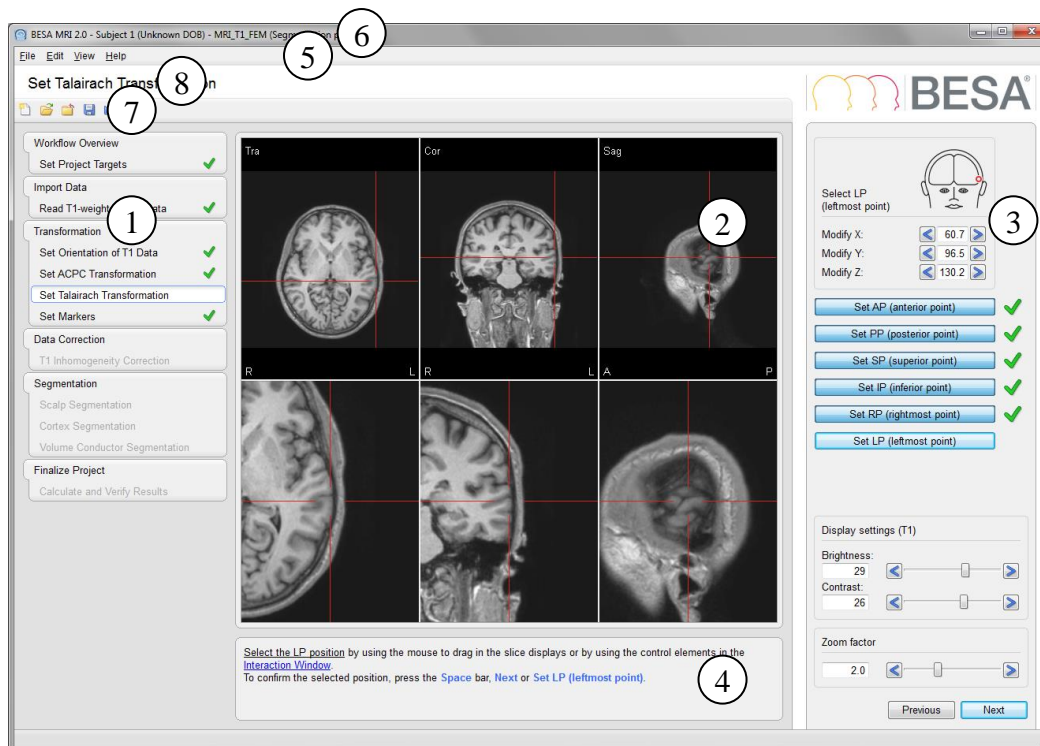
Stored projects can be viewed by selecting the menu item **File → Open Project**, using the open button in the toolbar, or pressing the **Open Segmentation / Coregistration Project** buttons on the start screen. After opening a stored completed project, the final workflow result is displayed in a special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

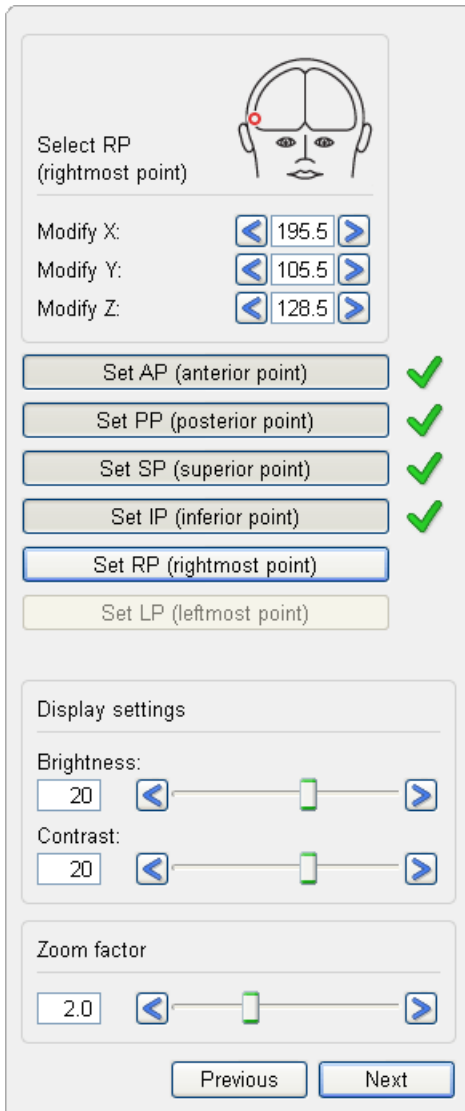
The current workstep is highlighted. This step is also shown in the caption.

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 is a panel on the left side of the software interface. It contains several sections:

- Select RP (rightmost point):** A diagram of a human head with a red dot on the right side of the forehead.
- 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 stack of buttons: "Set AP (anterior point)", "Set PP (posterior point)", "Set SP (superior point)", "Set IP (inferior point)", "Set RP (rightmost point)", and "Set LP (leftmost point)". The "Set RP" button is highlighted with a blue border and has a green checkmark to its right. The other buttons have green checkmarks to their right.
- Display settings:** A section with sliders for "Brightness" and "Contrast", both set to 20. Each slider has a numeric input field and left/right arrow buttons.
- Zoom factor:** A section with a slider set to 2.0, with a numeric input field and left/right arrow buttons.
- 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
Create New Project	Start a new project.
Open Project	Load an existing project (see chapter 6.4.2).
Close Project	Close currently active project. Show the Select Project Page (see chapter 6.1.2).
Save	Save the currently active project.
Save As...	Specify a filename for currently active project and save it (see chapter 6.4.3).
Delete Projects...	Select one or multiple projects that shall be deleted (see chapter 6.4.4).
Select Data Folder	Select the folder to be used as BESA MRI Data Folder (see chapter 7.1).
Update Data Folder Info	Update the information file in the BESA MRI Data Folder (see chapter 7.2).
Exit	Terminate the BESA MRI program.

5.5.2. Edit Menu

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

Edit menu item	Description
Undo	Undo the last step completed in the current workstep.
Redo	Redo the last step that was undone in the current workstep.
Finalize Current Project	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.
Finalize All Segmentation Projects	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
Show Workflow Window	By selecting or deselecting this menu item the Workflow Menu is displayed or hidden (see chapter 5.1).
Show Information Window	By selecting or deselecting this menu item the Information Window is displayed or hidden (see chapter 5.4).
Standard Font Size, Large Font Size, Extra Large Font Size	Select one of these menu items to specify the size of the font to be used in BESA MRI.

5.5.4. Help Menu

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

Help menu item	Description
BESA MRI Help	Open the program help.
About...	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

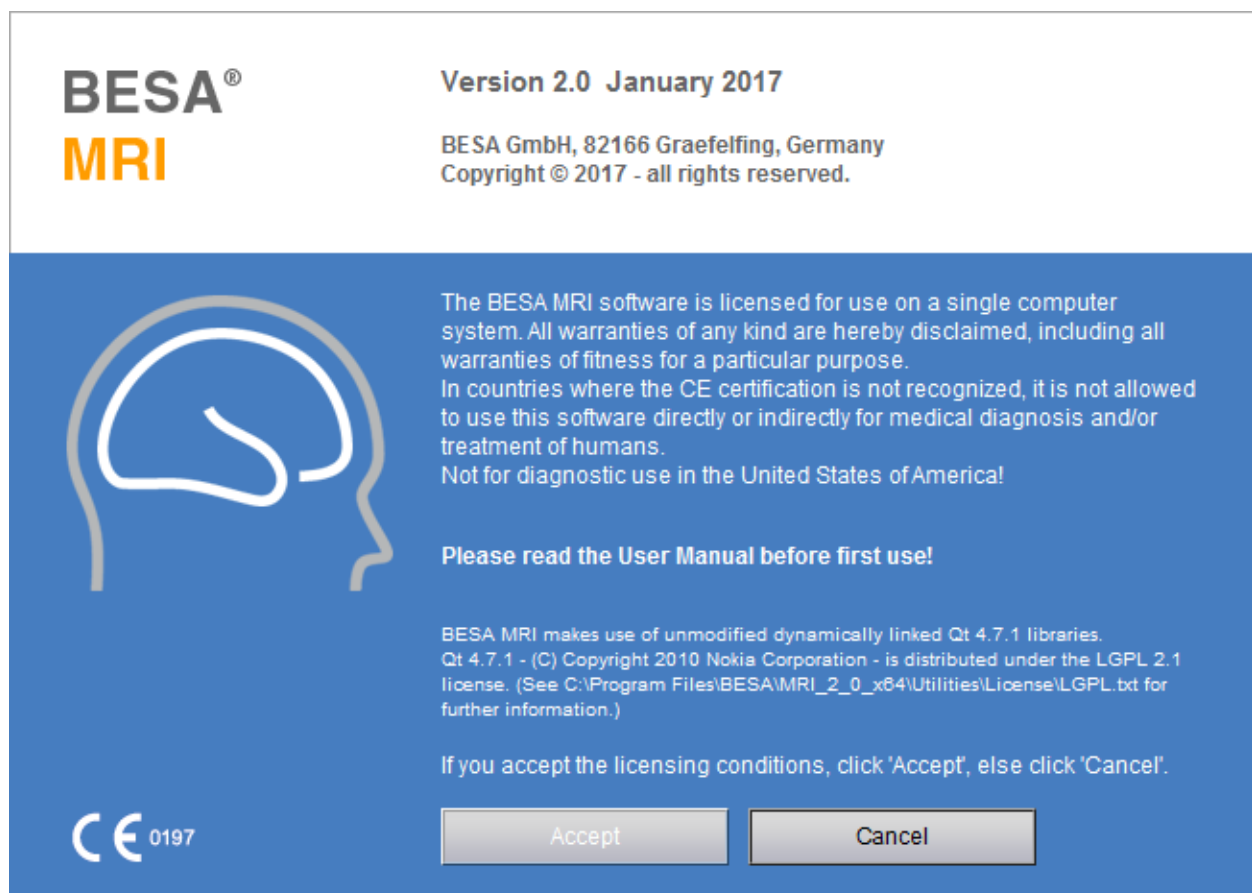
Before working with BESA MRI, please read chapter 4 on the workflow concept. Consult chapter 5 on the elements of the BESA MRI screen while starting to use the program.

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.

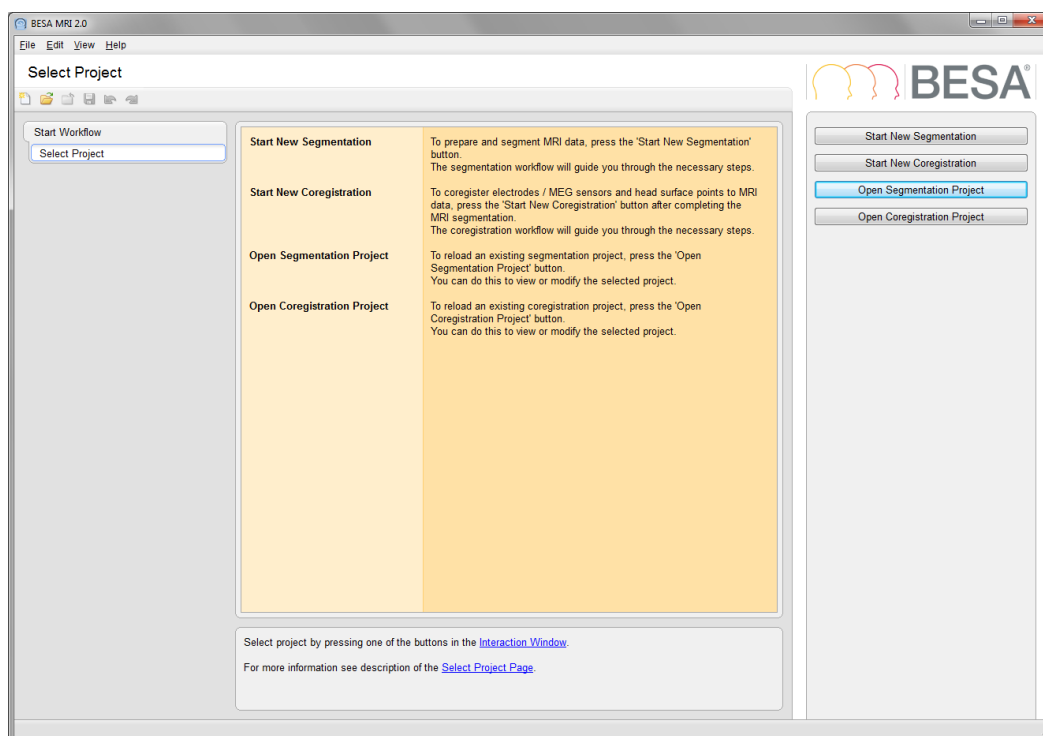
When starting BESA MRI, a welcome screen appears. It provides some information on the BESA MRI program including the current version number and date:



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 (scalp, skull, CSF and brain) needed for finite element modeling (FEM). Once the head tissues are segmented, a 4-layer FEM model is generated based on the segmented volumes. The FEM 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 is to be created, the option **Run Volume Conductor Segmentation** 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.

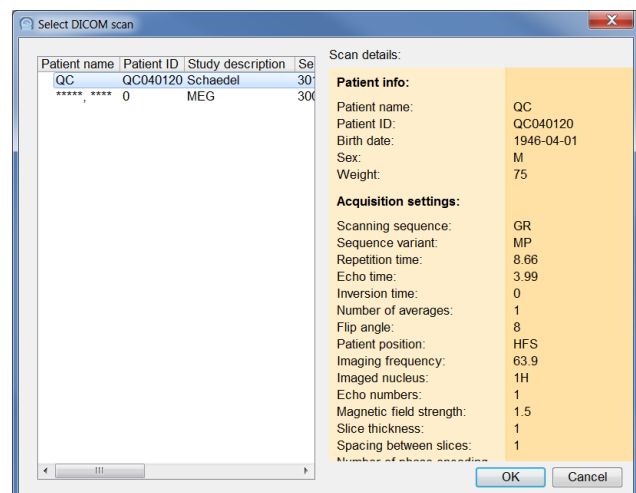
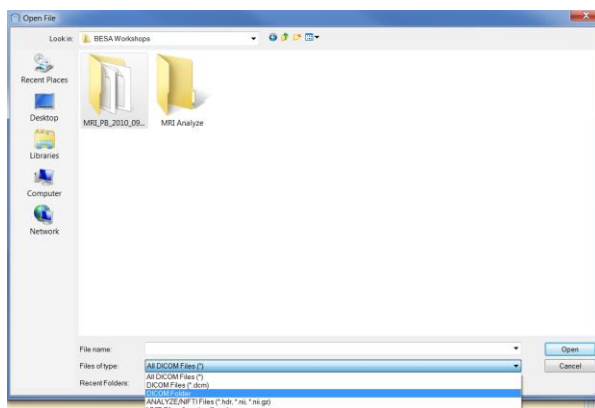
The header information of the DICOM files is evaluated and displayed in the Main Window. Check if subject and sequence are correct and hit **Space** or press **Next** to continue the workflow.

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.



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.

Anonymize data

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

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. Still, 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.



6.2.1.4. Set Orientation of T1Data

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 point)	Transversal	Coronal	Frontal brain
PP (posterior point)	Transversal	Coronal	Occipital brain
SP (superior point)	Coronal	Transversal	Top gyri
IP (inferior point)	Coronal	Transversal	Temporal poles
LP (leftmost point)	Coronal	Sagittal	Lateral temporal cortex
RP (rightmost point)	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.

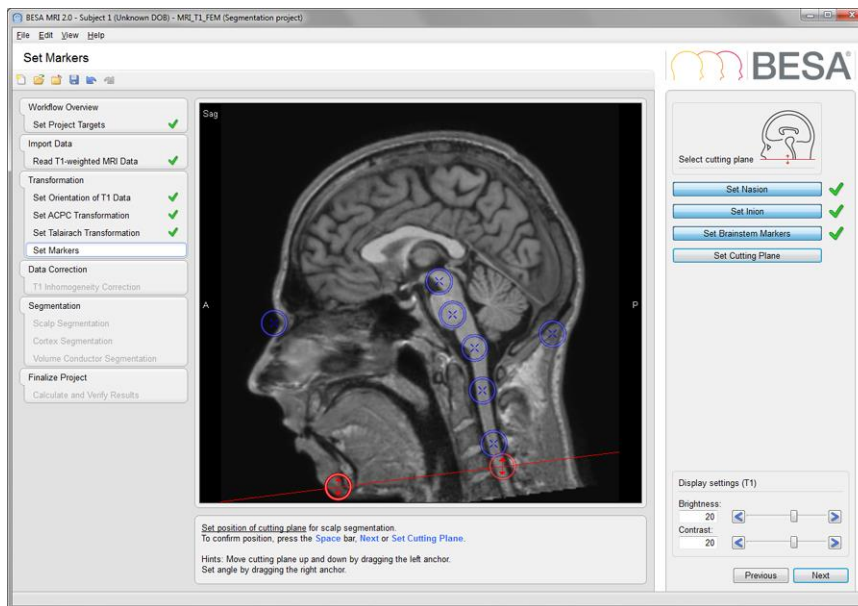
Corrections can be made by unpressing any substep button in the Interaction Window on the right and hitting **Space** or pressing **Next** to continue. For more details on setting or modifying markers see chapter 6.3.2.

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). Mutual information (Wells) 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.

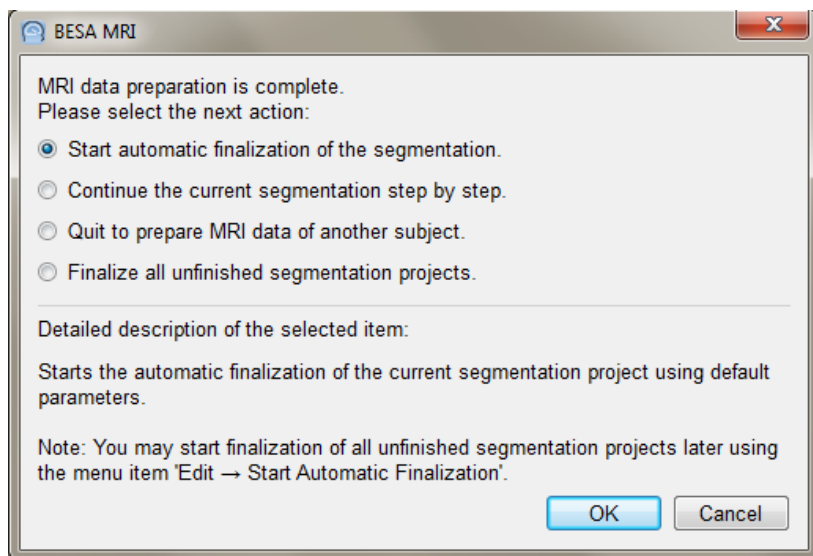
Hit **Space** or click **Next** to continue.

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:

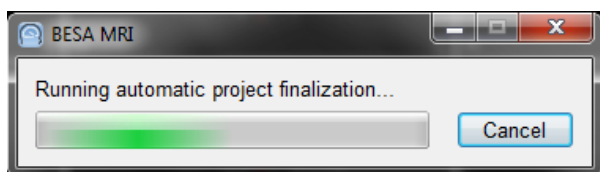


Since the correction and segmentation worksteps take about 20-30 minutes per MRI data set, it is recommended to use Automatic Finalization and inspect the results before deciding whether parameter adjustment is needed.

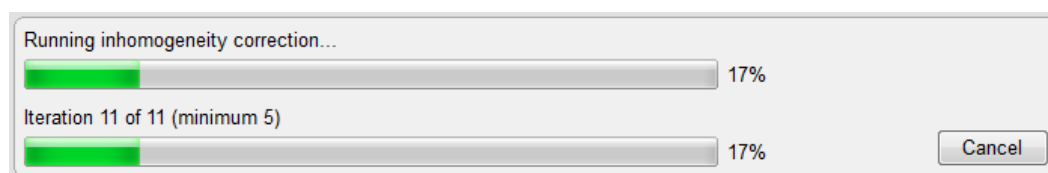
If the default segmentation results are inadequate, you may return to the segmentation worksteps using the Workflow Window or by pressing the **Previous** button. Then, modify the required segmentation parameter(s) and continue the segmentation step by step.

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 algorithm enhanced by incorporating anatomical template masks. For more details on the AFCM algorithm (Adaptive Fuzzy C-Means) see (Pham).

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). 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.

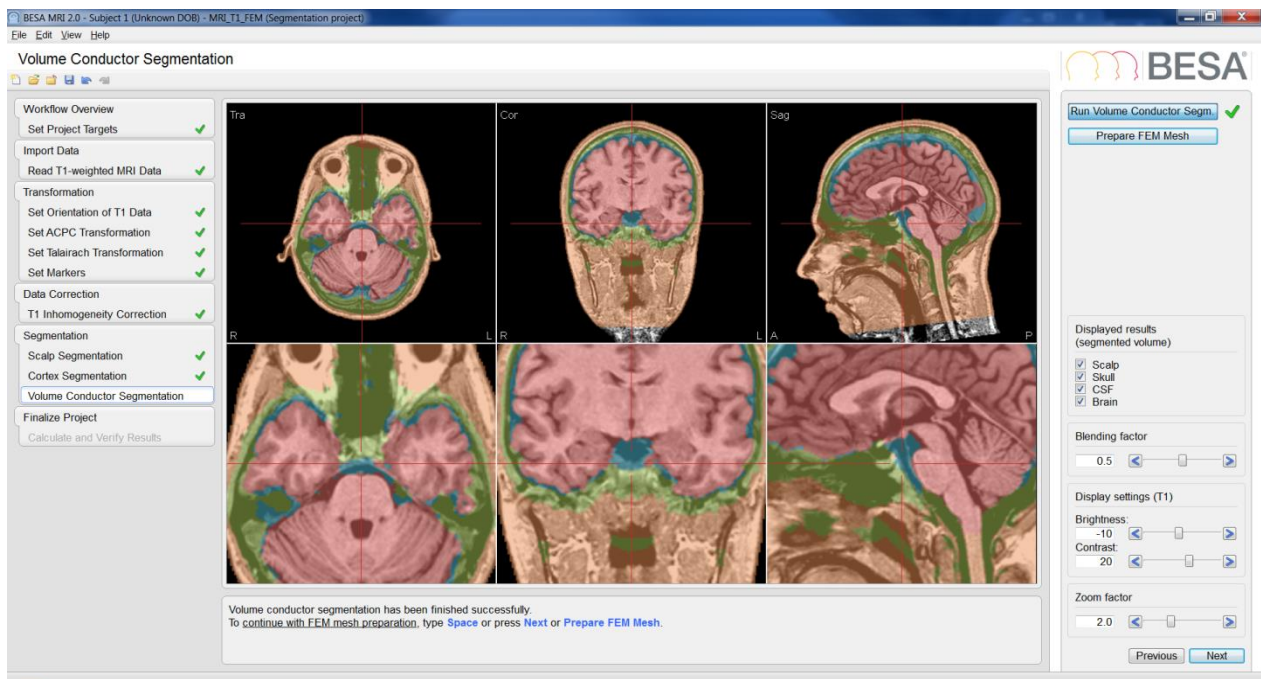
Currently, cortical surface reconstruction and inflation are done by fully automated procedures not requiring the user to define specific parameters.

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: <http://besa.de/contact/support/form.php>, 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) 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.

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.

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) **Head symbol buttons** in the **Set main window display** section at the lower right of the Interaction Window. The FEM 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.

Also, standard electrodes can be 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. Please note that in case a FEM model was created that is to be used in BESA Research or for exporting, the option **Generate FEM EEG Leadfield** or **Generate FEM 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.

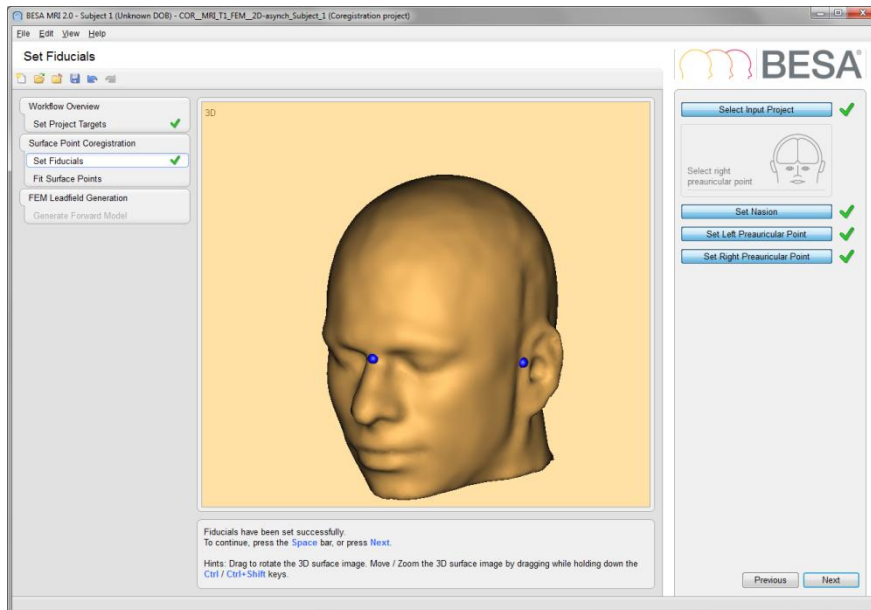
To confirm the position, hit **Space** or press **Next** or **Set Left Preauricular Point**.

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.

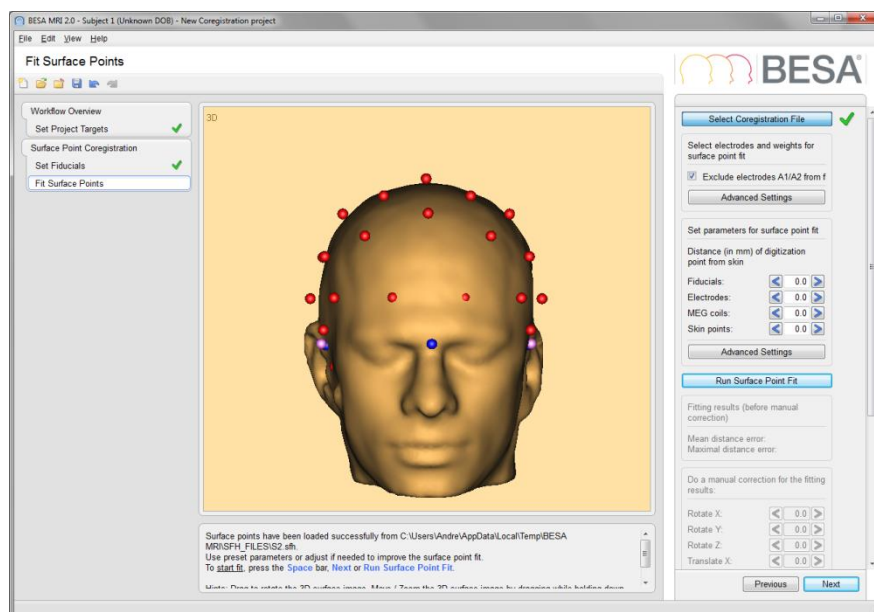
6.2.2.3. Fit Surface Points

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).

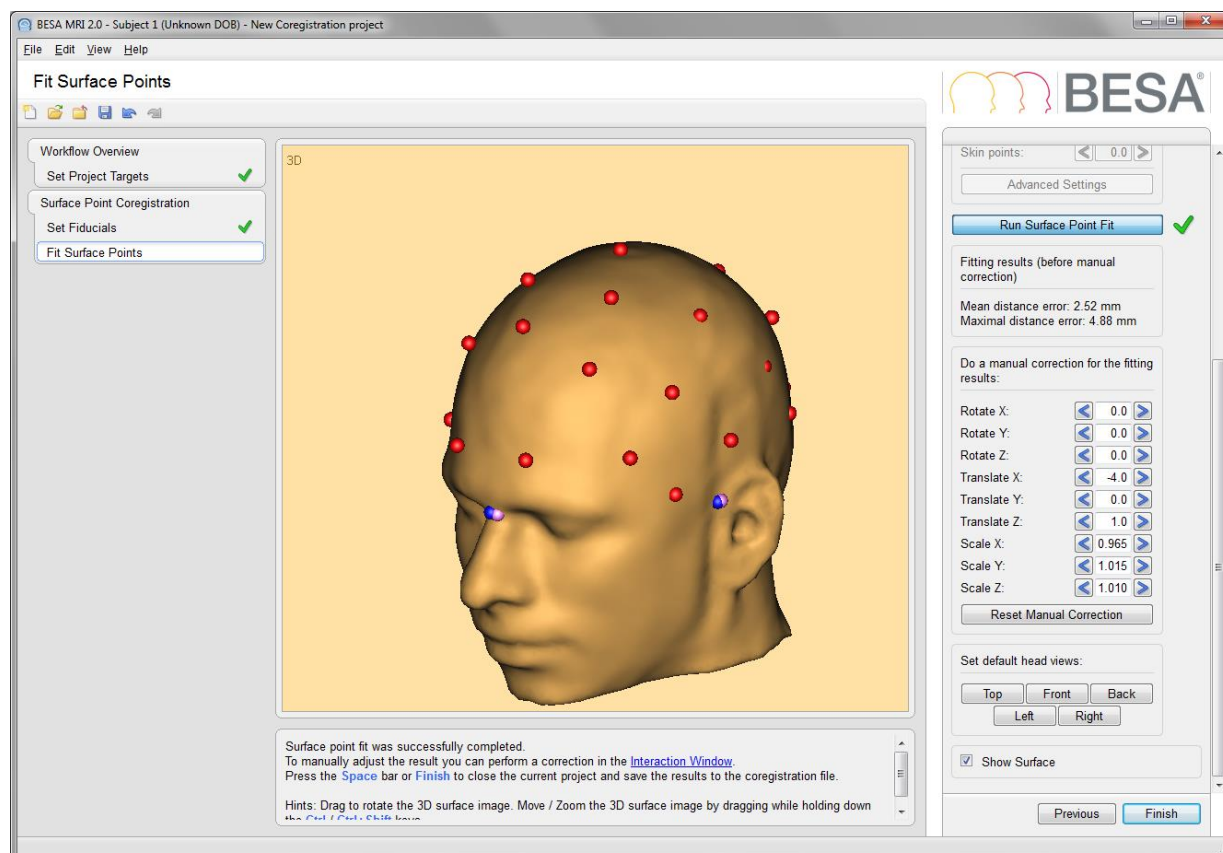
The **Open File** box comes up. Select the appropriate coregistration file (*.sfh) and open.

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 & surface points optimally to the MRI surface. For this fitting process, **only electrodes and surface points higher than A1/A2 ($z \geq -10$ mm in the head coordinate system)) are used** while a variable elastic bound is attached to the fiducials to preserve their closeness.

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



fitting process uses default parameter settings. 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.

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.

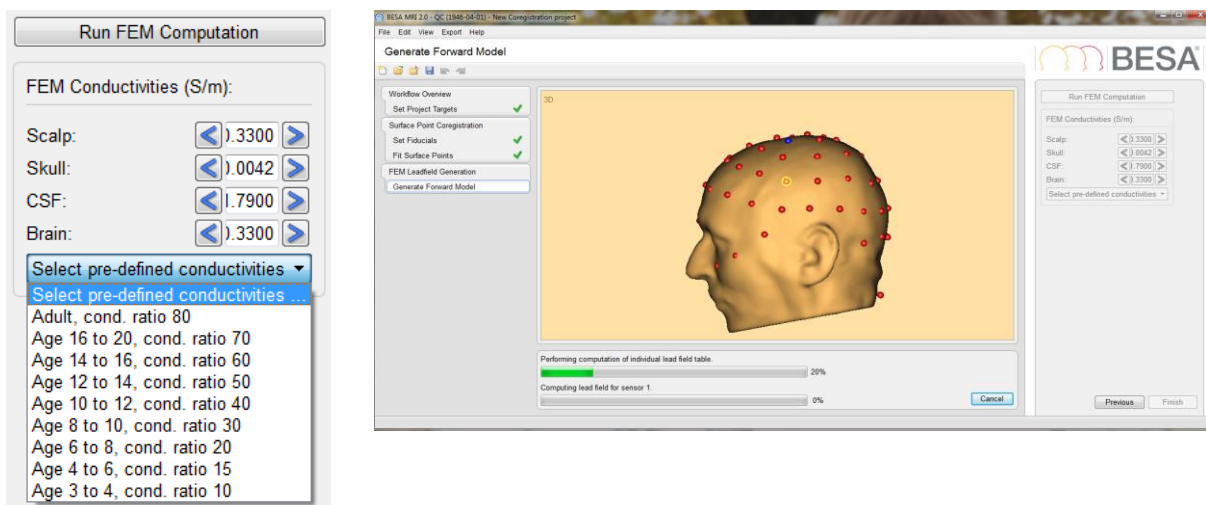
Alternatively, alas less directly, one can also tune the automatic surface point by unpressing the button **Run Surface Point Fit** and changing the parameters in **Advanced Settings**. This can be done either in the upper section of the Interaction Window (e.g. to change weights of fiducials vs. electrodes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

6.2.2.4. Generate Forward Model

If the option **Generate FEM EEG Leadfields** or **Generate FEM 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**) or to manually adjust conductivity settings for Scalp, Skull, CSF, and brain.



Please note that this step can take a while to compute, depending on the number of electrodes / sensors in the channel layout. The electrode / sensor, for which the leadfield is currently computed is highlighted in orange. 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:

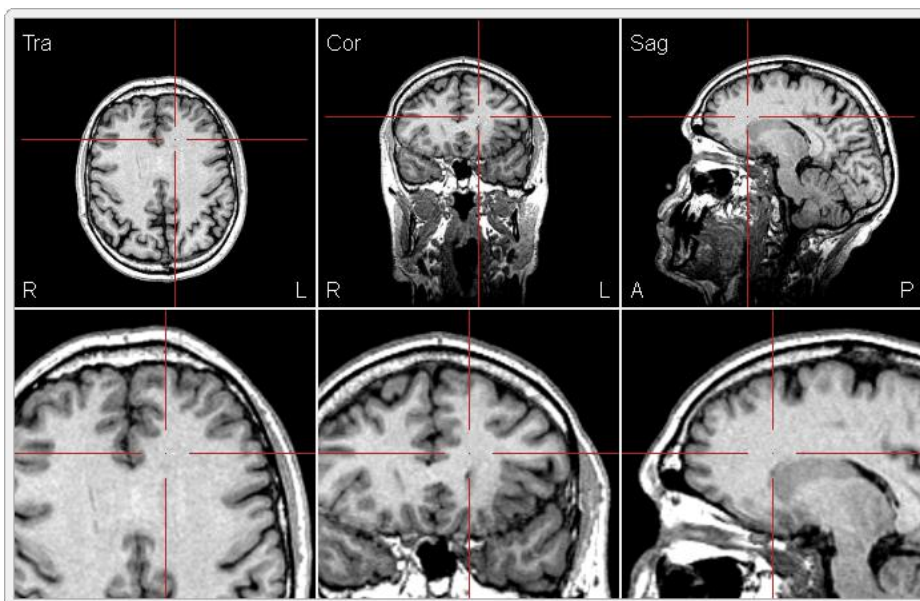
1. The loaded coregistration file will be modified, i.e. the current coordinate transformations and MRI output file information are added to the end of the file when saving the project. When refitting with modified parameters, and saving, it is modified again.

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.

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:

	No 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:

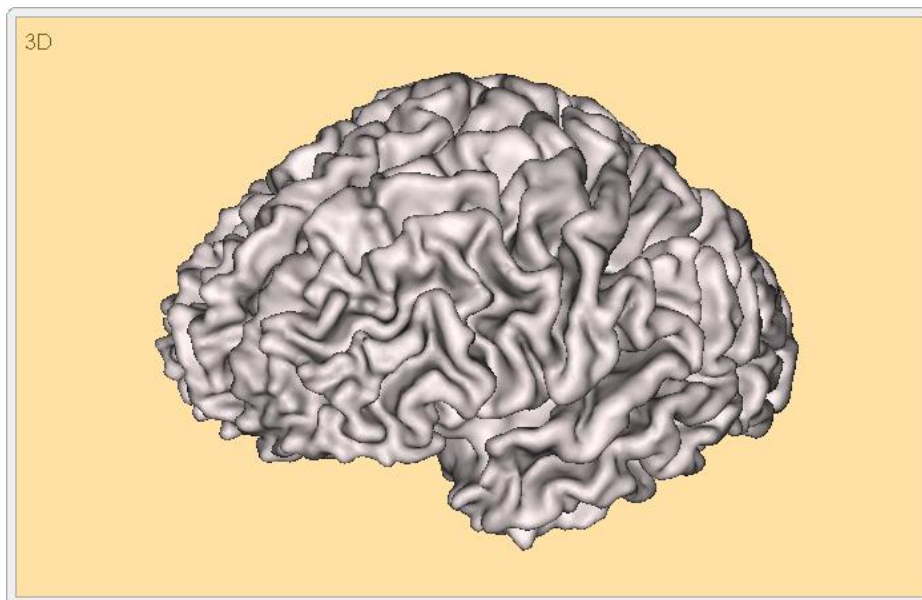


Set marker.

Select or move marker under cursor.

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:



Rotate 3D image or set marker.

Move 3D image.



Zoom 3D image.

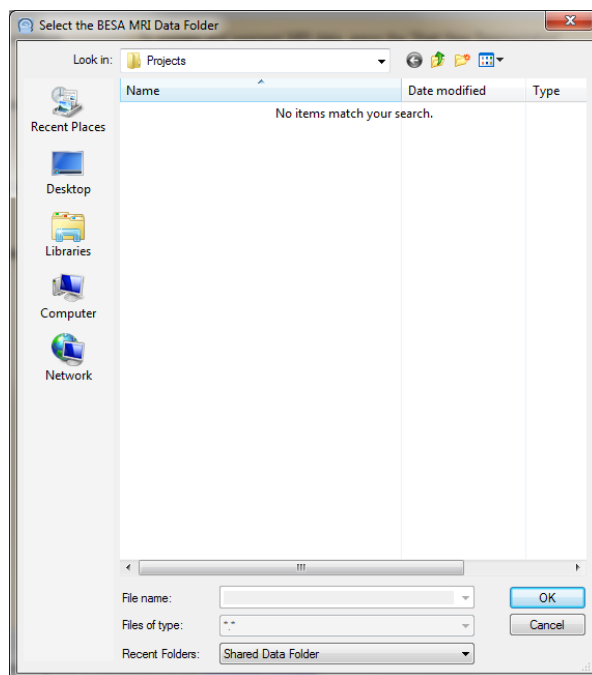
Select or move marker under cursor.

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):



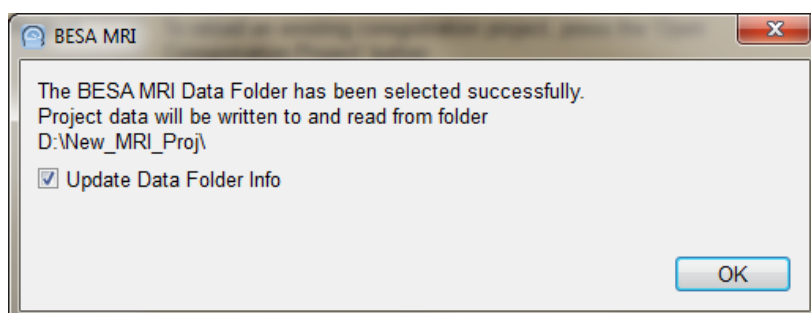
Select a folder in this dialog and press **OK** to set this folder as the current BESA MRI Data Folder.

The **Recent Folders** selection box at the bottom of the dialog can be used to reselect one of the BESA MRI Data folders used previously.

By using the **Shared Data Folder** entry, the default BESA MRI Data Folder can be selected (see chapter 7.1).

Note: To create a new folder, select drive and path, press the create folder button (), then select the folder, and press **OK**.

After selecting a new BESA MRI Data Folder, the following confirmation dialog appears:



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

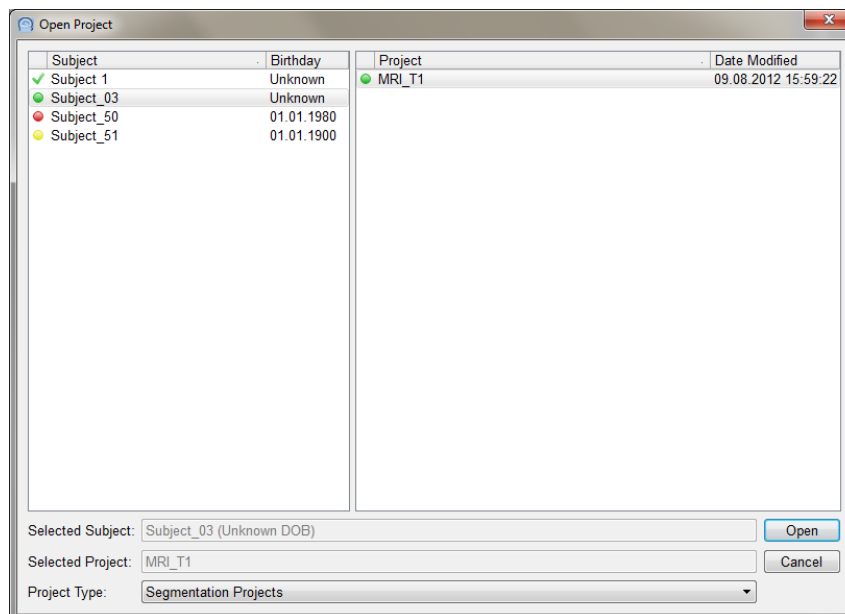
It is recommended to leave the tick mark on to update all existing projects in the new BESA MRI Data folder, if you switch between folders (see chapter 7.1).

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:



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

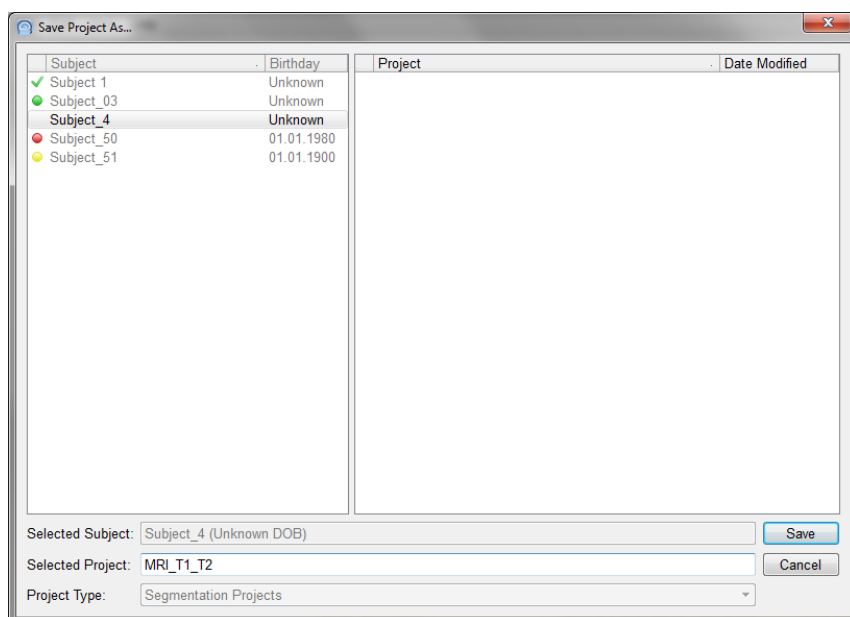
6.4.3.1. Finish a project

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.

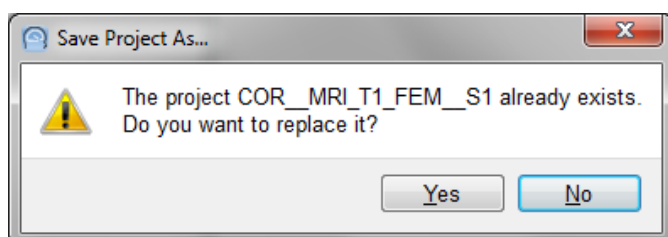
The selected subject and proposed project names are highlighted automatically. To save under a different project name, enter a new project name in the **Selected Project** edit field.

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.

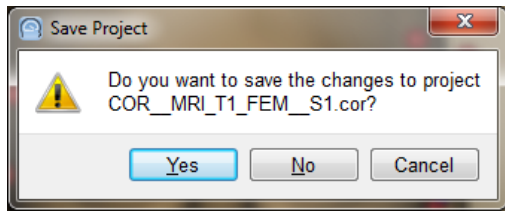
This workstep is complete when the Select Projects page comes up again offering to select another project or exit the BESA MRI program.

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

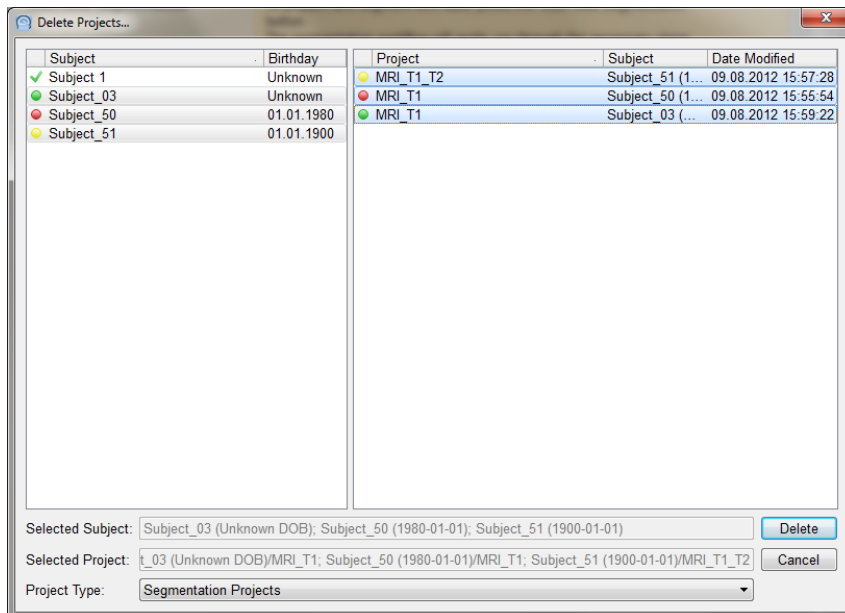
At any time during the workflow, data can be saved by selecting the menu item **File → Save** or typing **Ctrl+S**. However, previously stored data will be overwritten automatically.

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.

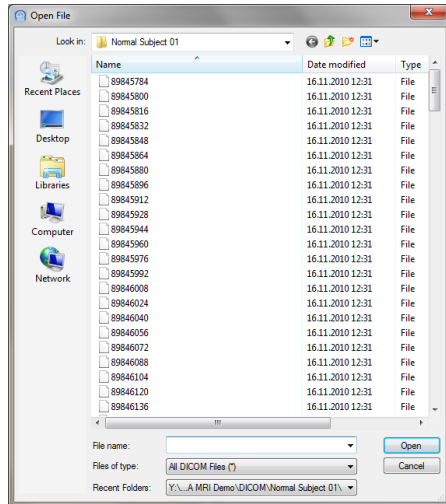
Mark all subjects for whom project data shall be deleted in the **Subjects** selection box. Then select the projects to be deleted in the **Projects** selection box (multiple subjects or projects can be selected by holding the **Ctrl** or **Shift** key while selecting).

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. 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**.

Use the **Recent Folders** selection box at the bottom to open a folder previously used for input to speed up navigation.

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 3.2.4), 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 7: **C:\Users\Public\Public Documents\BESA MRI\Projects**
- Windows Vista: **C:\Users\Public\Public Documents\BESA MRI\Projects**
- Windows XP: **C:\Documents and Settings\All Users\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 (see chapter 3.2.4).

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.

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The CE marking certifies that the BESA product as shown here fulfills
the basic requirements of the Medical Devices Directive MDD 93/42/EEC.

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