



## **BESA MRI**

User Manual





# **BESA<sup>®</sup>**

## **MRI 1.0**

# **User Manual**

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# Table of Contents

<b>Table of Contents .....</b>	<b>2</b>
<b>Notes.....</b>	<b>4</b>
<b>Symbols.....</b>	<b>4</b>
<b>1. Indications for Use .....</b>	<b>5</b>
<b>2. Introduction.....</b>	<b>5</b>
2.1. Features of BESA MRI .....	7
2.2. Product Classification.....	8
2.3. Certification .....	8
2.4. System Requirements.....	8
2.5. Application Environment .....	9
2.6. Disposal Information .....	9
<b>3. Installation and Initial Setup.....</b>	<b>11</b>
3.1. Installation .....	11
3.2. Initial setup .....	11
3.2.1. Connect the BESA Dongle .....	11
3.2.2. Start the Program .....	13
3.2.3. Specify the BESA MRI Data Folder.....	13
<b>4. The Workflow Concept.....</b>	<b>15</b>
<b>5. Elements of the BESA MRI Screen .....</b>	<b>17</b>
5.1. Workflow Window.....	18
5.2. Main Window.....	18
5.3. Interaction Window.....	18
5.4. Information Window .....	19
5.5. Menu Bar.....	19
5.5.1. File Menu.....	19
5.5.2. Edit Menu .....	20
5.5.3. View Menu.....	20
5.5.4. Help Menu .....	20
5.6. Title Bar .....	20
5.7. Toolbar .....	21
5.8. Caption .....	21

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<b>6.</b>	<b>How to use BESA MRI .....</b>	<b>23</b>
6.1.	Starting BESA MRI .....	23
6.1.1.	Welcome Screen .....	23
6.1.2.	The Select Project Page .....	24
6.2.	The Workflows of BESA MRI .....	25
6.2.1.	The Segmentation Workflow .....	25
6.2.2.	The Coregistration Workflow .....	30
6.3.	User Interaction in Main Window .....	34
6.3.1.	How to use the Slice Displays .....	34
6.3.2.	Setting Markers in Slice Displays .....	35
6.3.3.	How to use 3D Surface Displays .....	35
6.4.	Important Dialogs .....	36
6.4.1.	Select the BESA MRI Data Folder .....	36
6.4.2.	Open Projects .....	37
6.4.3.	Finish, Save and Close Projects .....	37
6.4.4.	Delete Projects .....	40
6.4.5.	Select Files .....	41
<b>7.</b>	<b>Appendix .....</b>	<b>43</b>
7.1.	The BESA MRI Data Folder .....	43
7.2.	The BESA MRI Data Folder Information File .....	43
7.3.	Subject-based Data Management .....	44

## 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 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.

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## 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. Indications for Use

BESA MRI is a software-only product compatible with personal computers running under a Windows operating system or an emulator thereof. The software is intended to help users visualize and analyze electrical activity of the human brain by fusing a variety of previously acquired, adult or pediatric ( $\geq 10$  years of age), electroencephalographic (EEG) and/or magnetoencephalographic (MEG) data with Magnetic Resonance (MRI) and/or Computed Tomography (CT) images. The intended user is a qualified neuroscientist who will exercise professional judgement in using the information.

The segmentation component of BESA MRI imports digital MRI data, segments and labels different brain tissues, transforms the MRI data into ACPC- and Talairach spaces, and renders the scalp and cortical surfaces.

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.

The device does not provide any diagnostic conclusion about the subject's condition.

It is not allowed to use the BESA MRI software directly or indirectly for medical diagnosis and/or treatment of humans. MEGIS is not liable for the use of the software beyond the intended research purpose.

The BESA MRI software is licensed for research use only.







## 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 reader
- Easy definition of ACPC- and Talairach points and other markers
- Automated inhomogeneity correction and reconstruction of individual scalp and cortical surfaces
- 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 standard electrodes (10-20 or 10-10 system) to the individual scalp
- Output of coregistration and MRI files for source analysis programs, e.g. BESA Research

The integrated segmentation workflow guides quickly 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 guides quickly 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 0). All results are stored in subject-related subfolders. Several segmentation and coregistration projects can be managed for each subject.

## 2.2. Product Classification

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.

According to safety classifications in **DIN/EN IEC 62304:2006**, BESA MRI is a **Class A** product (class A: no injury or damage to health is possible).

The product is noninvasive since it is stand-alone software and does not control any equipment physically connected to the patient. 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 patient, for example, during the recording of data, can therefore be excluded.

According to **DIN EN IEC 60601-1:2005**, BESA MRI does not affect the possibility of using the computer within the patient environment. BESA MRI does not interfere with other programs or hardware connected to the computer (third-party equipment)

According to **UMDNS/DIMDI**, BESA MRI is classified with the following codes:

UMDNS code: 16-307

GMDN code: CT112 (Software, application program)

## 2.3. Certification



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

The number 1275 represents the identification number of the Notified Body that carried out testing and certification.

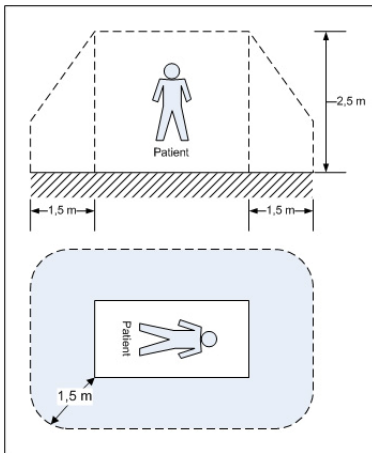
## 2.4. System Requirements

- Operating system: Windows® 7  
Windows® Vista  
Windows® XP Service Pack 2
- CPU: Minimum 2 GHz
- RAM: Minimum 2 GB
- Display resolution: Minimum 1280x800 pixels
- Graphics card: OpenGL 1.1 with 16 MB RAM or more

## 2.5. Application Environment

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 3<sup>rd</sup> Edition) e.g. by an isolating transformer fixed at the PC, or mobile isolating devices for Notebooks.

The patient environment is defined as follows:



## 2.6. Disposal Information

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



## 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 3<sup>rd</sup> Edition) e.g. by an isolating transformer fixed at the PC, or mobile isolating devices for Notebooks.



### 3.1. Installation

1. Start Windows and insert the installation disk into the CD-ROM drive.
2. If the PC permits auto start from the CD drive, the installation starts automatically after a short time. If the PC does not permit auto start, please run **Setup.exe** from the CD. The file is located in the **Setup** folder.
3. Please follow the on-screen instructions.
4. Once the installation is complete, proceed with the initial setup as explained in the following chapter.

### 3.2. Initial setup

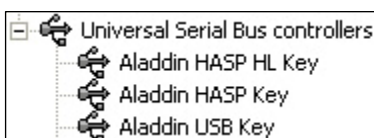
This section explains the steps to be done for an initial setup of BESA MRI.

#### 3.2.1. Connect the BESA Dongle

BESA MRI is protected by a licensing scheme developed by Aladdin Knowledge Systems. 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.

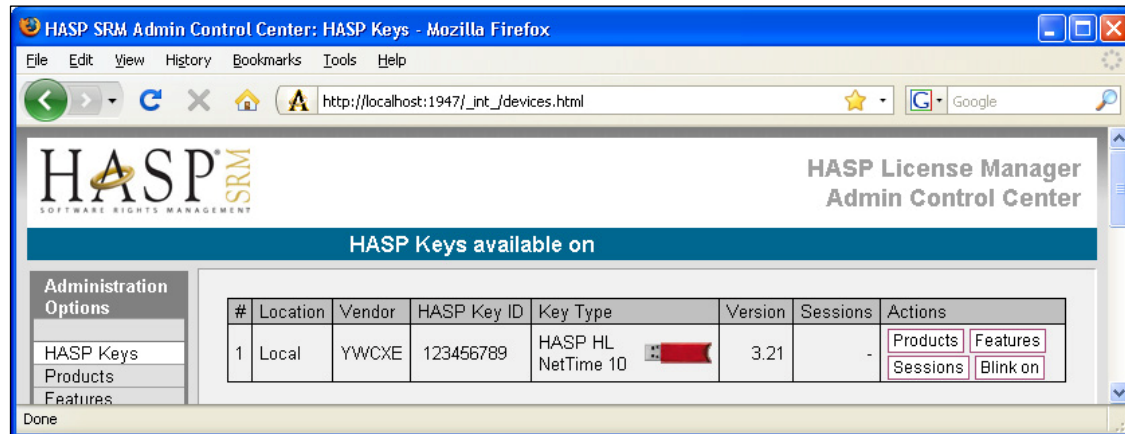
If the dongle is installed correctly, the Windows Device Manager reports three items in the “Universal Serial Bus controllers” section: Aladdin HASP HL Key, Aladdin HASP Key and Aladdin USB Key.



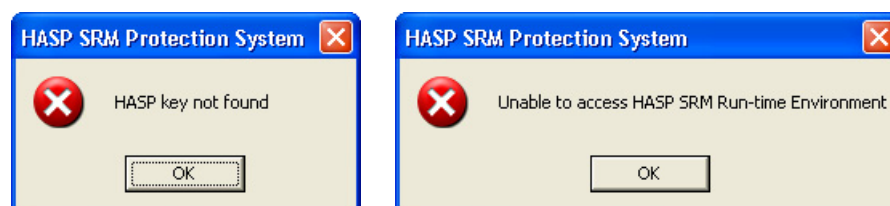
The Aladdin HASP key installer includes the HASP License Manager application:

**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**)

### 3.2.2. Start the Program

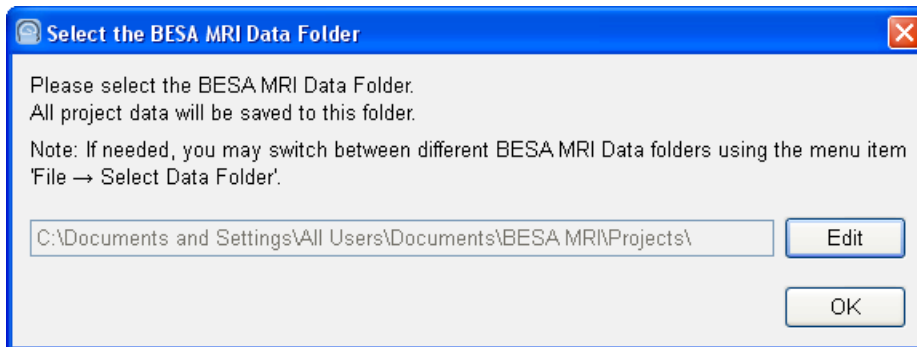


Start BESA MRI using the shortcut created on the desktop or run **BESA MRI.exe** from the **All Programs → BESA → MRI 1.0** folder in Startup menu. First, the Welcome Screen appears (cf. 6.1.1). Press **Accept** to start BESA MRI.

### 3.2.3. Specify the BESA MRI Data Folder

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

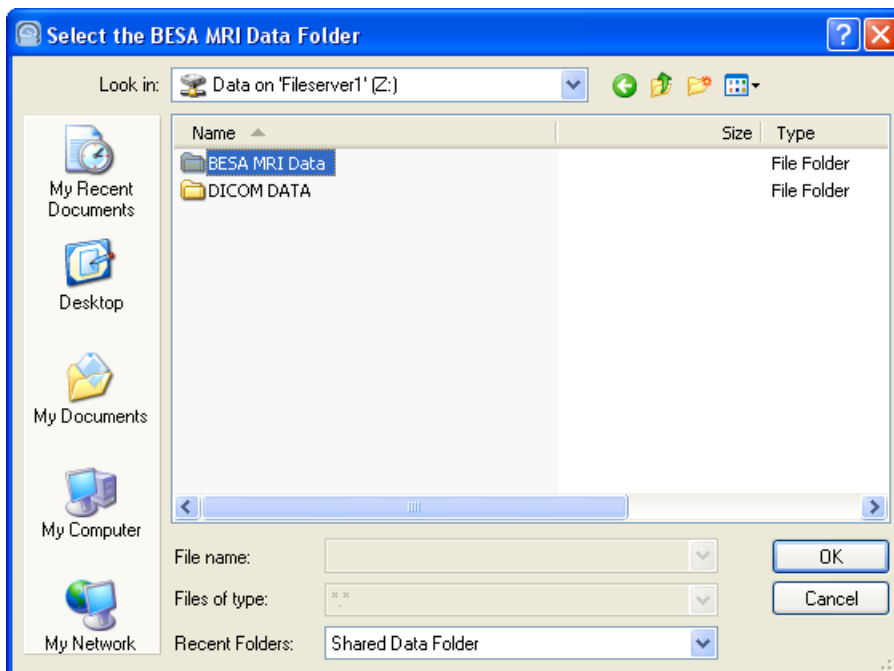
When starting the program for the first time, the following dialog box appears:



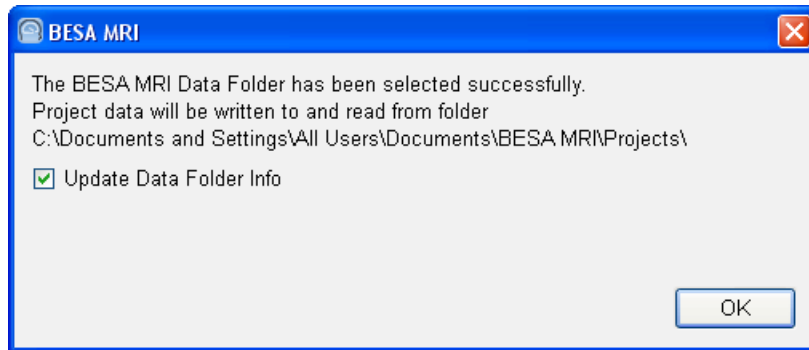
The BESA MRI Data Folder is preselected to All Users on the local PC (shown above for Windows XP). However, it is recommended to create the BESA MRI Data Folder on your server where it is accessible to all users from anywhere in the local network. For more details, see chapters 6.4.1 and 7.1.

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 the server **Z:\** as below:



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



Press the **OK** button.

BESA MRI is now configured to start projects.

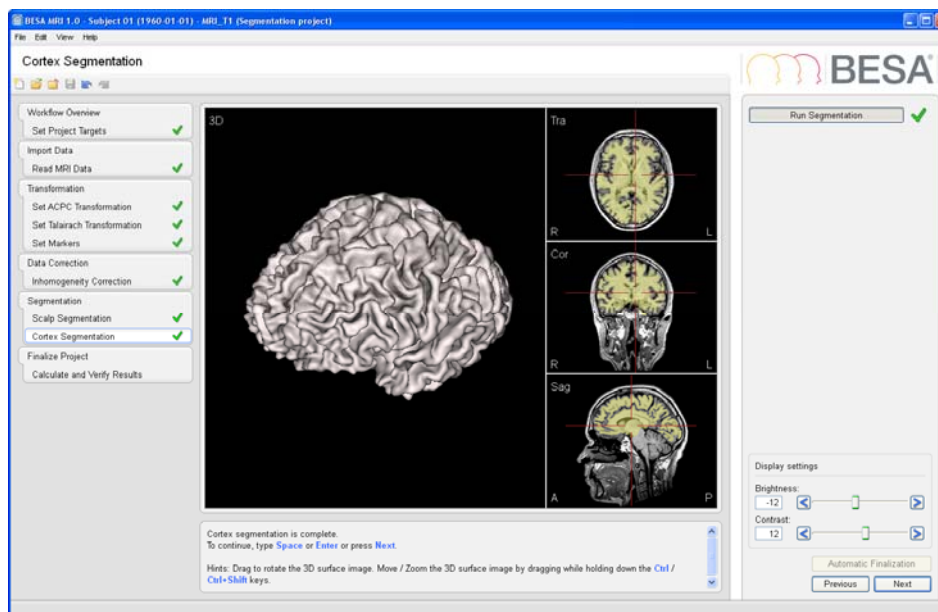
**Notes:**

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 (cf. 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.

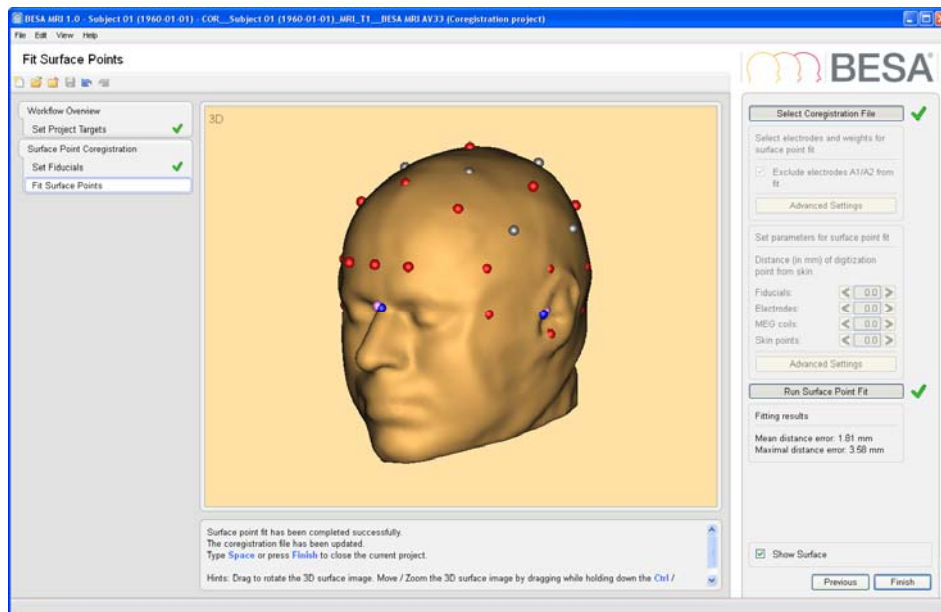
A workflow consists of a series of worksteps that have to be done to finalize a project. Each workstep realizes a set of user interactions needed to achieve the workstep-specific result. Some worksteps can be run in automated processing mode with preset parameters, e.g. inhomogeneity correction and segmentation.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

When pressing the **Next** button or **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 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 (cf. 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 (cf. 5.2). The **Information Window** below (cf. 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 (cf. 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 **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.



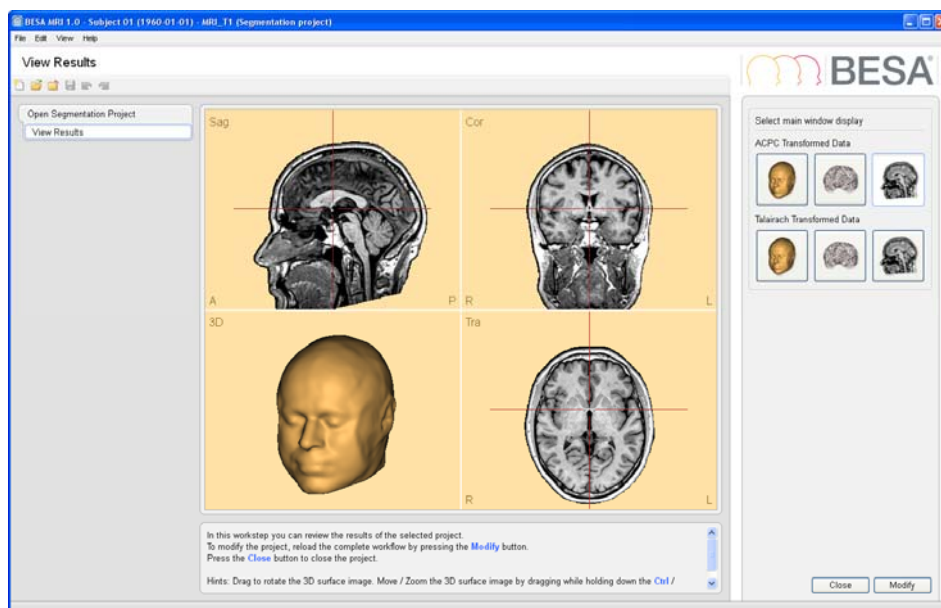
BESA MRI offers two different workflows associated with the following projects:

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

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

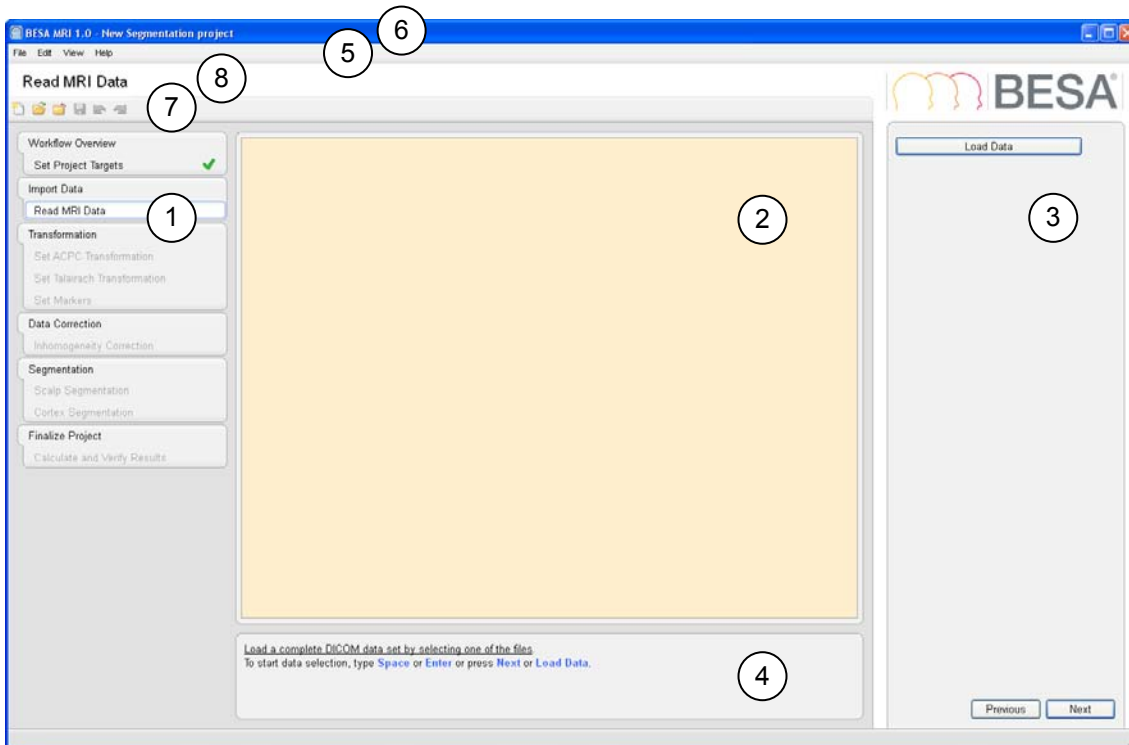
Stored projects can be viewed by selecting the menu item **File → Open Project**, using the open button in the toolbar, or pressing the **Open Segmentation / Coregistration Project** buttons on the start screen. After opening a stored completed project, the final workflow result is displayed in a special viewer workflow (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 cf. 6.2). Steps already completed are marked with a green OK sign. ✓

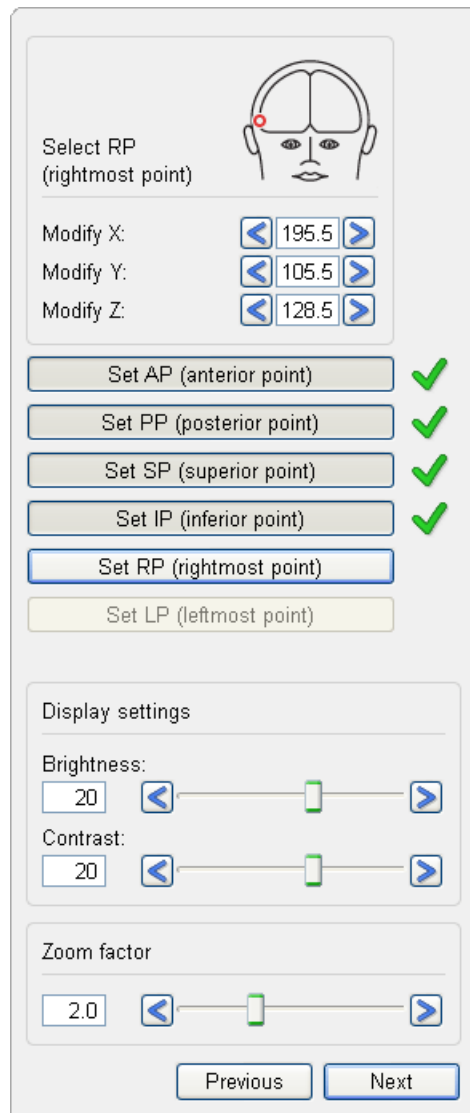
The current workstep is highlighted. This step is also shown in the caption.

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), and Set LP (leftmost point). Green checkmarks are shown to the right of the first four buttons.
- 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 typing **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 (cf. 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 typing **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 (cf. 0). 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 (cf. 6.4.2).
<a href="#">Close Project</a>	Close currently active project. Show the Select Project Page (cf. 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 (cf. 6.4.3).
<a href="#">Delete Projects...</a>	Select one or multiple projects that shall be deleted (cf. 6.4.4).
<a href="#">Select Data Folder</a>	Select the folder to be used as BESA MRI Data Folder (cf. 7.1).
<a href="#">Update Data Folder Info</a>	Update the information file in the BESA MRI Data Folder (cf. 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 is 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 (cf. 5.1).
<b>Show Information Window</b>	By selecting or deselecting this menu item the Information Window is displayed or hidden (cf. 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. 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

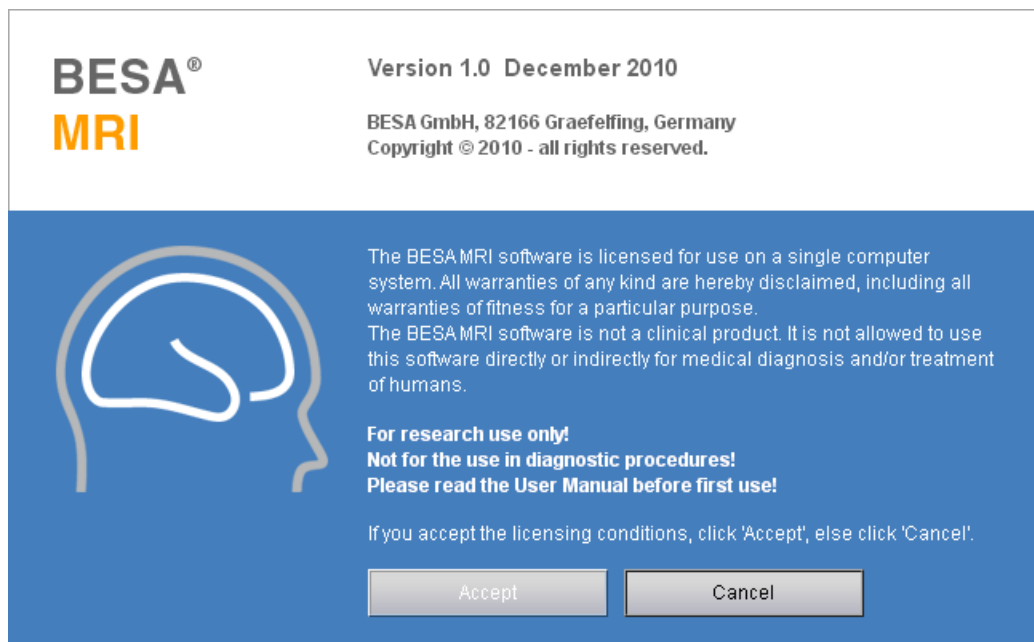
Before working with BESA MRI, please read chapter 4 on the workflow concept. Consult chapter 5 on the elements of the BESA MRI screen while starting to use the program.

### 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.

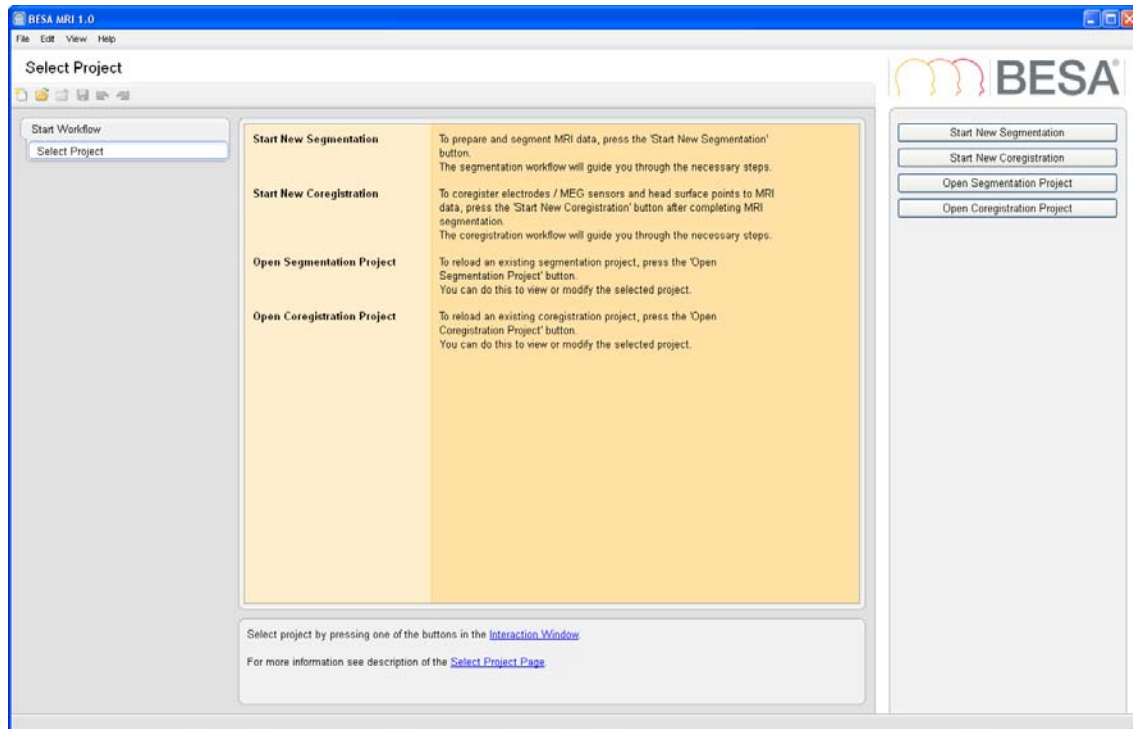
When starting BESA MRI, a welcome screen appears. It provides some information on the BESA MRI program including the current version number and date:



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 (cf. 6.2.1).

Press **Start New Coregistration** to create a new coregistration project. The Coregistration Workflow opens (cf. 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 (cf. 4).

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

The Segmentation Workflow realizes the preparation and correction of individual MRI data, the segmentation of the different head tissues for finite element modeling (FEM), and the rendering of scalp and cortical surfaces. 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, black tick marks relate to optional worksteps.

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

#### 6.2.1.2. Read MRI Data

In this workstep, the MRI data is imported. 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 MRI data is 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.



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

**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 to reload the project data later independently of the original DICOM data.

#### 6.2.1.3. 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 cf. 6.3.1). You may also adjust the crosshair in half millimeter steps using the interaction elements in the Interaction Window on the right.

Type **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.

Type **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.

Type **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.

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

#### 6.2.1.4. 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.

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

#### 6.2.1.5. 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. Type **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 typing **Space** or pressing **Next** to continue. For more details on setting or modifying markers cf. 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 on the next page, the Set Markers workstep is illustrated at its end before confirming the Cutting Plane.

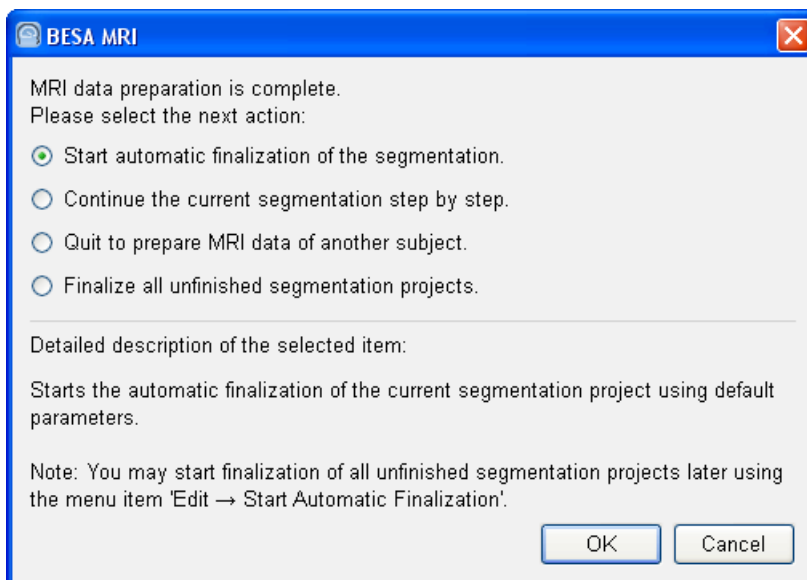


### 6.2.1.6. Automatic Finalization

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 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:

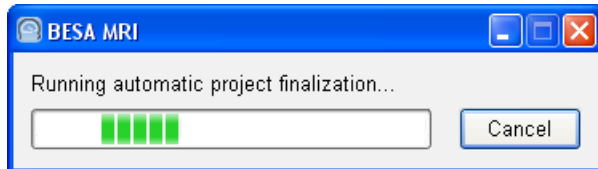


Since the correction and segmentation worksteps take about 20-30 minutes per MRI data set, it is recommended to use Automatic Finalization and inspect the results before deciding whether parameter adjustment is needed.

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 **Automatic Finalization** button at the lower right of the Interaction window, by pressing the **F9** key, or by selecting the menu item **Edit → Finalize Current Project** (or All Segmentation Projects).

#### 6.2.1.7. 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, D. & Prince, J. (1999), 'An Adaptive Fuzzy Segmentation Algorithm for Three-Dimensional Magnetic Resonance Images', *Information Processing in Medical Imaging*, 140–153.

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.

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

#### 6.2.1.8. 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, T. & Vese, L. (2001), 'Active contours without edges', *Image Processing, IEEE Transactions on* 10(2), 266–277. 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.

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 type **Space** to recalculate this segmentation workstep.

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

#### 6.2.1.9. Cortex Segmentation

In this automated workstep the cortical surface is reconstructed in several steps. First, a voxel-based classification of the white matter is performed. Then, using the level set algorithm again, 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.

Currently, cortical surface reconstruction is done by a fully automated procedure not requiring the user to define specific parameters.

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

**Note:** Cortex segmentation was tested and optimized for a large number of data sets acquired on current MRI systems. We appreciate your feedback to [mri-support@besa.de](mailto:mri-support@besa.de), if you are not getting sufficient results with older MRI data sets.

#### 6.2.1.10. 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.

Type **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. 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 or Talairach **Head symbol buttons** in the **Set main window display** section at the lower right of the Interaction Window. 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.

Type **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 (cf. 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, black tick marks relate to optional worksteps.

Type **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, type **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, type **Space** or press **Next** or **Set Nasion**.

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, type **Space** or press **Next** or **Set Left Preauricular Point**.

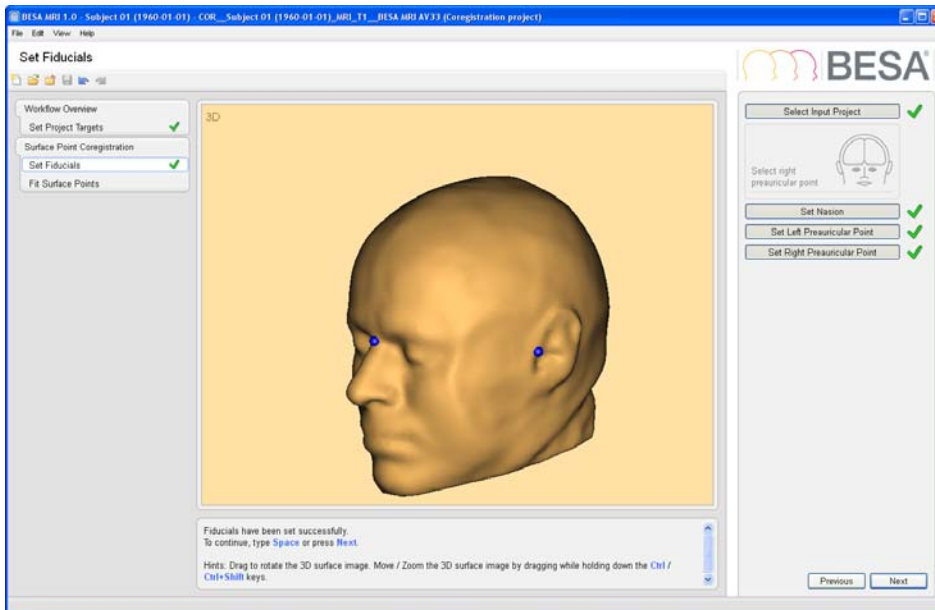
The head now turns to show the right side for marking the next fiducial. Click onto the surface to mark the right preauricular point. You may adjust by dragging the marker with the mouse.

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

Rotate the head to reinspect the positions of the 3 markers (cf. 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:



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

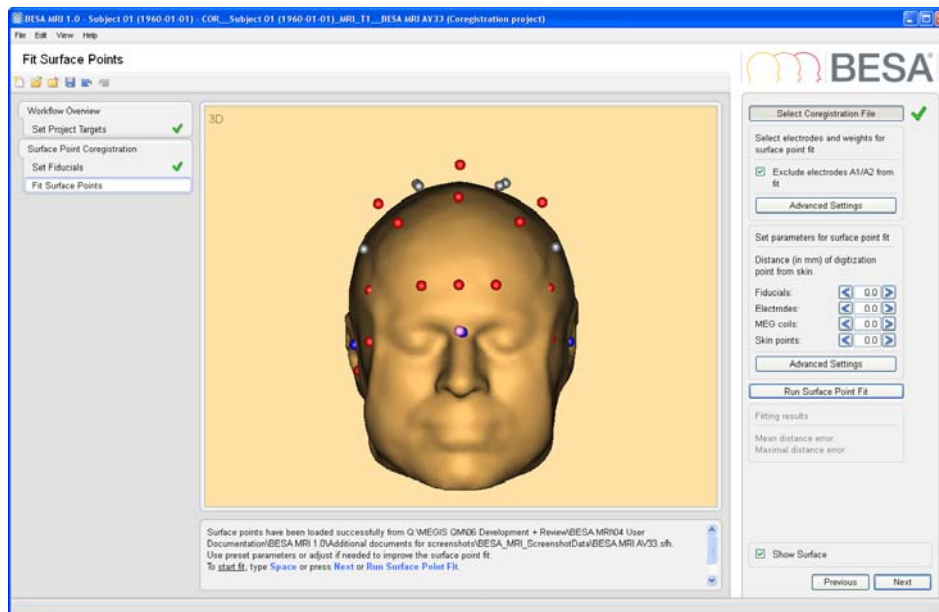
### 6.2.2.3. Fit Surface Points

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.

Type **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.

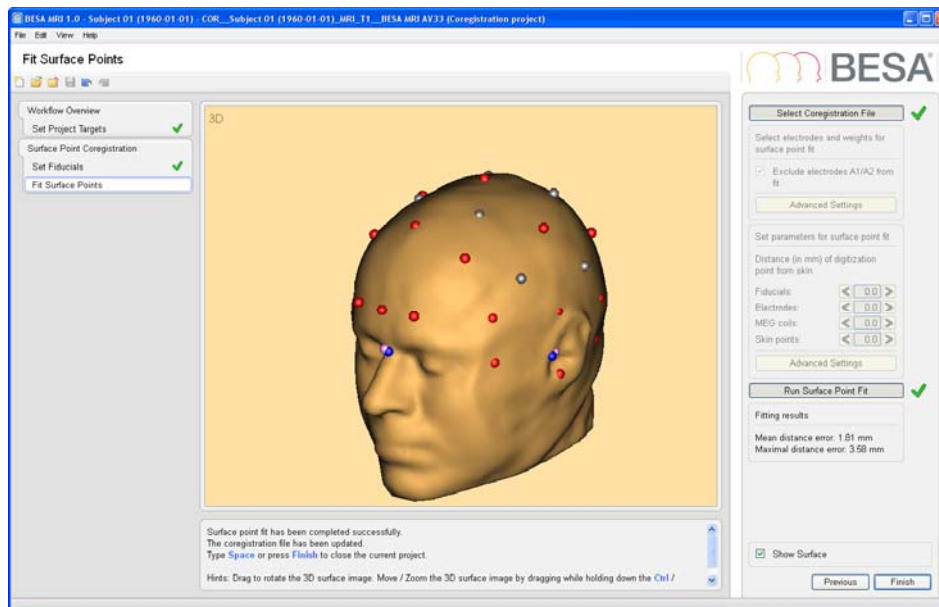
After loading the .sfh file, an initial coordinate transformation is calculated to match and align the three fiducials marked on the MRI scalp surface with the fiducial positions stored in the .sfh file. The loaded surface positions are displayed using this transformation:



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, type **Space** or press **Next** or **Run Surface Point Fit**.

This 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 coregistration is adequate, type **Space** or press **Finish** to complete the coregistration workflow. Follow the dialogs to save all data of the coregistration project (cf. 6.4.3).

If not adequate, unpress the button **Run Surface Point Fit** and change the parameters by pressing **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.

**Notes:**

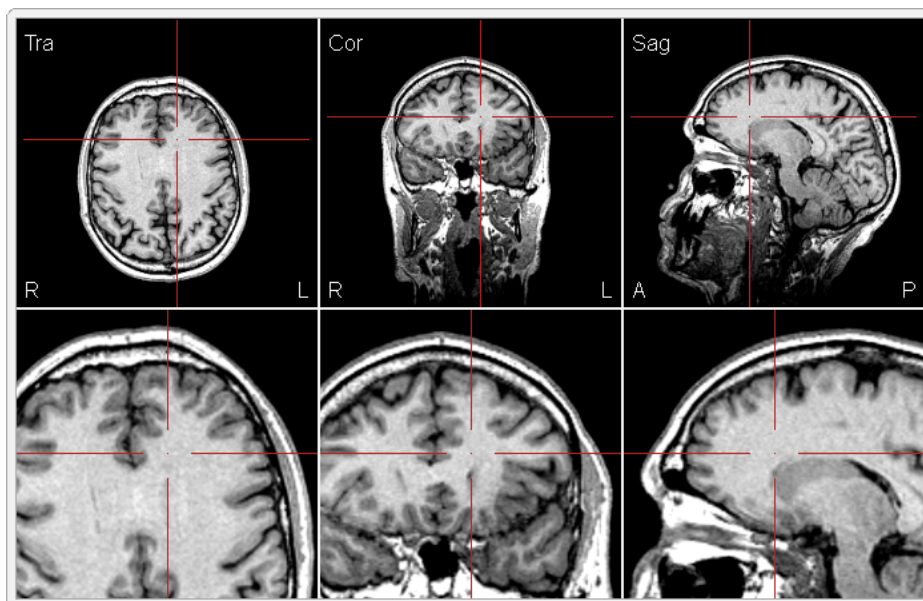
1. The loaded coregistration file will be modified automatically after fitting the surface points, i.e. the current coordinate transformations and MRI output file information are added at the end of the file. When refitting with modified parameters, it is modified again.
2. If you have several coregistration files of the same subject, e.g. from data sets with different digitization protocols, you may not want to finish the project but go back to the Set Fiducials workstep to load each coregistration file and fit the surface points. Thus, each file is modified to contain the complete coregistration information. When finishing the project, the last file information is stored together with the project data.

## 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.

Click to set slice center (anywhere in slice).

Click to move slice center (only up-down).

Click to move slice center (only right-left).



Rotate the slice (around fixed mid-position).

Move the slice.

Move the slice (only left-right).

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:

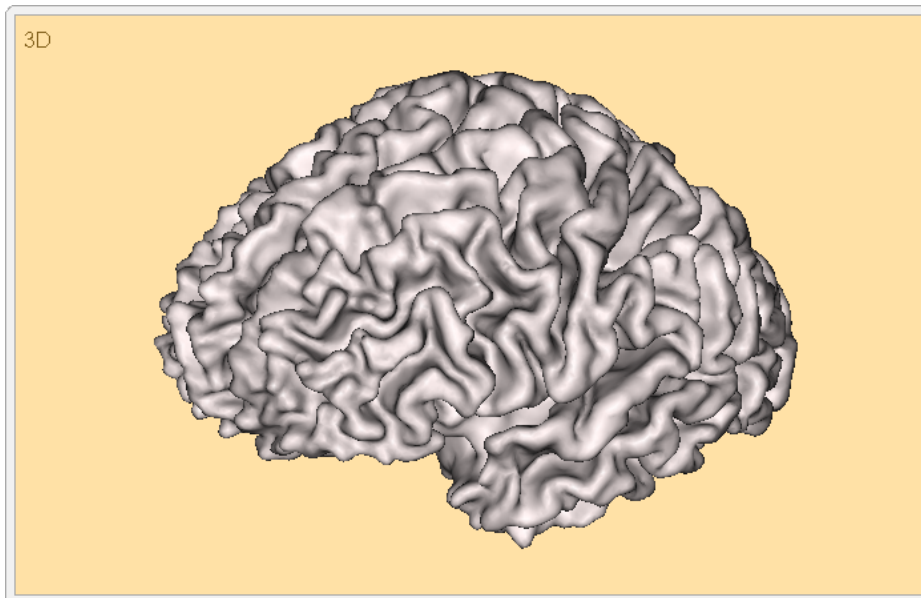


Set marker.

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.

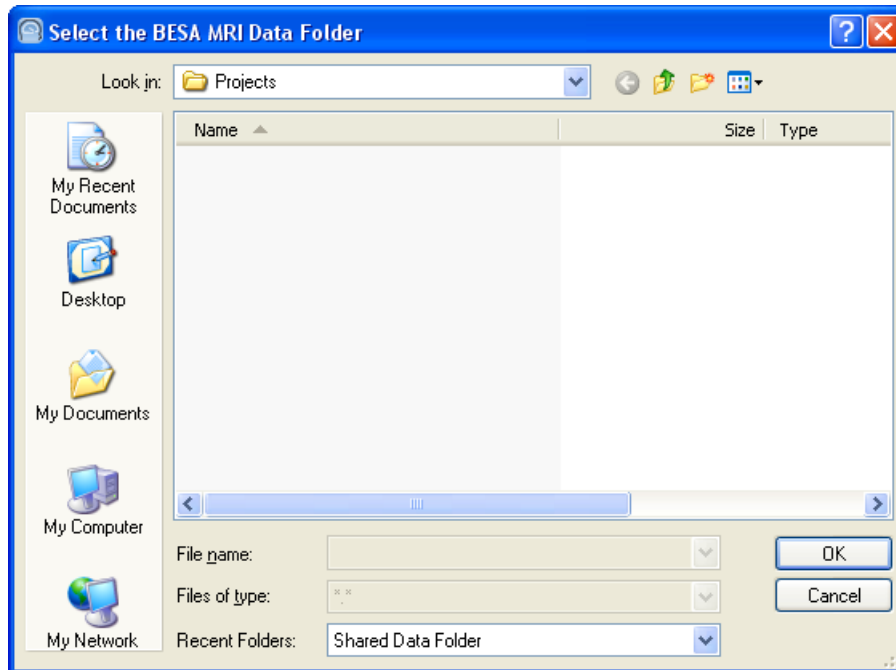
Select or move marker under cursor.

## 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 (cf. 7.1):



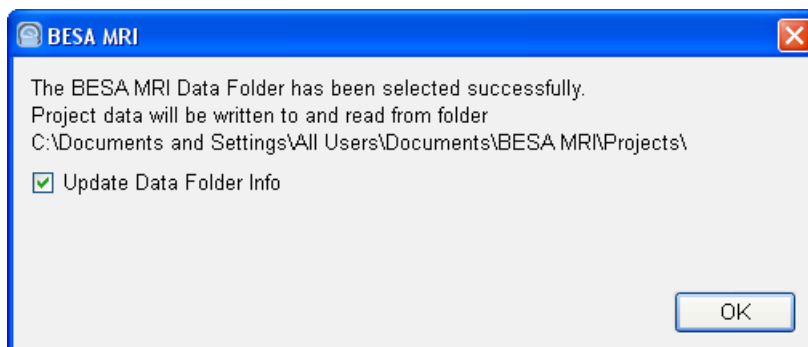
Select a folder in this dialog and press **OK** to set this folder as the current BESA MRI Data Folder.

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 (cf. 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.

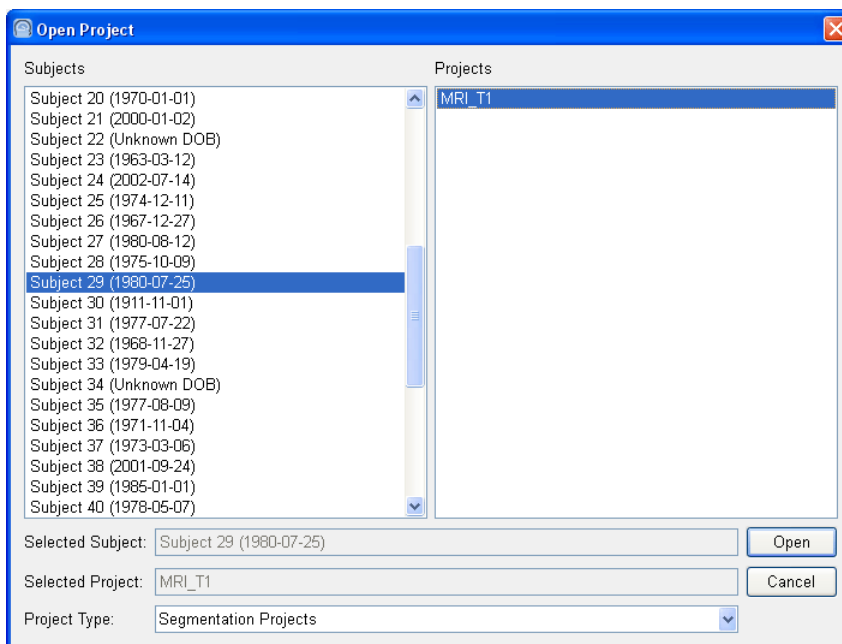
It is recommended to leave the tick mark on to update all existing projects in the new BESA MRI Data folder, if you switch between folders (cf. 7.1).

**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 (cf. 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

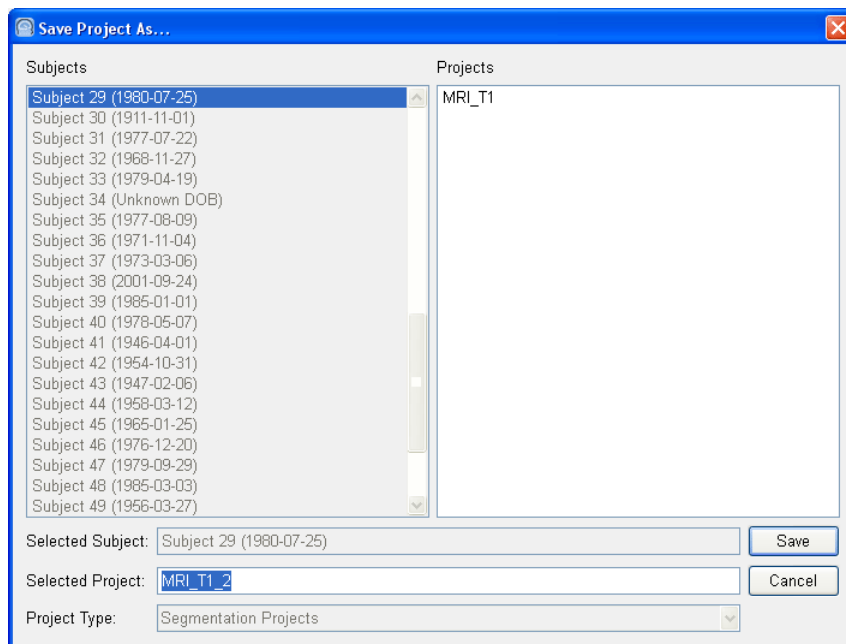
The last step in any workflow is finishing the project by typing **Space** or pressing **Finish**. This last action ensures that the project data with all result files are stored in the BESA MRI Data Folder.

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.

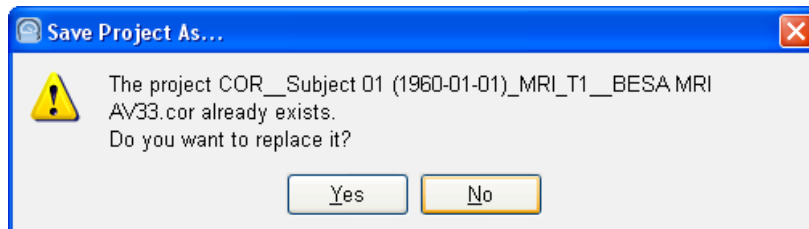
Press **Save** to store the project data including all volume and surface data sets.





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.

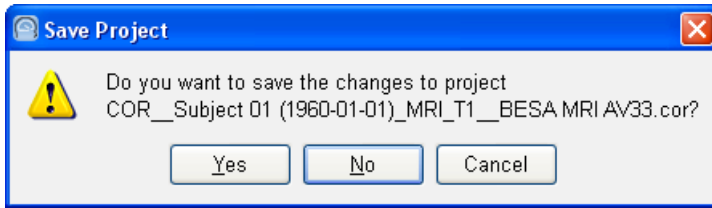
**Note:** You may get to the Save Project As... dialog box at any time during the workflow using the menu item **File → Save As**, e.g. if you want to store the current data preparation under a specific project name to be completed later by Automatic Finalization.

#### 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

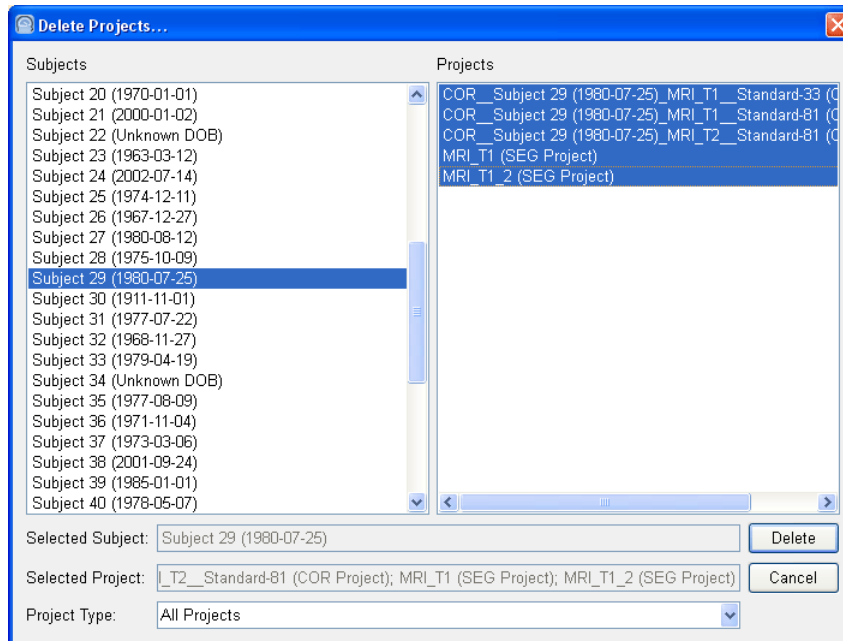
At any time during the workflow, data can be saved by selecting the menu item **File → Save** or typing **Ctrl+S**. However, previously stored data will be overwritten automatically.

##### 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.

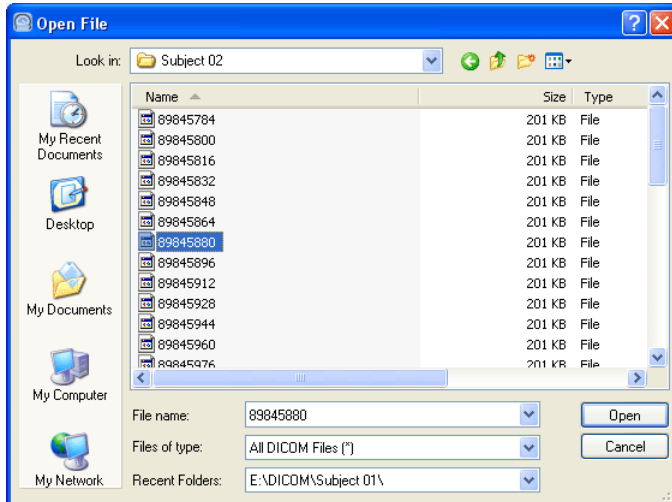
Mark all subjects for whom project data shall be deleted in the **Subjects** selection box. Then select the projects to be deleted in the **Projects** selection box (multiple subjects or projects can be selected by holding the **Ctrl** or **Shift** key while selecting).

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 (e.g. original MRI DICOM data for segmentation or a coregistration file), the following dialog appears:



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 (cf. 3.2.3), 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 (cf 3.2.3).

**Note:** If you have a multi-license installation, make sure that two user 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 (cf. 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 (cf. 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 (cf. 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 this product fulfills the basic requirements of the Medical Devices Directive MDD 93/42/EEC. The number 1275 represents the identification number of the Notified Body which carried out testing and certification.

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