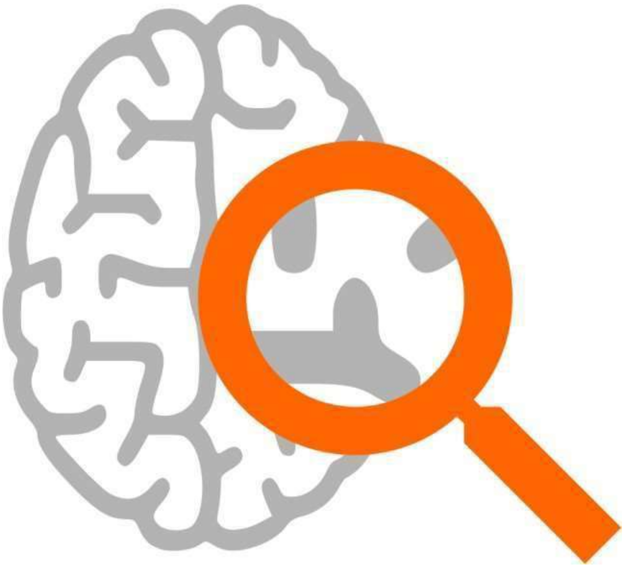
User Manual



Multi-modal Imaging for Neurological Diagnostics

Medical Imaging Visualization Software

DISCLAIMER: This software product was developed at ‘Stichting Kempenhaeghe’ as part of the “Advancing Smart Optical Imaging and Sensing for Health" (ASTONISH) project that has received funding from ECSEL Joint Undertaking (grant no 692470).

DISCLAIMER: Please note that the results obtained by using MIND do not in any way constitute medical advice and Clinical Neuro-Science projects cannot be held liable for any consequences (including any damages) resulting from a misinterpretation of the results by the user.

I. Preliminaries

Installation

The software is written in C++. The software was developed using state-of-the-art code libraries for analysis and visualization using stable releases, which are possible to be updated when bugfixes or improvements become available. The following opensource libraries or tools were used for MIND: Visualization Toolkit (VTK) and Insight Toolkit (ITK) by Kitware, NiftyReg by Center for Medical Imaging Computing, and Robust Brain Extraction (ROBEX) available on NITRC.

The software can be installed by using provided installers. The pre-compiled packages include all dependencies and have been prepared for:

Windows 7* or higher	64-bit	MIND_install_win64.exe

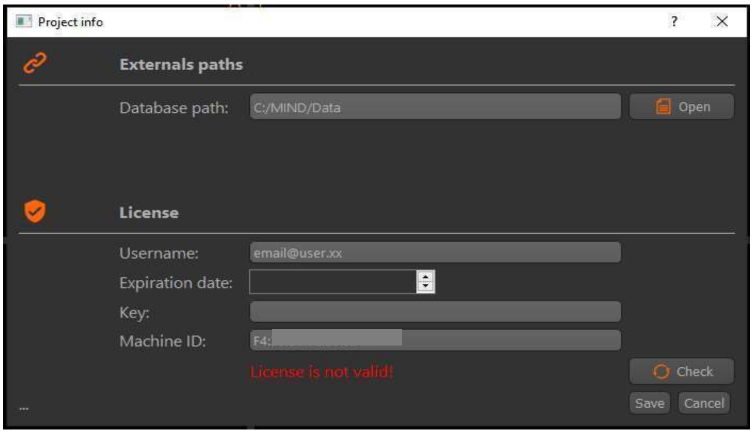
*Microsoft C++ Redistributable 2019.

The best equipment for visualisation of the medical imaging datasets by MIND is listed here:

- Operating System: Windows 7 or higher, 64bit
- CPU: any modern Multi-Core CPU (like Intel i5 or i7 processors)
- Memory RAM: 8 GB or more
- Graphics Card: dedicated video card with memory 256MB or more
- Hard Drive: any modern choice will do (SSD improves performance processing large data sets)
- Monitor: 1600×1200 or more (full HD 1920 x 1080 is recommended)
- Wheel mouse

License

Before the software can be used, it has to be configured correctly in terms of user information and license. When the software is started for the first time, a settings window will appear for providing a valid license in order to be used. After providing the license username, expiration date and key, click the **Check** button to verify the license information. After successful verification, the software can be used.



Database path: C:/MIND/Data

Username: email@user.xx

Expiration date:

Key:

Machine ID: F4:[redacted]

License is not valid!

When the license is about to expire within 30 days, a warning will be displayed during start- up. For obtaining a (new) license, please contact: info@cnsprojects.nl.

Intended use and conceptual Design

MIND is developed for bringing together brain images in the same co-ordinate system, for exploration (browsing) of these data and for visualization in support of minimally invasive treatment of neurological disorders. No prerequisite knowledge of the internal workings of the software or medical data pre-processing is required. The software provides neuroscientists also with a perfect tool to visualize in a multi-modal fashion brain images acquired as result of their studies using distinct imaging modalities. Therefore, the intended users are clinical staff (neurologists, neurophysiologists, neurosurgeons) of worldwide hospitals and mental health institutes and staff of research academies, centres specialized in neurological (epilepsy) research and treatment and neuroscience institutes or departments.

The conceptual design of the application distinguishes three different domains of the software, each designed to be used by a different user group: Data Preparation, Exploration and Visualization, see Figure 1.

Figure 1 - Conceptual design of the application.

Data Preparation

At the preparation step the required data is collected, pre-processed and included in a project file together with the patient info. Pre-processing steps include: co-registration, brain extraction and verification of the data. The result of the pre-processing steps can be saved in the project file of the patient.

Data Exploration

During the exploration step, the clinician can browse through the medical imaging datasets and inspect the images. Moreover, more advanced visualization of externally processeddatasets can be created, such as evolvement in time of source mapping results in 4D, in a given voxel or in a specified Region of Interest (ROI). Next, the clinician is able to select the 3D-images that are essential in the pre-operative decision-making process.

Data Visualization

In the data visualization step, all previously selected images that are relevant to the planning of the surgery are imported. The user is able to add or remove multiple images together into a multi-modal visualization. Additionally, the user is able to export datasets as DICOM files or as objects for Virtual Reality applications.

Data I/O

This section describes the different types of data that can be imported and exported by the application. An overview of the data input and output is shown in Figure 2.

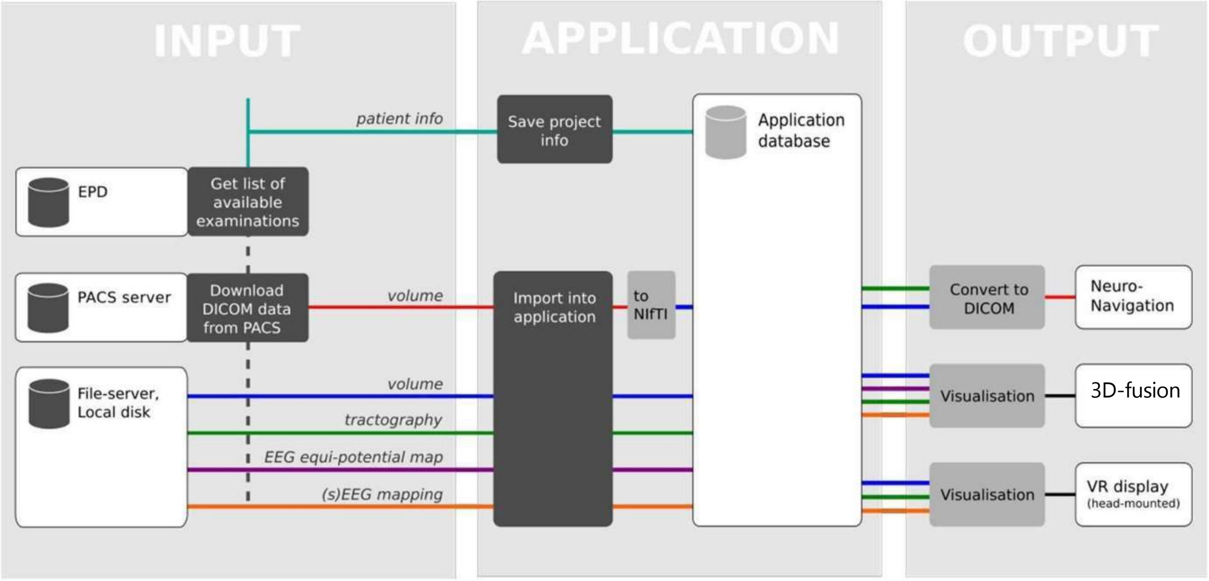


Figure 2 - Overview of data input and output

Data input

🟦 Patient information, such as patient name, date of birth and ID. This information is stored in the application database and used to save and access all imported datasets of the given patient.

🟥 Medical imaging datasets, such MRI, CT, PET, SPECT, EEG/MEG source maps, fNIRs maps in either

DICOM or NIfTI format

🟩 Tractography data, in .vtk format. The dataset should a series of lines describing the tracts. Additionally, the dataset may contain scalar values on each position.

🟪 EEG equipotential map, in text format. The dataset should contain EEG contacts labels and their matching values. When available, the position information of the electrodes is also used.

- SEEG source mapping of depth electrodes. Externally generated source mapping data can be imported and visualised on the detected electrodes. This requires the data to be saved in a .csv or .txt based text file, containing the intensities per depth electrode and contact point.

Application

When importing data, the application saves a copy of the dataset in the application data base. In the case of a DICOM series, the data is first converted into a NIfTI file before being copied to the database. Patient and project information is also saved in the database, together with the copied datasets.

Data output

- DICOM files for Neuro-navigation applications. Imported NIfTI volumes can be exported as DICOM files. This allows for data export to commercial neuro-navigation software used in the planning of epilepsy surgery.
- Multi-modal visualizations. The multi-modal visualizations in the 2D and 3D viewports created in the application can be exported as images (.png format).
- Objects for Virtual Reality applications. Models generated from the imported data can be exported for VR applications. This includes models of the patient's skull and cortex as well as tractography data and detected depth electrodes.

Database structure

All imported datasets and patient information are saved in the application database (Figure 3). Each project is saved as a folder, which contains all the patient's data. The folder is labelled based on the patient ID and date of birth.

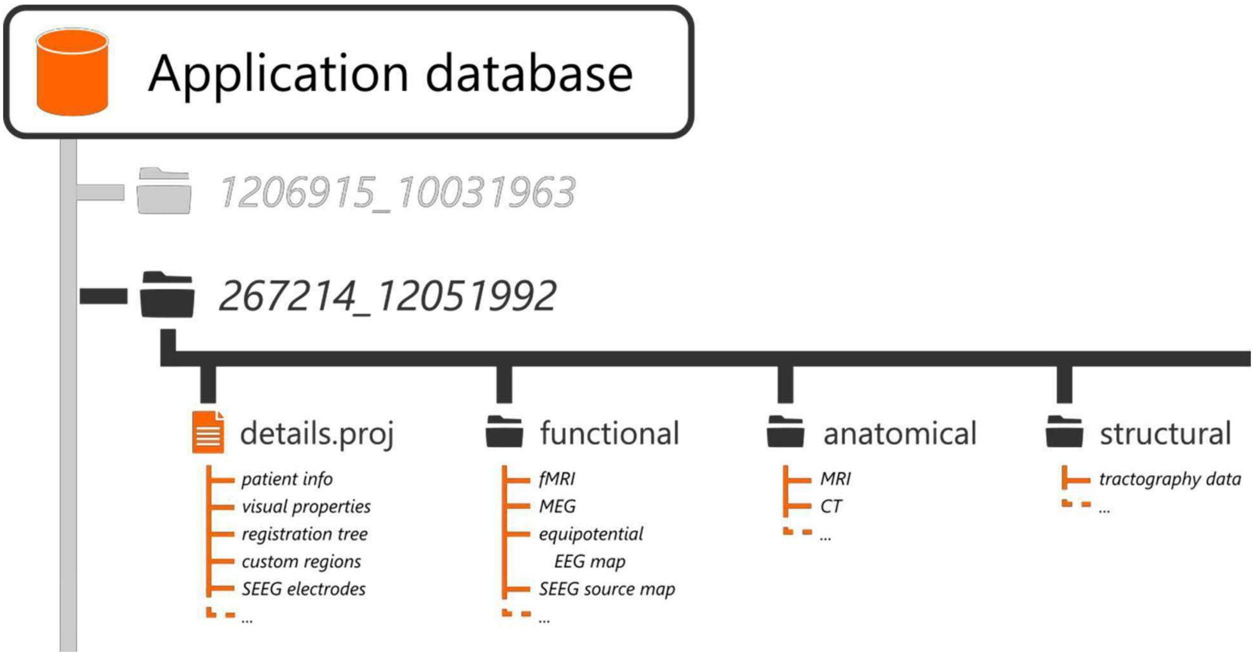


Figure 3 – Schematic overview of the application database structure.

Project file (details.proj)

The project file in each entry contains the patient information (name, ID, date of birth, etc.) as well as the project information (project ID and description). Furthermore, the project file contains a list of references to all the imported data, together with their visual settings and registration information. In the case of manually created regions or detected depth electrodes, the information of the datasets is saved in the project file itself.

Functional

This folder contains all the imported functional datasets, such as: 4D tomography volumes, EEG equipotential maps and SEEG source mapping data.

Anatomical

This folder contains all the imported anatomical datasets, such as: MRI or CT tomography volumes.

Structural

This folder contains all the imported structural datasets, such as tractography dataset

User interface

The main user interface of the application is shown in Figure 4. It consists of three 2D viewports and a 3D viewport that visualize the imported datasets. Each of the three 2D-viewports shows an anatomical plane slicing the datasets with a specific orientation, providing sagittal, coronal and axial views that are commonly used in medical visualization software. The 3D-viewport shows renderings of patient-specific models, e.g. the cortex, the skull or orthogonal slices of the volumes as shown in Figure 4.

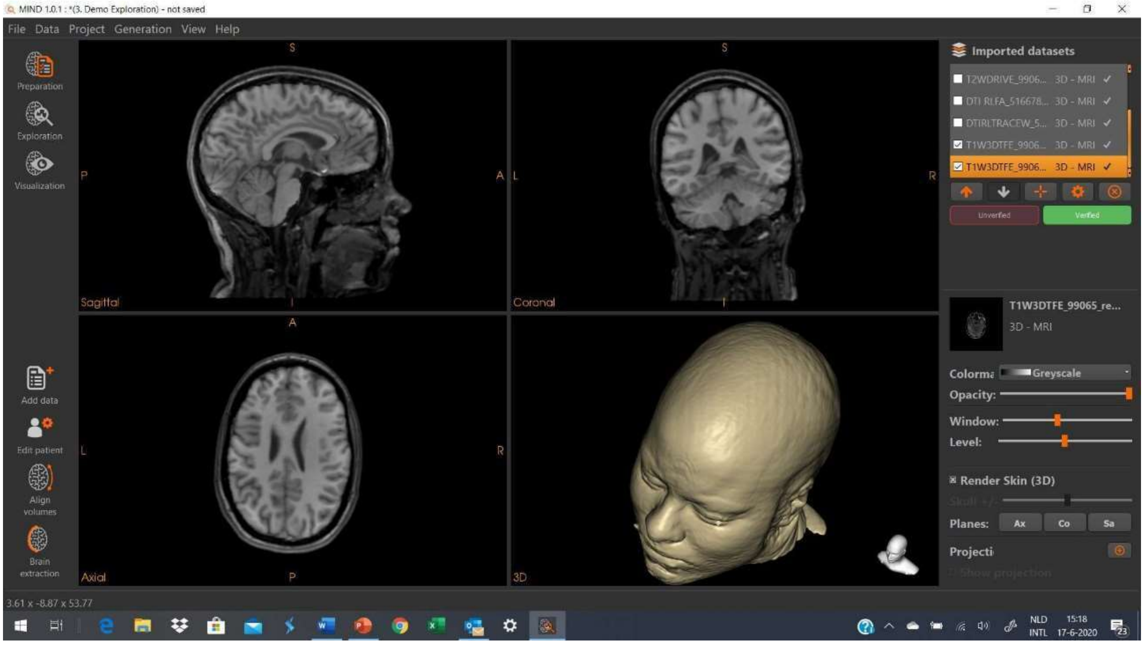
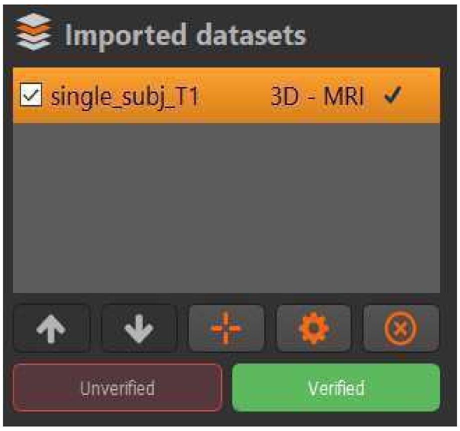


Figure 4 - Main user interface of the application, showing three 2D-viewports and a 3D-viewport and the supporting controls.

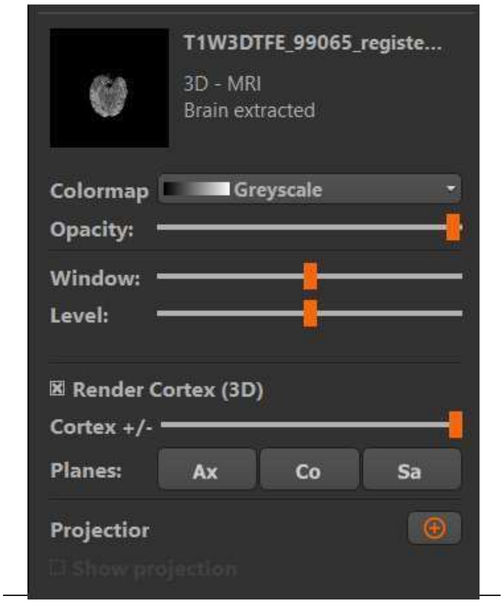
Data overview



☑ single_subj_T1 3D - MRI ✓

The panel in the top-right corner of the interface displays a list of selectable datasets that added or removed from the current visualization. The overview also displays the data type and status of each dataset. The buttons below the list can be used to re-order, focus, edit or remove the currently selected dataset. Reordering the datasets will reorder their visualizations in the viewports accordingly.

Visual settings



T1W3DTFE_99065_registe...
3D - MRI
Brain extracted

Colormap: Greyscale

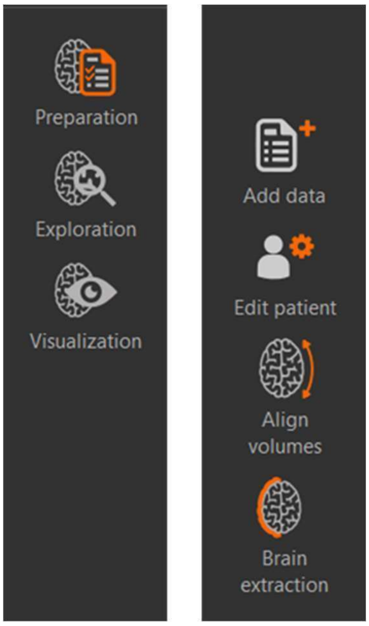
☒ Render Cortex (3D)

☐ Show projection

The panel in the bottom-right corner of the interface contains the visualization settings for the currently selected dataset. Specific settings are available for each type of dataset. For more details, see Appendix: Visualization details on page 42.

The status bar at the bottom of the interface is used to display current position in the 2D viewports, together with messages to the user.

Toolbar



The toolbar at the left of the interface includes controls for switching between the three user modes (preparation, exploration and visualization). It provides quick navigation to the most commonly used functionalities of the software. Depending on the currently active user mode, the toolbar will show different functionalities, as shown in the right column for the Preparation mode.

Instructions

This following chapters of this document are structured as separate sections describing specific tasks that can be performed with the software. The sections are listed under their corresponding user mode. Each task section contains a list of instructions for performing the specific task, together with a figure showing the most important elements in the user interface. The sections also contain additional information on the task and possible issues that can be encountered.

Test cases and data

It is recommended to prepare a test case that includes the most important tasks of the three different modes and can be run with the example data in the folder 'test_data' of the installation folder, containing at least the following datasets: an MRI, an DWI and a functional image (PET, SPECT, fMRI, an MEG/EEG source map etc.). Test cases are:

- Data Preparation	page 13
- Data Exploration	page 22
- Data Visualization	page 32

II. Data preparation

Project creation

1. Go to **Preparation mode.**

   This opens a project creation dialog.

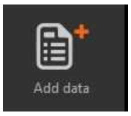
Data import

2. **Click** on the **Folder** import button**.**

   Select the folder to import files from.

   After specifying a folder, the software will scan the folder and show a list of importable data including previews of the visualizations.

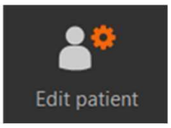
3. Import datasets by clicking at the Add data button in the left toolbar**.**



   a. When importing 3D NIfTI files, the user will be asked to specify what type of data is being imported. The options are: CT, MRI or Functional. Additionally, the user can also label the dataset as brain-extracted.

   b. When importing DICOM files, the user will be asked whether to use available patient information from the DICOM file.

4. Patient Info: Press **Edit.**
5. **Specify patient information.**



   a. The information cannot contain special characters (!@#$%^&*()_+-=`~).

   b. The following patient information is required to continue: patient name, ID and date of birth. The patient ID2 is not required.

6. Press **Ok.**
7. When all data has been imported, press **Ok** again.

   The software will now start importing all the selected data into the application and create an project file in the application database.

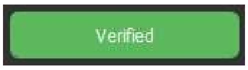
Labelling a dataset as verified

Labelling a dataset as verified indicates to the software and other users that this dataset is correct and can safely be used in further steps of the application. This action is required in order to continue to Data Exploration or Data Visualization mode.

Things to check include:

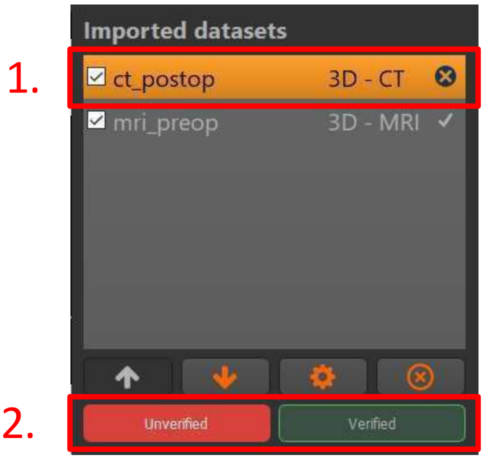
- Left-right correctness
- Alignment with other datasets
- Sufficient image quality

1. Select dataset
2. Click on **Verify**.



Note that the icon next to the selected dataset will change depending on its status.

When not all currently loaded datasets are verified, a warning will be shown in the status bar at the bottom of the interface. Additionally, when a project is opened that contains one or more unverified dataset.



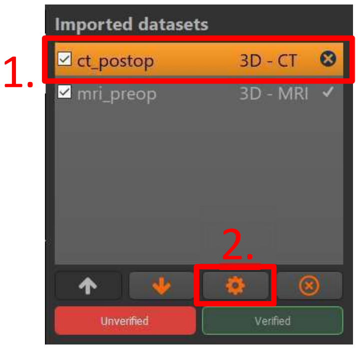
Changing the label of a dataset

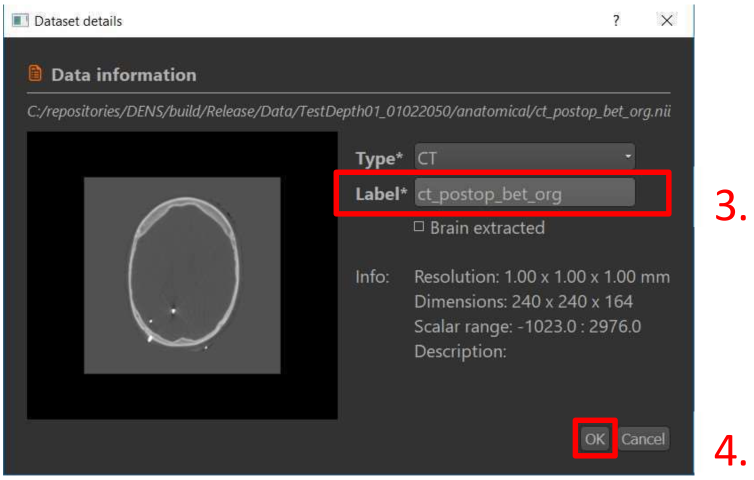
The label of an imported dataset set by default to its filename. It is recommended to change this to a more readable name.

1. **Select** the dataset.
2. Click on the **Rename** button.
3. Provide a new **label**.
   a. Note that the label has to be unique: no other datasets can have the same label.
   b. Special characters are not allowed (!@#$%^&*()_+-=`~).
4. Click **Ok**.

   The label of the selected dataset will be updated in the overview.

Note that the datasets 'Depth electrodes', 'Custom markers' and 'Custom regions' cannot be renamed. These datasets often contain multiple data parts, of which the label can be changed by double clicking on their label in the second, lower overview or by clicking on the corresponding rename button.





Data information

C:/repositories/DENS/build/Release/Data/TestDepth01_01022050/anatomical/ct_postop_bet_org.nii

Type* CT

Label* ct_postop_bet_org

☐ Brain extracted

Info: Resolution: 1.00 x 1.00 x 1.00 mm
Dimensions: 240 x 240 x 164
Scalar range: -1023.0 : 2976.0
Description:

Changing the modality of a dataset

The type of 3D rendering that can be generated from volume is dependent of its modality. Three options are supported: CT, MRI or functional data. The value for brain-extraction can be set for only the CT and MRI volumes.

1. **Select** the dataset**.**
2. Click on the **Edit** button**.** 
3. Provide a new **modality.** 

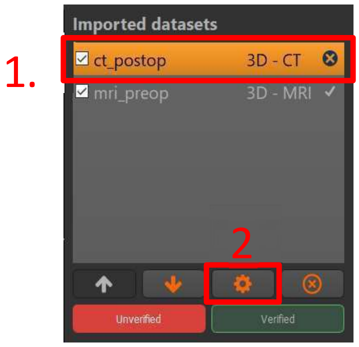
   Type* MRI

   Three options are supported: CT, MRI or Functional.
4. Provide a new value for **brain-extracted.** 

   ☒ Brain extracted

   This can only be set for MRI or CT Volumes.
5. Click **Ok.**

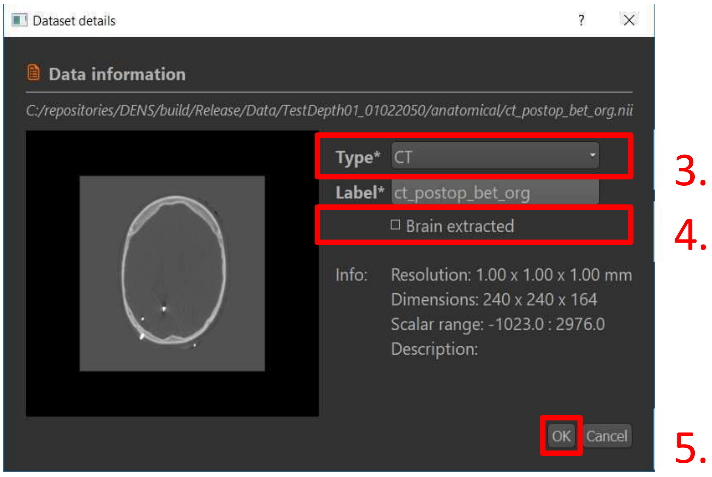
   The type of the selected dataset will be updated in the overview.



Imported datasets

☑ ct_postop 3D - CT

☑ mri_preop 3D - MRI



Data information

C:/repositories/DENS/build/Release/Data/TestDepth01_01022050/anatomical/ct_postop_bet_org.nii

Type* CT

Label* ct_postop_bet_org

☐ Brain extracted

Info: Resolution: 1.00 x 1.00 x 1.00 mm
Dimensions: 240 x 240 x 164
Scalar range: -1023.0 : 2976.0
Description:

Depending on the selected option, different rendering options will be available:

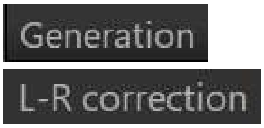
- CT: skin rendering
- MRI: skin rendering
- MRI (brain extracted): brain cortex rendering
- Functional: functional region rendering

In the case of cortex and functional region renderings, an additional control is available for shrinking/growing the rendering (see Appendix).

Correcting a left-right flip in a dataset

When working with NIfTI datasets, the correctness of left and right is not guaranteed and must be verified. When these datasets are flipped with respected to left and right, this has to be corrected before continuing to other steps.

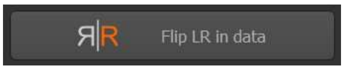
1. **Menu bar → Generation → L-R correction.**
   A dialog will appear.



2. **Select the volume** for correction.

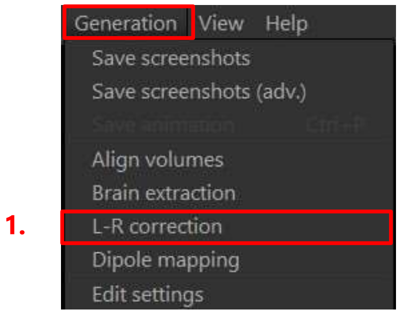

Volume: ct_postop_bet

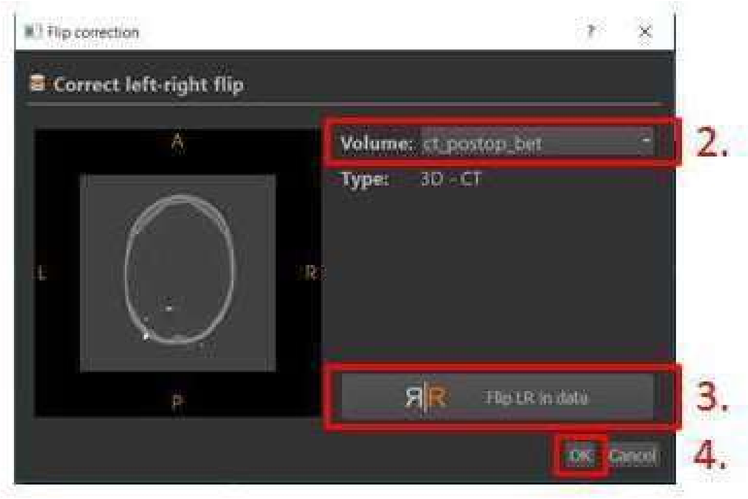
3. **Click** on the **flip button**.
   The thumbnail on the left will be updated.



4. Press **Ok.**
   The software will now create a flipped version of the selected dataset.

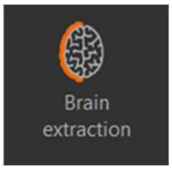
After the correction has finished, the newly created, flipped volume will be saved in the application database. After saving the file, the application will import the new, flipped volume and remove the old version from the application.





Volume: ct_postop_bet
Type: 3D - CT

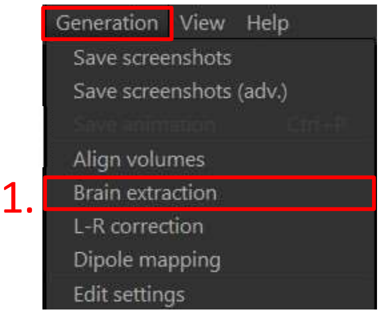
Brain extraction

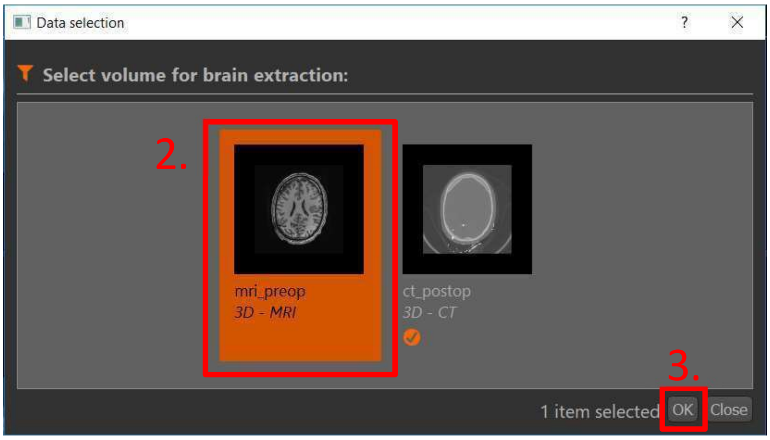


Brain extraction removes non-brain tissues from a volume. In the case of an MRI volume, the skull and skin are removed so that only a volume of the brain cortex remains. In the case of a CT volume, the skull is extracted from the volume, removing any electrode wiring.

1. **Menu bar → Generation → Brain Extraction**.

   A popup dialog will appear for selection.
2. **Select the volume** for brain extraction**.**
3. Press **Ok.**




Data selection

Select volume for brain extraction:

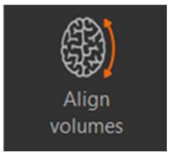
mri_preop
3D - MRI

ct_postop
3D - CT

1 item selected

When the brain extraction is finished, the newly created, brain-extracted volume will be saved in the application. If an output file already exists, the user is asked whether to override the file. After saving the file, the application will import the new volume. The quality of the extraction can be checked by inspecting the 3D rendering or by changing the opacity of the brain-extracted volume.

Co-registration

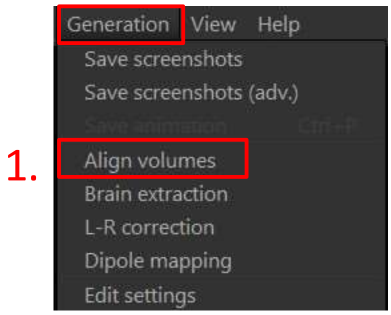


Co-registration will align volumes to match the selected **main image**. This step is required when volumes do not share the same coordinate space.

P.S. For co-registration choosing the main image is a crucial step, since all images available in a project should be aligned with the main image (i.e. are all brought in the same co-ordinate space as the main image). Switching of the main image is not possible for the patient-specific project that you are working on.

P.S. The brain extraction of the main image will be used to align functional volumes of the patient, such as PET, SPECT etc., as this gives the best registration result.

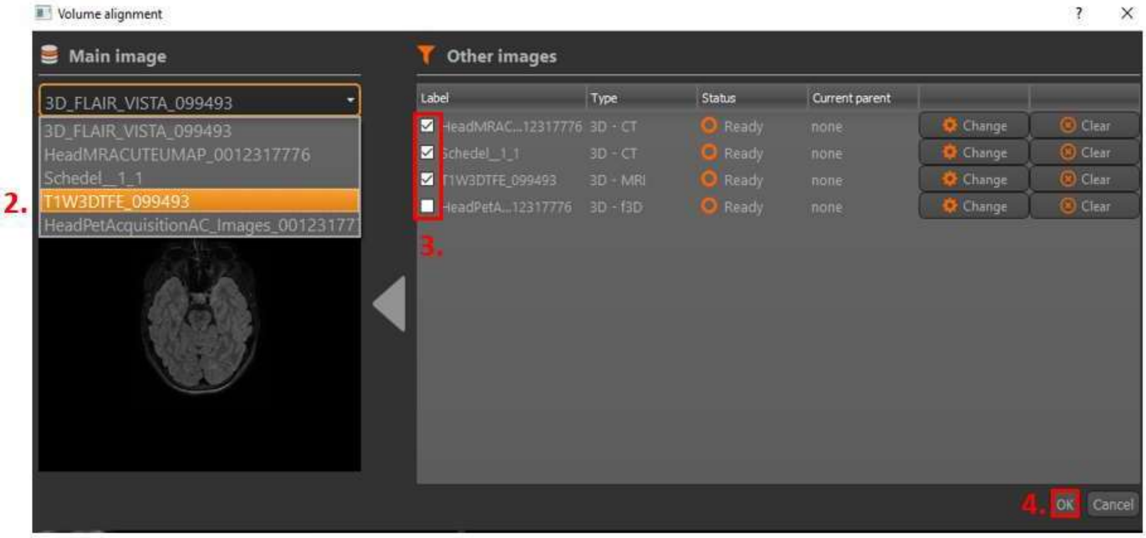
1. **Menu bar · Generation · Align volumes.**



2. **Select** the **main volume** out of the list with available imaging datasets.
   a. It is recommended to use an original (anatomical) MRI volume as the main volume to align anatomical (MRI etc.), structural (DWI) or voxel-based morphometry (VBM) volumes, as this gives the best registration result.
   b. It is recommended to use the brain extraction of the original MRI volume as the main volume to align functional volumes, such as PET, SPECT etc., as this gives the best registration result. If there is (not yet) a brain extraction of the main image available, the functional datasets are not selected for alignment.

3. **Check the volumes** which have to be **registered**.
   The selected volumes will be moved to the coordinate space of the main image.

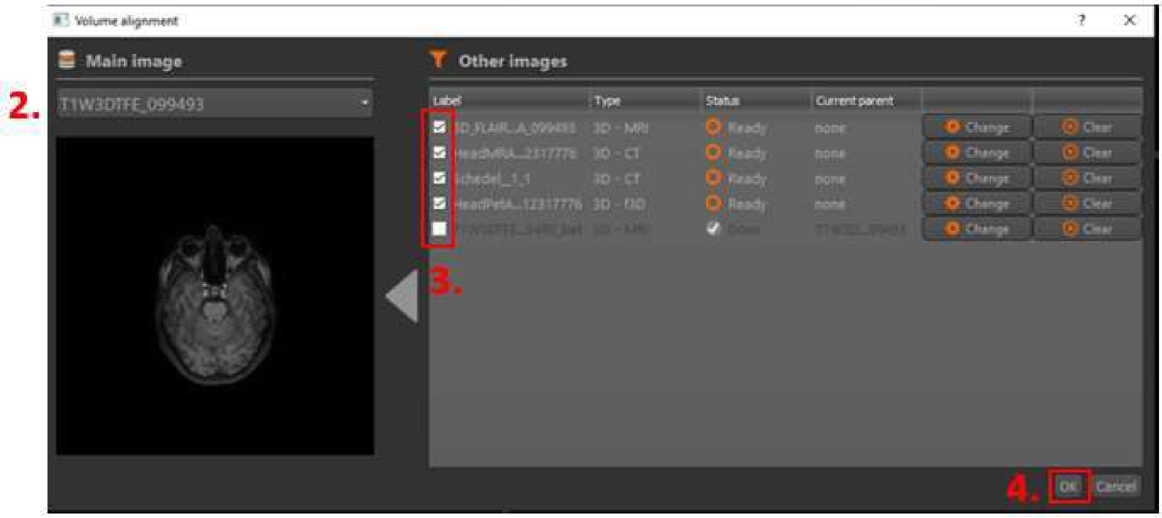
4. Press **Ok** to start the algorithm**.**



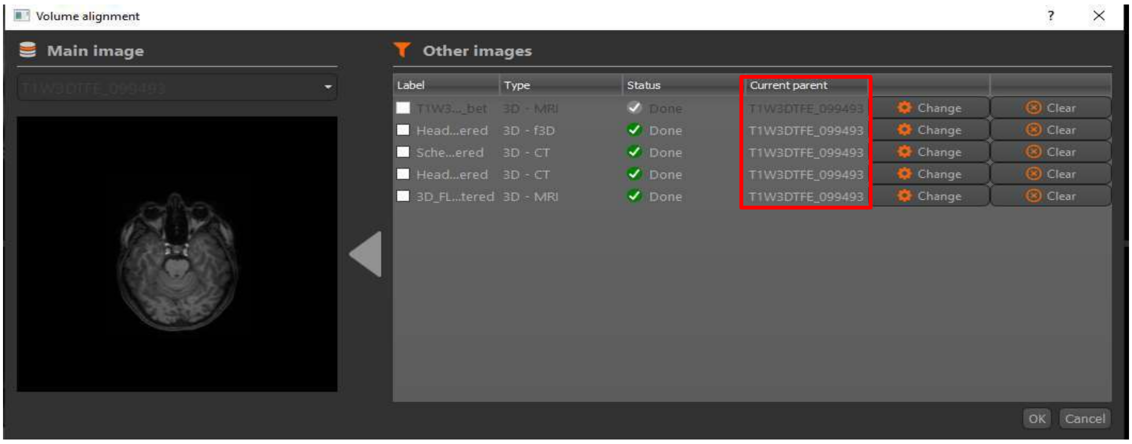
- 3D_FLAIR_VISTA_099493
- HeadMRACUTEUMAP_0012317776
- Schedel__1_1
- T1W3DTFE_099493
- HeadPetAcquisitionAC_Images_00123177

Label	Type	Status	Current parent		
☑ HeadMRAC...12317776	3D - CT	Ready	none	Change	Clear
☑ Schedel_1_1	3D - CT	Ready	none	Change	Clear
☑ T1W3DTFE_099493	3D - MRI	Ready	none	Change	Clear
☐ HeadPetA...12317776	3D - f3D	Ready	none	Change	Clear

c. If there is a brain extraction of the main image available, the main image will be chosen automatically, while the brain extraction of the main image (bet) will be used automatically to align with the functional datasets.



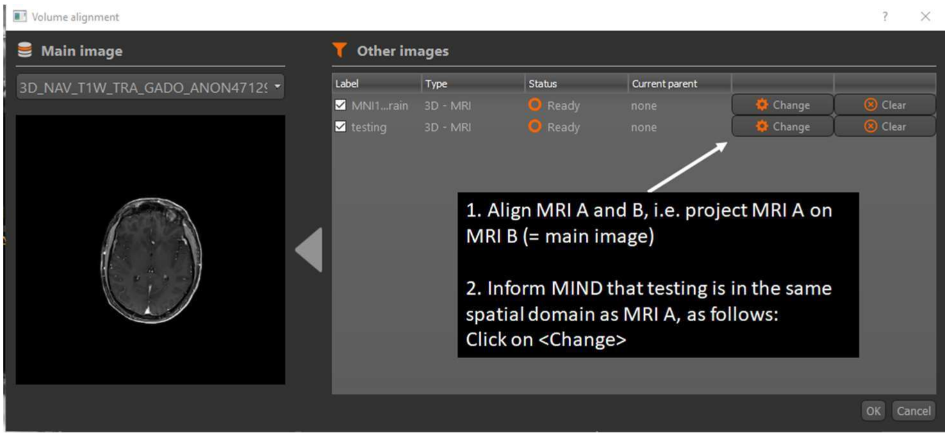
d. After co-registration of the available imaging datasets the main image is disabled (cannot be changed anymore)and all imaging datasets have as current parent the main image.



Label	Type	Status	Current parent		
☐ T1W3..._bet	3D - MRI	Done	T1W3DTFE_099493	Change	Clear
☐ Head...ered	3D - f3D	Done	T1W3DTFE_099493	Change	Clear
☐ Sche...ered	3D - CT	Done	T1W3DTFE_099493	Change	Clear
☐ Head...ered	3D - CT	Done	T1W3DTFE_099493	Change	Clear
☐ 3D_FL...tered	3D - MRI	Done	T1W3DTFE_099493	Change	Clear

e. When **thresholded volumes have already been registered** to a **different volume**, this information can be provided by using the 'Change' button Change and selecting the parent volume.

For example, available in the project file of MIND is **MRI A** and **MRI B**. A third image named **'testing'** which is aligned with MRI A was added (e.g. a processed fMRI image). Follow the next steps to align the volumes:

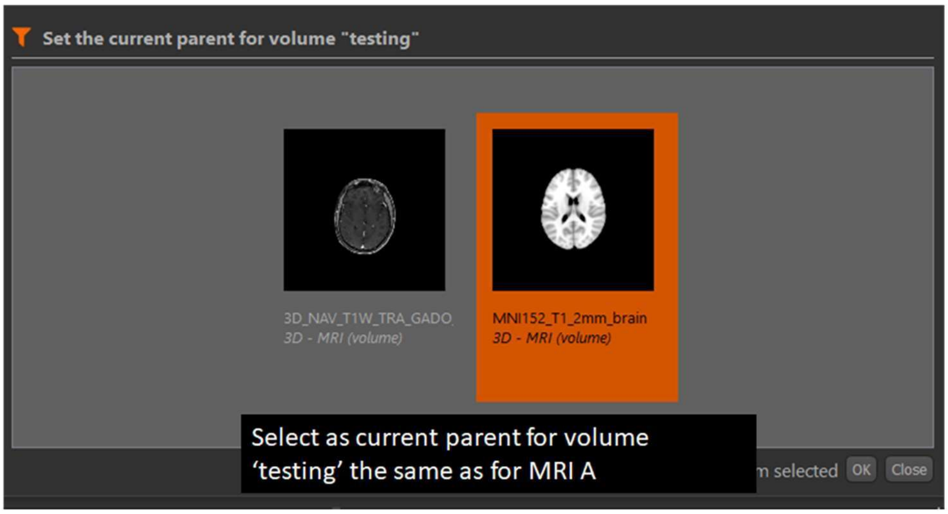


Label	Type	Status	Current parent		
☑ MNI1...rain	3D - MRI	Ready	none	Change	Clear
☑ testing	3D - MRI	Ready	none	Change	Clear

1. Align MRI A and B, i.e. project MRI A on MRI B (= main image)

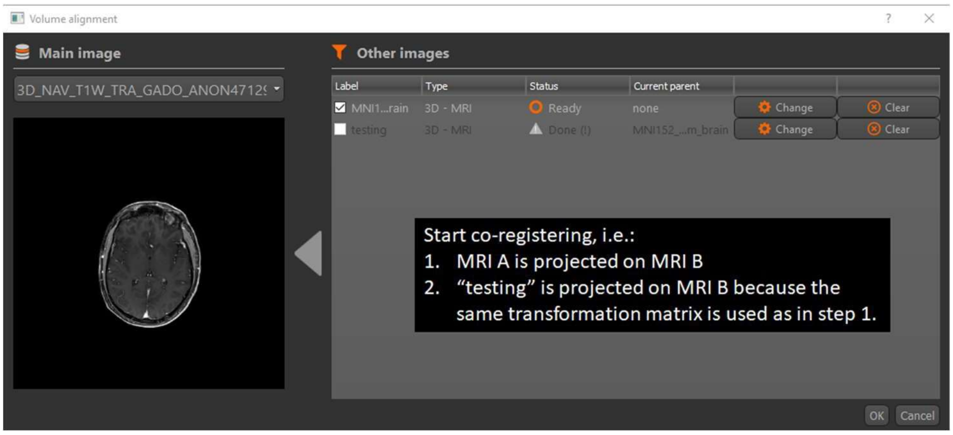
2. Inform MIND that testing is in the same spatial domain as MRI A, as follows: Click on <Change>

P.S. This action can also be reversed by clicking the 'Clear' button.



Select as current parent for volume 'testing' the same as for MRI A

P.S. Providing this information will ensure that the volume is transformed together with its parent volume, ensuring that the current alignment is not lost after registration.



3D_NAV_T1W_TRA_GADO_ANON4712(

Label	Type	Status	Current parent
☑ MNI1...rain	3D - MRI	Ready	none
☐ testing	3D - MRI	Done (!)	MNI152_...m_brain

Start co-registering, i.e.:

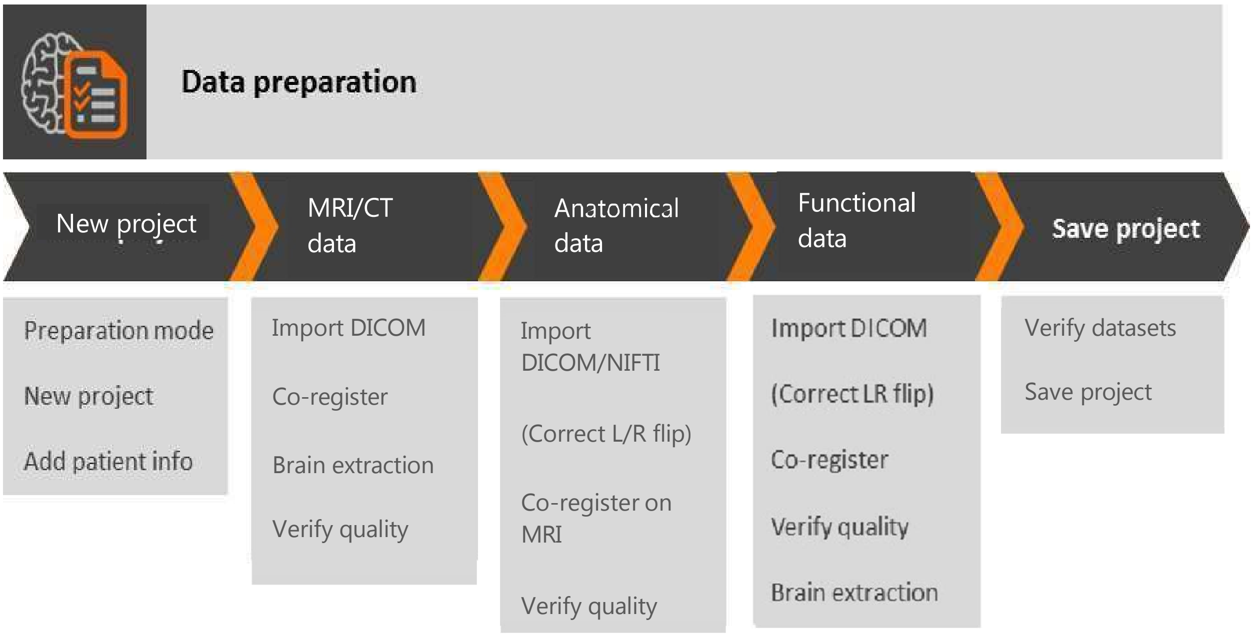
1. MRI A is projected on MRI B
2. "testing" is projected on MRI B because the same transformation matrix is used as in step 1.

P.S. When the co-registration is finished, the registered version of the volumes will be saved in the application. If a file already exists, the user is asked whether to override the file. After saving the file, the application will import the new volumes and remove to old version from the application.

The quality of the registration can be checked by changing the opacity of the registered volume.

Complete test case: Data Preparation

This section describes a test scenario that contains all important tasks in the Data Preparation mode. It can be performed using, for example, the test datasets <MRI, DWI, PET or SPECT or fMRI and if available MEG/EEG source mapping data>.



Data preparation

New project
- Preparation mode
- New project
- Add patient info

MRI/CT data
- Import DICOM
- Co-register
- Brain extraction
- Verify quality

Anatomical data
- Import DICOM/NIFTI
- (Correct L/R flip)
- Co-register on MRI
- Verify quality

Functional data
- Import DICOM
- (Correct LR flip)
- Co-register
- Verify quality
- Brain extraction

Save project
- Verify datasets
- Save project

New project

- Start the application, in preparation mode page 13
- Create a new project with patient data

MRI/CT data

- Import a DICOM MRI and (if available) CT dataset page 13
- Verify the quality and correctness of the MRI dataset page 14
- Run co-registration on the CT and MRI volume page 18
- Perform brain extraction on the MRI volume page 19

Anatomical (structural) data

- Import either as DICOM or NIFTI anatomical c.q. structural datasets: diffusion datasets, SWI, proton scan etc. page 13
- Run co-registration on the anatomical datasets and the MRI page 18
- If needed, correct the LR flip in the datasets compared to the MRI page 17

Functional data

- Import either as DICOM or NIFTI functional datasets: fMRI, PET, SPECT etc. page 13
- Run **co-registration** on the **functional datasets** and the **Brain extracted MRI** volume page 18
- If needed, correct the LR flip in the datasets compared to the MRI page 17

Save project

- Select for all datasets < Verify> page 14
- Save the project

III. Data exploration

Exploration of 3D volume’s

The user interface in the exploration mode (Figure 5) provides:

- quick navigation to the most commonly used functionalities in this mode (lower part of the left column);
- the three 2D-viewports and a 3D-viewport with the orthogonal MRI-slices and the rendering of the cortex,
- in the upper part of the right column the data overview and the buttons below to re-order, centralize (focus), edit or remove the currently selected dataset
- and in the lower part of the right column the supporting controls.

- **Multi-modal explorations**
- The panel in the top-right corner of the interface displays a list of selectable datasets that can be added or removed from the current visualization (Figure 6). The arrows can bring the datasets up- or downwards, thus moving the datasets from front to the back and vice versa of the multi- modal visualization. By selecting the Planes (bottom right column) of the medical imaging datasets selected in the Ax, Co and Sa direction, these datasets are viewed as a 3D-image.

Figure 5 – User interface in the Exploration mode.

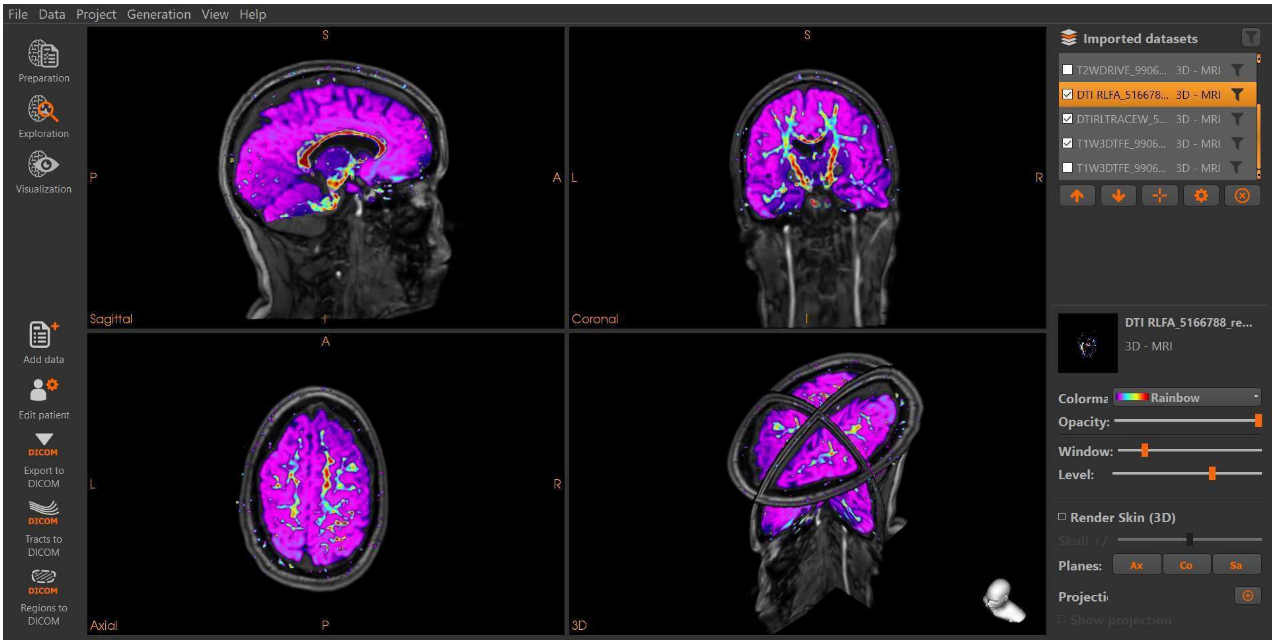


Figure 6 – 2D/3D exploration of diffusion weighted imaging (ADC/FA) datasets.

Exploration of the fMRI datasets

If the fMRI dataset contains positive and negative values (1) set based on the color bar (2) the threshold (3) for display (Figure 7).

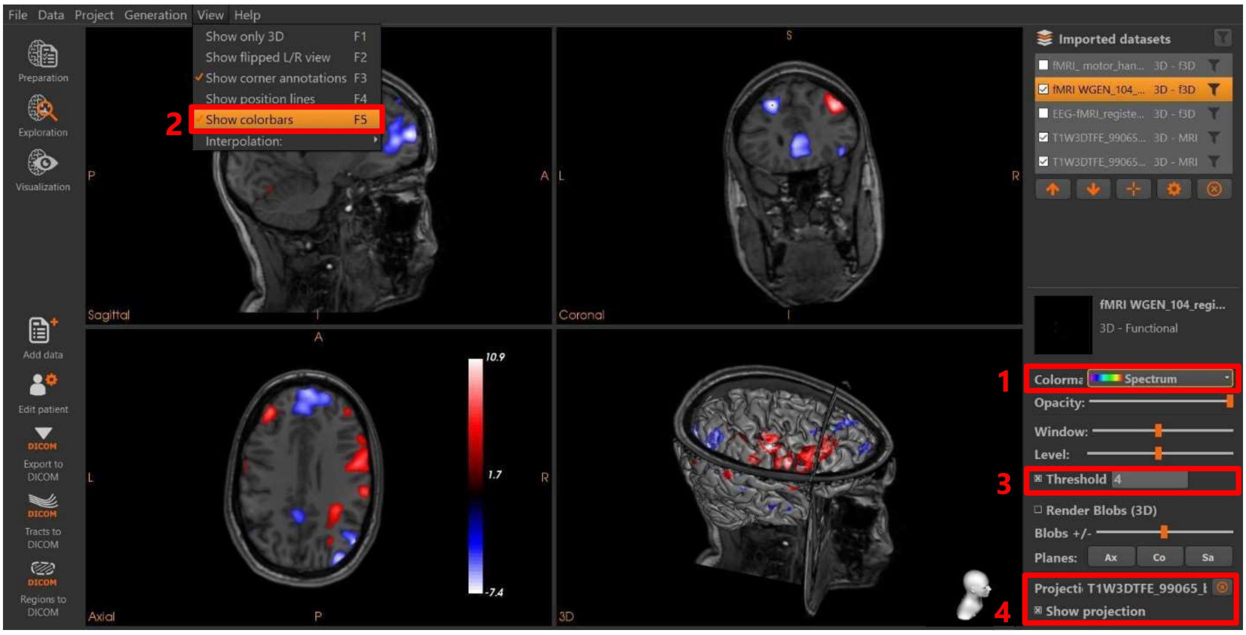
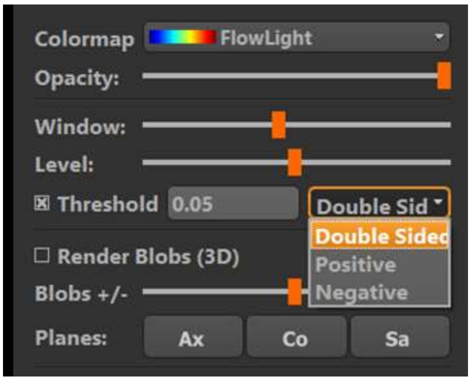


Figure 7 – 2D/3D visualization of fMRI (word generation) dataset.

- For thresholding you may choose either Double Sided, Positive and Negative thresholding (see the Combi-box in the next figure).



Creating a cortical projection

In case of a cortical projection (see Figure 7) the intensities of the functional dataset are projected on the surface of a cortex rendering. Datasets that can be used to create a projection are: 3D volumes and EEG source maps.

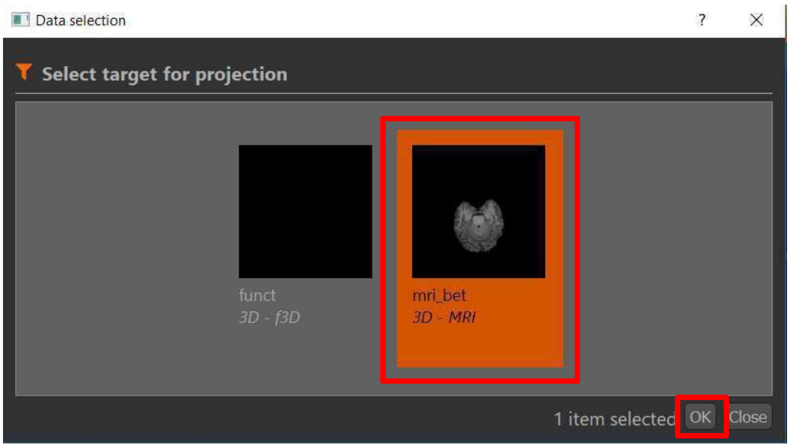
1. **Select** the functional dataset (3D functional or EEG source maps)**.**

2. **Click** on the **'New projection'** button**.** ⊕

   This will open a selection dialog, showing the available datasets that can be used as a target for the projection.

3. **Select** the **target** dataset in the **dialog.**

   The targeted dataset can be a CT or MRI volume, resulting in a projection on skull or skin, respectively. When a brain-extracted MRI is the target the result is a projection on the patient's cortex.



4. **Click** on **Ok.**

   Notice that after creating the projection, the 'New' button changes to a delete button. Clicking this will remove the projection.

Creating regions of interest

MIND allows the user to create custom regions (ROIs) to mark (pathologic) abnormalities at the MRI, as shown in Figure 8, abnormalities visible at anatomical images or deviations of functionality according to the functional images. The fused images of the medical imaging datasets, together with the custom regions support the clinician to come to a clinical hypothesis with regard to the optimal treatment of the patient.

1. **Go to a position** where the region approximately needs to be placed**.**
2. Go in the menu to **<Data>** and select **<Add custom regions>**

This will add a new dataset 'Custom regions' to the Data overview.

3. **Click** on the **'New region'** button.

This will place a contour on the current position, after which it can be moved and resized.

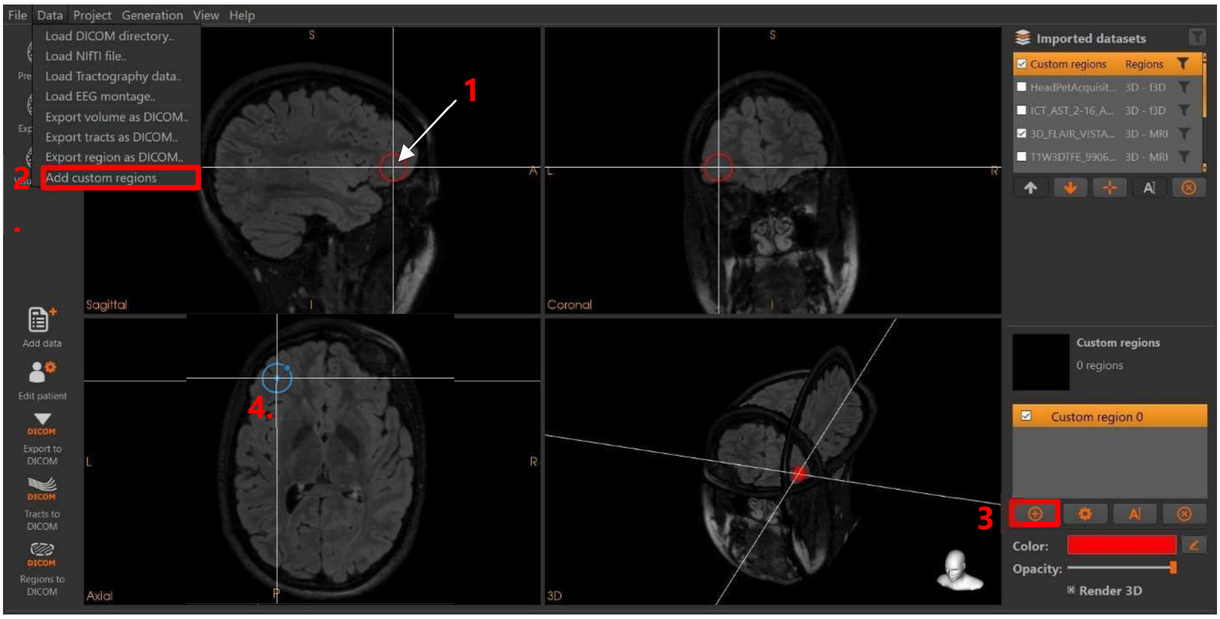
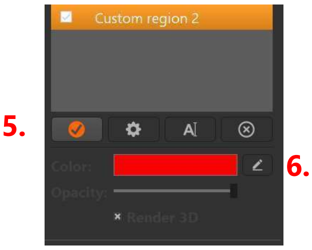


Figure 8 – Setting of custom regions indicating abnormalities visible at MRI.

4. **Move and resize** the **region** as desired in the 2D viewports.

The selected volumes will be moved to the coordinate space of the main image.

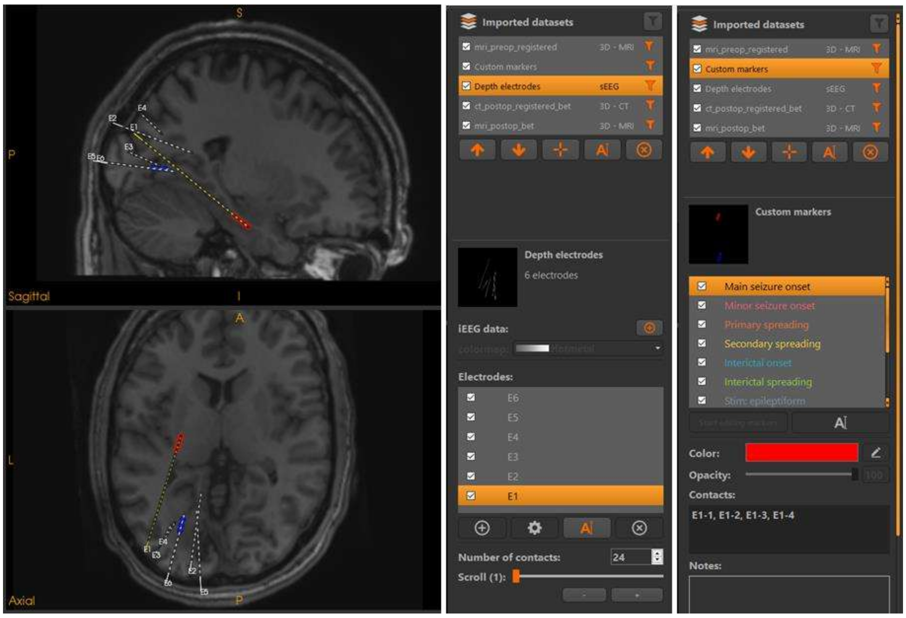
5. **Press** the **Finish button.**
6. Adjust the **color** of the custom region



Visualise depth electrodes and annotations

In MIND the project files including depth electrodes and custom markers can be visualized (Fig, left panel).

- The labels of the depth electrodes can be adapted, the number of Contacts and the user is able to scroll through the electrodes, using either a slider or the +/- button (Fig. middle panel).



Number of contacts: 24

Scroll (1):

Contacts: E1-1, E1-2, E1-3, E1-4

- For the custom markers, the interface shows the list of annotations, and for the annotation selected, the following information is visible: color coding, Contacts, and notes given as input with these contacts, nothing can be changed (Fig. right panel).

Source mapping

Voxel-based source analysis results

For the visualization of distributed source mapping results the following datasets need to be imported in the preparation domain, either as DICOM or NIFTI files:

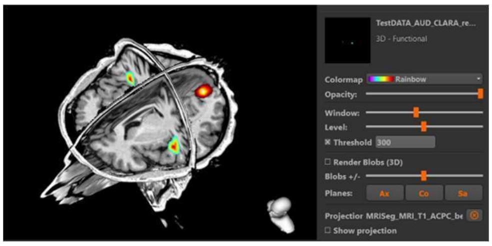
- a 3D-MRI dataset of the head;

- a 3D-(voxel-based) source map.

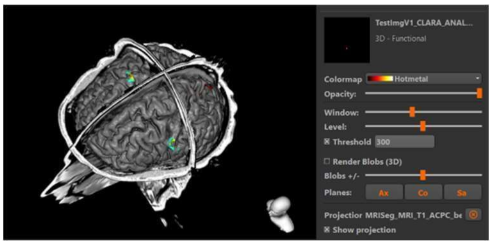
1. Perform a brain extraction of the MRI Brain extraction

2. Align the source map with the brain extracted MRI dataset. Align volumes

3. Go to the Exploration domain and create a 3D-image of the datasets, as shown for the source maps of bilateral auditory responses and of a visual response, in 3 orthogonal planes (left) and as cortical projection (right).



TestDATA_AUD_CLARA_re...
3D - Functional
Colormap Rainbow
Opacity:
Window:
Level:
☒ Threshold 300
☐ Render Blobs (3D)
Blobs +/-
Planes: Ax Co Sa
Projectior MRISeg_MRI_T1_ACPC_be
☐ Show projection



TestImgV1_CLARA_ANAL...
3D - Functional
Colormap Hotmetal
Opacity:
Window:
Level:
☒ Threshold 300
☐ Render Blobs (3D)
Blobs +/-
Planes: Ax Co Sa
Projectior MRISeg_MRI_T1_ACPC_be
☒ Show projection

Single dipole source mapping

For the visualization of dipole sources the following datasets need to be imported in the preparation domain (Figure 9), either as DICOM or NIFTI files:

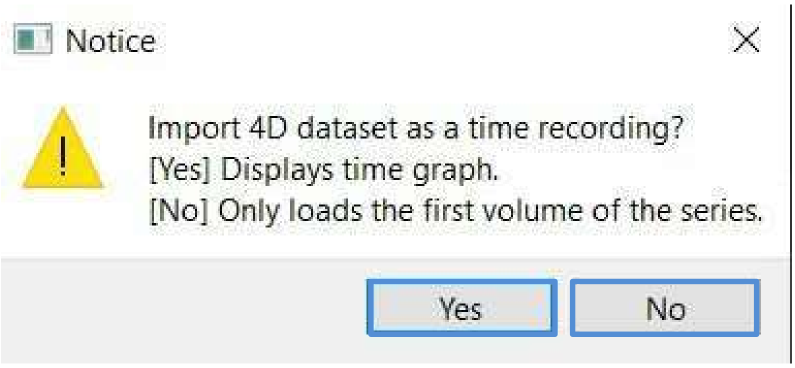
- a 3D-MRI dataset of the head;
- a file containing the positions and orientations of the dipoles (e.g. the *.bsa files created by the BESA software as shown here as result of the localization of bilateral auditory responses).

"Notice that the dipole localizations should be in the same co-ordinate system as the MRI of the patient's head."

Figure 9 – Import and visualization of text files with the dipole parameters.

Exploration of a 4D volume

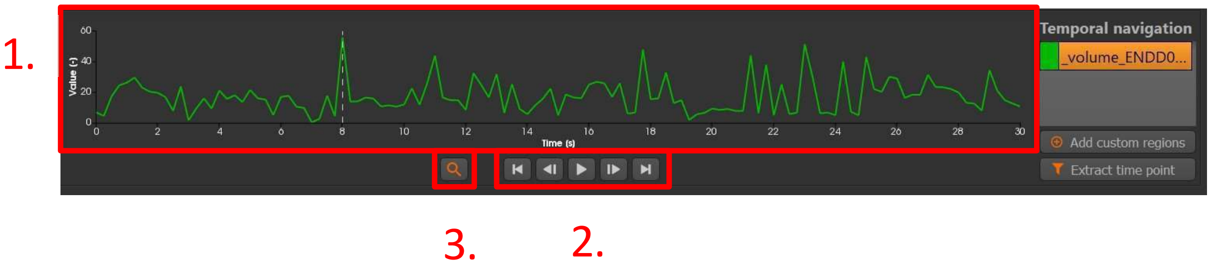
A 4D dataset contains multiple values per voxel. When reading a dataset with multiple values per voxel a pop-up window appears with the following options for input:



Import 4D dataset as a time recording?
[Yes] Displays time graph.
[No] Only loads the first volume of the series.

A number of datasets (DWI, fMRI, PET etc.) may contain multiple values per voxel, for example, DWI-datasets may contain multiple values per voxel obtained with four different b-values. These datasets do not represent time recordings, therefore select <No>. MIND will import a 3D dataset related by default to the first value and save this 3D dataset in the project file.

In the case of EEG source mapping data, this is often a time series. Select <Yes> in the pop-up window and a 4D dataset will be imported and an additional **panel** will appear which shows the **time series** for the selected position in the 2D MRI viewports **(1)**.



✓ Select location

Click on the desired **position** in the 2D viewports and the application will show the time series for the newly selected voxel of the brain.

✓ Select time-point

Click on the desired **time point** in the graph and the application will show the source map of the current time point in the 2D and 3D viewports. The vertical, dashed line indicate what time point currently has been selected.

2. Use the **button controls**.

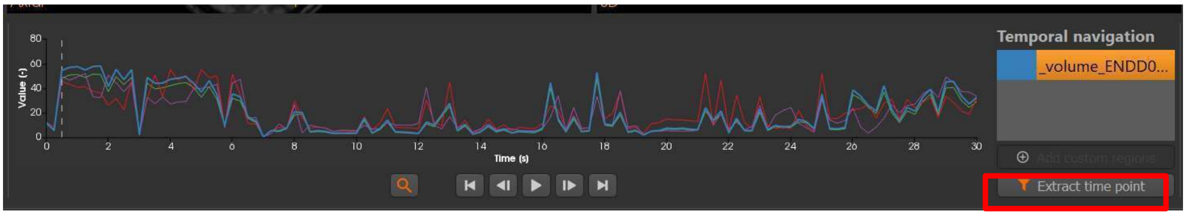
The buttons on the bottom of the graph can be used to go to different time points. The play button will start an animation through the different time points.

✓ Adjust plot

3. **Zoom** in on graph.

In order to best visualize the graph of the time series, the zoom button on the left can be clicked. This will adjust the view of the graph to best fit its contents.

A common exploration task for functional 4D data is to investigate the average time series for different regions. After manually creating different custom regions (see section “ Creating regions of interest’, page 25) , the software will show the corresponding average times series in the graph so that they can be compared.



Extracting a 3D volume from a 4D volume

During the exploration of a 4D dataset (page 28), several interesting time-points may be noticed. These time points can be extracted, saved and imported as a separate dataset.

1. **Go to a time point** to be extracted**.**

For more details, see page 29.

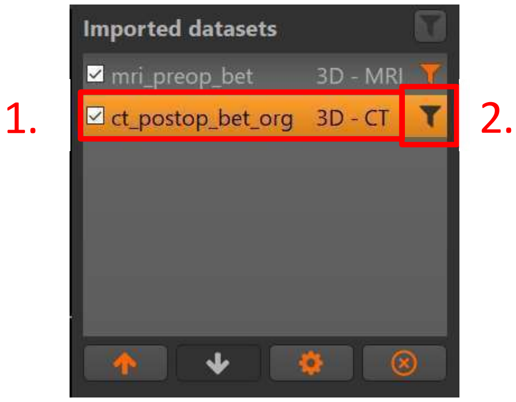
2. **Click** on the **‘Extract time point’** button**.**

The software will now extract the time point, save and open it as a new 3D dataset. During the extraction a 3D NIFTI volume will be created and saved in the project file, alongside the original dataset.

The extracted dataset requires significantly less memory and can be imported and visualized more easily. Moreover, the extracted 3D dataset can be processed e.g. realigned with other datasets, whereas this is not possible for a 4D dataset. It is recommended to extract the interesting time points of a 4D dataset before continuing to the Data Visualization step.

Labelling a dataset as final

1. **Select** the dataset**.**
2. Click on the **Final button.** **or**

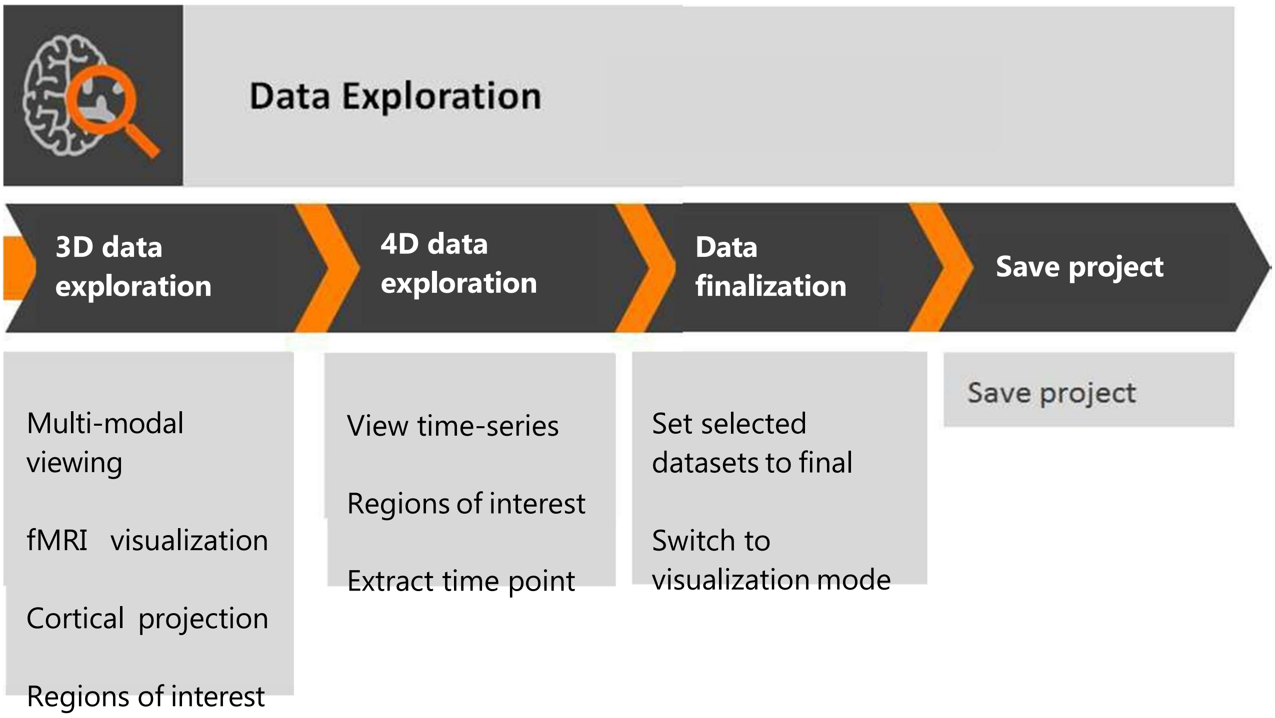


3. Go to the **visualization mode**

During the Data Visualization mode only the datasets that have been labelled as final will be loaded into the application.

Complete test case: Data Exploration

This section describes a test scenario that contains the essential tasks in the Data Exploration mode. It can be performed using, for example, the test datasets <MRI, DWI, PET or SPECT or fMRI and if available MEG/EEG source mapping data>.



Data Exploration

3D data exploration
- Multi-modal viewing
- fMRI visualization
- Cortical projection
- Regions of interest

4D data exploration
- View time-series
- Regions of interest
- Extract time point

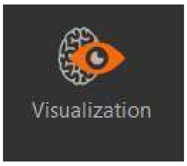
Data finalization
- Set selected datasets to final
- Switch to visualization mode

Save project
- Save project

Load project

- Start in **Data Exploration** mode with an existing project file data page 22
- Explore the medical imaging datasets
- Create regions of interest
- Inspect the voxel time-series of the 4D dataset at different positions
- Create regions of interest and view the averaged time-series
- Extract a time-point
- Label the selected datasets as final
- Save the project

IV. Data visualization



Creating multi-modal visualizations

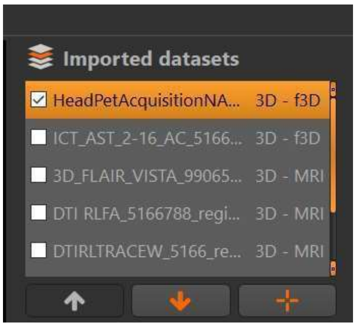
When the visualization mode is selected only these datasets will be listed which were marked as Final

Multi-modal visualization of medical imaging datasets

When multiple datasets have been loaded, they can be visualized together in a multi-modal visualization.

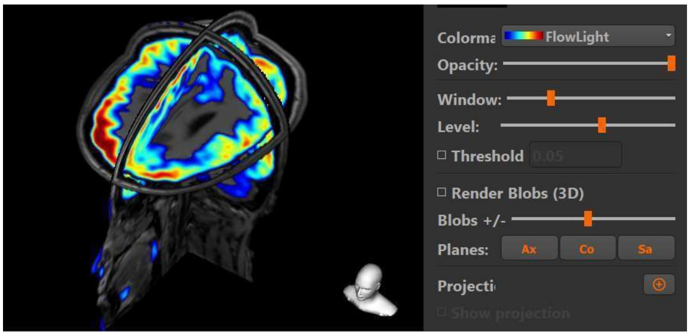
1. **Show the medical imaging datasets** by turning the datasets on in the overview.
2. **Adjust the visual settings** of the anatomical datasets**.**
   - Enable the 3D anatomical planes.
   - Set a color map and adjust if needed the settings for visualization, e.g change the visualization of the image (i.e. the amount of activated voxels shown) by using the slicer <Window> and <level> or give as input a threshold.

1.



Imported datasets

☑ HeadPetAcquisitionNA... 3D - f3D
☐ ICT_AST_2-16_AC_5166... 3D - f3D
☐ 3D_FLAIR_VISTA_99065... 3D - MRI
☐ DTI RLFA_5166788_regi... 3D - MRI
☐ DTIRLTRACEW_5166_re... 3D - MRI



Colorma FlowLight
Opacity:
Window:
Level:
☐ Threshold 0.05
☐ Render Blobs (3D)
Blobs +/-
Planes: Ax Co Sa
Projecti
☐ Show projection

2.

- For a functional 3D volume: enable the 3D rendering or alternatively, a projection on an anatomical dataset can be created.
- The opacity of the volume can be changed in order to view multiple volumes together.

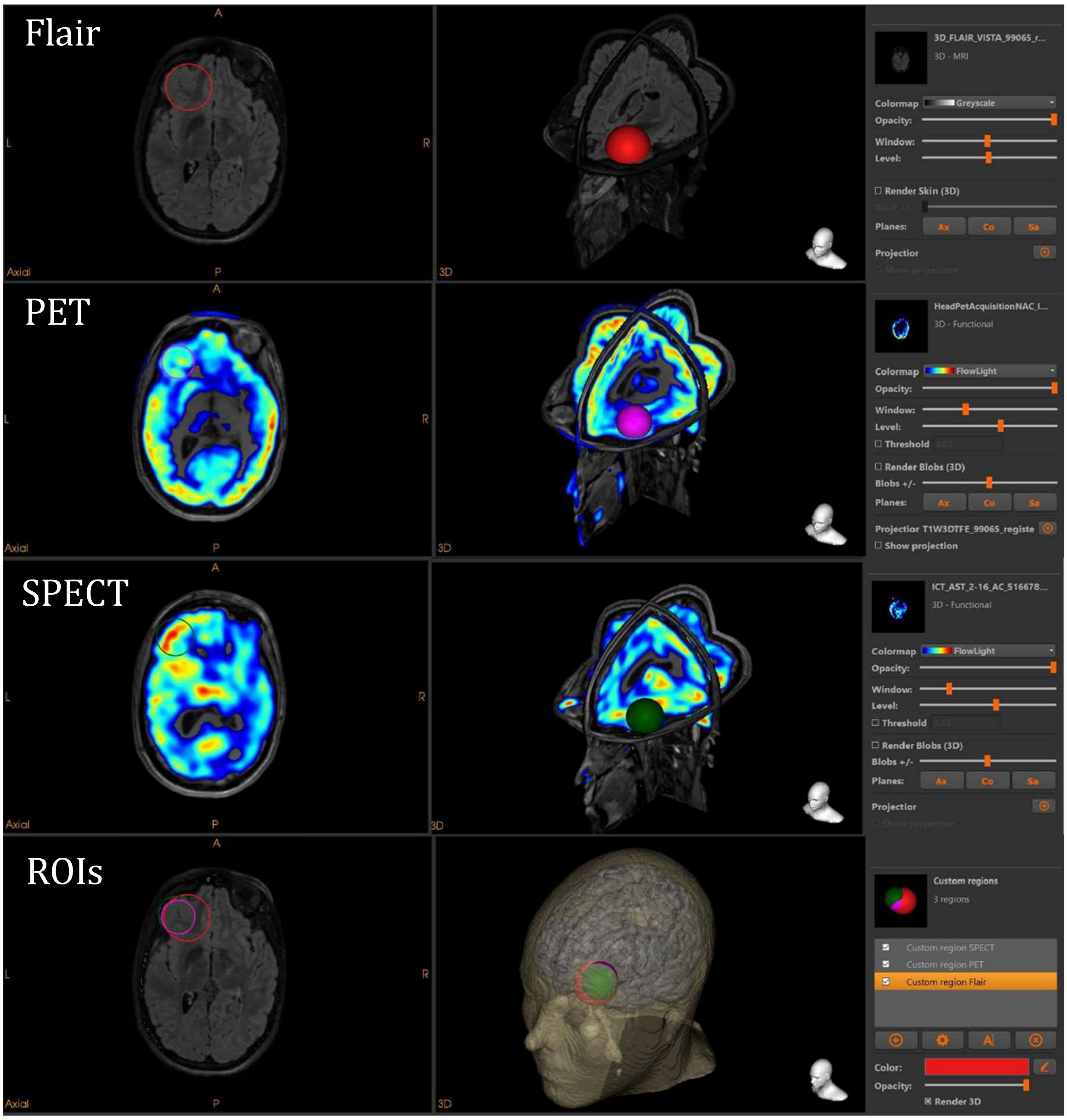


Figure 10 – Fusion of images of the medical imaging datasets

- The custom regions (ROIs) for the distinct medical imaging datasets created during the exploration phase can be visualized as a fused image in a 2D-MRI viewport or in 3D-renderings, as shown in the bottom row of Figure 10. The visualization of the custom regions can be manipulated by changing colors and changing the opacity of the custom regions.

3. **Change the camera** of the 3D viewport to view the data optimally.

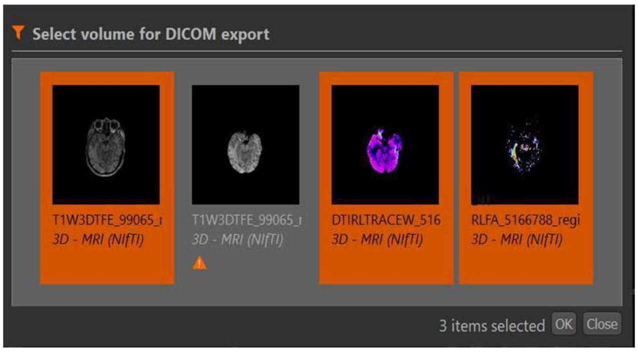
Exporting volumes as DICOM

Three dimensional volumes can be exported as DICOM files. This allows for data export to other software, including commercial neuro-navigation software used in the planning of epilepsy surgery.

Export datasets in DICOM format

1. **Click** on **Export to DICOM.**

2. **Select** the **volumes** for export.



For some volume datasets, a conversion of values is needed in order to export the data as DICOM format. In these cases, a warning will appear indicating the values will be converted.

3. **Click Ok**.
4. **Select** an output directory

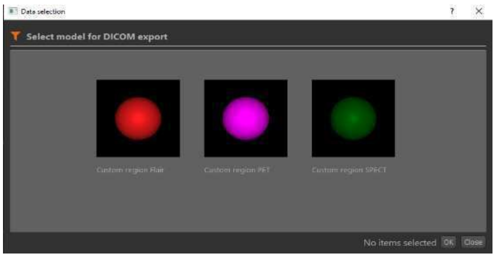
Be aware that the DICOM-files will be saved by default in the directory of the project file. If the folder already files that might be overwritten, the user is asked to overwrite the files.

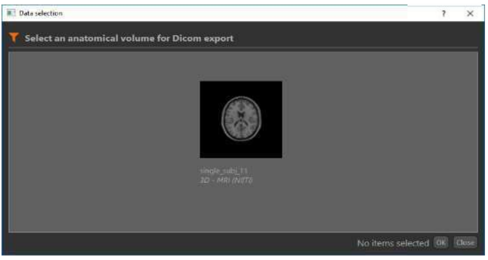
This method will add a custom region to an anatomical DICOM dataset, by overlaying the border of the region in white on top of the anatomy.

1. **Click** on **Regions to DICOM.**

2. **Select** the **Region** for export and **Click Ok**.

3. **Select** the **Anatomical dataset** for export and **Click Ok**.





4. **Select** an output directory and press **Ok.**

   If the folder already CONTAINS files that might be overwritten, the user is asked whether to overwrite the files.

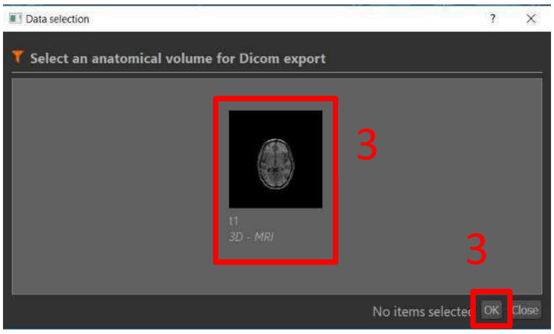
The DICOM files will be exported with their location in the application. This will ensure that aligned volumes will stay aligned after export.

Exporting tractography as DICOM

This method will add a tractography to an anatomical DICOM dataset, by overlaying the tractography in white on top of the anatomy. This step requires:

- An imported anatomical dataset
- An imported tractography dataset

1. **Click** on **Tracts to DICOM.**
2. **Select** the **Tractography dataset** for export and **Click Ok**.
3. **Select** the **Anatomical dataset** for export and **Click Ok**.



For some volume datasets, a conversion of values is needed in order to export the data as DICOM format. In these cases, a warning will appear indicating the values will be converted.

4. **Select** an output directory and press **Ok.**

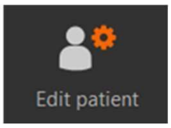
If the folder already files that might be overwritten, the user is asked whether to overwrite the files.

The DICOM files will be exported with their location in the application. This will ensure that aligned volumes will stay aligned after export.

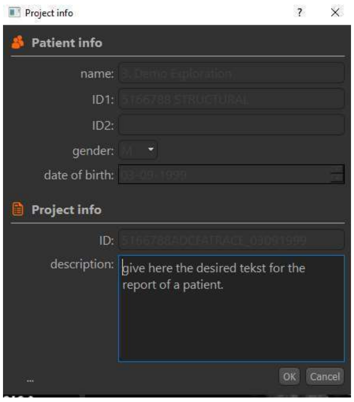
Create a patient report

1. Create a pdf report of the patient.
    - The patient report contains the patient ID etc, which was saved in the project file
    - A further description can be provided in the Patient info window

- Select the button

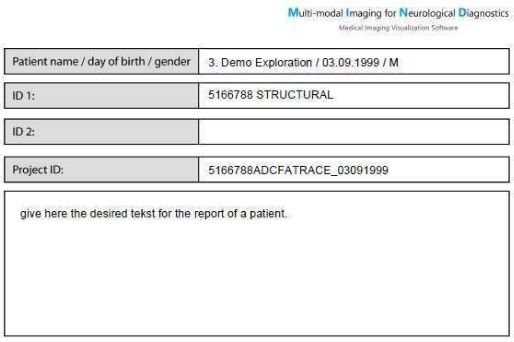


- Provide the textual input in the Patient info window



name: 3. Demo Exploration
ID1: 5166788 STRUCTURAL
ID2:
gender: M
date of birth: 03-09-1999
ID: 5166788ADCFATRACE_03091999
description: give here the desired tekst for the report of a patient.

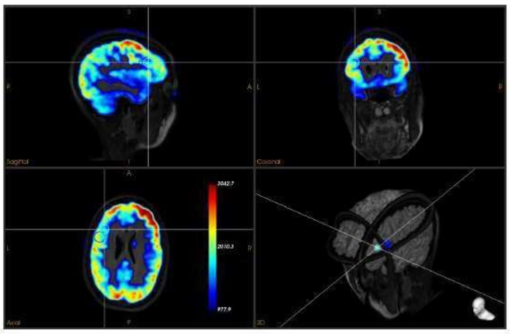
- The current visualization of the 2D/3D MRI viewport is saved together with the patient information.



Multi-modal Imaging for Neurological Diagnostics
Medical Imaging Visualization Software

Patient name / day of birth / gender	3. Demo Exploration / 03.09.1999 / M
ID 1:	5166788 STRUCTURAL
ID 2:	
Project ID:	5166788ADCFATRACE_03091999

give here the desired tekst for the report of a patient.

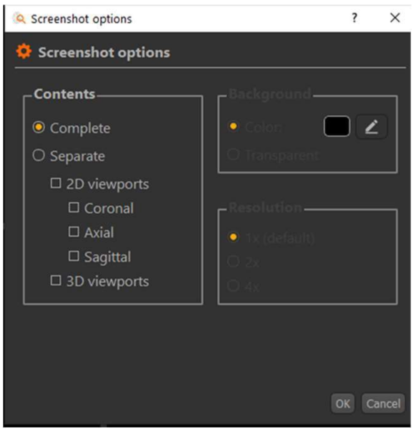


This report was generated on: di jun 23 2020, 13:49:01

2. Add if needed screenshots of the visualizations

- **Save screenshots** by following the menu item

< Generation/Save screenshots>, giving the shown options.



Screenshot options

Screenshot options

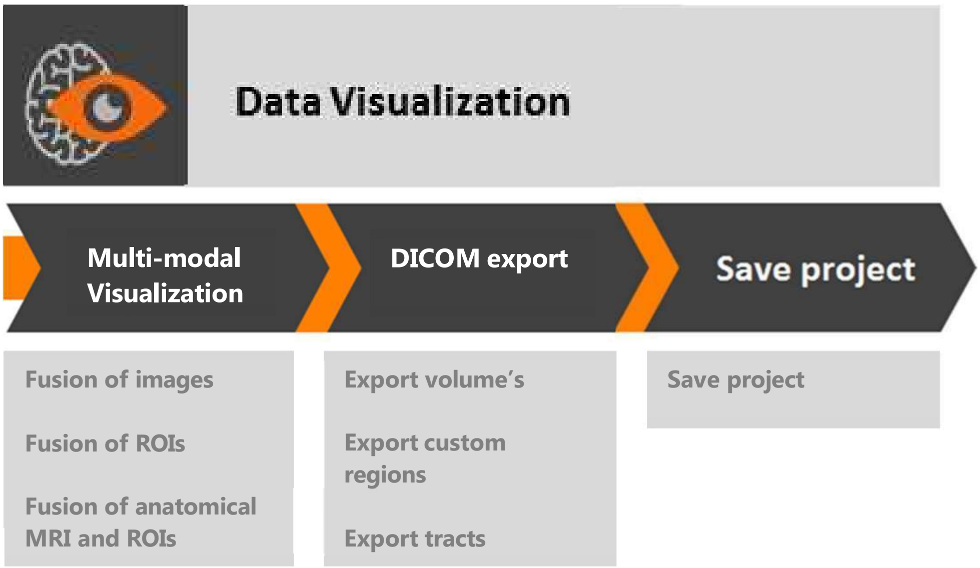
Contents
● Complete
○ Separate
☐ 2D viewports
☐ Coronal
☐ Axial
☐ Sagittal
☐ 3D viewports

Background
● Color:
○ Transparent

Resolution
● 1x (default)
○ 2x
○ 4x

Complete test case: Data Visualization

This section describes a test scenario that contains the essential tasks in the Data Visualization mode. It can be performed using, for example, as test datasets the 3D volumes of <MRI, DWI, PET or SPECT or fMRI and if available MEG/EEG source mapping data and custom regions>.



Continue to **Data Visualization** mode with the existing data

- Create a multi-modal visualization
- Export volume as DICOM
- Export tractography data as DICOM
- Create a pdf (patient report)
- Save the project

Appendix: Integrate with depth electrodes.

In most of the institutes were epilepsy surgery candidates are evaluated the patients go through an extensive work-up followed for a selection of patients by invasive EEG assessment. The processing of these data in MIND and DENS (Depth Electrode Navigator Software) depends on the workflow of the user, with as options 1. 'Create a project file in MIND' and detect the depth electrodes in DENS, and 2. 'Create a project file in DENS, detect de depth electrodes and visualize these together with the other medical datasets in MIND.

Create a project file in MIND

Save the project file containing the medical imaging datasets as shown in Figure 10 while MIND is in the preparation mode.

1. Select the button Add data and import a post-implantation CT dataset and if available a post-implantation MRI (either as DICOM or NIFTI).
2. Align both datasets with the pre-implantation MRI. Align volumes
3. Perform brain extraction for both the post-implantation CT and MRI dataset Brain extraction
4. Verify all the datasets (see Page 19) and save the project file in the exploration mode.
5. Import the project file in DENS and detect automatically the positions of the depth electrodes and save - after checking the positions of the depth electrodes versus the cortical anatomy – the project file.
6. Import the project file in MIND and visualize the medical imaging datasets together with the depth electrodes in the 2D/3D-MRI viewports (Figure 12).

Create a project file in DENS

1. Import and pre-process the post-implantation CT, the pre-implantation MRI and if available the post-implantation MRI using DENS and detect automatically detect the positions of the depth electrodes and save - after checking the positions of the depth electrodes versus the cortical anatomy – the project file.

2. Import the project file in MIND in the preparation mode and add the medical imaging datasets either as DICOM or NIFTI

3. Align the medical imaging datasets with the pre-implantation MRI. Align volumes
   Note: realign functional dataset with the brain extracted pre-implantation MRI

4. Perform brain extraction for both the post-implantation CT and MRI dataset Brain extraction

5. Verify all the datasets (see Page 19), select the datasets for visualization and save the project file in the exploration mode.

6. Select the visualization mode and visualize the medical imaging datasets together with the depth electrodes in the 2D/3D-MRI viewports (see Figure 12).

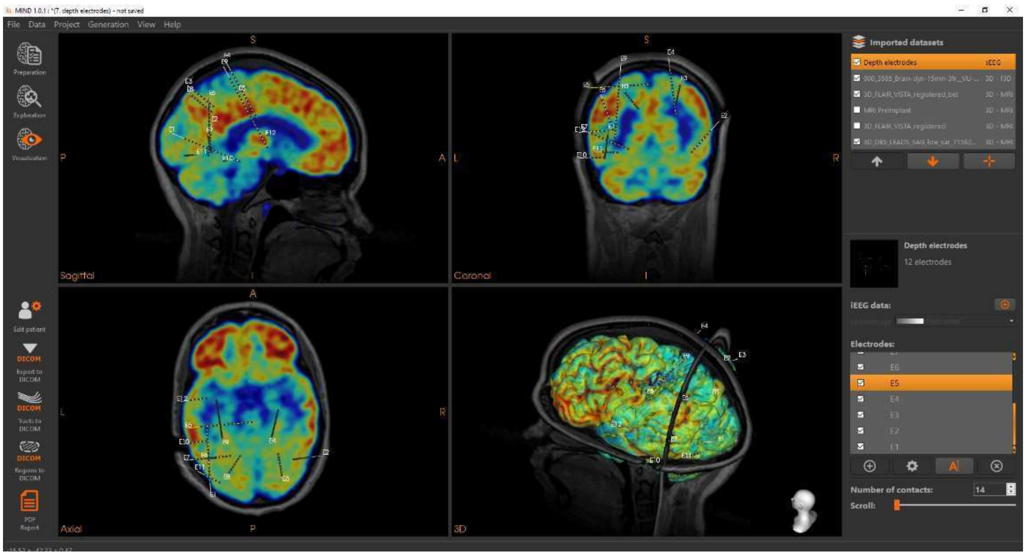
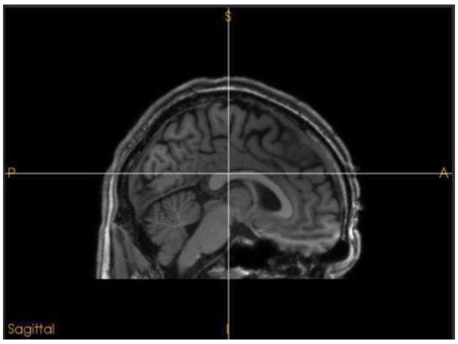


Figure 12 – Visualization in MIND of the depth electrodes fused with the imaging datasets.

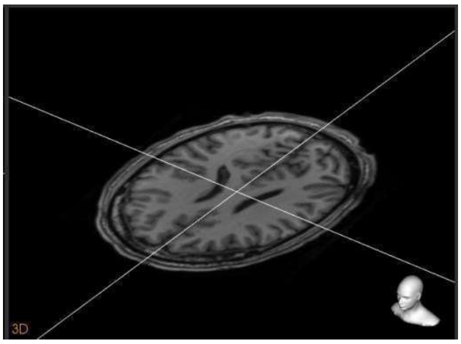
Appendix: Visualization details

3D volumes and 4D volumes

This section describes the different visualizations options and settings for 3D volume datasets.



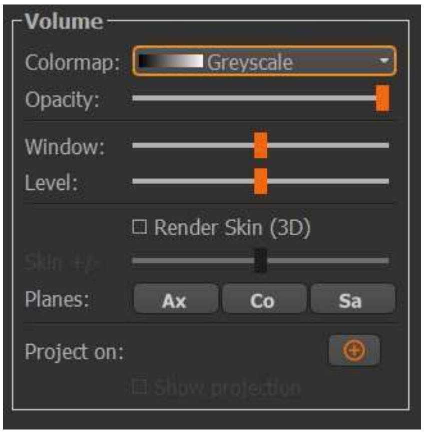
2D visualization



3D visualization

Volume datasets are visualized in the 3D viewport by a 3D rendering and/or anatomical planes. Slices through the datasets are shown in the 2D viewports.

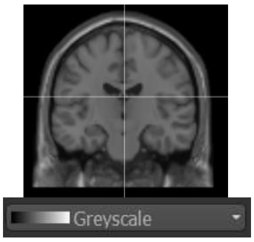
Some of the visualization options depend on the modality of the dataset.

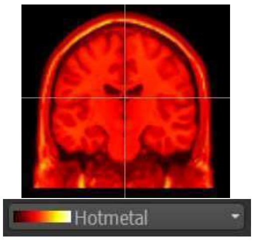


Colormap

Changes the color mapping of the values in the dataset.

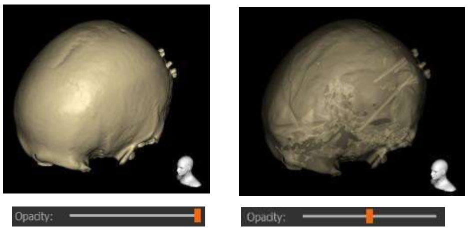
When a Colormap starts from black, the lowest intensity will be set to transparent.





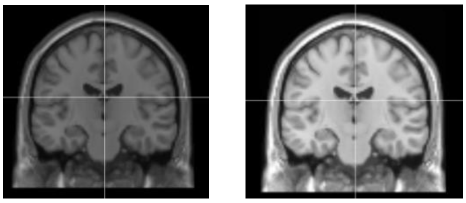
Opacity

Changes the transparency or opacity of the dataset. A value of 100% means no transparency. This setting affects all the visuals of the dataset, including its 3D renderings.



Window, Level

Changes the contrast and saturation of the dataset. Indirectly changes the values used in the color mapping.



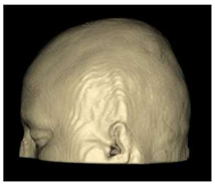
Render 3D (Skin, Cortex, Functional region)

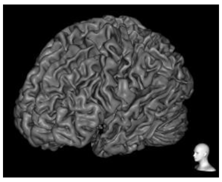
Shows or hides the 3D rendering of the dataset. The type of 3D rendering depends on the modality of the dataset: -

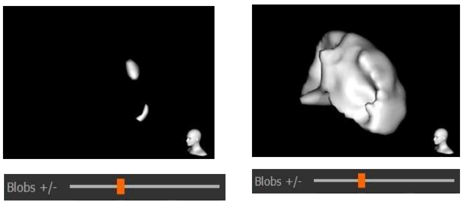
Skin (CT, MRI)

Cortex (brain-extracted MRI)

Functional region (Functional data)

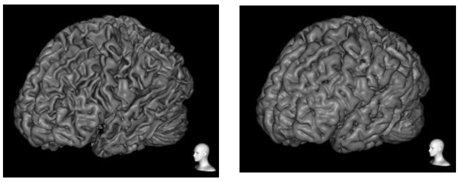

Skin


Cortex

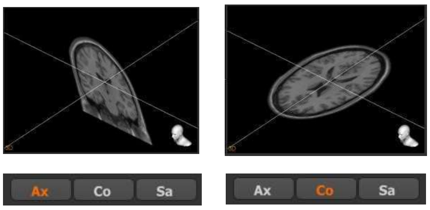


Render +/- (Cortex, Functional region)

Increases or decreases the size of the 3D rendering. This is only available for the Cortex and Functional region renderings. In the case of a Cortex rendering, it can be set to include more or fewer cortex structures. In the case of a Functional region rendering, it can be set to threshold the data resulting in larger or smaller regions.



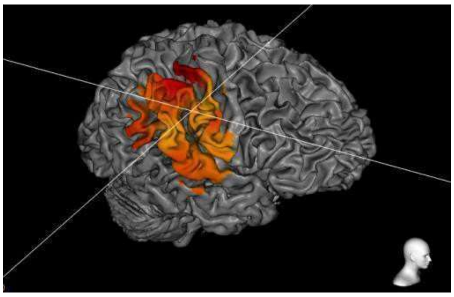
Planes



Shows or hides a splice plane in the 3D viewport. A plane can be shown for each anatomical direction: axial, coronal and sagittal.

When depth electrodes have been imported, an additional option is available that shows a slice orthogonal to the currently selected electrode.

Projection



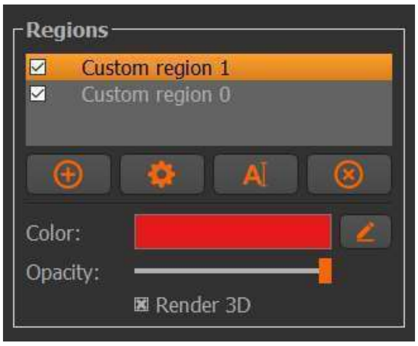
Creates or removes a projection on a volume.

Show projection

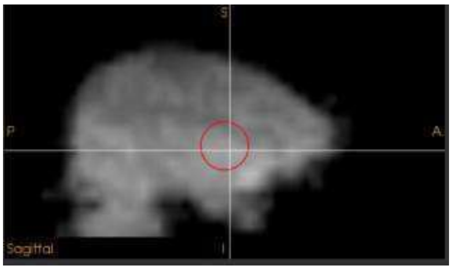
Shows or hides the current projection

Regions

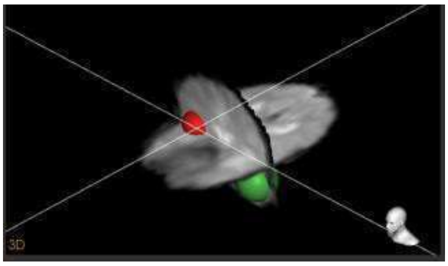
This section describes the different visualization options and settings for regions



Regions are visualised in the 3D viewport as a spherical object. The 3D viewports show slices through this object as contours.



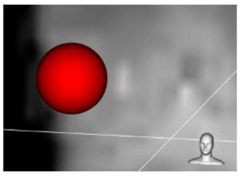
2D visualization



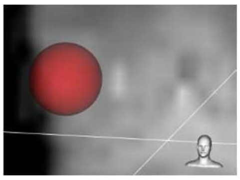
3D visualization

Opacity

Changes the transparency or opacity of the dataset. A value of 100% means no transparency. This setting affects all the visuals of the dataset in the 2D viewports.



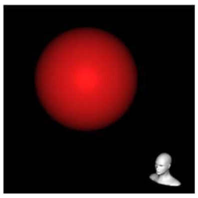
Opacity: 100%

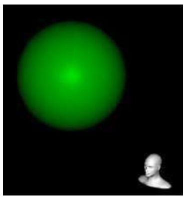


Opacity: 50%

Color

Changes the color of the rendering. This setting affects all the visuals of the dataset in the 2D viewports.

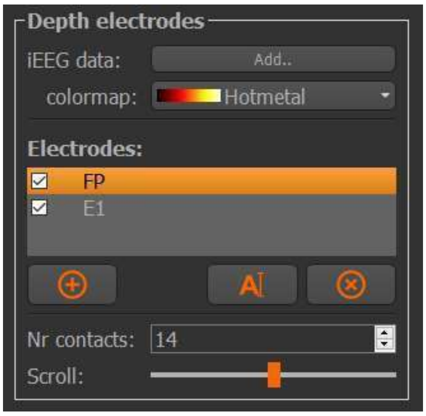




Render 3D

Shows or hides the rendering in the 3D viewport.

Depth Electrodes



Depth electrodes

iEEG data: Add..

colormap: Hotmetal

Electrodes:

☑ FP

☑ E1

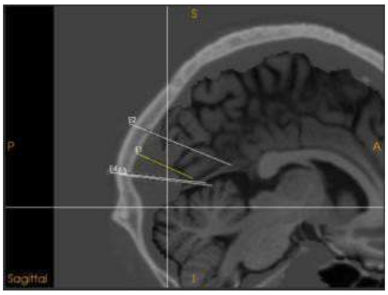
Nr contacts: 14

Scroll:

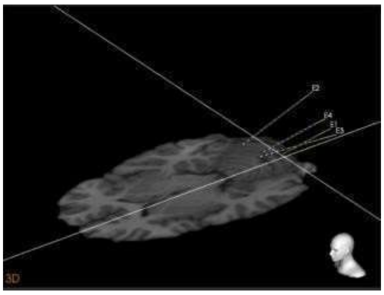
This section describes the different visualization options and settings for depth electrodes.

This step requires:

- An imported, project file created by the Depth Electrode Navigator Software – DENS



2D visualization

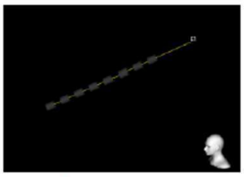


3D visualization

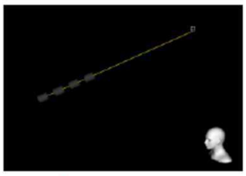
Depth electrodes are visualized as a thin line containing a number of contacts. This visualization is shown in all four viewports similarly.

Number of contacts (electrode)

The number of contacts can be changed.



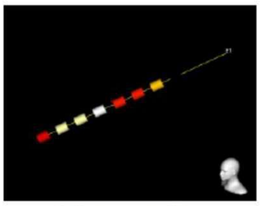
8 contacts



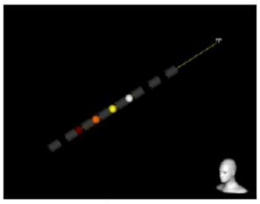
4 contacts

iEEG data

Source mapping data (iEEG data) can be visualized on the electrodes. In the case of monopolar data, the values are visualized on the contacts. For bipolar data, the values are visualized as a sphere between the contacts.



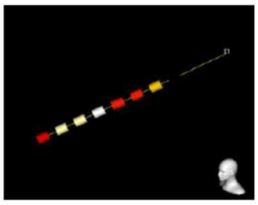
Monopolar



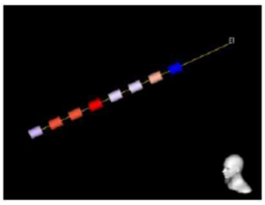
Bipolar

Colormap

Changes the color mapping of the values in the iEEG data.



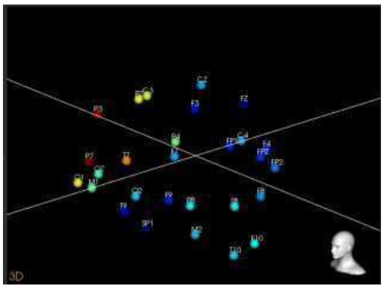
'Hotmetal'



'Temperature'

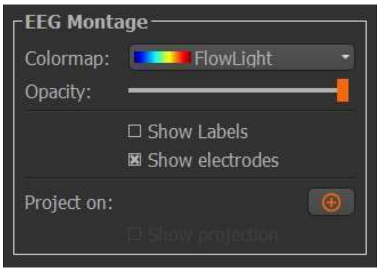
EEG equipotential maps

This section describes the different visualization options and settings for EEG equipotential maps.



3D visualization

EEG equipotential maps are only visualised in the 3D viewport. The default visualization includes the electrodes with a color mapping and their corresponding label. When available an equipotential map can be projected onto another volume.



EEG Montage

Colormap: FlowLight

Opacity:

☐ Show Labels

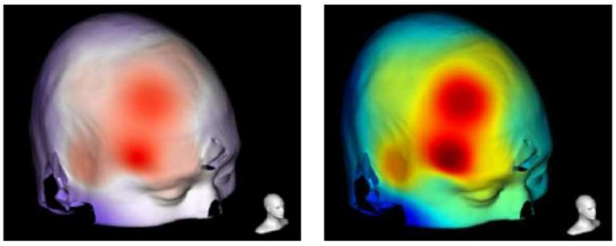
☒ Show electrodes

Project on:

☐ Show projection

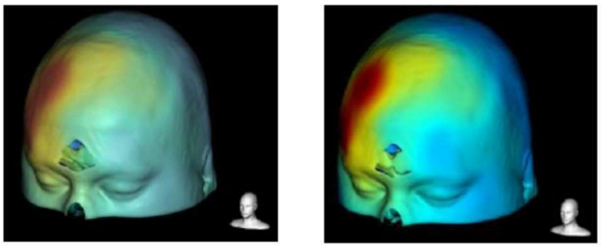
Colormap

Changes the color mapping of the values in the iEEG data.



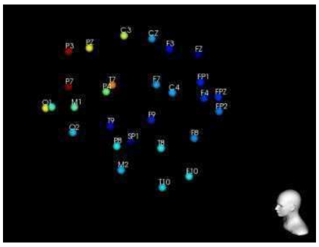
Opacity

Changes the transparency or opacity of the dataset. A value of 100% means no transparency. This setting affects all the visuals of the dataset, including its electrodes and projection.



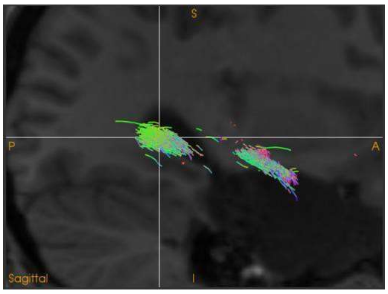
Show labels / electrodes / projection

Shows or hides the labels/electrodes/projection in the 3D viewport.

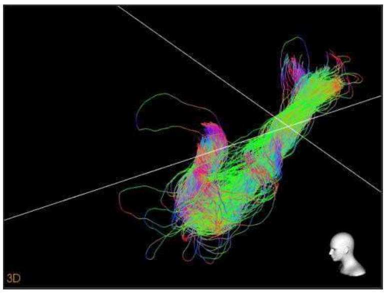


Tractography

This section describes the different visualization options and settings for tractography datasets.



2D visualization



3D visualization

Tractography datasets are visualized in the 3D viewport by rendering all individual lines simultaneously. Slices through the datasets are shown in the 2D viewports.

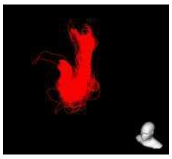
Some of the visualization options are only available when the dataset contains scalar values on each point. These options are the Colormap and threshold settings.

Tractography
Rendering: Color
color:
Opacity:
Crop size:

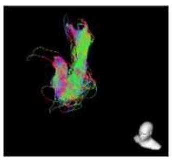
Rendering

Three render options are available:

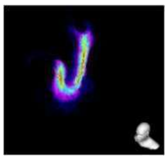
- Color: renders the entire datasets with a single color.
- Orientation: Colors the points based on the local orientation.
- Scalar mapping: Colors the points based on the scalar values.



Color



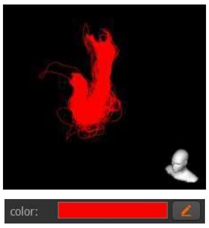
Orientation

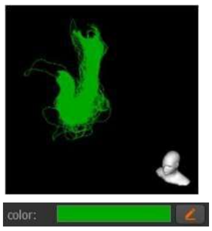


Scalars

Color

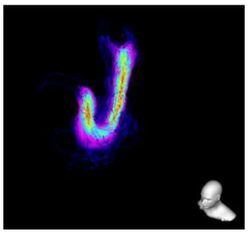
Changes the line color of the rendering.

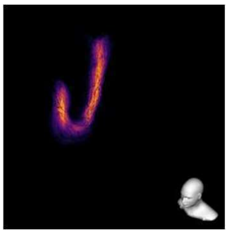




Colormap

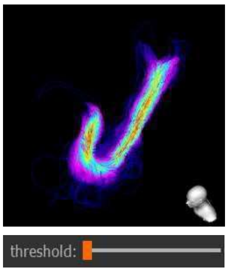
Changes the color mapping of the values in the dataset.

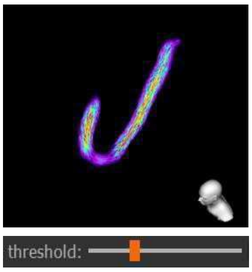




Threshold

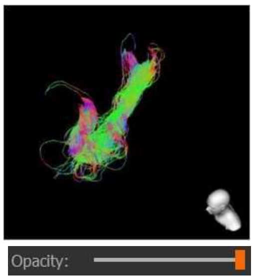
Removes parts of the dataset where the scalar values are below the threshold.

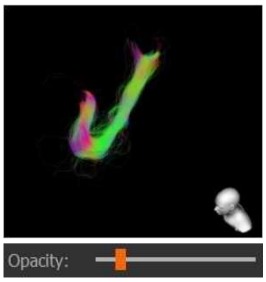




Opacity

Changes the transparency or opacity of the dataset. A value of 100% means no transparency. This setting affects all the visuals of the dataset, including its 3D rendering and slices





Crop size

Changes the contrast and saturation of the dataset. Indirectly changes the values used in the color mapping.