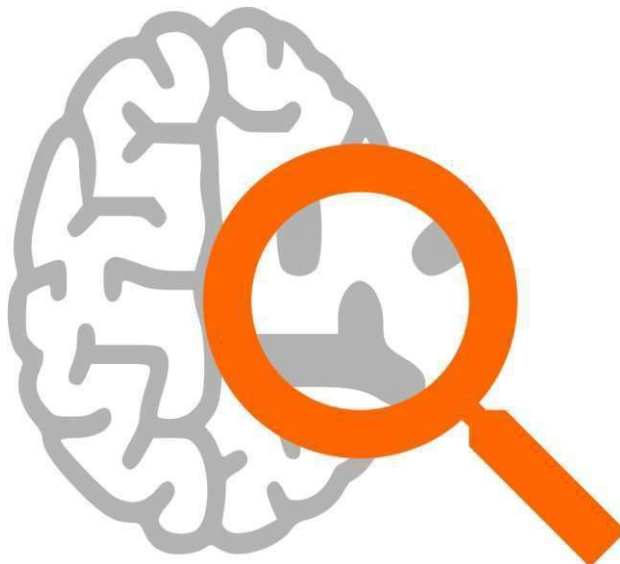


# User Manual



## VIEWER

Medical Imaging Visualization Software

DISCLAIMER: This software product was developed at 'Stichting Kempenhaeghe' as part of the Devices for NeuroControl and NeuroRehabilitation (DeNeCor) project that has received funding from ENIAC Joint Undertaking (grant no. 692470) and 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 VIEWER 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.

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# 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 VIEWER: Visualization Toolkit (VTK) and Insight Toolkit (ITK) by Kitware.

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

<b>Windows 7*</b> or higher	64-bit	MIND_install_win64.exe
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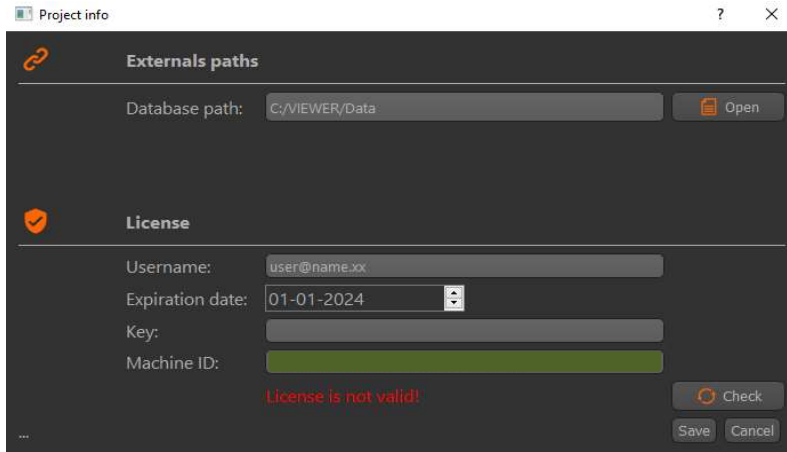
\*Microsoft C++ Redistributable 2019.

The best equipment for visualization of the medical imaging datasets by VIEWER 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

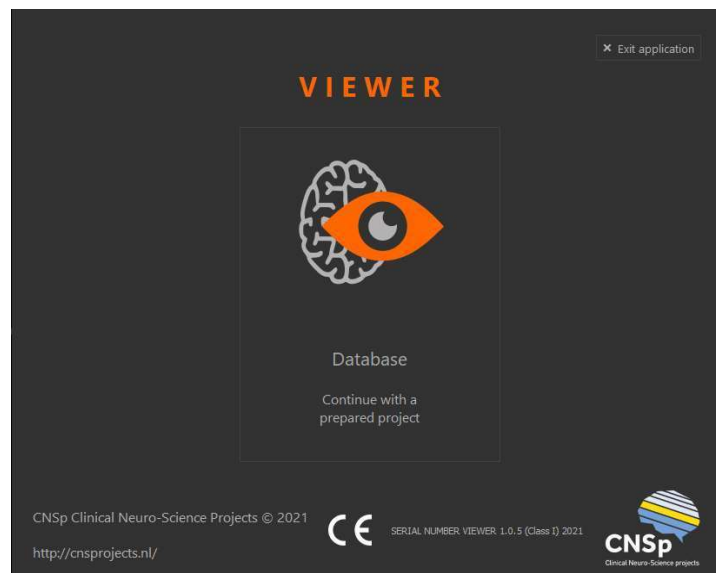
Before the software can be used, it has to be configured correctly in terms of user information and license. When the software is started for the first time, a settings window will appear for providing a valid license in order to be used. After providing the license username, expiration date and key,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



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](mailto:info@cnsprojects.nl).

## Intended use

The intended use of the viewer software (VIEWER) is that multiple users are able to visualize the content of a prepared project. For example, VIEWER can be used by the clinicians for fine tuning of a prepared project, for example while discussing a patient with colleagues at the patient management meeting, when deciding about invasive treatment, and VIEWER is very well suited for patient counselling. The difference with MIND and DENS is that with VIEWER you cannot create a project file and you cannot add datasets. You can open a prepared project that contains all the medical imaging datasets of a patient (Figure 1).



**Figure 1 – Open a prepared project in VIEWER**

## Database structure

All imported datasets and patient information are saved in the application database (Figure 2). 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.

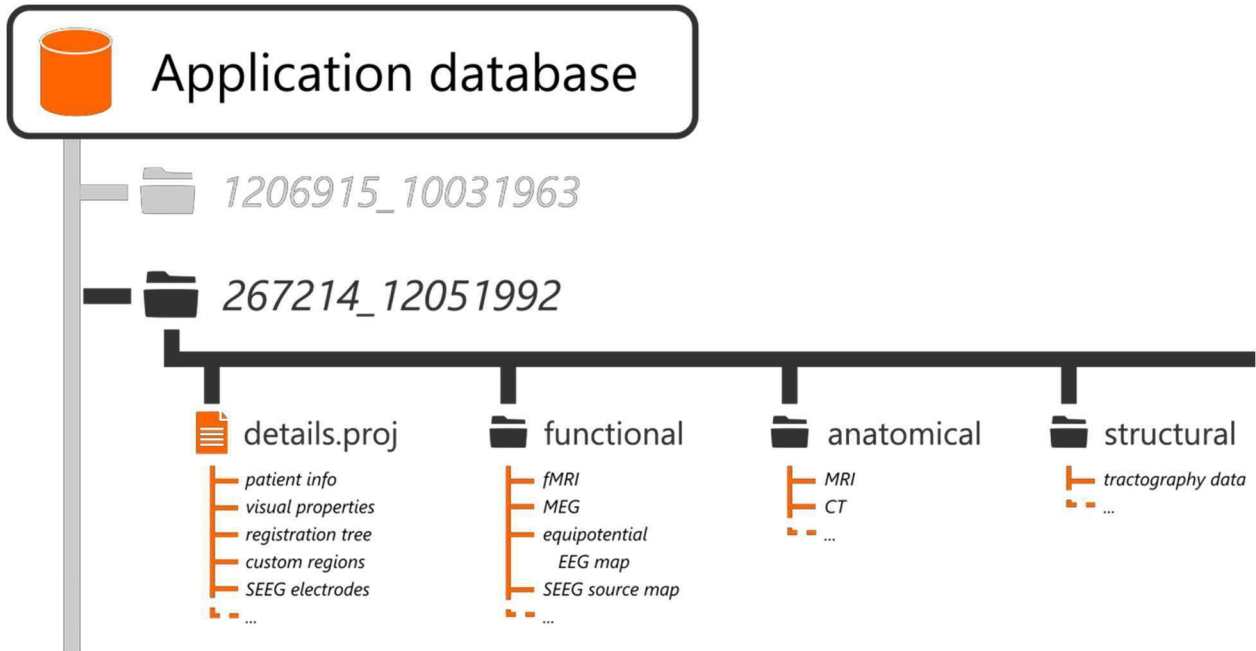


Figure 2 – Schematic overview of the application database structure.

### 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

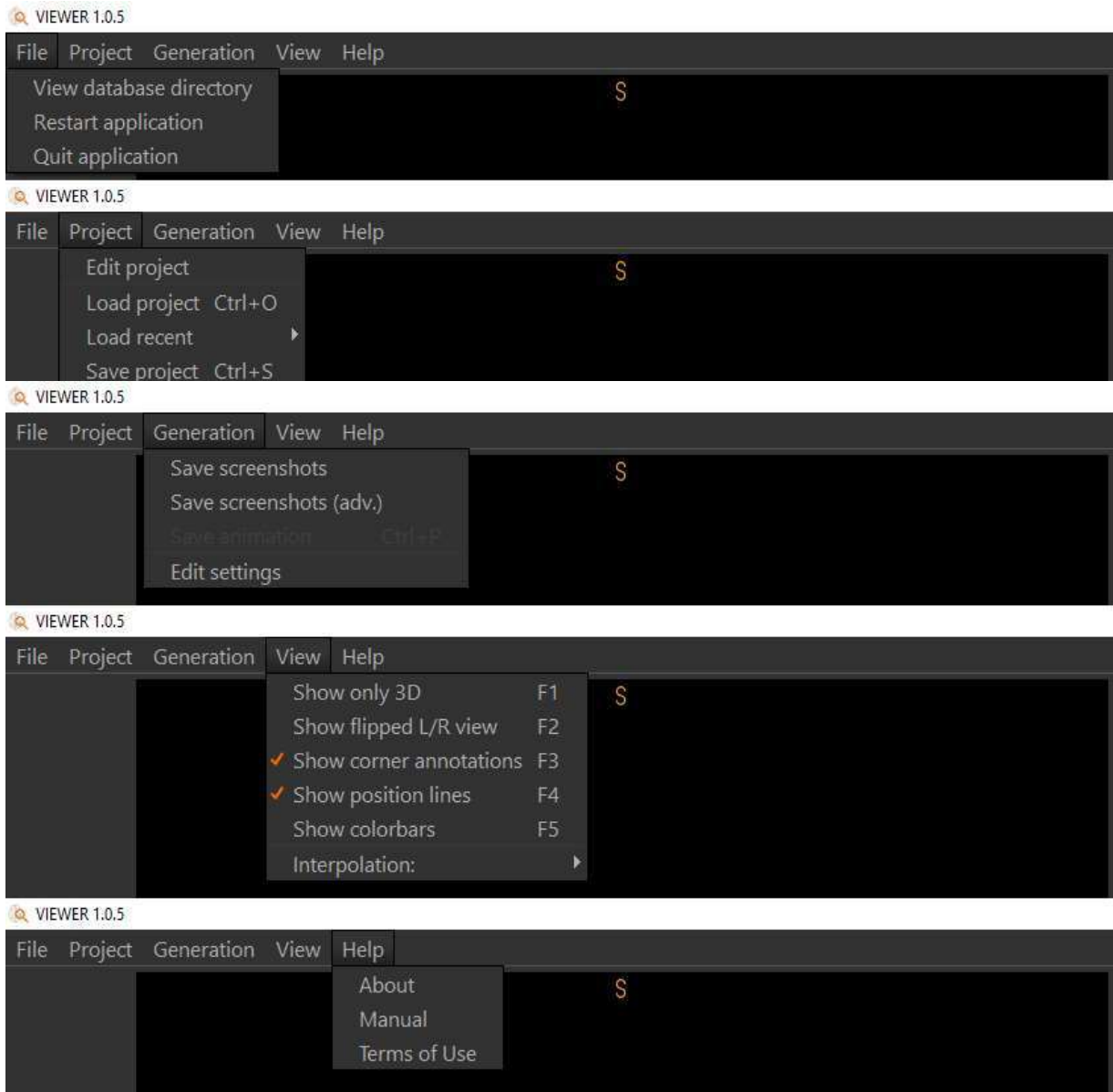
This folder contains all the imported anatomical datasets, such as: MRI, CT or tomography volumes.

### Structural

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

## User interface

Compared to the MIND software, in VIEWER the menu item < Data> is missing. Furthermore, in the scroll down menu of <Project> the option <New folder> is missing and in the scroll down menu of <Generation > the options are missing that allow preprocessing of the medical imaging datasets.



**Figure 3 – Menu items of VIEWER, from left to right: <File>, <Project>, <Generation>, <View> and <Help>, with from top to bottom the scroll down menu of each of the items.**

The main user interface of the application is shown in Figure 4a. 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 the sagittal, coronal and axial slices perpendicularly.

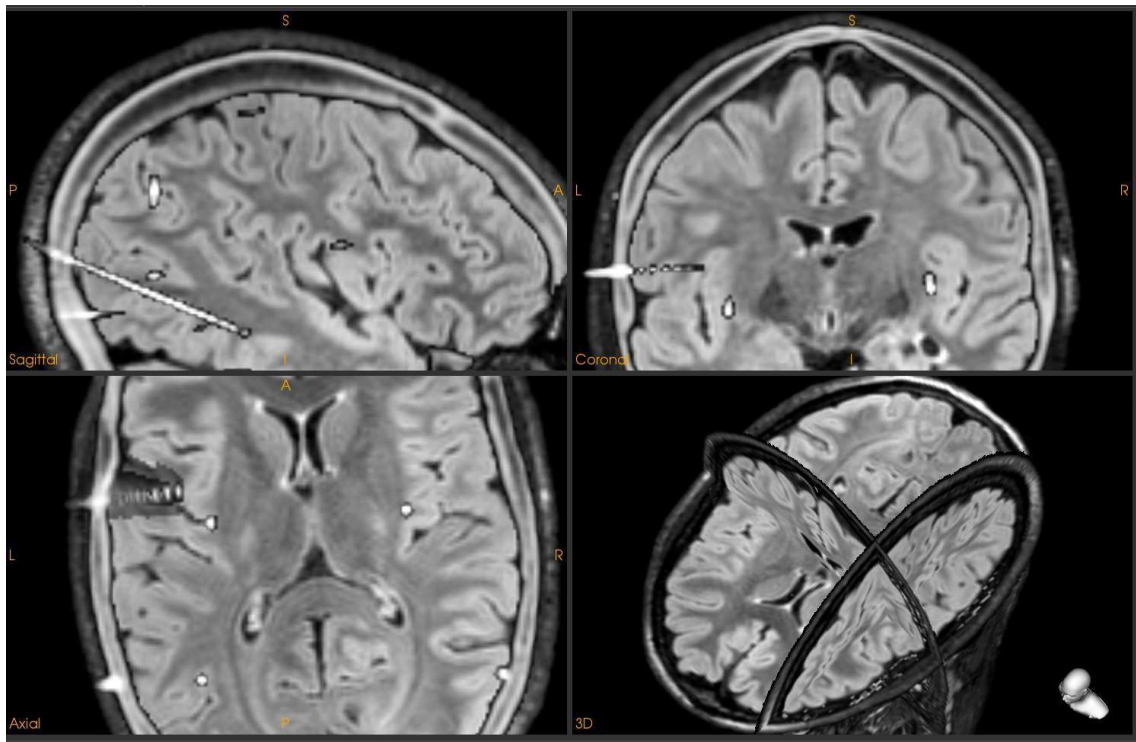


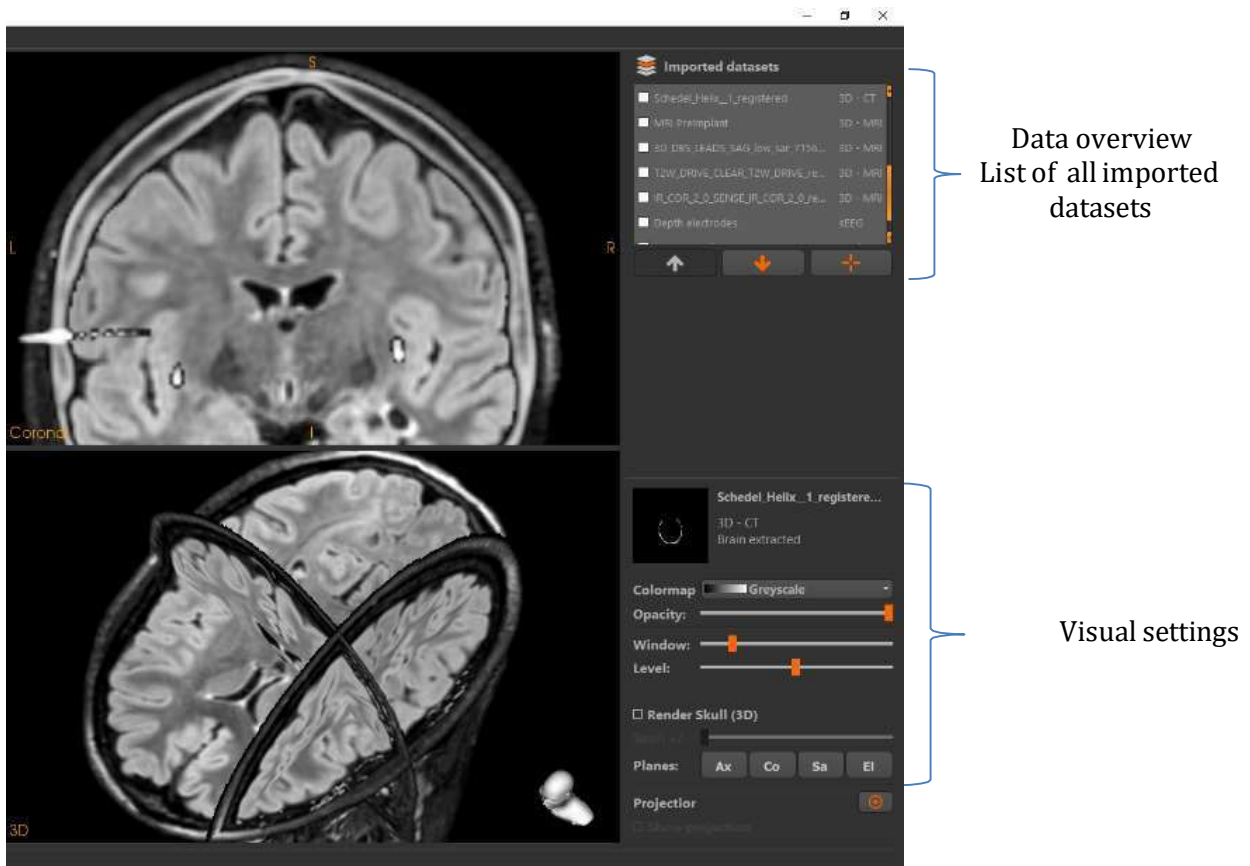
Figure 4a – 2D/3D MRI viewport.

### Data overview

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. The overview also displays the data type 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

The panel in the bottom-right corner of the interface contains the settings for visualization of the selected dataset (Figure 4b). Specific settings are available for each type of dataset. For more details, see Appendix: Visualization details on page 27.

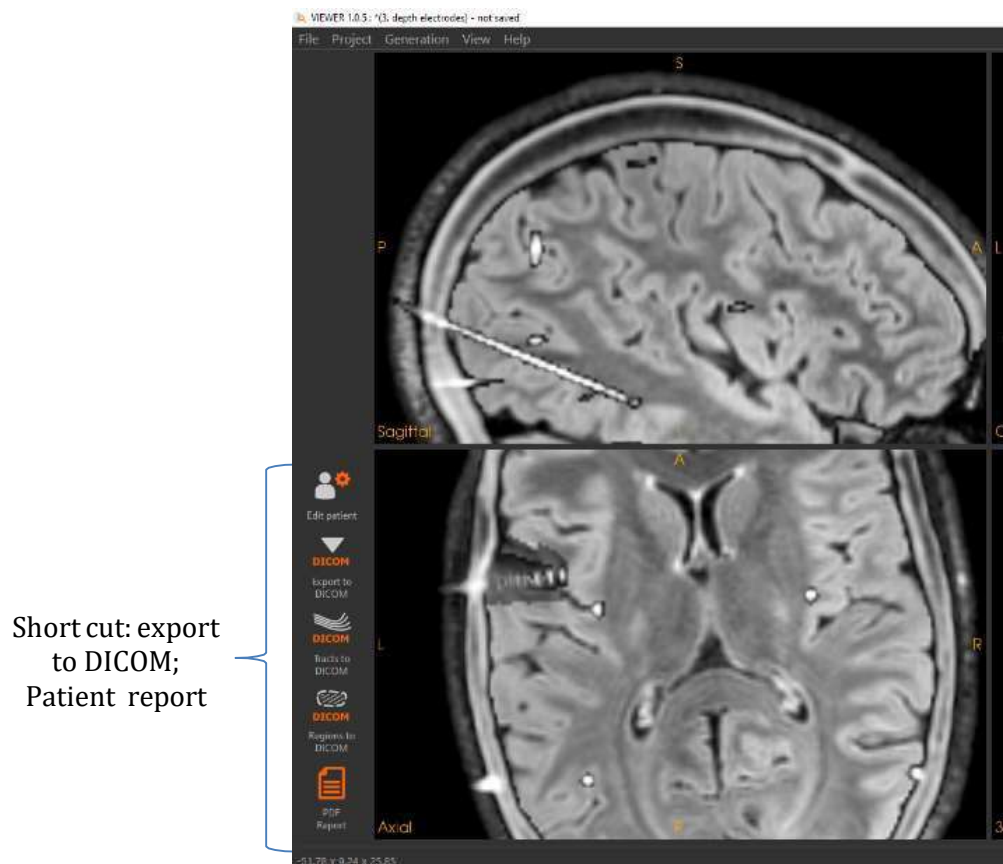


**Figure 4b – 2D/3D MRI viewport with the data overview (upper right corner) and visual settings (bottom right corner).**

## Toolbar

The toolbar at the left of the 2D/3D MRI viewport (Figure 4c) includes short cuts to control the output controls, including the button <edit patient> to give as input further information about the patient, which will be included together with the patient ID in the patient report. The buttons DICOM control the output of the medical images as DICOM files, of tracts to DICOM files and of Regions (ROIs) to DICOM files.





**Figure 4c – 2D MRI viewport with in the left panel the short cuts to create output i.e. DICOM output and a patient report.**

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

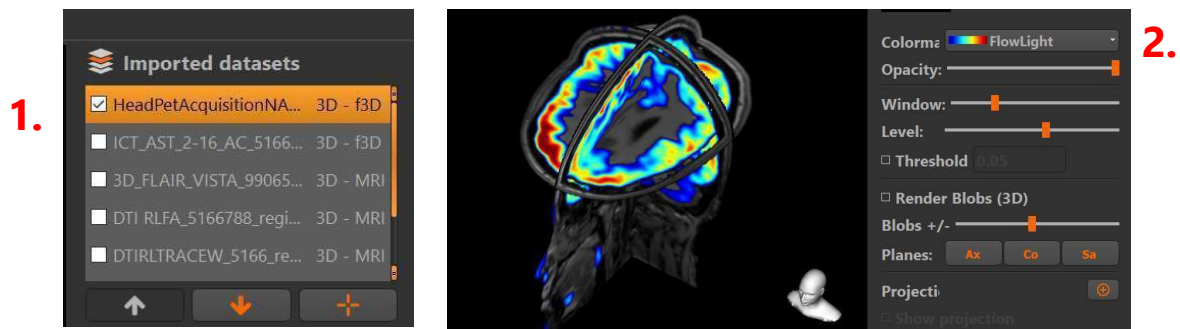
## II. Functionality of VIEWER

In VIEWER you can view the medical imaging datasets in a multi-modal fashion and adapt the visualization of each of the images which are imported by the clinician as part of a prepared project.

### Multi-modal visualizations

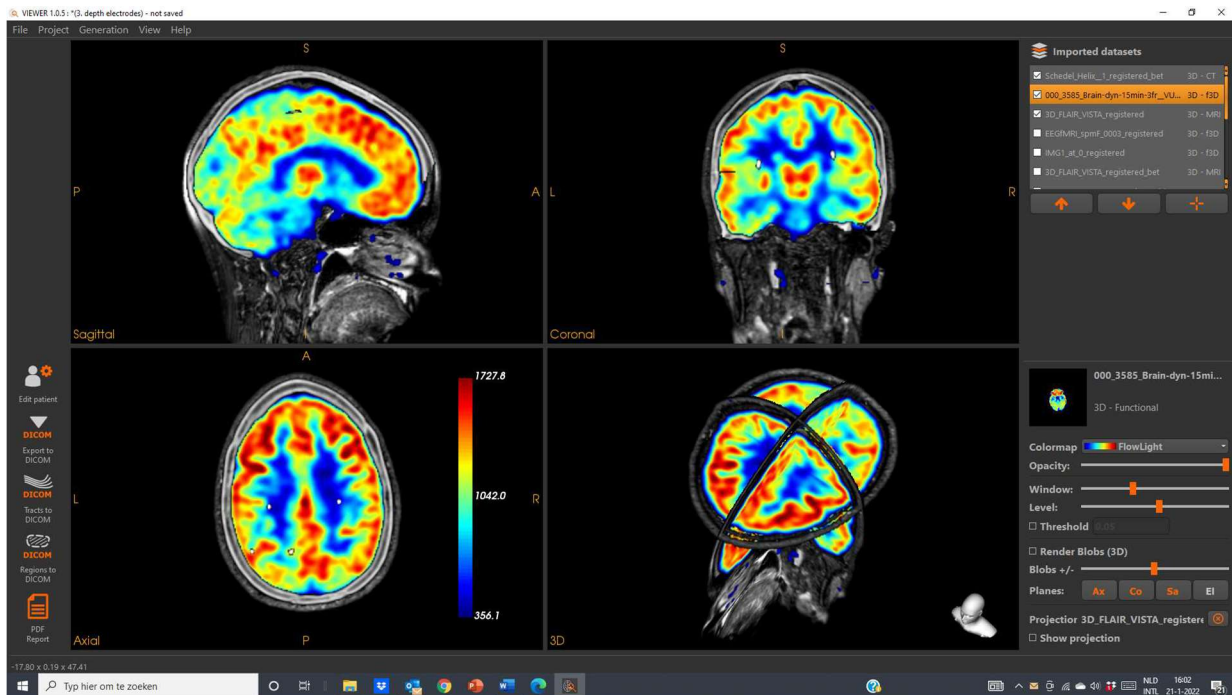
When multiple datasets have been loaded, they can be visualized together in a multi-modal visualization.

1. **Show the medical imaging datasets** by turning the datasets on in the overview. 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.
2. **Adjust the visual settings** of the anatomical datasets.
  - Enable the 3D anatomical planes by selecting Ax, Co and Sa.
  - 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.



- 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 5 displays the complete user interface with visualization in the 2D/3D MRI viewport the CT, Flair MRI and PET in the patient specific co-ordinate system.



**Figure 5 – 2D/3D visualization of CT, Flair MRI and PET in the patient specific co-ordinate system.**

## Creating a cortical projection

In case of a cortical projection (see Figure 6) the intensities of the functional dataset are projected on the surface of a cortical rendering (based on the brain extracted MRI). Datasets that can be used to create a projection are: functional 3D-datasets such as fMRI and EEG/MEG source maps.

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

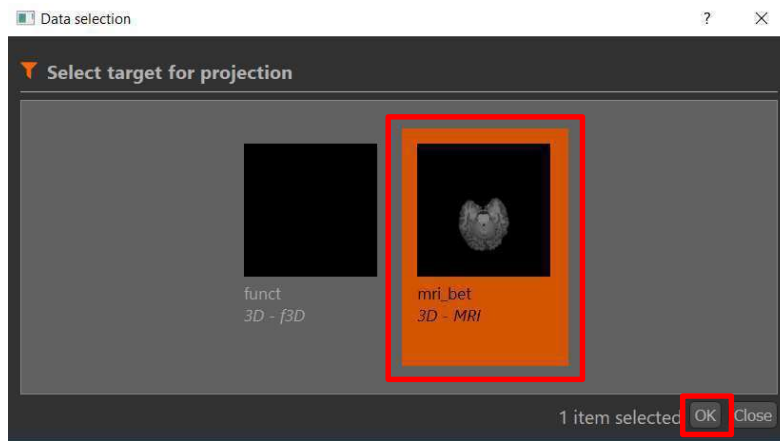
**2. Click** on the 'New projection' button.




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 'Show' button changes to a delete button.  this will remove the projection.

### Visualization of the fMRI datasets

Select the fMRI dataset in the panel of the top right part of the interface. Choose for color mapping 'Spectrum' (1) and set based on the color bar (2) the threshold (3) for display (Figure 6). In the 3D- MRI viewport the orthogonal planes of CT and MRI are displayed, together with the cortical rendering. The intensity distribution of the fMRI activation map is projected on the surface of the cortical rendering (4).

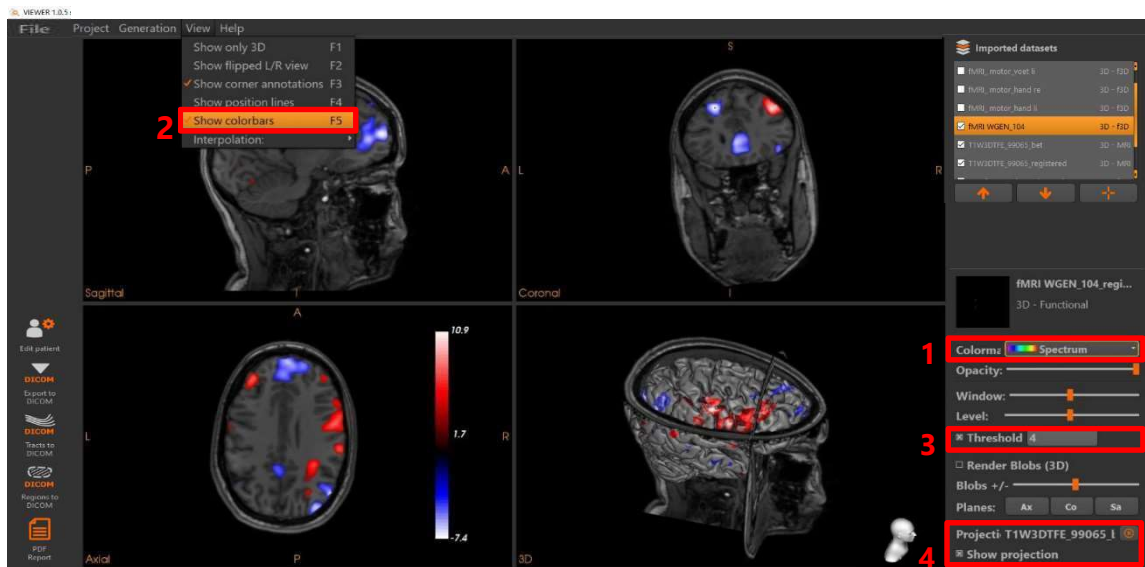
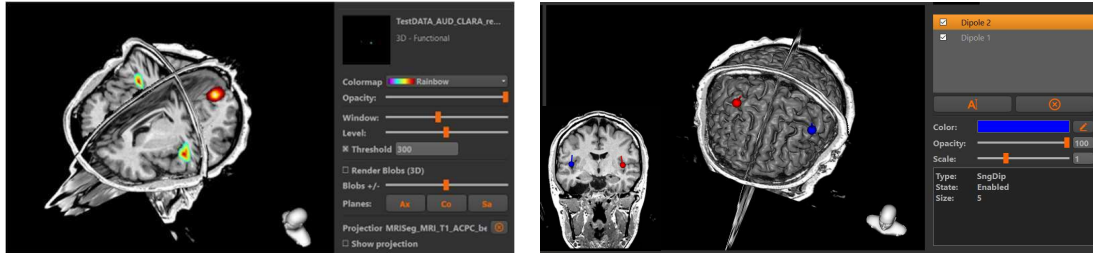


Figure 6 – 2D/3D visualization of fMRI (word generation) dataset.

## Source mapping

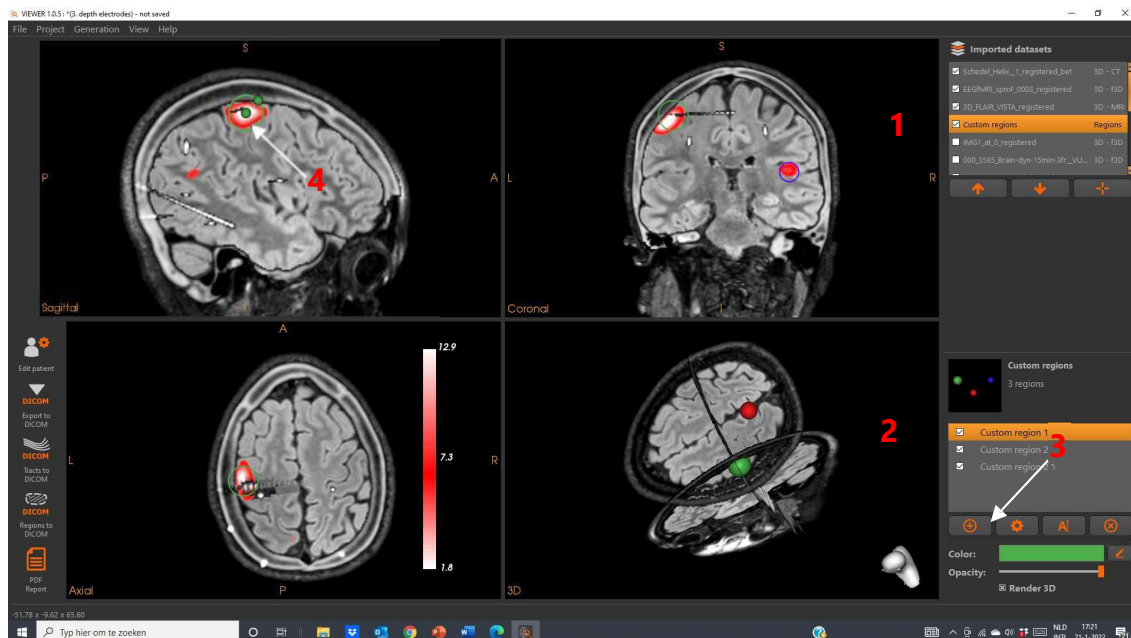
For the visualization of distributed source mapping results the source maps need to be co-registered with the 3D-MRI dataset in the patient specific brain. Shown are the 3D-images of the source maps of bilateral auditory responses and of a visual response, in 3 orthogonal planes (left) and as cortical projection (right).



Notice that dipole sources generated by the BESA research software can be visualized and marked by custom regions in MIND and visualized in VIEWER. The custom regions can be exported imbedded in the MRI as DICOM files.

## Edit regions of interest

You can edit and remove or add custom regions or regions of interest in VIEWER. For example to indicate abnormalities at MRI or edit in VIEWER the custom regions that mark the most relevant activation spots of the EEG-fMRI activation map (Figure 7).



**Figure 7 – Edit and add or remove custom regions to identify interesting findings at the functional images.**

1. **Select the dataset** <custom regions>.
2. Select < custom region 1>
3. Press the wheel to edit the custom region
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 Confirm button.**

6. **Adjust the color** of the custom region



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



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

## Edit depth electrodes

### Correcting depth electrode detection results

VIEWER enables the clinician to check the accuracy of the detection of the base and tip of the depth electrode and of the number of detected contact points which can be manually corrected or improved and of course enables to edit the labels of the depth electrodes.

Check the position of the depth electrodes one by one by scrolling through the depth electrode, from base (upper row) to tip (middle row) and check the number of contact points versus the anatomy (bottom row). Follow the next steps for editing the position of the electrodes and number of contact points.

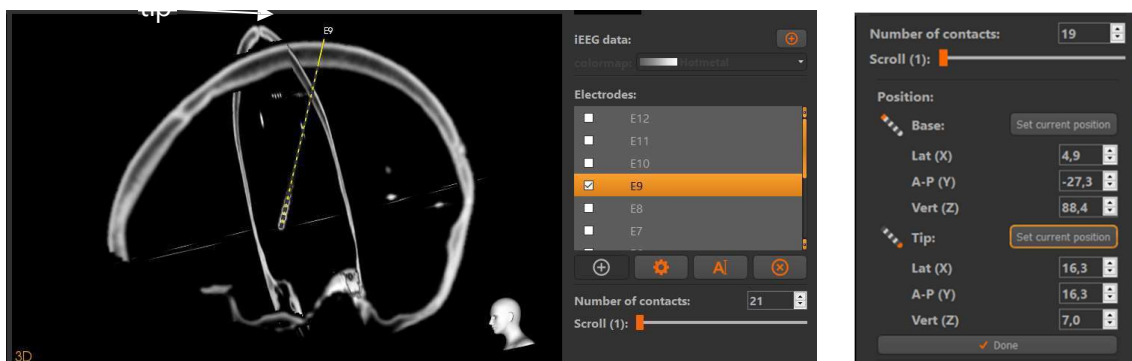
1. Press after selecting the electrode to be edited the wheel that opens the panel for editing the positions of the depth electrodes.



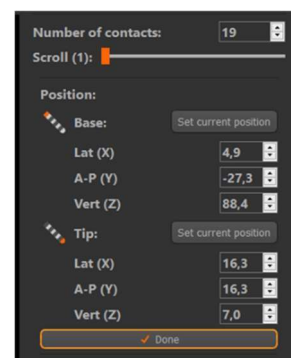
- Identify based on the CT-artefact that crosses with the skull the base of the depth electrode and select the base: Press in the panel at the right bottom of the interface <Set current position>.



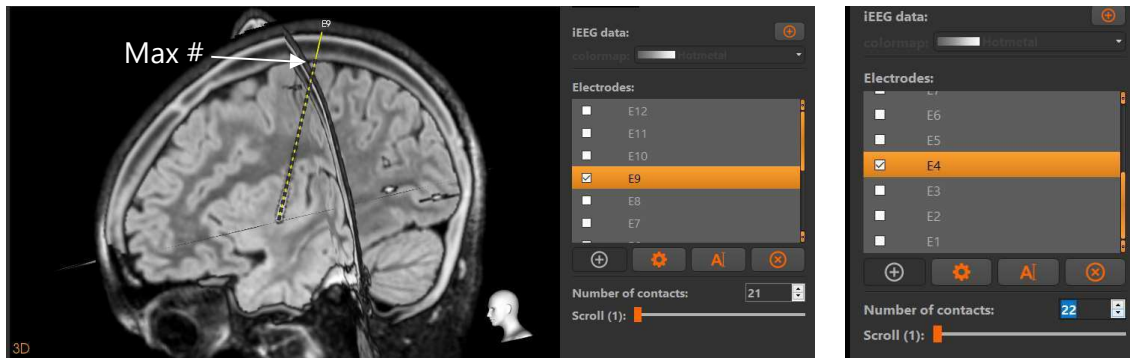
- Identify based on the CT-artefact the tip of the electrode and select the tip: Press in the panel at the right bottom of the interface <Set current position>.



- When satisfied about the position of the depth electrode press <Done> (bottom).



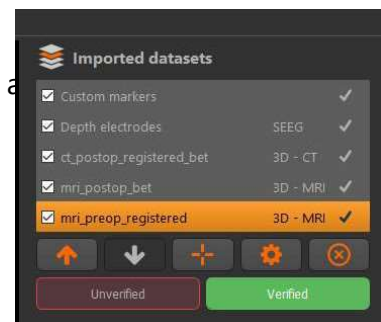
- To check the estimated number of electrode contacts select in the panel of the right upper part of the interface the MRI and adapt the number manually if needed.



## Edit annotations of depth electrode recordings

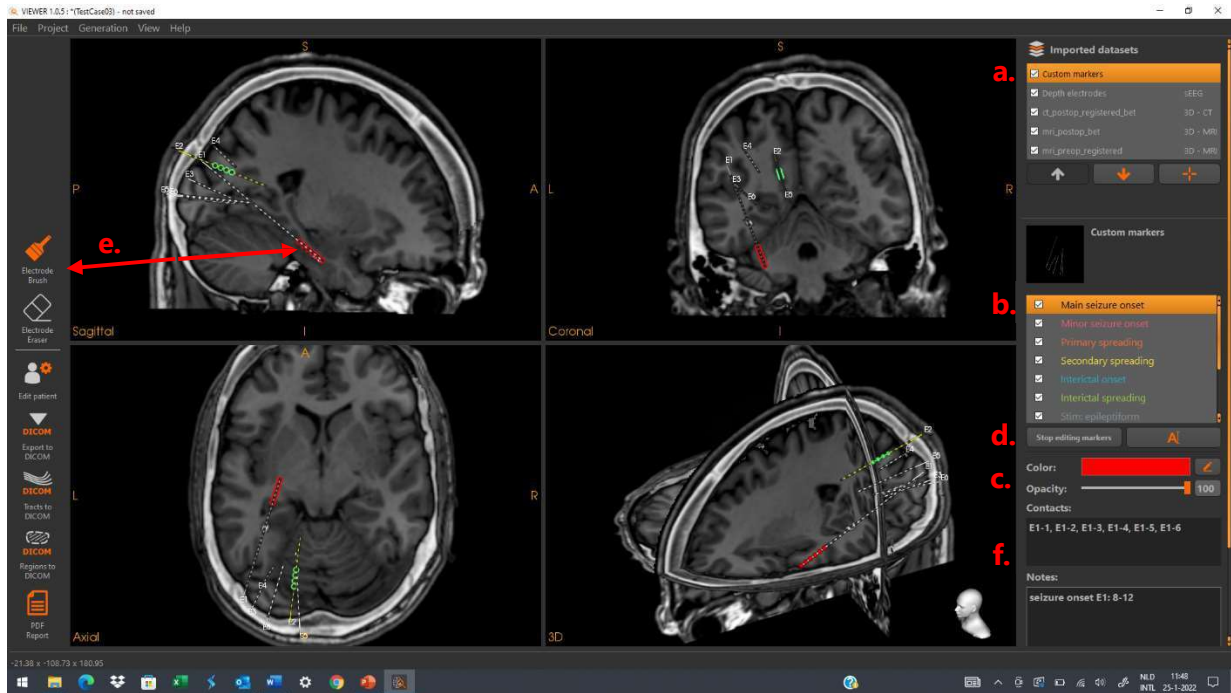
You can check and edit the annotations added to the depth electrodes: you also can do this in real time, e.g. when discussing the treatment options of a patient at a patient management meeting.

- In DENS the dataset < Custom markers > was created to add a dataset for depth electrodes. Verify the dataset < Custom markers > before the project file is saved.



- Open the project file in VIEWER
- Option I: follow in Figure 8 steps -a till f - to add the annotations:
  - Select in the list of datasets the dataset < Custom markers >
  - Select the category e.g. Main seizure onset.
  - Adapt if needed color or opacity
  - Select the button < Start editing markers > (is a toggle). In the left panel the buttons appear: Electrode brush for adding markers and Electrode erase, for erasing markers.
  - Brush the contact points of the electrode searched for in the 2D/3D MRI viewpoints.
  - An update of the names of the electrodes and the numbers of the contact points is listed in the right panel of the user interface, below the heading Contact points. In the panel < Notes >, add free text.





**Figure 8 – Option I: Edit annotations by searching in the 2D/3D MRI viewports for the contact points of a depth electrode to add or remove annotations.**

4. Option II: If electrodes are close or even crossing it will be difficult to add annotations by identifying through slicing of the 2D/3D-MRI viewports the contact points of your choice. Follow in this case, the procedure as illustrated in Figure 9:
  - a. Select the dataset <Electrodes> and select the electrode to be annotated, e.g. E2 as indicated in Figure 9 and scroll to the contact point.
  - b. Select the dataset < Custom markers>.
  - c. Select the category e.g. Stim: Motor (i.e. response to motor stimulation) and change the label to Stim:Visual.
  - d. Select the button <Electrode brush> and brush the contact points of E2.
  - e. Add free text.
  - f. If you are ready press <Stop editing markers>.



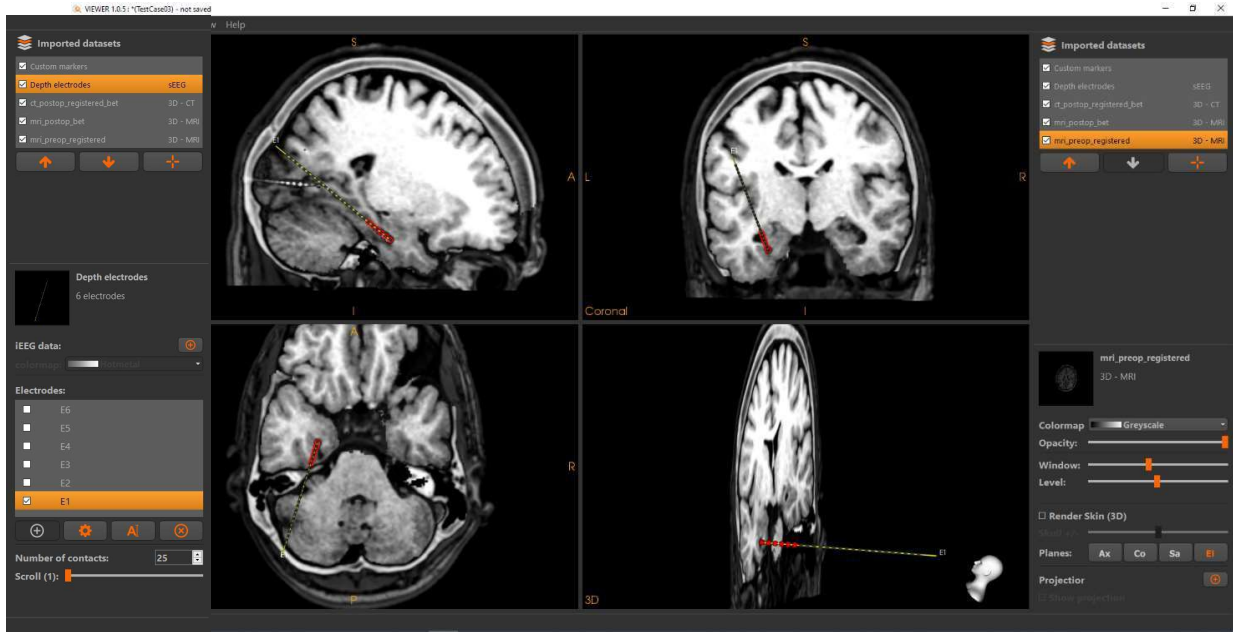
**Figure 9 – Option II: Add annotations after selecting the electrode and contact point of your choice.**

## Check the targeting of the depth electrodes

In case of thermocoagulation it is useful to know what the targeting of the depth electrode is in relation to the cortical anatomy.

1. Select in the list of the Imported datasets the dataset Depth Electrodes and double click on electrode E1 to visualize only this particular electrode (left panel of Figure 10).
2. Select the pre-operative MRI and select as one of the Planes **E1** (right panel of Figure 10)

As result of step 1 and 2 the electrode of interest, with annotations marking the seizure onset, is visualized in the tangential plane (in the sagittal slice) and in the 3D-viewport perpendicular to the axial slice.

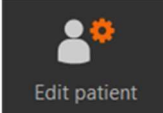


**Figure 10 – Check the target of the depth electrode of your choice versus the cortical anatomy of a patient.**

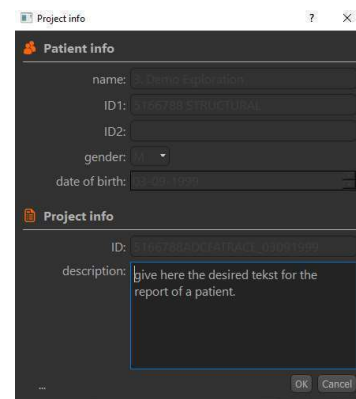
### III. Create output

#### 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 of the case can be provided in the Patient info window

- Select the button 

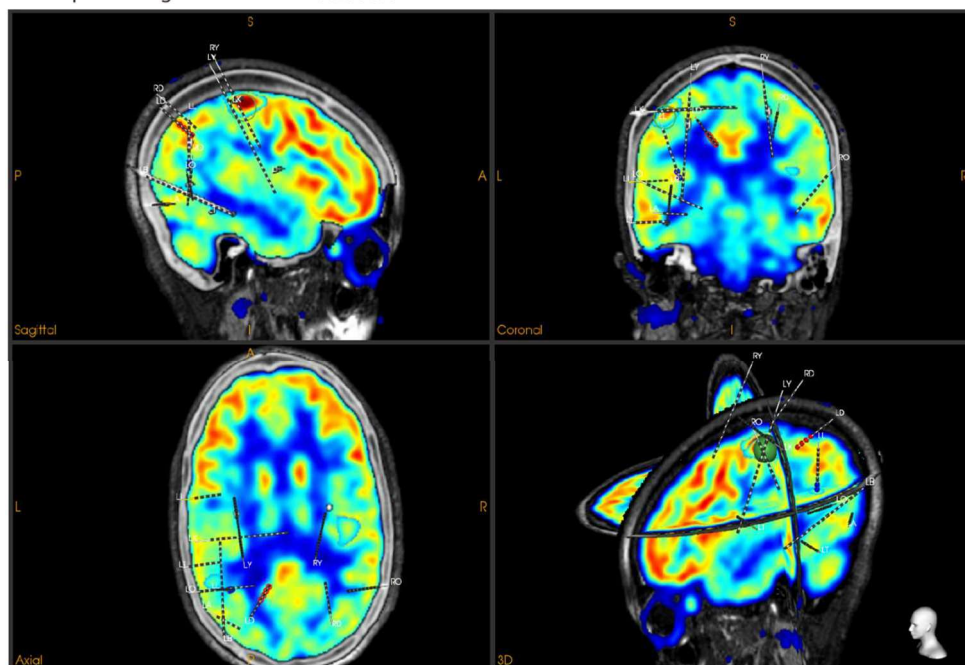
- Provide the textual input in the Patient info window



- The current visualization of the 2D/3D MRI viewport is saved together with the following information:
  - patient information given as input in the window <Patient info>
  - The listing of the electrode contacts and the textual input given as notes describing the annotations at the electrode contacts.

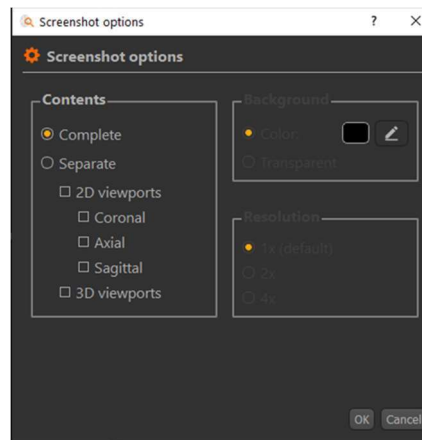
Patient name / day of birth / gender	3. depth electrodes / 01.01.1900 / M
ID 1:	Patient3
ID 2:	
Project ID:	3_20190903
Secondary spreading(LL-2, LL-1): Main seizure onset(LD-1, LD-2, LD-3, LD-4):	

This report was generated with VIEWER



This report was generated on: di Jan 25 2022, 16:44:21

2. Add if needed screenshots of the visualizations
- **Save screenshots** by following the menu item < Generation/Savescreenshots>, giving the shown options.



## Exporting volumes as DICOM

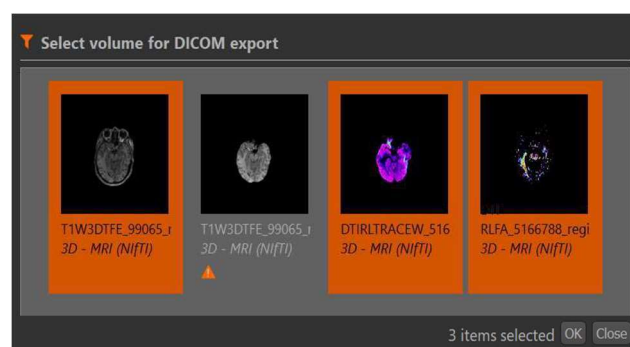
Three dimensional volumes can be exported as DICOM files. This allows for data export to other software, including commercial neuro-navigation software used in the planning of epilepsy surgery.

### 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 contains files that might be overwritten, the user is asked to overwrite the files.

## Exporting custom regions as DICOM

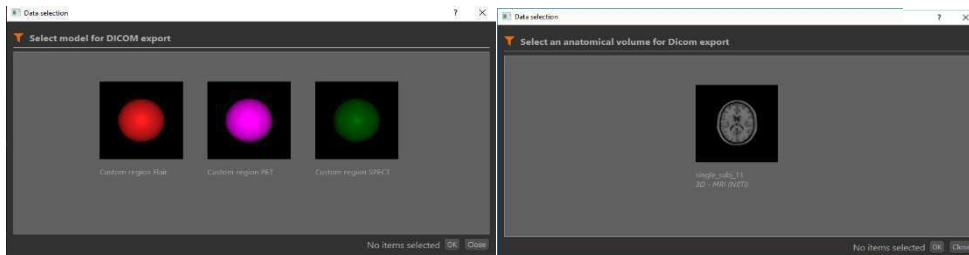
Custom regions will be added to an anatomical DICOM dataset, by overlaying the border of the region in white on top of the anatomy.

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**.



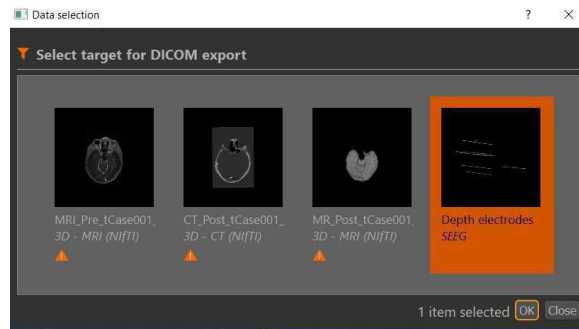
4. Select an output directory and press **Ok**.

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

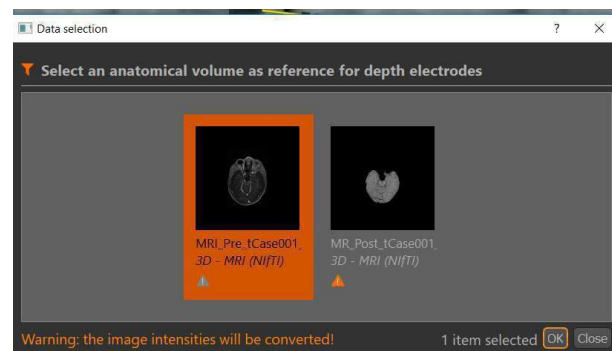
The DICOM files will be exported with their location in the application. This will ensure that aligned volumes will stay aligned after export.

## Exporting depth electrodes as DICOM

1. Click on **Electrodes to DICOM** (button left panel interface).
2. Select the dataset **Depth electrodes** for export.



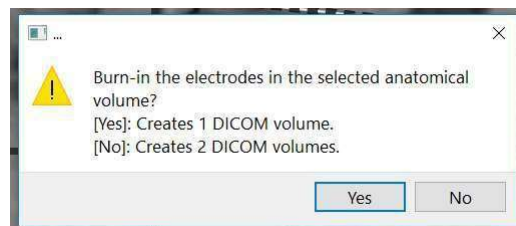
3. **Click Ok** and select in the pop/up window an **output directory**



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

*"The DICOM files will be exported while their volumes will stay aligned after export."*

5. **Click OK** and select in the pop up window **one of the options**:

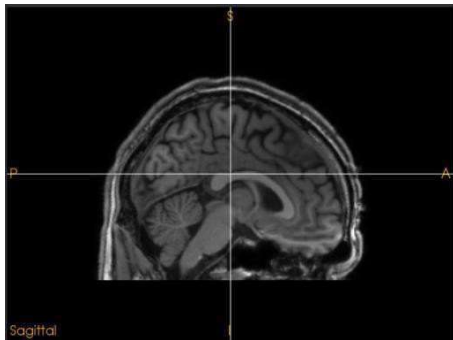


- Yes: a DICOM is created with the electrodes imbedded in the MRI
- No: two DICOMS are created, one with the MRI and the other with the depth electrodes, thus enabling the overlay of the electrodes.

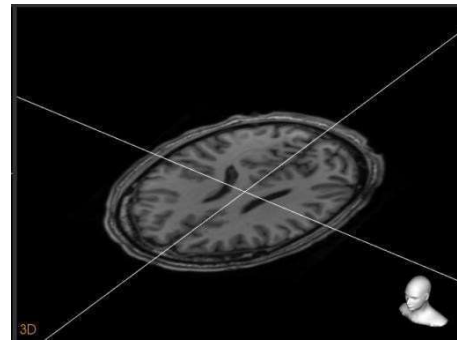
## Appendix: Visualization details

### 3D volumes

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



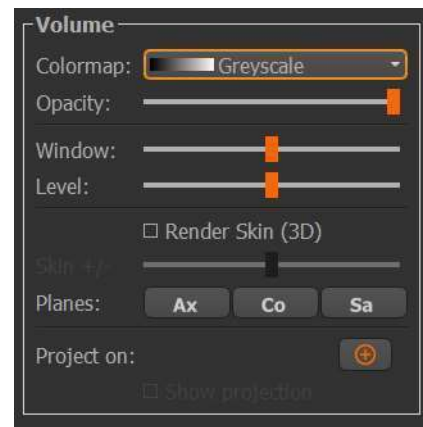
2D visualization



3D visualization

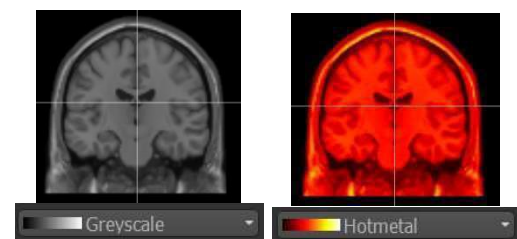
Volume datasets are visualized in the 3D viewport by a 3D rendering and/or anatomical planes. Slices through the datasets are shown in the 2D viewports.

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



#### Colormap

Changes the color mapping of the values in the dataset.

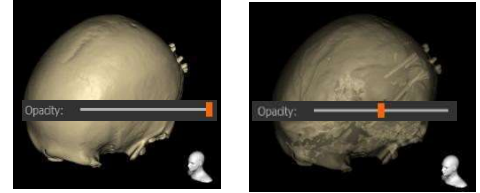


When a Colormap starts from black, the lowest intensity will be set to transparent.



## 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

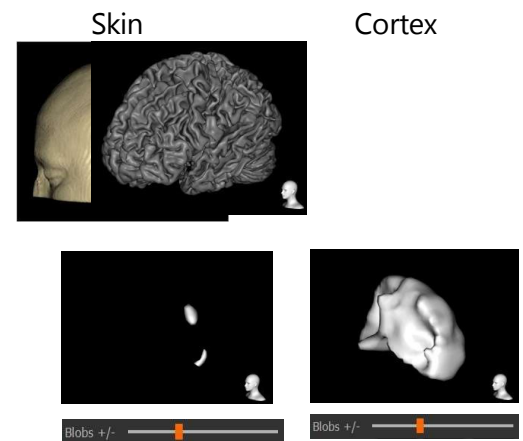
Changes the contrast and saturation of the dataset. Indirectly changes the values used in the color mapping.



## Render 3D (Skin, Cortex, Functional region)

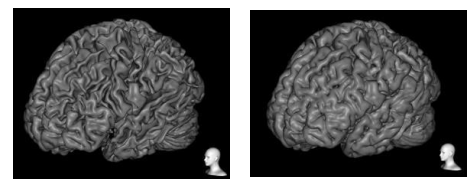
Shows or hides the 3D rendering of the dataset. The type of 3D rendering depends on the modality of the dataset: - Skin (CT, MRI)

Cortex (brain-extracted MRI) Functional region (Functional data)



## Render +/- (Cortex, Functional region)

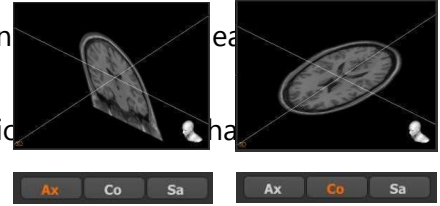
Increases or decreases the size of the 3D rendering. This is only available for the Cortex and Functional region renderings. In the case of a Cortex rendering, it can be set to include more or fewer cortex structures. In the case of a Functional region rendering, it can be set to threshold the data resulting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



### Planes

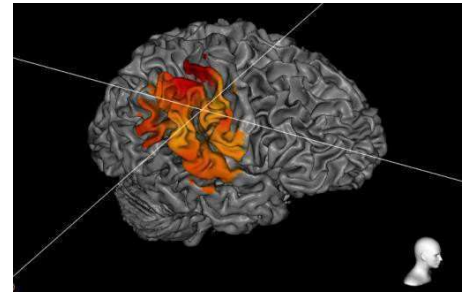
Shows or hides a splice plane in the 3D viewport. A plane can be selected in three directions: axial, coronal and sagittal.

When depth electrodes have been imported, an additional optical plane is shown, orthogonal to the currently selected electrode.



### Projection

Creates or removes a projection on a volume.



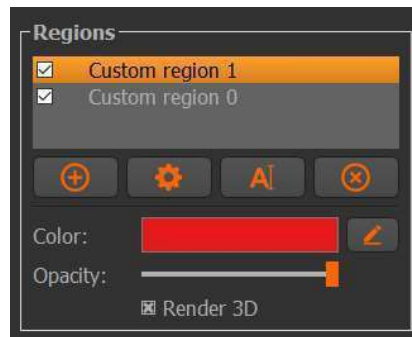
### Show projection

Shows or hides the current projection



### Regions

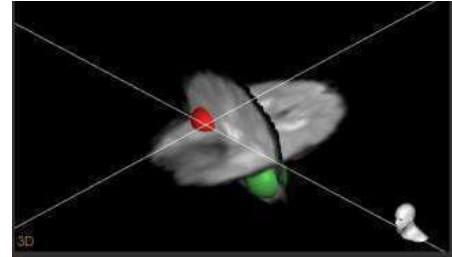
This section describes the different visualization options and settings for regions



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



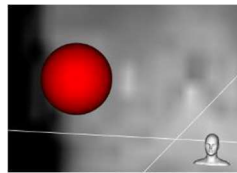
2D visualization



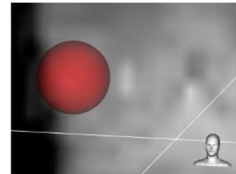
3D visualization

### 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.



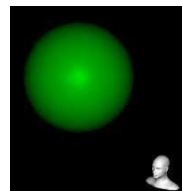
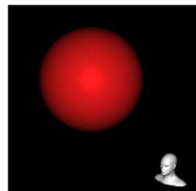
Opacity: 100%



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.

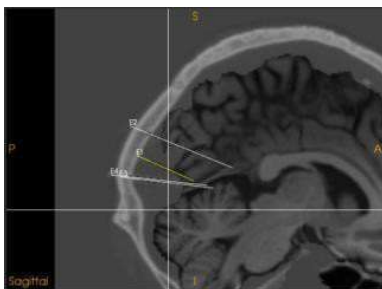
## Depth Electrodes

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

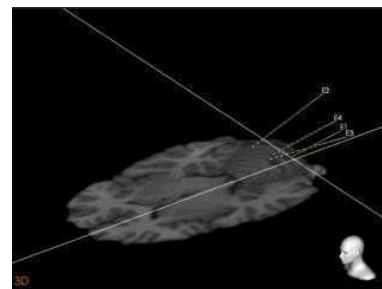


This step requires:

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



2D visualization

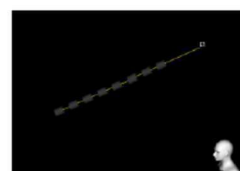


3D visualization

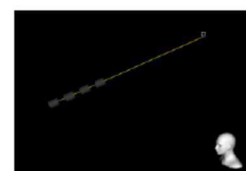
Depth electrodes are visualized as a thin line containing a number of contacts. This visualization is shown in all four viewports similarly.

### Number of contacts (electrode)

The number of contacts can be changed.



31 8 contacts



4 contacts