g·tec
GUGER
TECHNOLOGIES

g. *HReeg*

HIGH RESOLUTION EEG

advanced biosignal processing and analysis

http://www.gtec.at
office@gtec.at

VERSION 5.16.02

USER MANUAL

CONTENT:

To the Reader

Welcome to g.tec's world of medical and electrical engineering!
Discover the only professional biomedical signal processing platform under MATLAB and Simulink. Your ingenuity finds the appropriate tools in the g.tec elements and systems. Choose and combine flexibly the elements for biosignal amplification, signal processing and stimulation to perform even real-time feedback.

Our team is prepared to find the better solution for your needs.

Take advantage of our experience!

Dr. Christoph Guger   Dr. Guenter Edlinger

Researcher and Developer

Reduce development time for sophisticated real-time applications from month to hours.
Integrate g.tec's open platform seamlessly into your processing system.
g.tec's rapid prototyping environment encourages your creativity.

Scientist

Open new research fields with amazing feedback experiments.
Process your EEG/ECG/EMG/EOG data with g.tec's biosignal analyzing tools.
Concentrate on your core problems when relying on g.tec's new software features like ICA, AAR or online Hjorth's source derivation.

Study design and data analysis

You are planning an experimental study in the field of brain or life sciences? We can offer consultation in experimental planning, hardware and software selection and can even do the measurements for you. If you have already collected EEG/ECG/EMG/EOG, g.tec can analyze the data starting from artifact control, do feature extraction and prepare the results ready for publication.

Preface

This section includes the following topics:

Required Products

Using This Guide - Suggestions for reading the handbook

Conventions - Text formats in the handbook

Required Products

g®.HReeg uses:

g®.BSanalyze - the advanced biosignal analysis software package from g.tec

MATLAB - as basic matrix operation platform

Signal Processing Toolbox - to give access to standard signal analysis tools

Image Processing Toolbox - to generate scalp and brain boundaries from MRI/CT data

Using This Guide

Chapter "Generate ERD Maps" explains how to generate an electrode montage file and how to calculate event-related desynchronization (ERD) maps. The ERD maps are imported into g.HReeg and are shown with MRI/CT scalp and brain images.

Chapter "Generate Boundaries" shows the calculation of scalp and brain boundaries from MRI/CT data.

Chapter "Electrodes" shows how to import and show electrodes together with MRI/CT data and how to fit the electrodes to the MRI/CT data.

Chapter "Visualization" shows the 2D/3D visualization options for displaying the map-, scalp-, brain-data and electrodes. Furthermore, the manipulation of axis properties such as the rotation of the head is shown.

Chapter "Data Interpolation and Laplace Derivation" shows how to interpolate electrode positions and how to calculate a spline surface Laplace derivation.

Chapter "Help" explains the usage of the on-line help, the printable documentation and the function help.

Conventions

Item	Format	Example
MATLAB code	Courier	to start simulink, type `simulink`
String variables	*Courier italics*	`set(P_C,'`*`PropertyName`*`',...)`
Menu items	**Boldface**	Select **Save** from the **File** menu.

Hardware and Software Requirements

For Hardware and Software Requirements see the g.BSanalyze manual.

Generate ERD Maps

The Chapter **Generate ERD Maps** explains the following topics:

Create a Montage File

The Montage Creator is used to define electrode names and positions. The x-, y- and z-positions of the electrodes (e.g. measured by Polhemus Fastrak) can be loaded from files containing the coordinates in ASCII format (*.txt), boundary files (*.bnd) or can be entered manually. If the three dimensional coordinates are not available it is possible to estimate the coordinates from a planar electrode grid and using a spherical head model by performing the following steps:
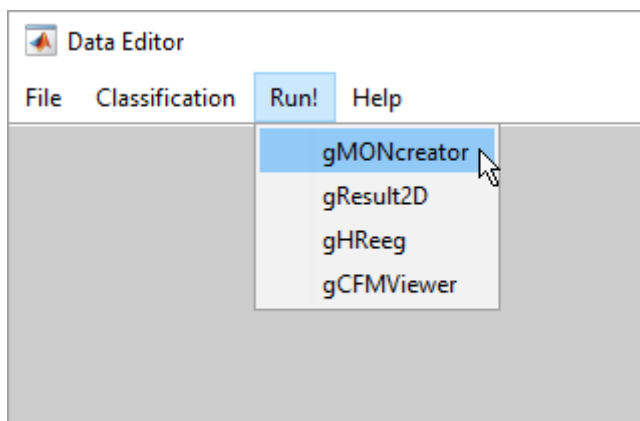
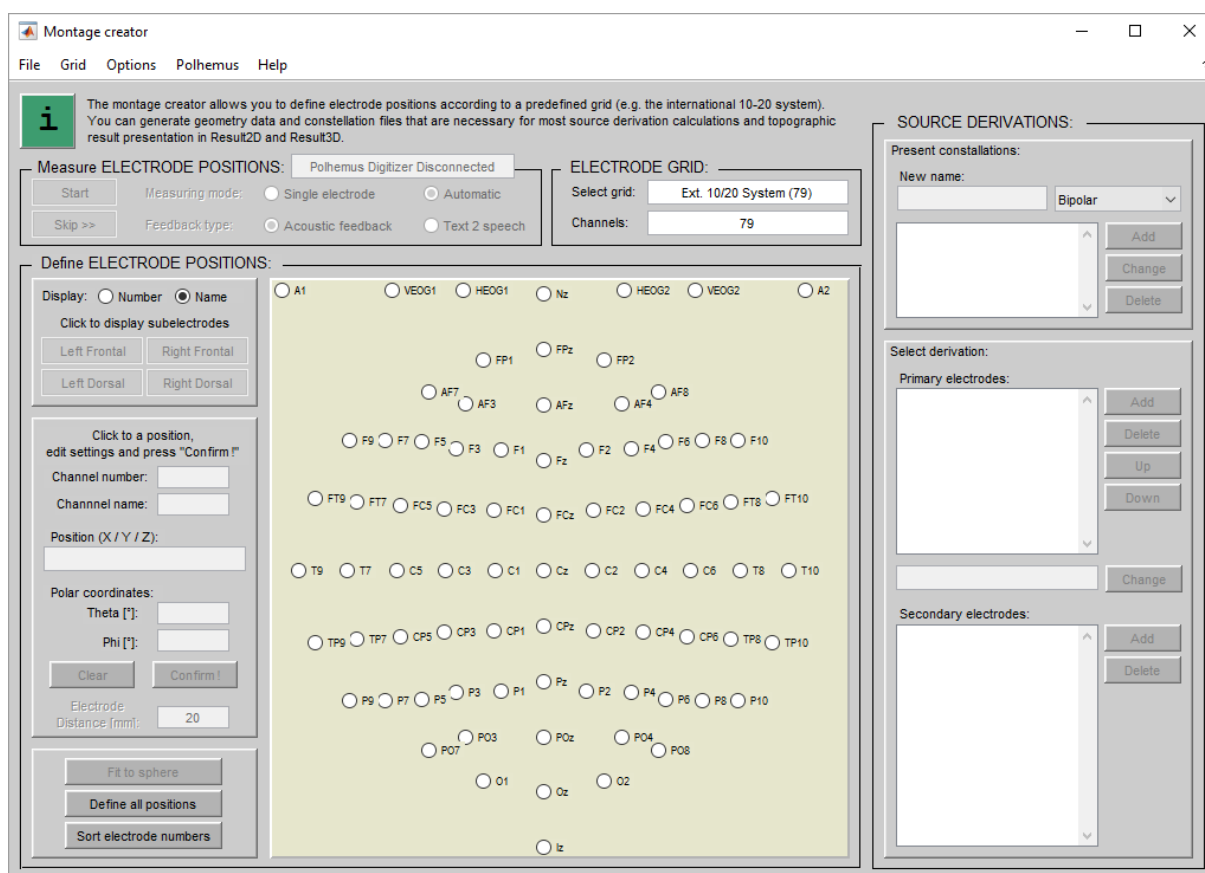1. After starting MATLAB and setting the correct path, type:

    `gbsanalyze`

    in the MATLAB command line
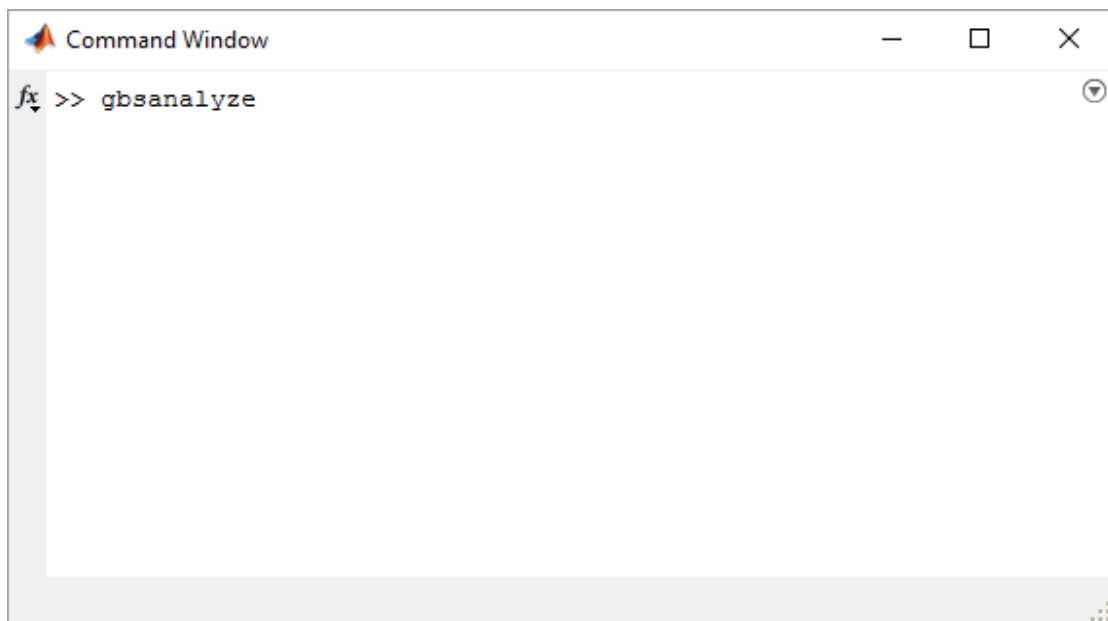
2. g.BSanalyze starts with a blank data window

3. Open **gMONcreator** from the **Run!** Menu

4. **gMONcreator** opens with the following window:

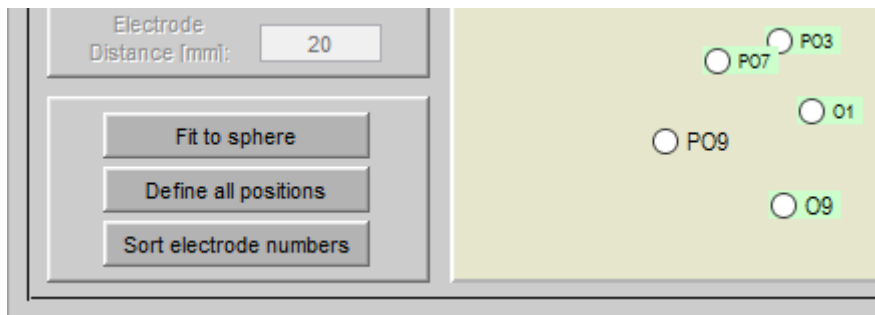## Fit the Electrodes to a Spherical Head Model

1. Click on **Load Montage** in the **File** menu and open `63ch_example.mat` from

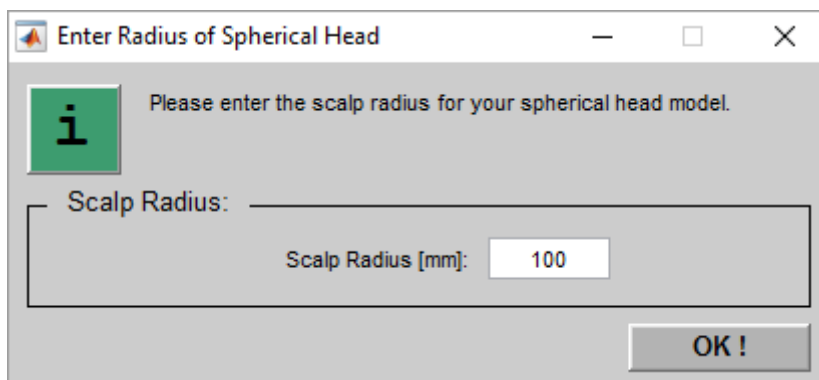   `Documents\gtec\gBSanalyze\testdata\montage`

   The Montage Creator shows a 10/10 System electrode grid with 63 defined electrodes.
   The electrode grid contains normalized x- y- and z- coordinates of the electrodes.
   Select e.g. the Cz electrode. The field **Position (X / Y / Z)** displays the coordinates:
   `0 / 0 / 1`.
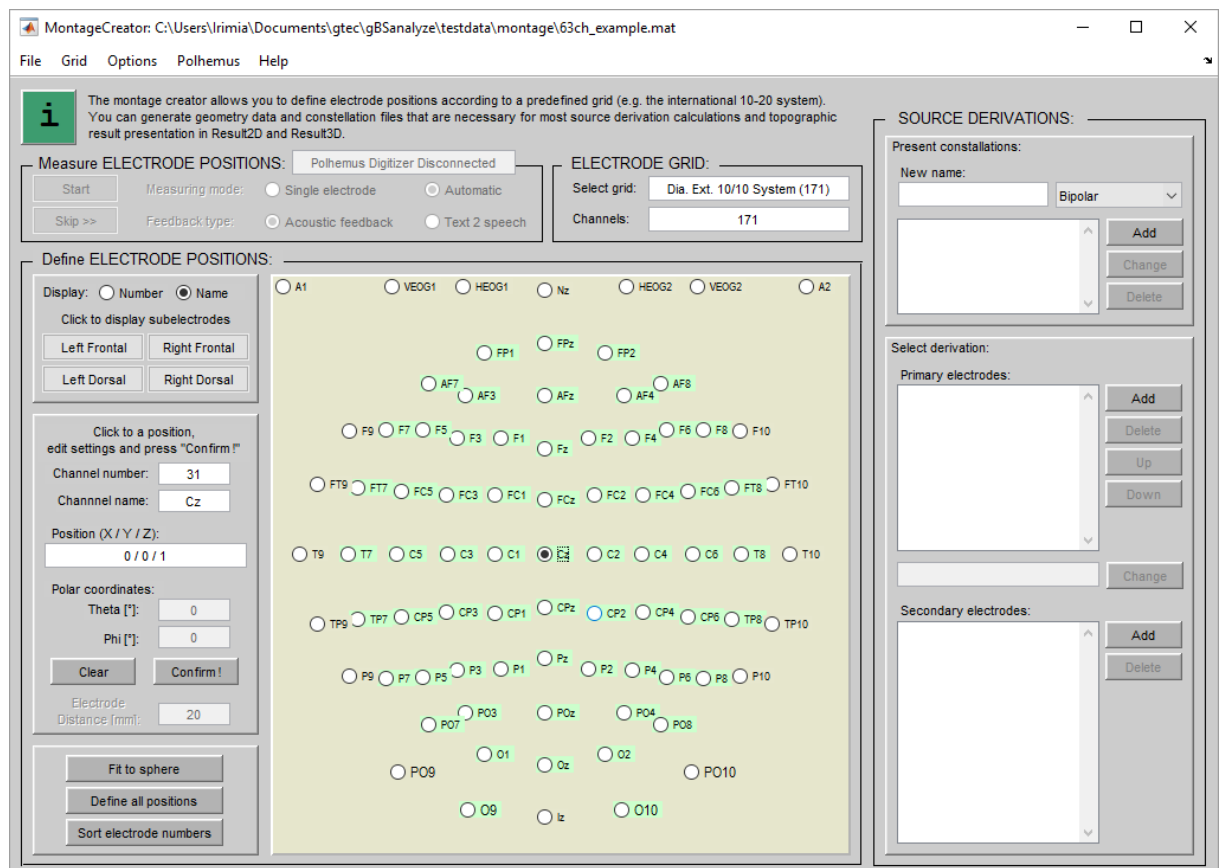
2. To fit the electrode coordinates onto a three dimensional spherical head model click on one of the defined electrodes and then press the **Fit to sphere** button

A window opens asking for the scalp radius for estimation

Enter `100` mm as the radius of the spherical head model and press **OK**.

The Montage Creator estimates the coordinates. Select e.g. the Cz electrode which has now the **Position (X / Y / Z):** `0 / 0 / 100` mm.

3. Select **Save montage as...** from the **File** menu and save the montage as `63ch_xyz.mat` under

`Documents\gtec\gBSanalyze\testdata\montage`

Load Electrode Positions

1. Click on **Load Montage** in the **File** menu and open `60ch_square.mat` from

    `Documents\gtec\gBSanalyze\testdata\montage`

    The Montage Creator shows a square electrode grid with 60 defined electrodes. The electrode grid contains only x- and y- coordinates of the electrodes.

2. Select the electrode of the montage which corresponds to Cz in the international 10/20 electrode system.

3. Enter the name `Cz` into the **Channel name** editor box and press the **Confirm** button.

4. Inspect the coordinates of the electrode in **Position (X / Y / Z):**, they are `0 / 0 / 0`.

5. Select the electrode that corresponds to Fz in the montage and assign the name `Fz` with the **Confirm** button.

6. Import x-, y- and z-coordinates from a boundary electrode file by opening **Import Positions** from the **File** menu and selecting `electrodes60.bnd` from

    `Documents\gtec\gBSanalyze\testdata\gHReeg\Electrodes`

7. Click e.g. on electrode Cz (electrode number 61) to inspect the coordinates again. They are now `-0.66115 / -15.813 / 81.4715`.
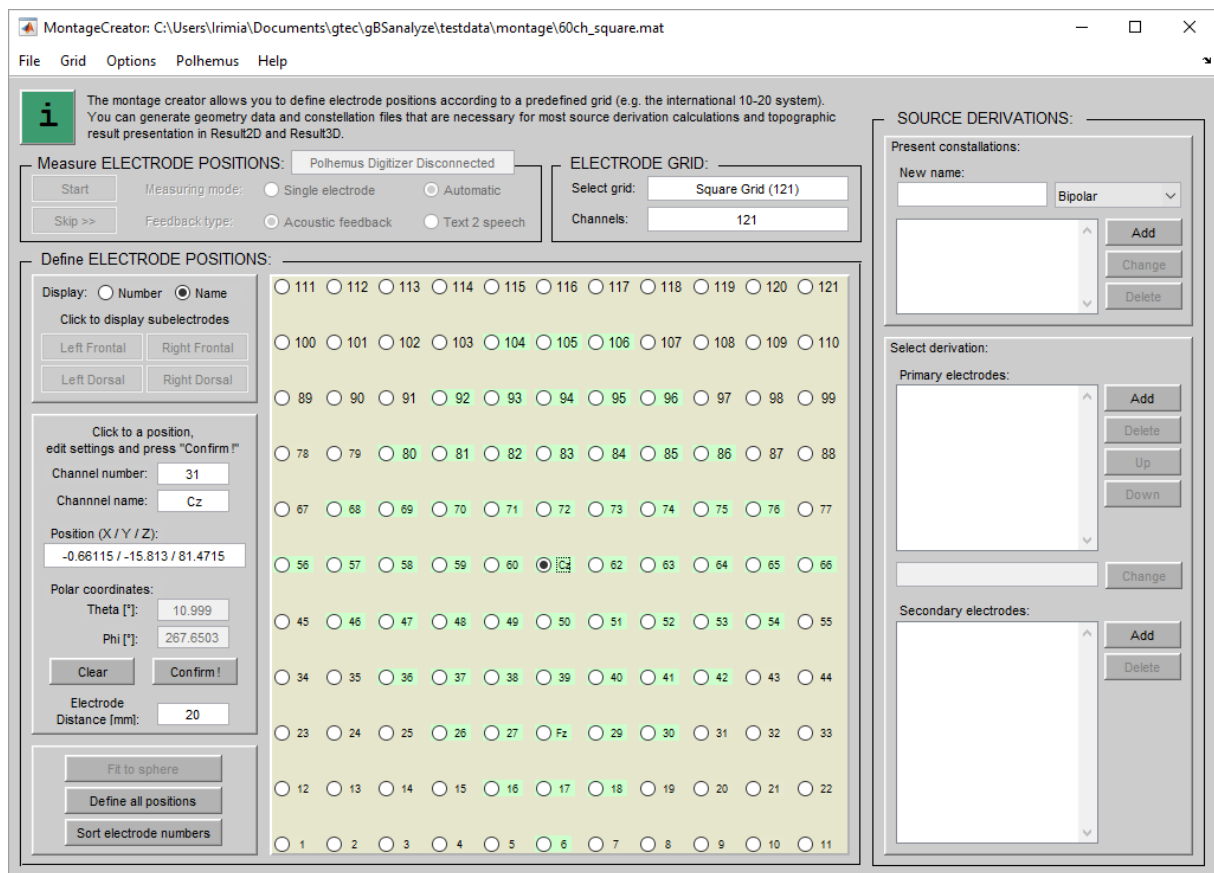
8. Save the montage as `electrodes60.mat` under

   `Documents\gtec\gBSanalyze\testdata\gHReeg\Electrodes`

9. Close the Montage Creator

Calculate a Spline Surface Laplace Derivation

Global approaches of surface Laplacian are based on analytical functions that describe the potential distribution on the scalp. These analytical functions are referred to as splines. This name comes from the flexible reeds used by ship-wrights to constrain wooden planks in a boat construction.

$$V(x, y, z) = U(x, y, z), \qquad \text{with} \quad U(x_i, y_i, z_i) = V_i. \tag{1}$$

The potential distribution V is given by the spline $U(x,y,z)$, and it should return the measured potential V_i at electrode i. Splines can be defined on either spherical or realistically shaped surfaces. The surface Laplacian is obtained by computing the second derivative with respect to the local head surface:

$$\nabla_s^2 V_i \cong \frac{\partial^2 U(x, y, z)}{\partial u^2} + \frac{\partial^2 U(x, y, z)}{\partial v^2}, \tag{2}$$

with u and v serving as the surface coordinates. Different implementations of the spline surface Laplacian, either for spherical of more realistic shaped surfaces, have been introduced (Perrin et al. 1989; Nunez and Pilgreen 1991; Law et al. 1993; Nunez et al. 1994; Babiloni et al. 1996; Babiloni et al. 1997).

An advantage of the spline-based surface Laplacian methods is that the potential distribution can be approximated rather than interpolated. This becomes a substantial advantage whenever the potential distribution is contaminated by noise. The amount of approximation can be set by a regularization parameter.

Perrin, F., Pernier, J., Bertrand, O., Echallier, J., 1989. Spherical splines for scalp potential and current density mapping. Electroencephalogr. Clin. Neurophysiol. 72, 184-187.

Nunez, P., Pilgreen, K., 1991. The spline-Laplacian in clinical neurophysiology: a method to improve eeg spatial resolution. J. Clin. Neurophysiol. 8 (4), 397-413.

Law, S., Nunez, P., Wijesinghe, R., 1993. High resolution EEG using spline generated surface Laplacians on spherical and ellipsoidal surfaces. IEEE Trans. Biomed. Eng. 40 (2), 145-153.

Nunez, P., Silberstein, R., Cadusch, P., Wijesinghe, R., Westdorp, A., Srinivasan, R., 1994. A theoretical and experimental study of high resolution EEG based on surface Laplacians and cortical imaging. Electroencephalogr. Clin. Neurophysiol. 90, 40-57.

Babiloni, F., Babiloni, C., Carducci, F., Fattorini, L., Onorati, P., Urbano, A., 1996. Spline Laplacian estimated of EEG potentials over a realistic magnetic resonance-constructed scalp surface model. Electroencephalogr. Clin. Neurophysiol. 98, 363-373.

Babiloni, F., Babiloni, C., Carducci, F., Gaudio, M.D., Onorati, P., Urbano, A., 1997. A high resolution EEG method based on the correction of the surface Laplacian estimate for the subject's variable scalp thickness. Electroencephalogr. Clin. Neurophysiol. 103, 486-492.

Perform the following steps:

1. Select **Import BKR** from the **File** menu of the Data Editor to load the file `FOOT.bkr` which is located in

    `Documents\gtec\gBSanaylze\testdata\gHReeg\`
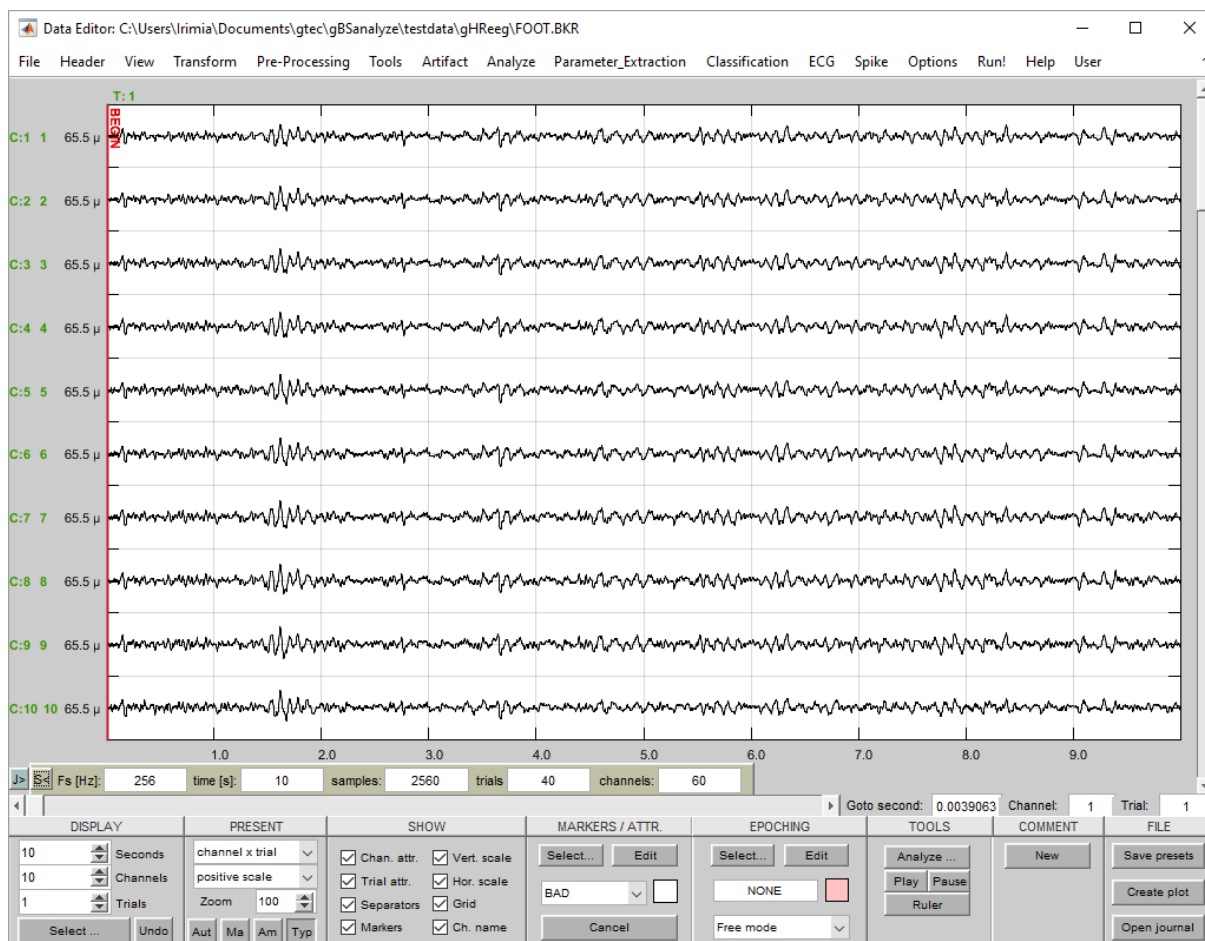
The Data Editor shows a 60 channel EEG data-set consisting of 40 trials (epochs) with 2560 samples each. The data was recorded with 256 Hz.

The subject performed a cue-paced foot movement imagination at second 3 of every trial. The end of imagination was indicated and the subject was instructed to perform the imagination until second 8 of each trial. The task was repeated 40 times.

2. Select **Spline Surface Laplace** under the **Pre-Processing** menu to open the following window:
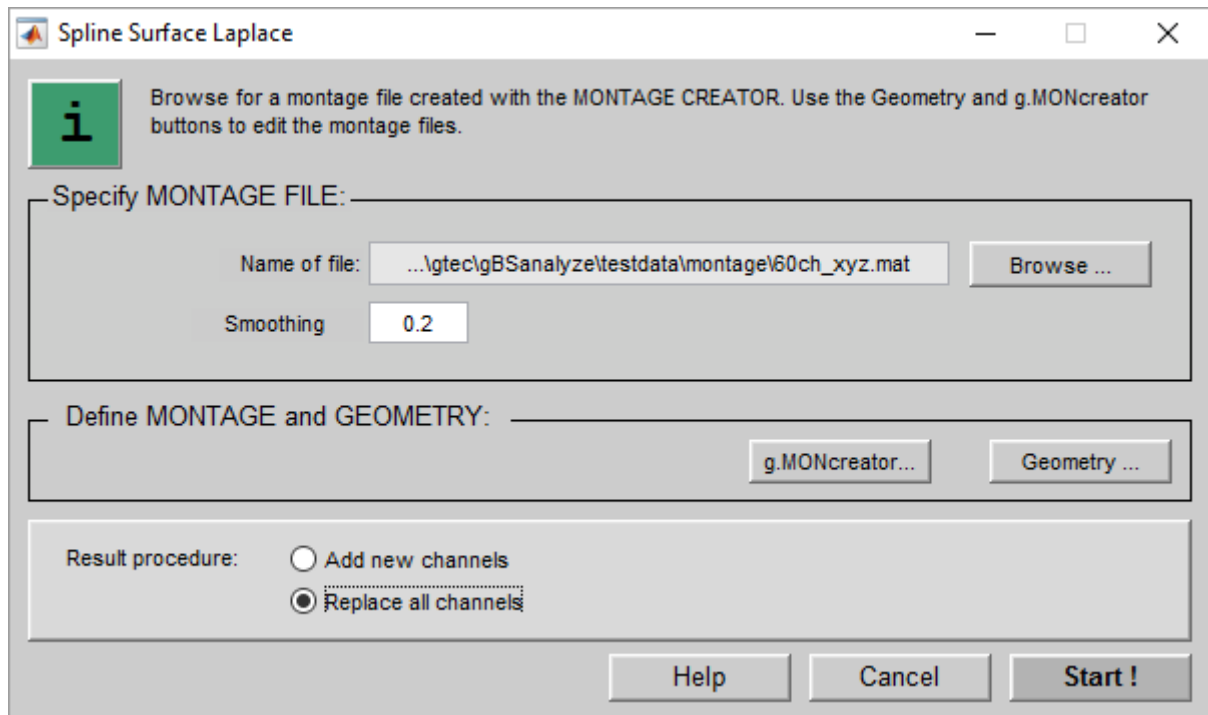
The window has the following entries:

Specify MONTAGE FILE:

Name of file – select a montage file with x-, y- and z-coordinates of the electrodes

Smoothing factor – enter a smoothing factor between 0 (no smoothing) and 1 (maximum smoothing)

Define MONTAGE and GEOMETRY:

g.MONcreator – open the Montage Creator to edit the montage file

Geometry – open the **Geometry** window to inspect and edit the coordinates

Result procedure – check the corresponding radio button to add the Spline Surface Laplace channels to the current data channels in the Data Editor or to replace all existing channels. The newly created channels get the attribute `SSL`.

3. Select e.g. the montage file 60ch_xyz.mat that was created in Section **Create a Montage File** and is stored under

   Documents\gtec\gBSanalyze\testdata\montage

4. Enter as **Smoothing factor** 0.2. The **Smoothing factor** can be between 0 (no smoothing) and 1 (maximum)

5. Select the radio button **Replace all channels** to view only the new calculated Spline Surface Laplace channels

6. Press **Start** to perform the calculation

The Data Editor is updated with the newly calculated channels.
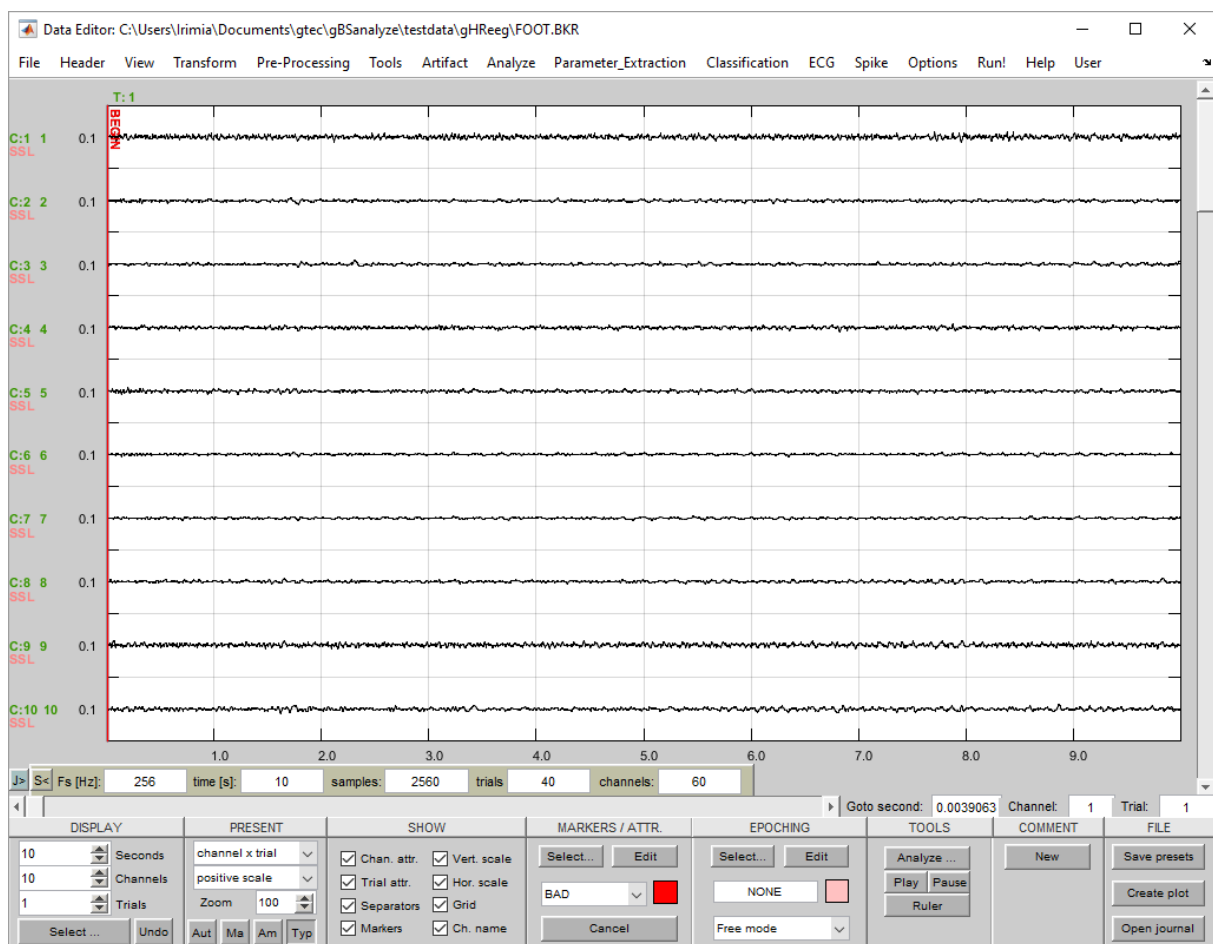
Calculate ERD

g.HReeg can show topographic maps of data that can be loaded into g.BSanalyze if they consist of only one trial (e.g. bandpower values, raw-data) and one of the following analyzes results:

Average – average data over trials e.g. used for evoked potentials (EP's)
ERD – Event Related Desynchronization – calculate ERD in percentage, absolute power, absolute amplitude or z-values (see the g.BSanalyze documentation for details)

To calculate the event-related desynchronization (ERD) and event-related synchronization (ERS) for a 60 channels data-set follow these steps:

1. Open the **ERD – Event Related Desynchronization** window from the **Analyze** menu in g.BSanalyze

2. Enter `500` ms into the editor box **Start of reference period at** and `1500` ms into **End of reference period at**

3. Select the `MU-2` filter to calculate the ERD from 11-13 Hz

4. Set the **Factor** for **Horizontal averaging** to `32`

5. Check the **Save results** box and enter as filename `SSLerd.mat` to save the calculated ERD results

6. Press the **Start** button to perform the analysis. g.Result2D opens with the calculation results.

7. Close the **ERD – Event Related Desynchronization** dialog.

8. Click on **Arrangement** in g.Result2D to open the following window:
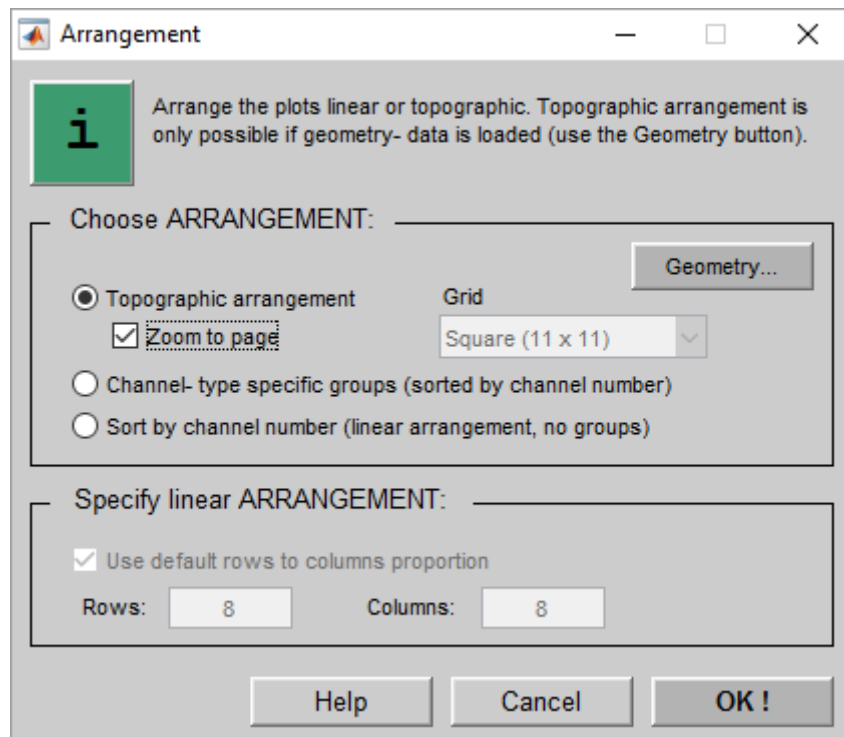
9. Select the **Grid** `Square (11 x 11)` and check **Zoom to page** to show the channels in the topographically correct arrangement
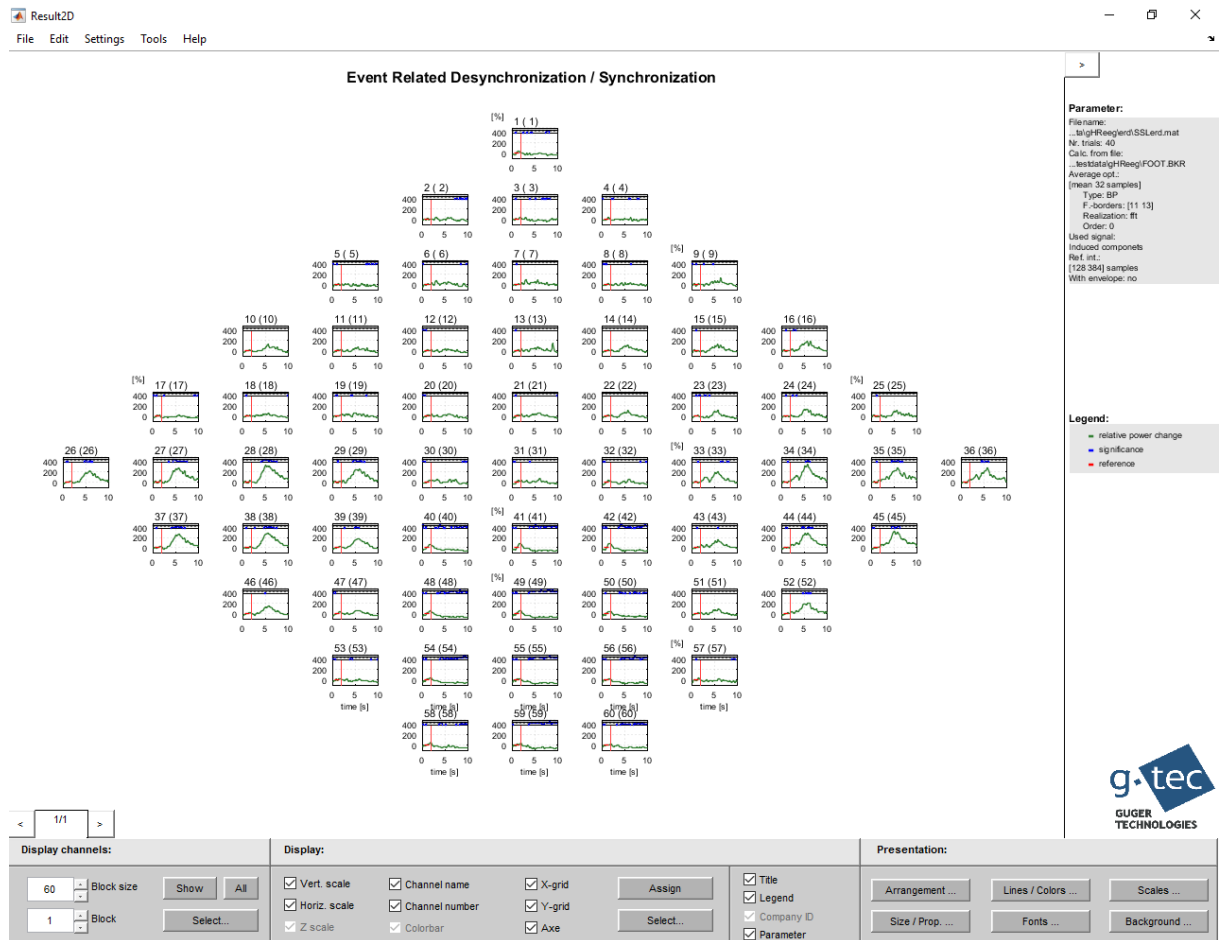
The plot shows an ERD on the parietal area (around channel 49) and an ERS around C3 (channel 28) and C4 (channel 34).
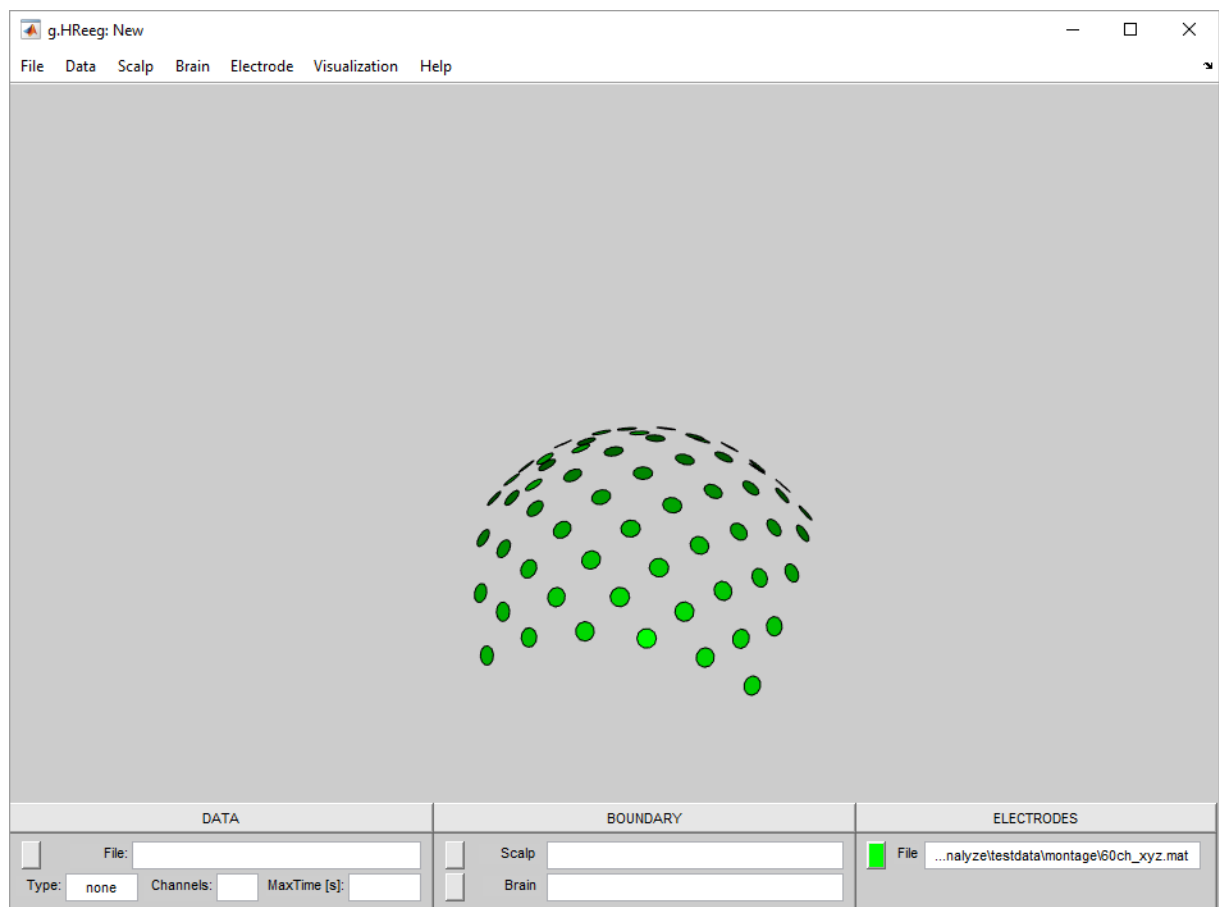
Load ERD Data

To show the calculated ERD with the corresponding electrodes in g.HReeg follow these steps:

1. Start **gHReeg** from the **Run!** menu of the Data Editor and click on **Load** under the
    Electrode menu. Select the montage file `60ch_xyz.mat` under
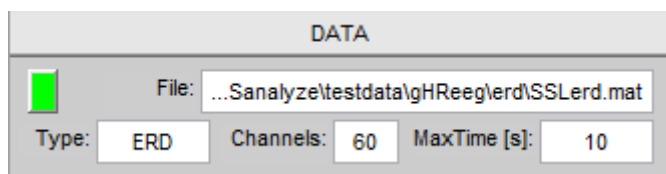
    `Documents\gtec\gBSanalyze\testdata\montage`
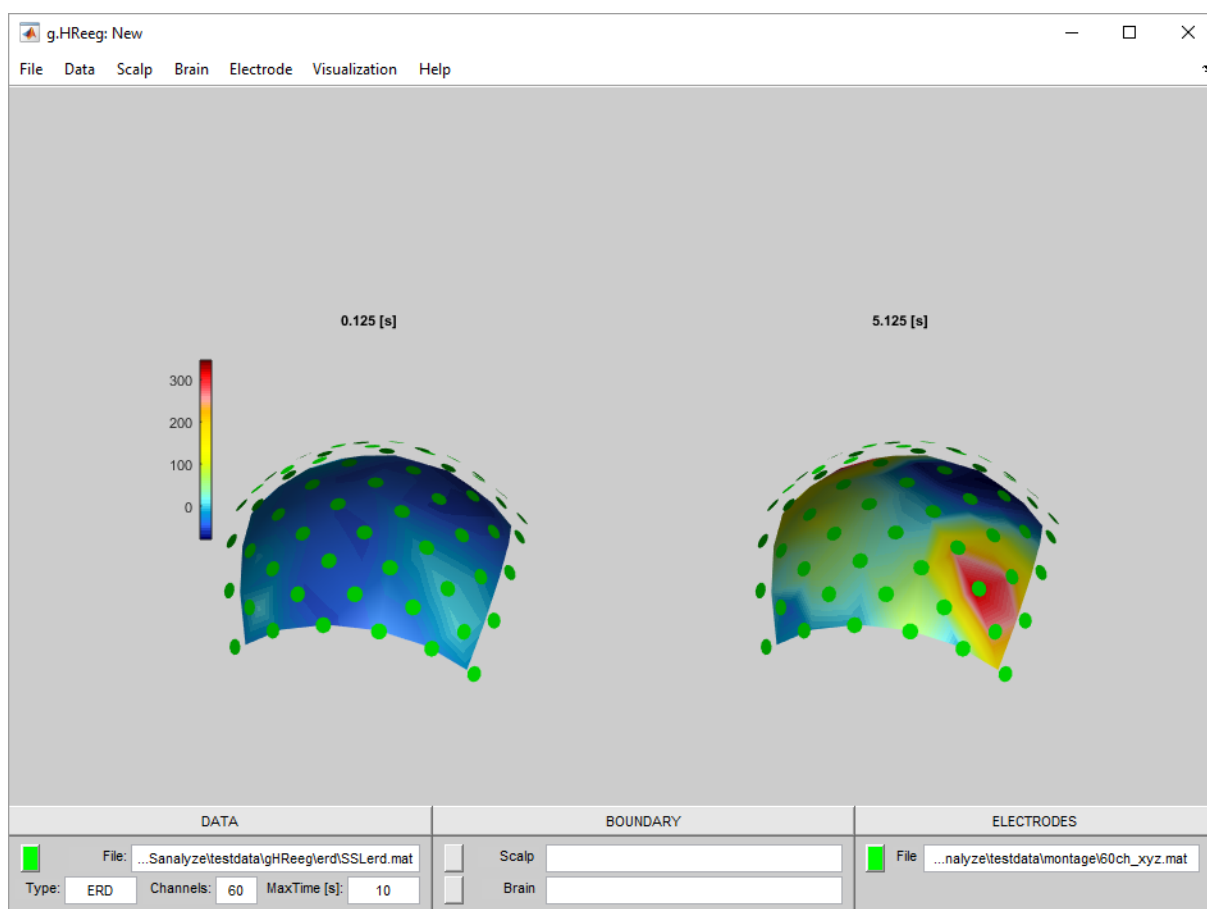
    g.HReeg shows the created montage.

2. Click the **Load** item from the **Data** menu and select the file `SSLerd.mat` from

    `Documents\gtec\gBSanalyze\testdata\gHReeg\erd`

g.HReeg shows in the status line the number of loaded **Channels**, the **Type** of signal – ERD and the data length – 10 seconds:

Furthermore the 60 electrodes and the data map are shown:

3. Click on the **Visualization** menu and select **Display Settings** to open the following window

4. Check the **Invert colormap** box in the **Set MAP parameters** field to show an amplitude attenuation (ERD) in red color and an amplitude enhancement (ERS) in blue color

5. Enable the **Confine to** box and set the **min** color value to `-120` and the **max** color value to `345`

6. Under the **Select ARRANGEMENT and TIME frame** area enter in **Nr. rows** 2 and in **Nr. cols** 4

7. Set the **Time steps from** editor box to 2, the **step** size to 1 and the **to** editor box to 8 seconds

8. Press the **Apply !** button

g.HReeg shows the maps from second 2 until second 8 to investigate the ERD evolution over time.
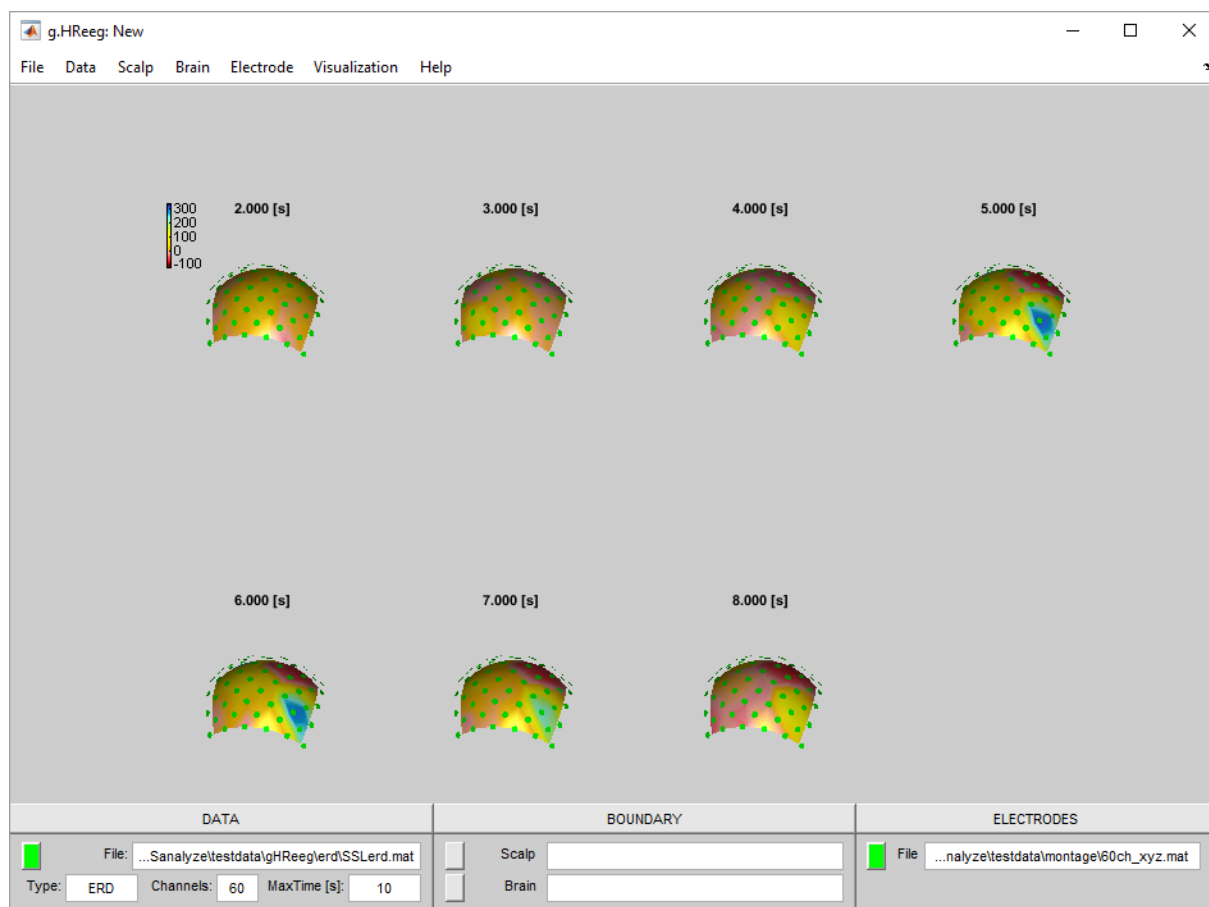
Add Scalp Data

1. To add scalp data to the ERD maps select **Load** from the **Scalp** menu

2. Select the file `subject1_scalp.bnd` from
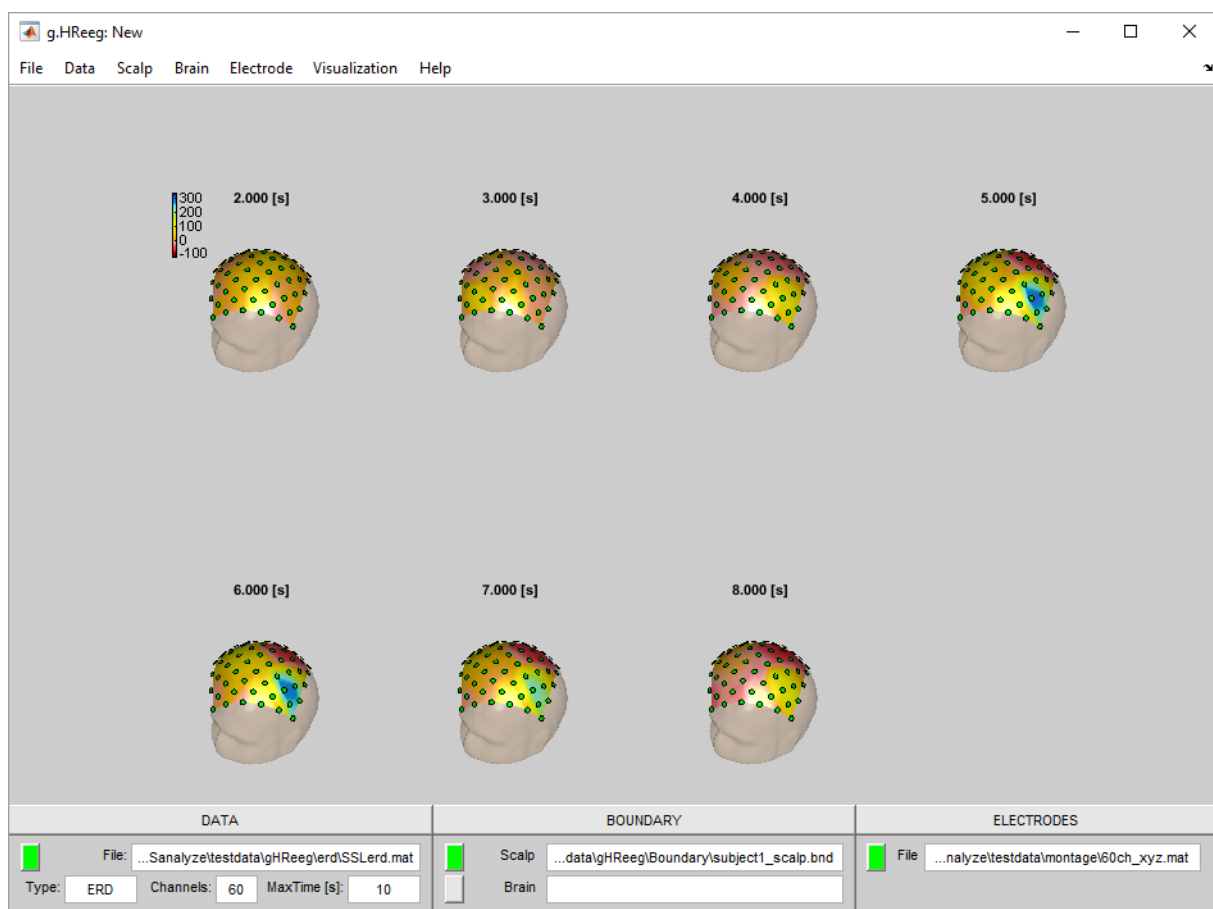
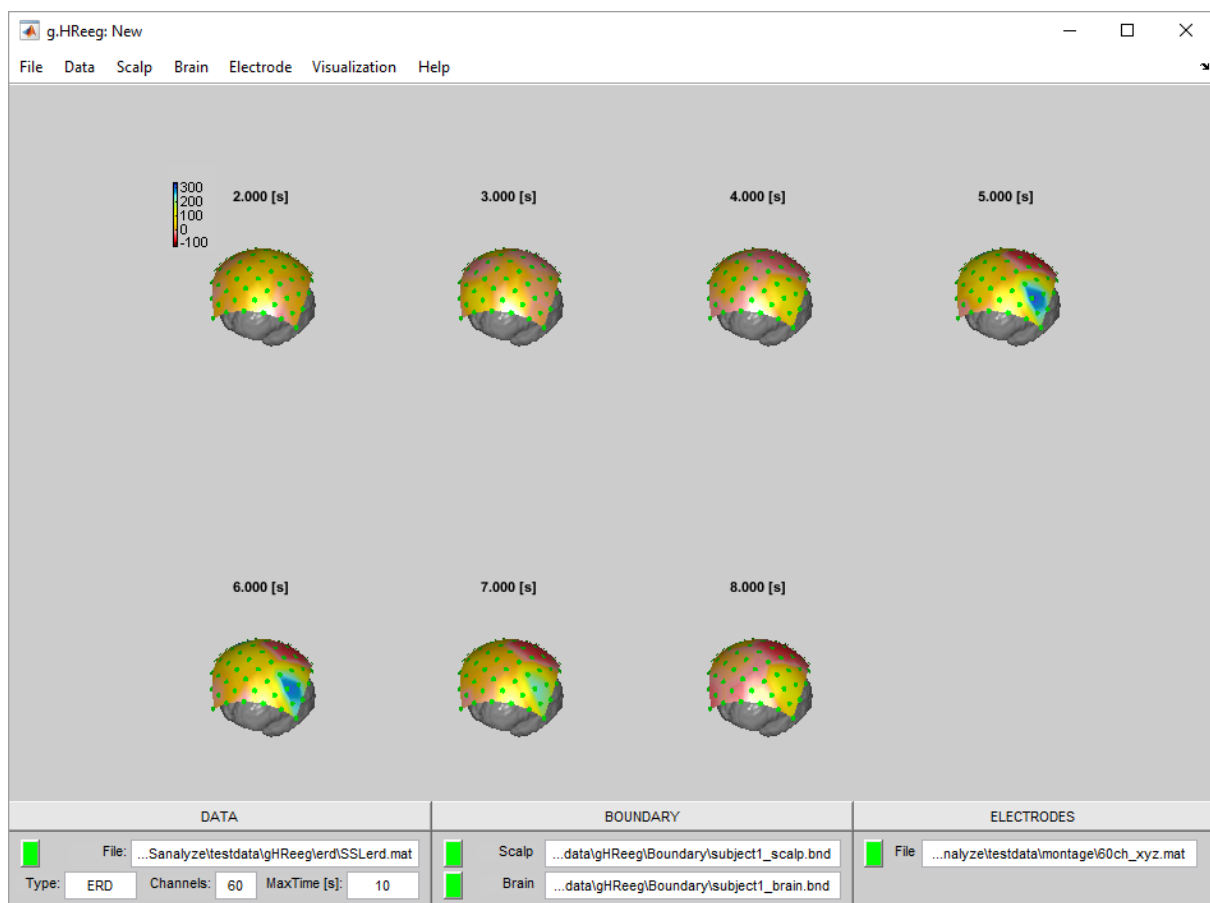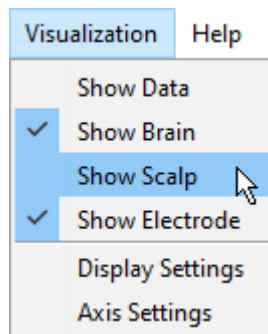   `Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`

Add Brain Data

To add brain data to the ERD maps select **Load** from the **Brain** menu. Select the file `subject1_brain.bnd` from
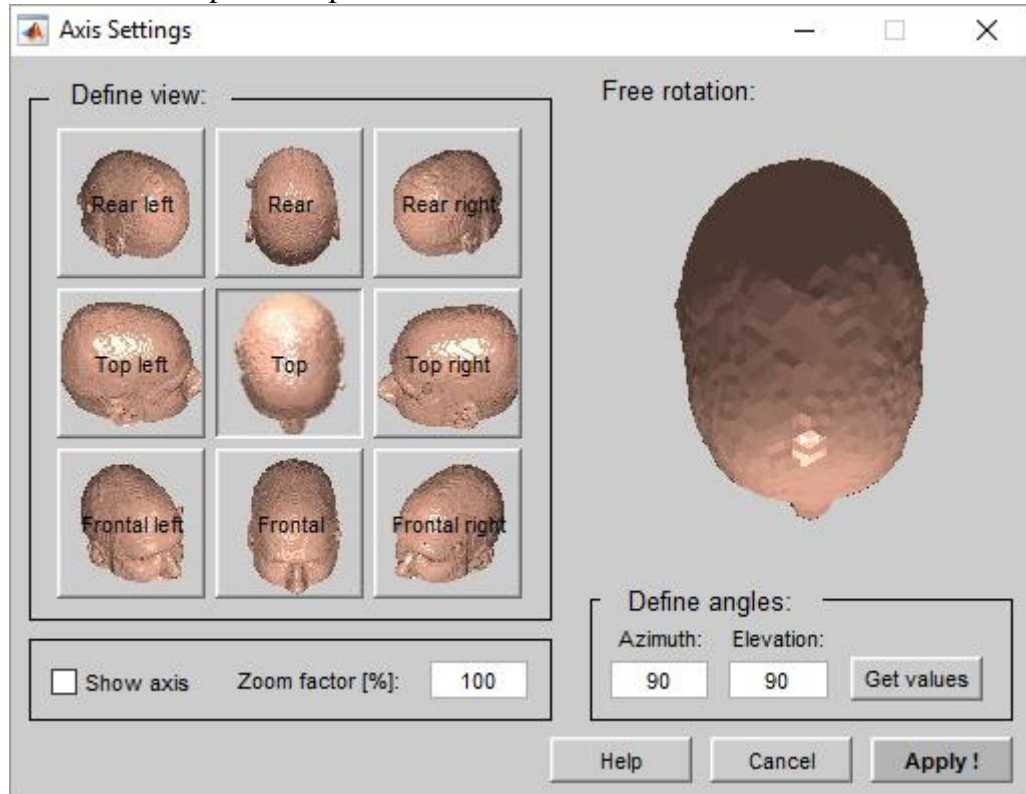
`Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`

1. Disable the **Show Scalp** entry under **Visualization** to show only the brain and the ERD maps.

Manipulate the Visualization

1. Open the **Axis Settings** window under the **Visualization** menu and press the **Top** button to view the scalp from top


2. Press **Apply !** to rotate the maps and close the window with **Cancel**

3. Check the **Show Scalp** item under **Visualization**

g.HReeg show the ERD maps and the scalp from top view. The ERD (red color) starts around second 3 on the parietal area. The ERS (blue color) can be found from second 5 to 7 around C3 and C4.
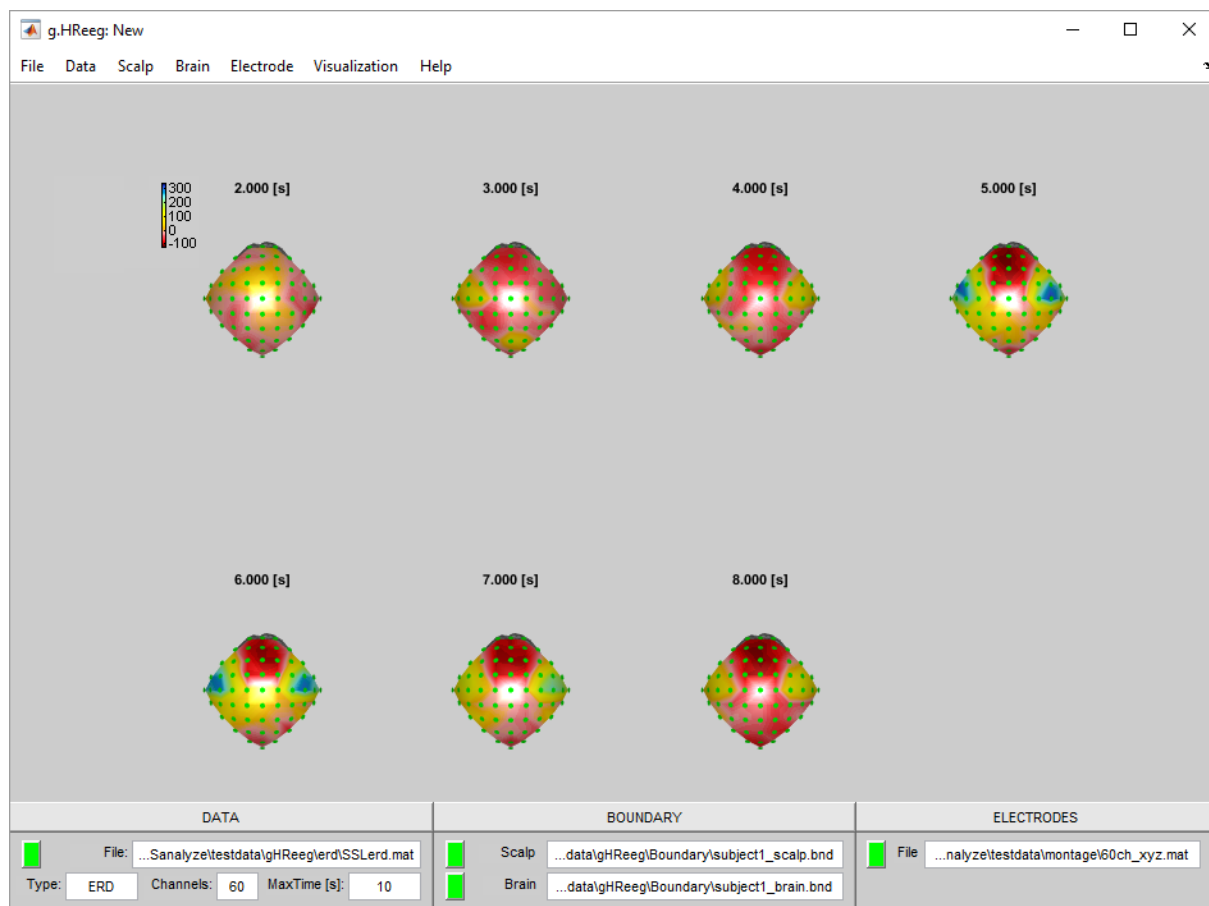
Print Results

Select **Print Preview** in the **File** menu to open the following window:
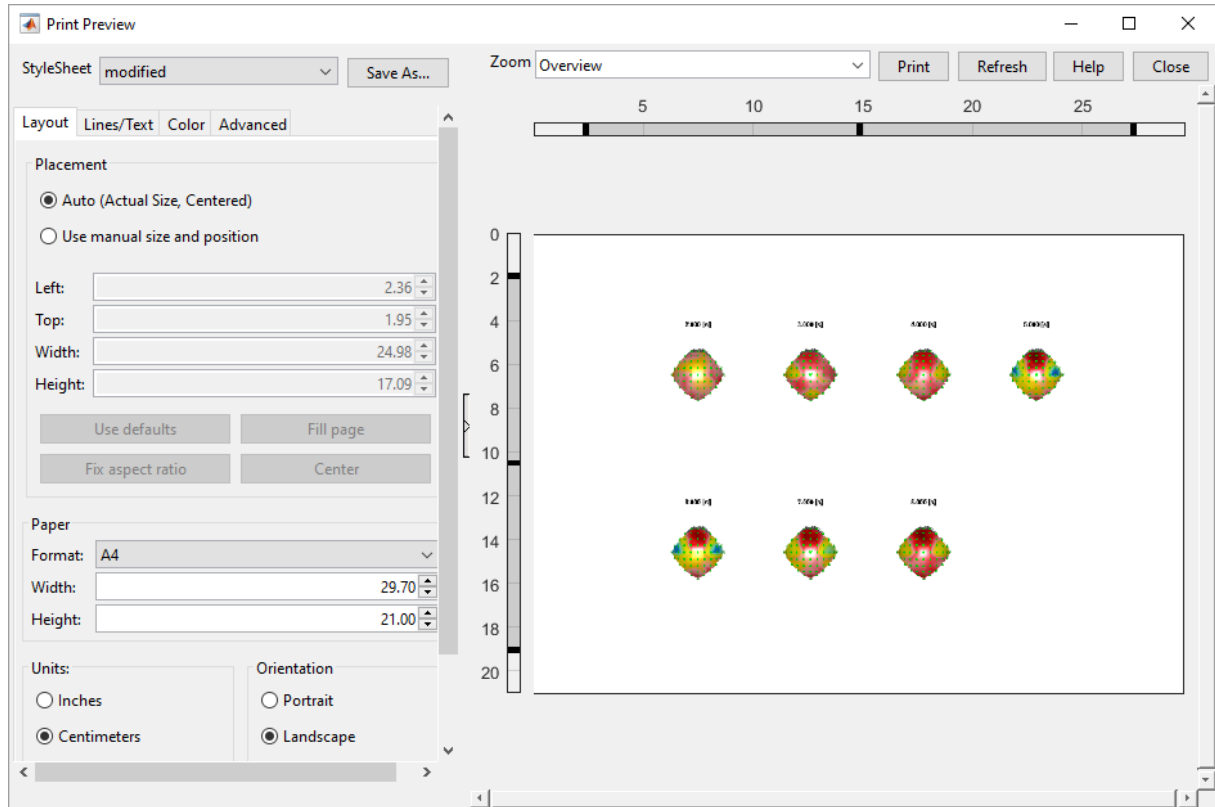
Press the **Print** button to start the printout of the data.

Save Data and Exit

1. To save the g.HReeg data (map, scalp, brain and electrodes) chose **Save as ...** under the **File** menu

2. Enter the name `Test.mat` and save it to the directory

   `Documents\gtec\gBSanaylze\testdata\gHReeg`

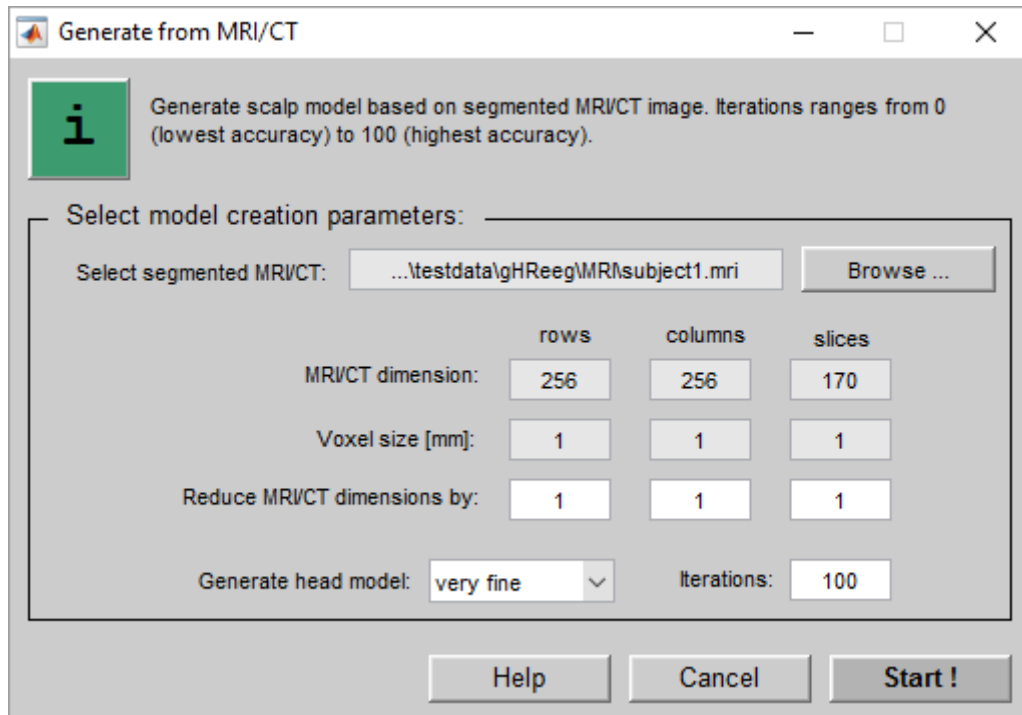3. Select **Exit** under **File** to close g.HReeg

Generate Boundaries

Chapter **Generate Boundaries** shows how to calculate scalp and brain boundaries of segmented MRI data files.

Scalp Boundary
Brain Boundary

Scalp Boundary

Scalp and Brain Boundaries can be generated from *.mri segmentation files.

The dialog box has the following entries:

Select segmented MRI/CT – chose the segmented MRI/CT file with the **Browse** button

MRI/CT dimension (status) – number of rows, columns and slices stored in the segmented MRI/CT file

Voxel size [mm] (status) – dimension of each voxel in the segmentation file

Reduce MRI/CT dimensions by – enter rows=1, columns=1 and slices=1 to take every voxel, enter rows=2, columns=2 and slices=2 to take every second voxel,…

Generate head model – select the resolution of the scalp model (8 steps from lowest to finest)

Iterations – enter the number of iterations for the calculation of the scalp model (range 0-100).

1. Click on **Generate from MRI/CT** under the **Scalp** menu and select the file `subject1.mri` from
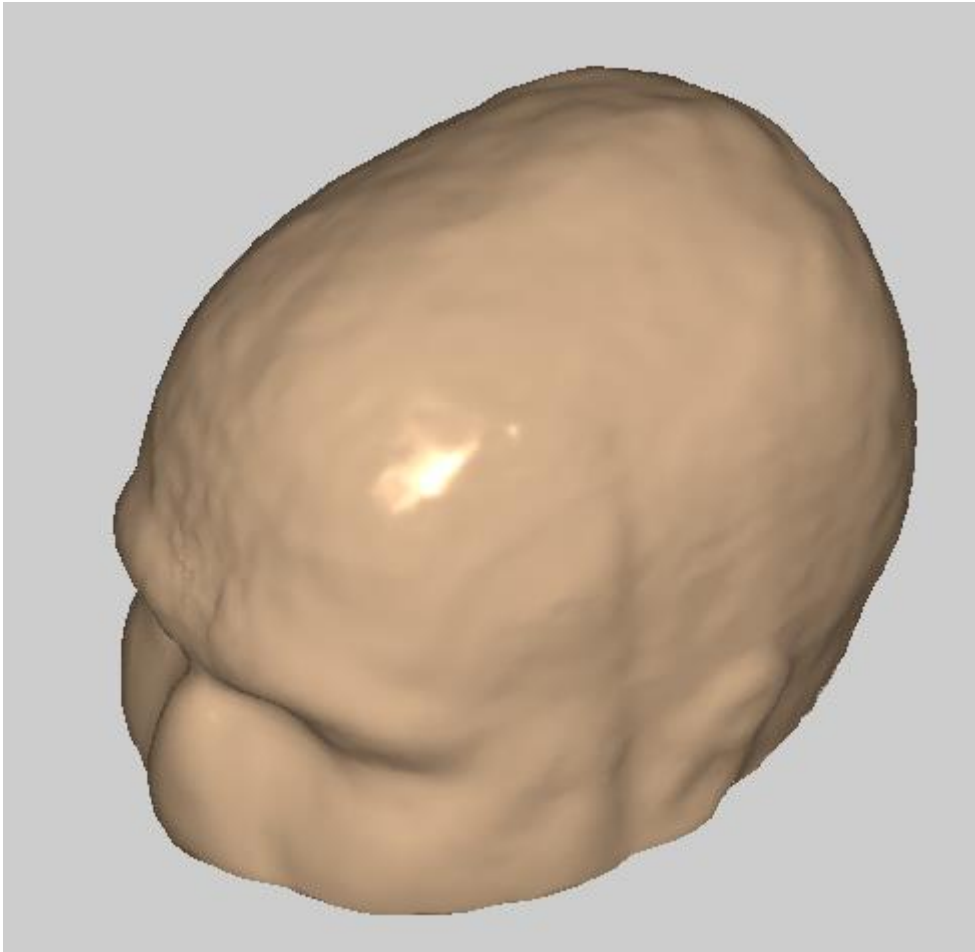
   `Documents\gtec\gBSanalyze\testdata\gHReeg\MRI`

   The segmentation file contains an MRI image with 256 rows, 256 columns and 170 slices.

The **Voxel size** is 1 mm x 1mm x 1mm.

2. Select `very fine` from the **Generate head model** pull down menu and enter `100` under **Iterations**

3. Press **Start** to generate the boundary file

The g.HReeg window opens with the scalp boundary:

4. Click on **Axis Settings** under the **Visualization** menu to open the following window:
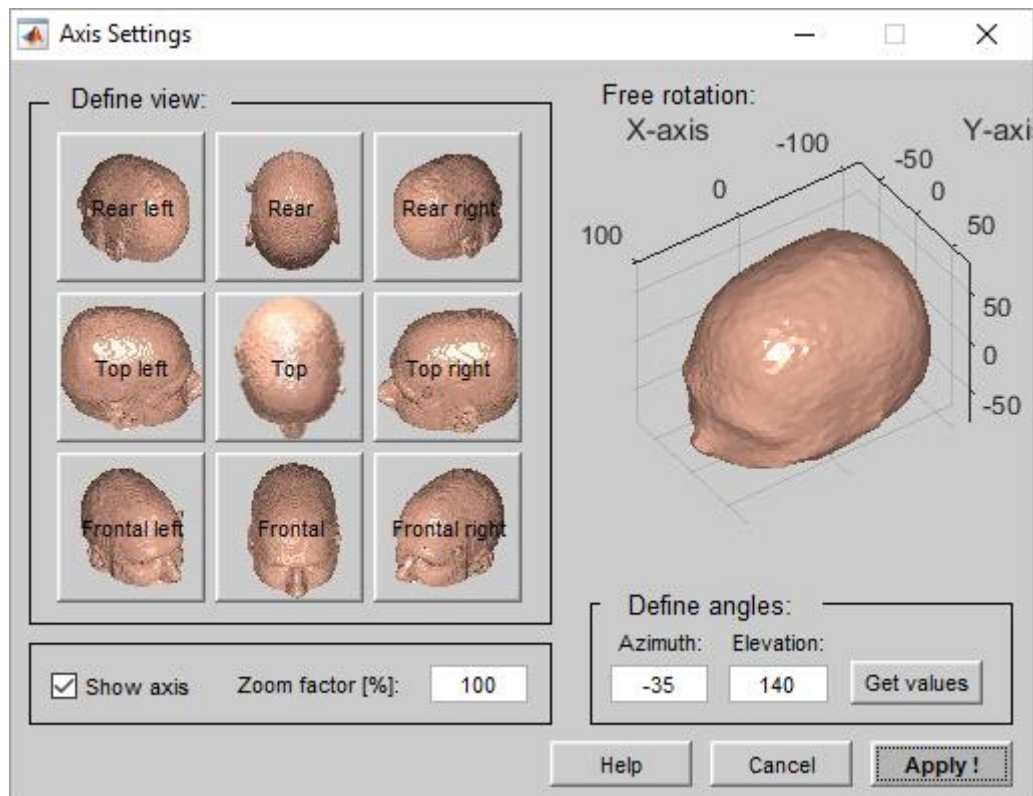
5. Check the **Show axis** box to indicate the range of the x-, y- and z-axis. Press **Apply !** and close the window with **Cancel**.

6. To reduce the number of triangles used for the scalp presentation open the **Manage Scalp** window from the **Scalp** menu
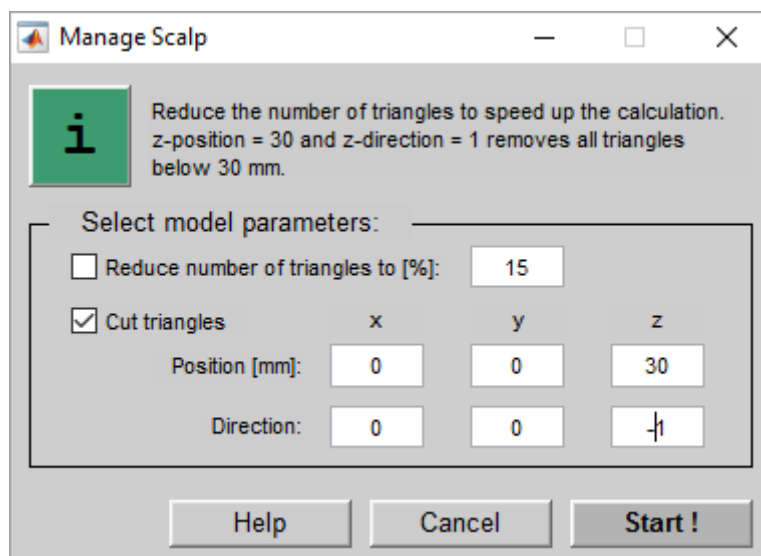
The window has the following entries:

**Reduce number of triangles to [%]** – remove a certain percentage of triangles from the boundary

Cut triangles – check the box to cut triangles above or below a certain plane

Position [mm] – enter the coordinates of the plane which is normal to the specified direction vector

Direction – enter the direction vector. **Direction** 1 means that the triangles below the plane are cut, **Direction** -1 means that triangles above the plane are cut.

7. Check the **Cut triangles** box and enter a **z-Position** value of 30 mm. Set the **z-Direction** to -1. This cuts all triangles above 30 mm.

8. Press **Start** to perform the operation
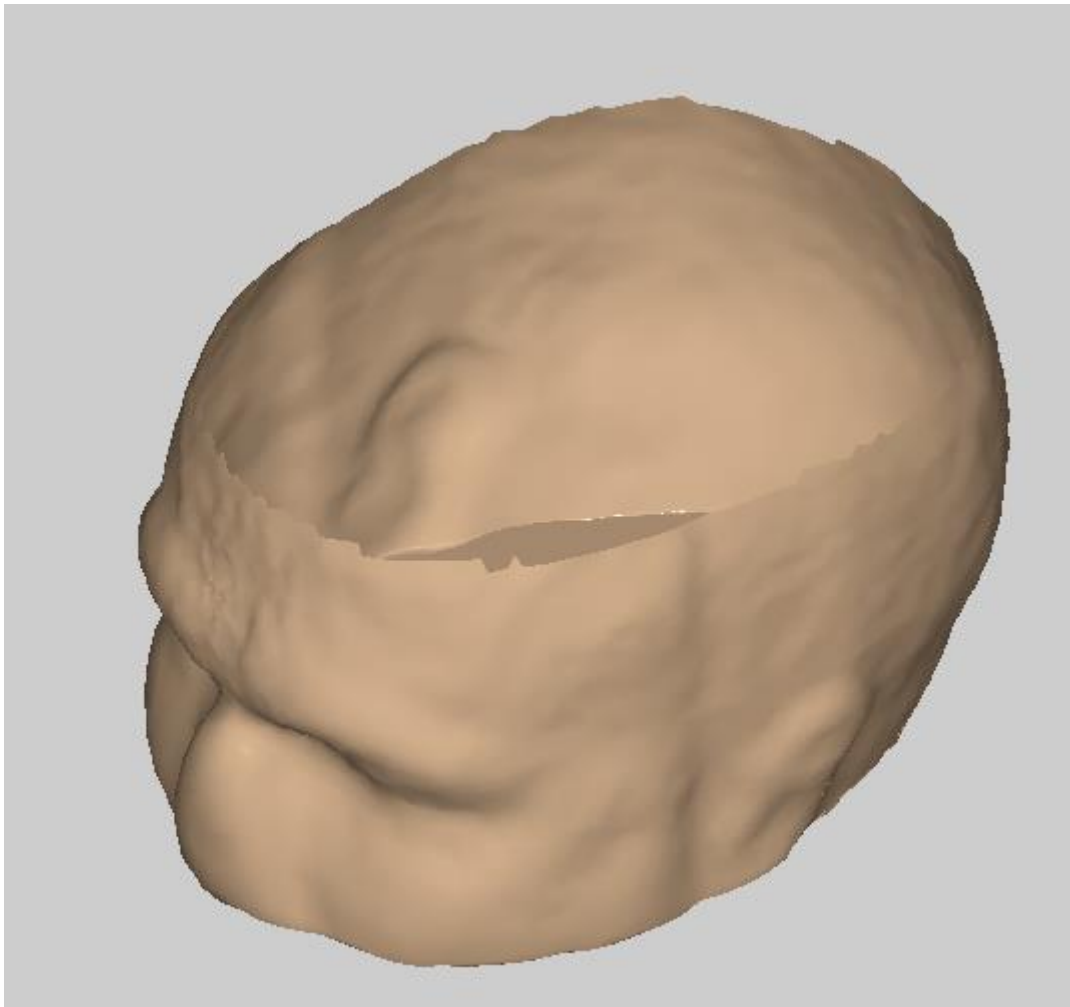
9. Select **Save as** from the **Scalp** menu, enter the name `scalp30mm.bnd` and set the path to

`Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`
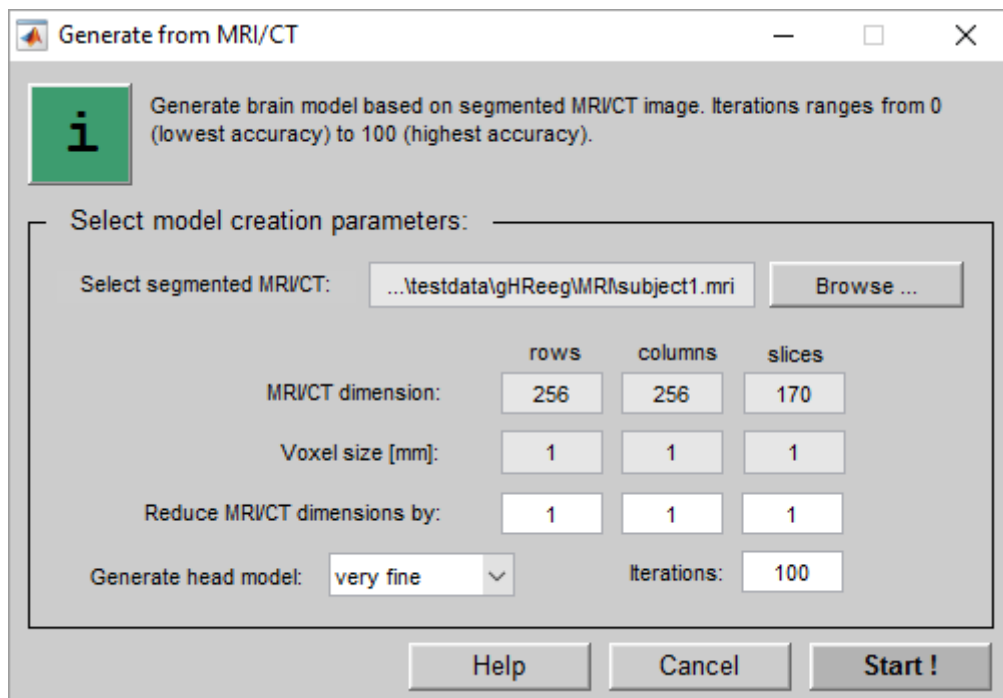
Brain Boundary

Brain Boundaries can be generated in the same way as Scalp boundaries:

1. Click on **Generate from MRI/CT** under the **Brain** menu and select the file `subject1.mri` from

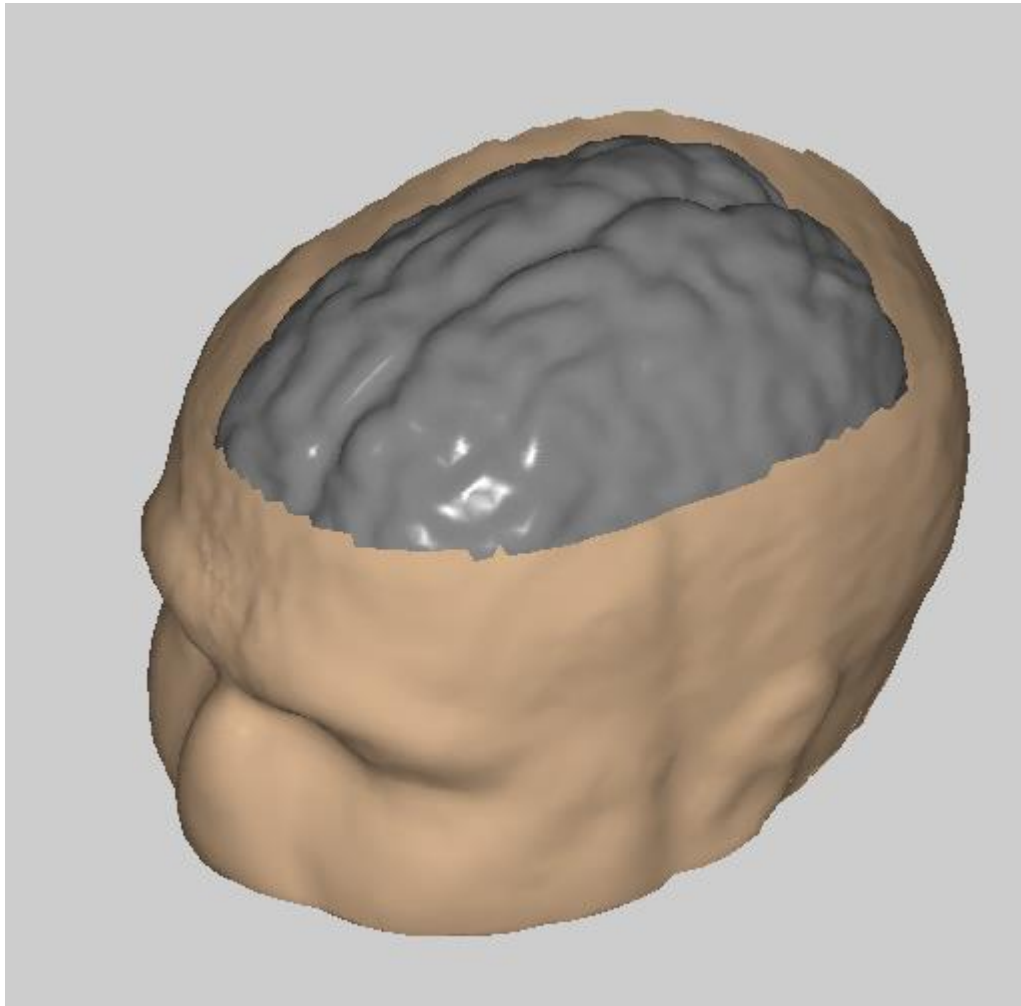   `Documents\gtec\gBSanalyze\testdata\gHReeg\MRI`

    The segmentation file contains an MRI image with 256 rows, 256 columns and 170 slices. The Voxel size is 1 mm x 1mm x 1mm.

2. Select `very fine` from the **Generate head model** pull down menu and enter `100` under **Iterations**
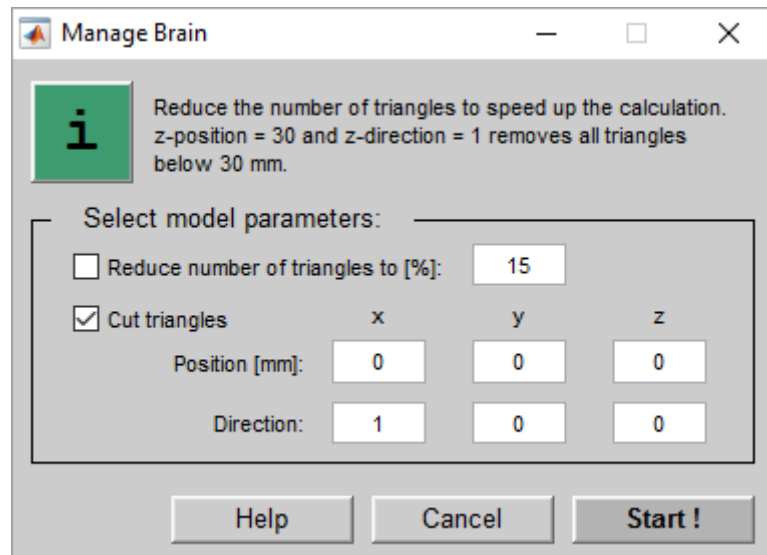

3. Press **Start !** to generate the boundary file

The g.HReeg window opens with the brain boundary:

4. To remove the back side of the brain boundary open the **Manage Brain** window from the **Brain** menu

5. Check the **Cut triangles** box and enter an **x-Position** value of 0 mm. Set the **x-Direction** to 1. This cuts all triangles below 0 mm in x-direction (opens the back side of the brain).

6. Press **Start !** to perform the operation

7. Open **Axis Settings** from the **Visualization** menu, press on the **Rear right** button and press **Apply !**
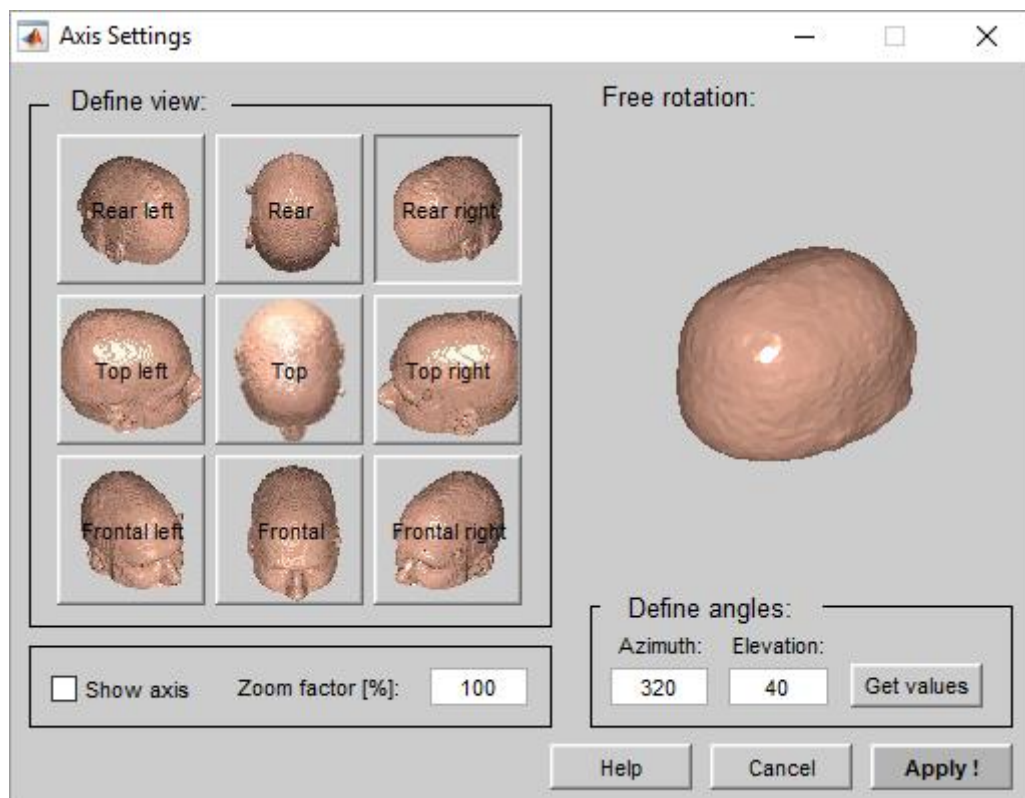
g.HReeg shows the brain from the back side:
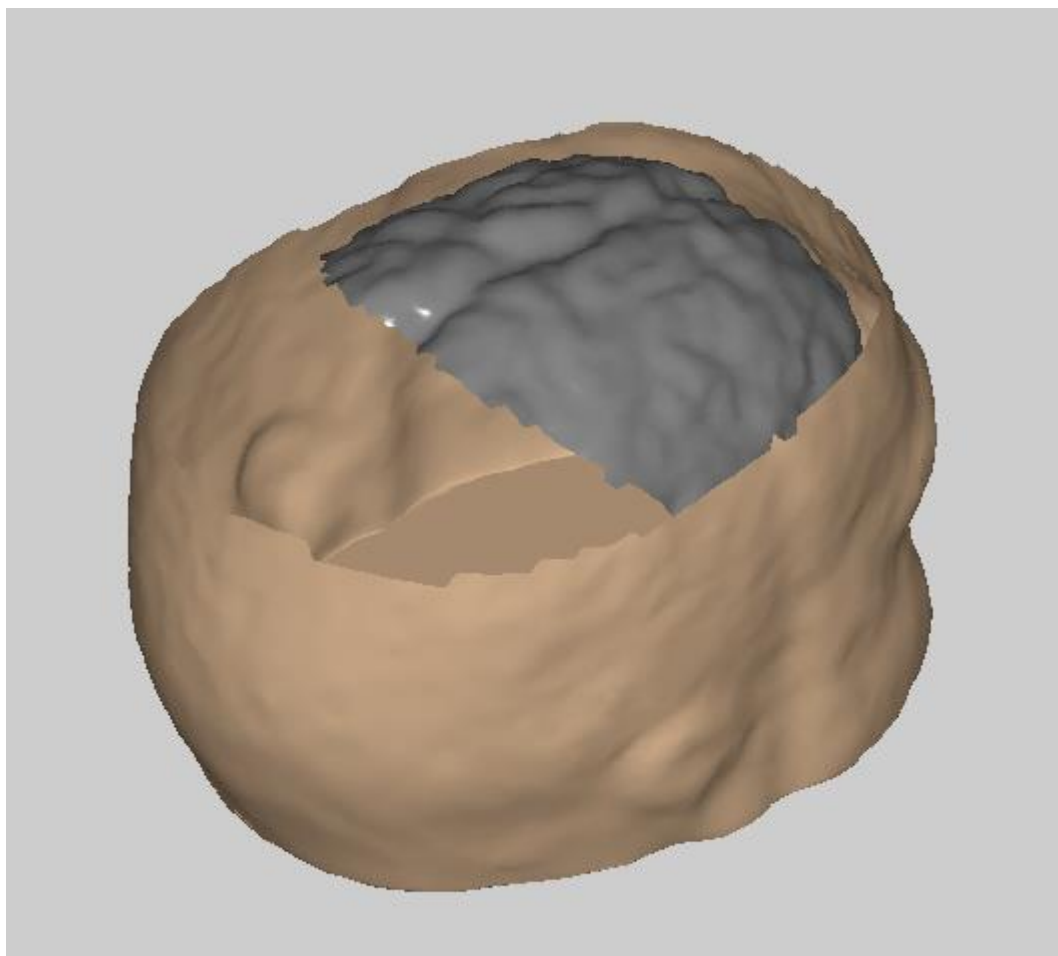
Electrodes

Chapter **Electrodes** shows how to load electrodes into g.HReeg and how to fit electrodes to the MRI/CT images.
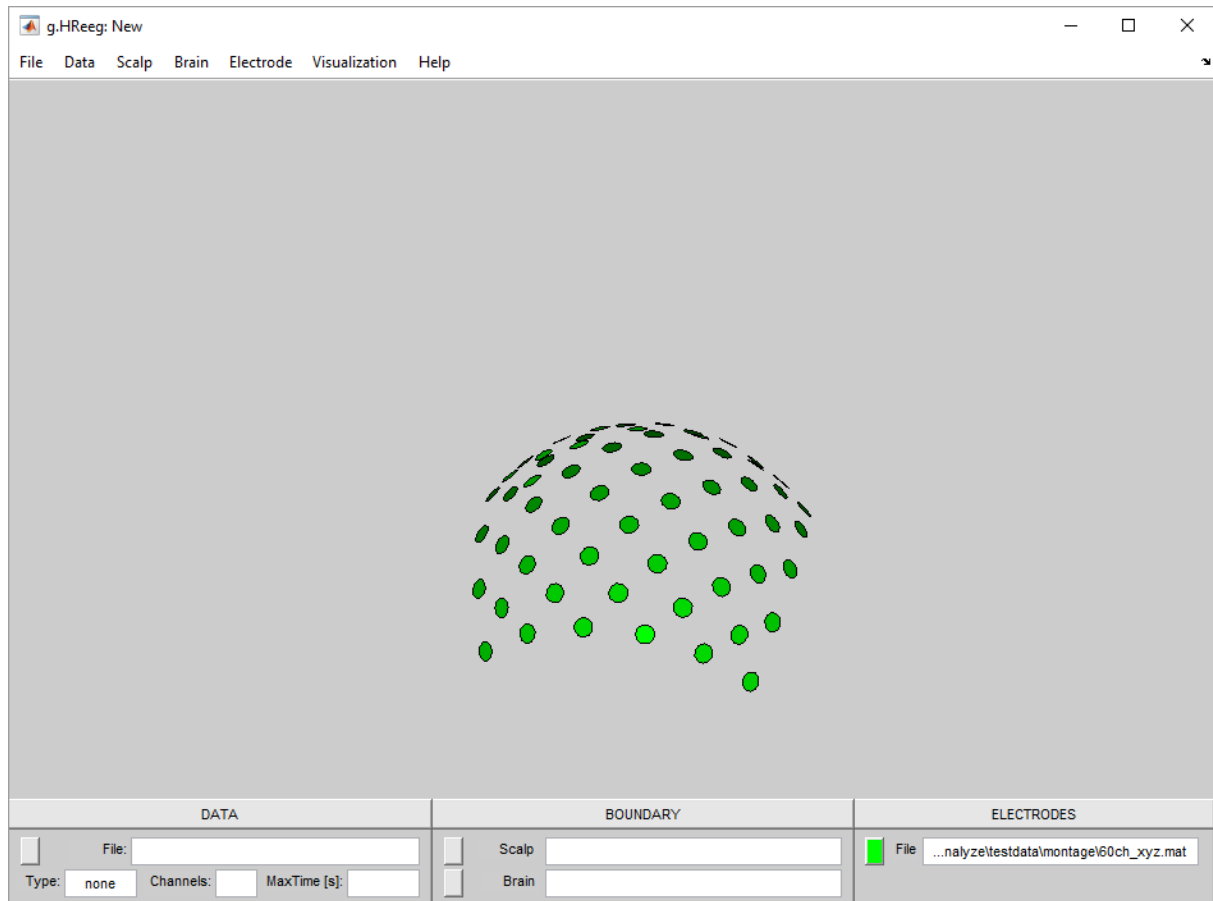
[Load and Visualize Electrodes](#)
[Fit Electrodes](#)

Load and Visualize Electrodes

1. Select **Load** under the **Electrode** menu and chose the file `60ch_xyz.mat` from

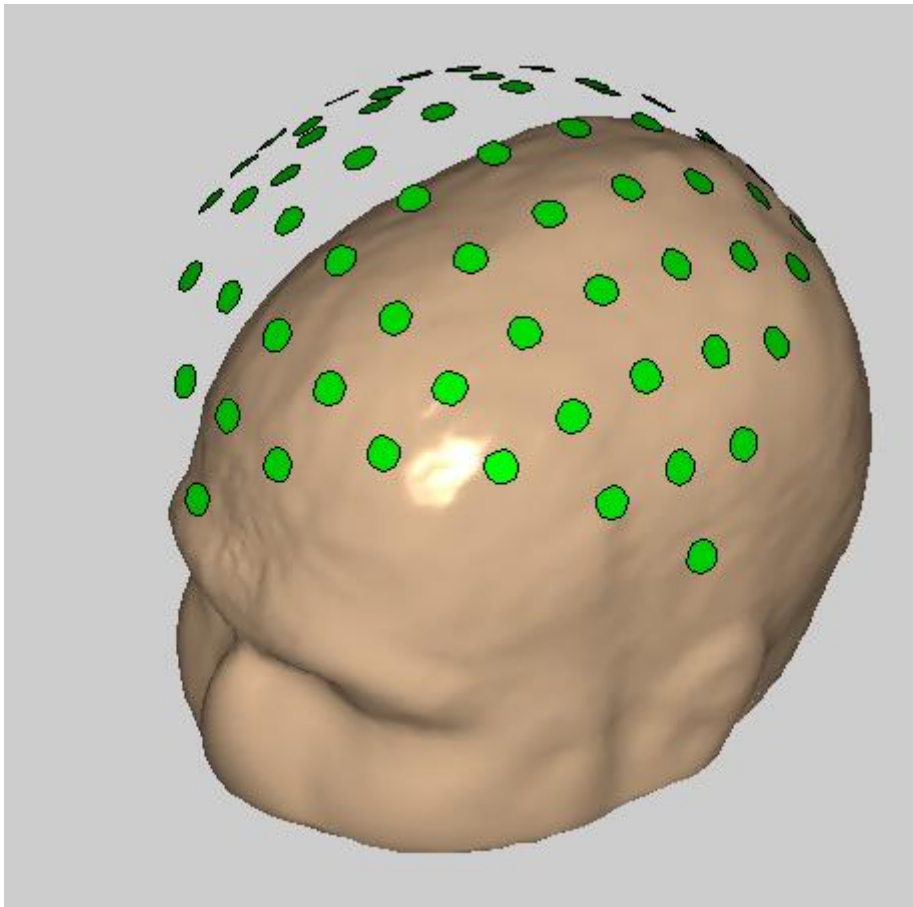   `Documents\gtec\gBSanalyze\testdata\montage`

    g.HReeg shows the electrode grid:

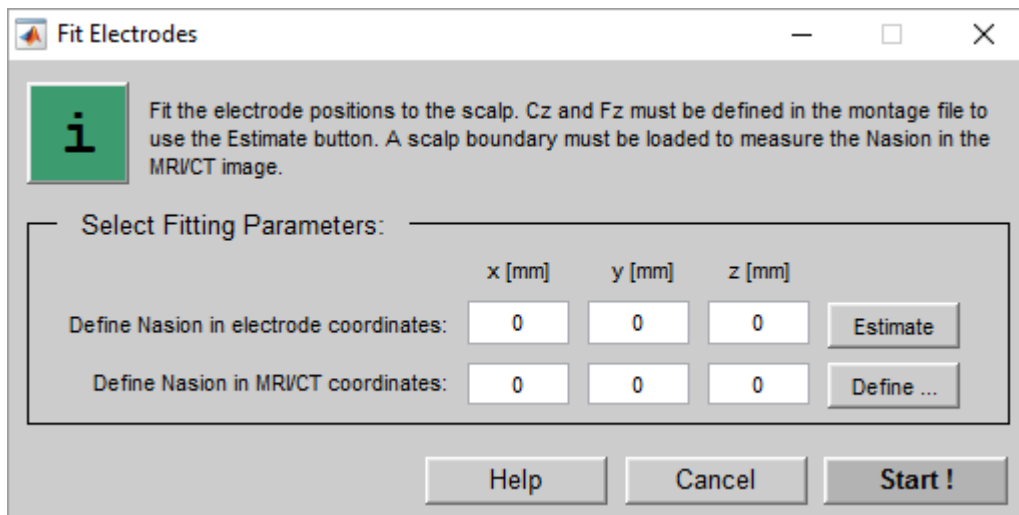2. From the **Scalp** menu open the scalp file `subject1_scalp.bnd` with **Load** from

    `Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`

g.HReeg show the scalp with the 60 electrodes. The electrodes are not fitted to the MRI/CT image.

Fit Electrodes

To fit the electrodes exactly to the MRI/CT image open **Fit Electrodes** under the **Electrode** menu.

The Nasion coordinates in the electrode coordinate system and in the MRI/CT coordinate system must be known to perform the operation. The coordinates can either be entered directly if known (e.g. from the Montage Creator or from Polhemus data) or can be estimated/defined.

The dialog window has the following entries:

Define Nasion in electrode coordinates – enter the x-, y-, and z-coordinates of the Nasion in the electrode montage system in mm. The coordinates can be viewed e.g. in the Montage Creator.

Estimate – press the button to estimate the Nasion position. This function works only if Cz and Fz are defined in the loaded electrode configuration file.

Define Nasion in MRI/CT coordinates – enter the Nasion coordinates in mm

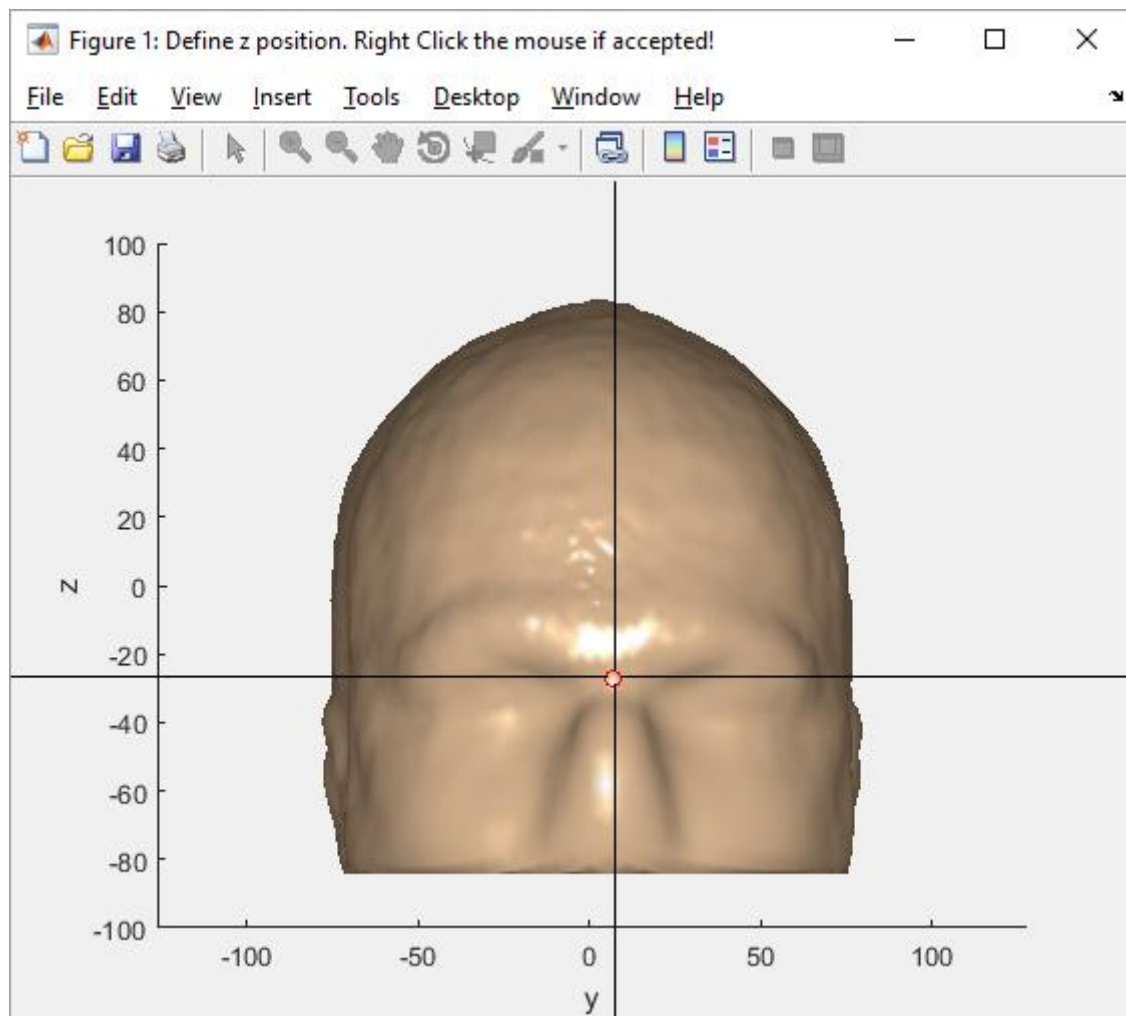**Define …** – press the button to measure the Nasion coordinates of the loaded scalp boundary

Perform the following steps:

1. Click on the **Estimate** button to calculate the Nasion coordinates for the electrodes. The estimation is done from the already defined Cz and Fz positions in the montage file (see Section **Create a Montage File**).

2. Click on the **Define …** button to measure the Nasion position of the MRI/CT image. A new figure opens with the scalp image. Try to find exactly the position of the Nasion and click with the left mouse button on it.
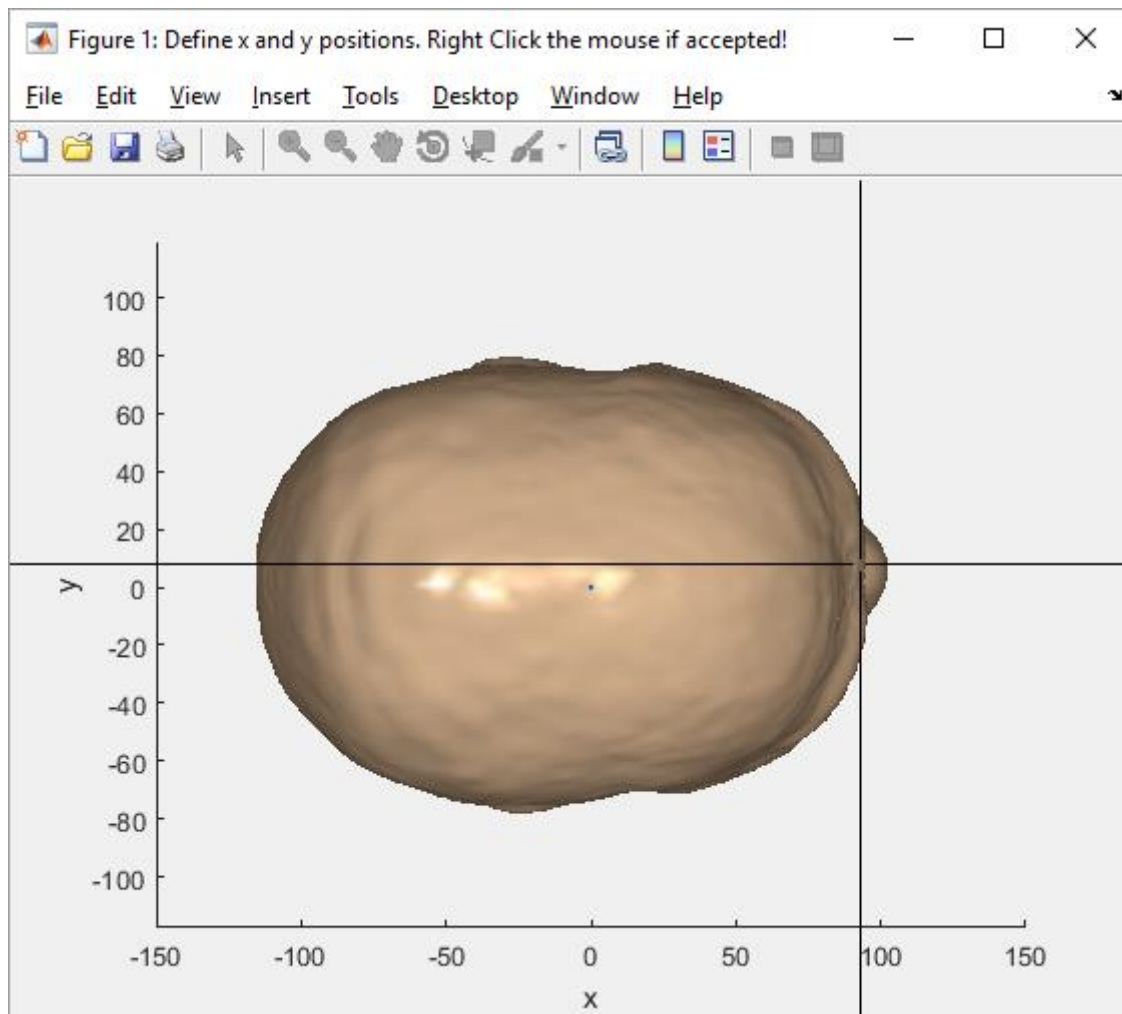
3. Then press the right mouse button to close this window

4. A new window opens which shows the front side of the boundary. Select the Nasion position again and press the left button of the mouse. Close the window with a right mouse click.
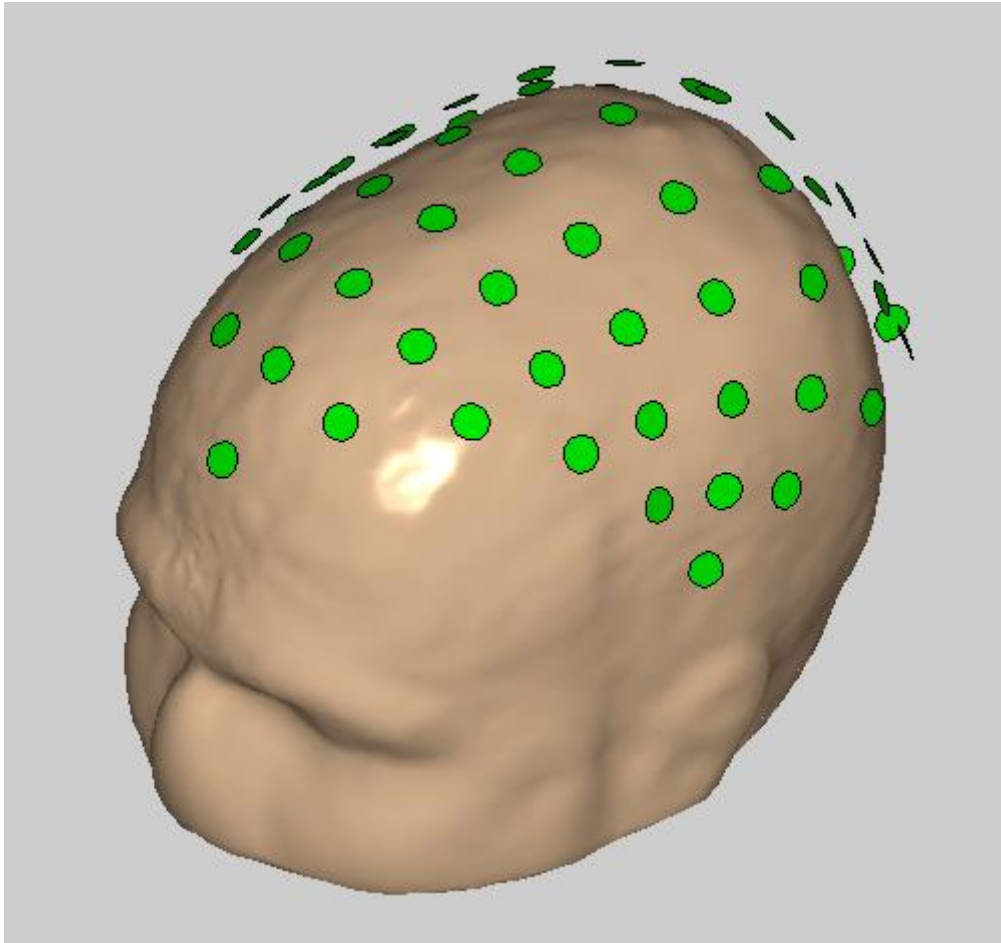

The Fit Electrodes window contains now the Nasion coordinates for both coordinate systems.

5. Press the **Start !** button

g.HReeg shows the fitted electrodes:

Visualization

Chapter **Visualization** explains the tools for changing the appearance of the data maps, of the scalp and brain boundaries and of the electrodes.
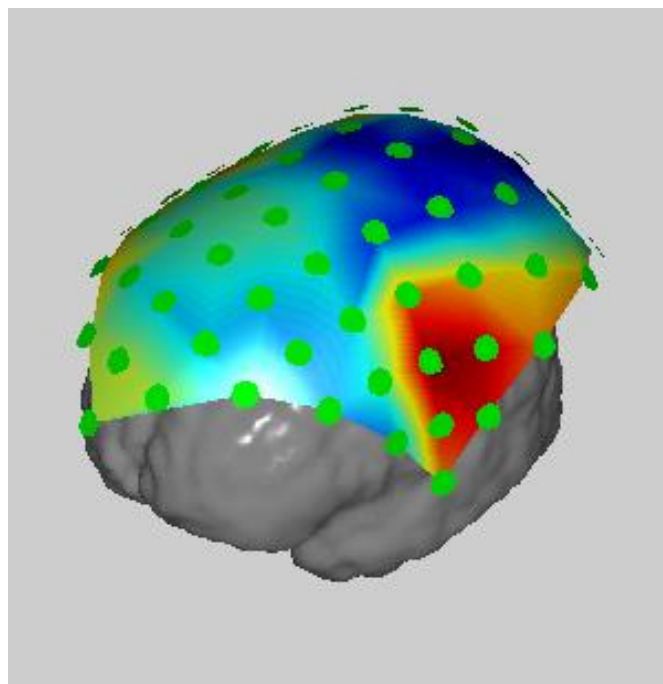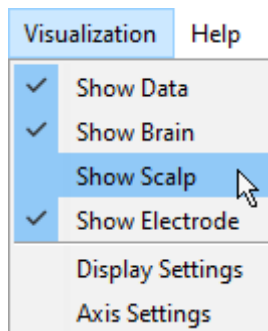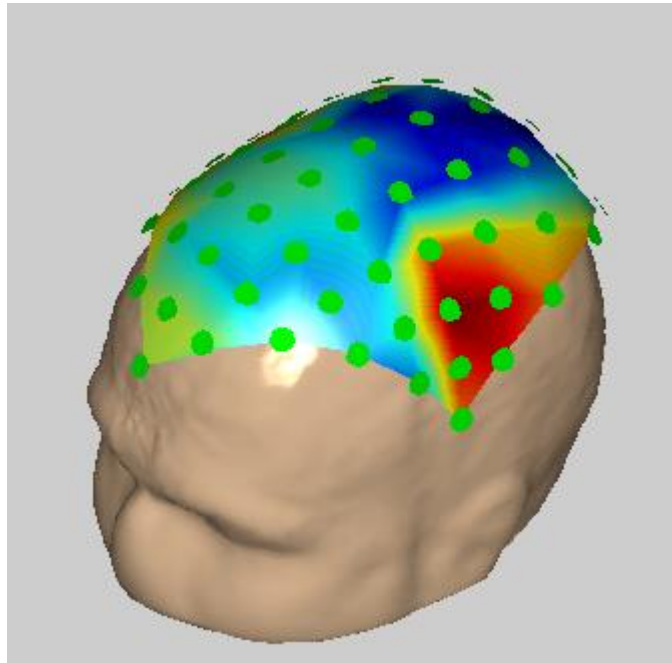
Visibility Settings
Display Settings
Axis Settings

Visibility Settings

The **Visualization** menu allows to change the visibility of the data maps, brain, scalp and electrodes.

Check or uncheck the corresponding item:
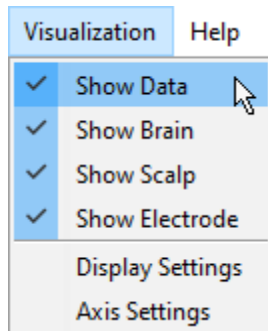
Display Settings

The **Display Settings** window has the following entries:

Set MAP parameters:

Transparency of map [%] - enter the transparency value for the data map (0 is not transparent, 100 is totally transparent)

Colormap - select a colormap for the data visualization

Nr. of colors - define the number of colors used for the colormap

Overall scaling - set the minimum and maximum equal for all maps

Individual scaling - calculate the minimum and maximum for each colormap separately

Confine to - enter manually the minimum and maximum values for all maps

Show colorbar - check to show the colorbar

Show times - check to show the time information for each map

Invert colormap - invert the minimum and maximum color of the map

Min-0-Max autoscale - use an equal amount of colors for the values below and above 0

Select ARRANGEMENT and TIME frame:

Rows / cols - enter the number of rows and columns for the visualization of the maps

Time steps [s] - enter the beginning and end time point in seconds for the visualization. The step size defines the number of maps which are shown.

Samples - same as Time steps but the unit is samples

Set SCALP parameters and **Set BRAIN parameters:**

Color … - define the color of the boundary

Transparency [%] - set the transparency of the boundary

Apply above z= - set the boundary to the transparency value above this z-coordinate

Set ELECTRODE parameters:

Color … - define the color of the electrodes

Size of electrode [mm] - set the size of the electrodes in mm

Axis Settings

The **Axis Settings** window can be used to change the view of the axis and has the following entries:

Define view – press the button to define the view angle

Free rotation – rotate the head to define the view angle

Define angles – enter the Azimuth and Elevation angle

Show axis – check to show the coordinates

Zoom factor [%] – enter the zoom factor to increase or decrease the visualization
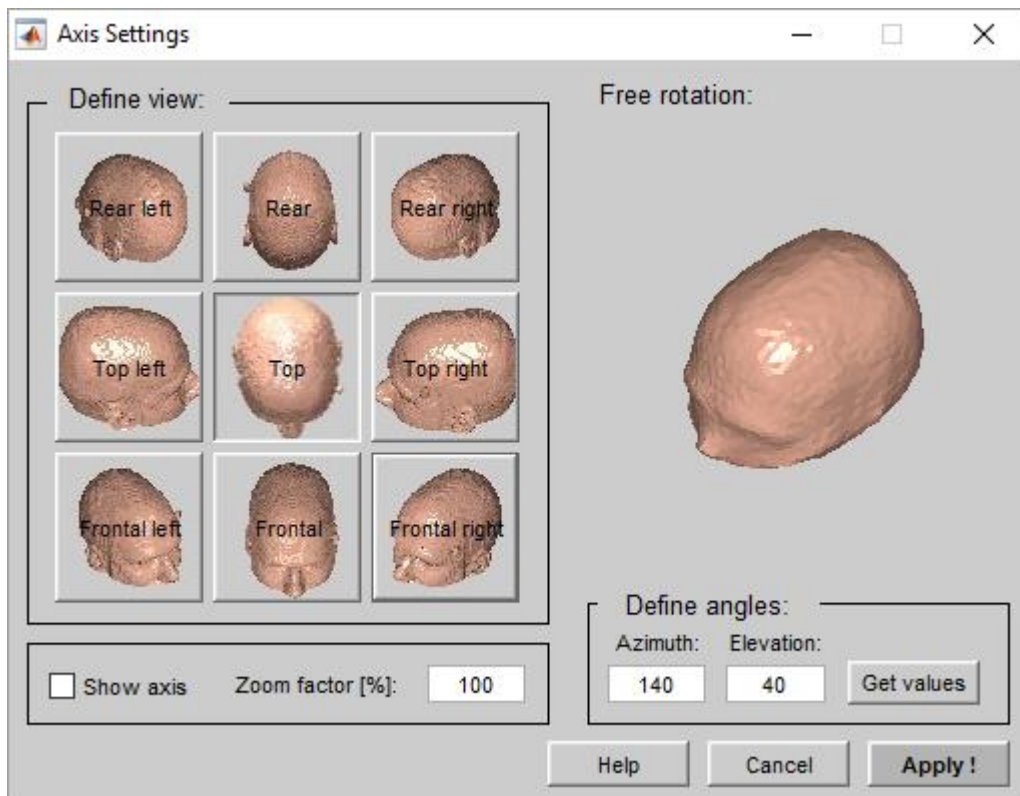
Data Interpolation and Laplace Derivation

Chapter **Data Interpolation and Laplace Derivation** explains how to interpolate the electrode positions and how to perform a spline surface Laplace derivation.

Interpolate Data
Calculate Laplace

Interpolate Data

Refine Electrode Positions

1. Load the data file `SSLerd.mat` in the **Data** menu with **Load** from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\erd`

2. With **Load** from the **Scalp** menu load the scalp boundary file `subject1_scalp.bnd` from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`

3. Add the electrode file `electrode60.mat` with **Load** from the **Electrode** menu from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\Electrodes`

4. Open **Display Setting** under the **Visualization** menu and show second 4 and 6 of the data file, invert the colormap and select **Confine to** to set the optimal scaling (**min**: `-120`; **max**: `346`).
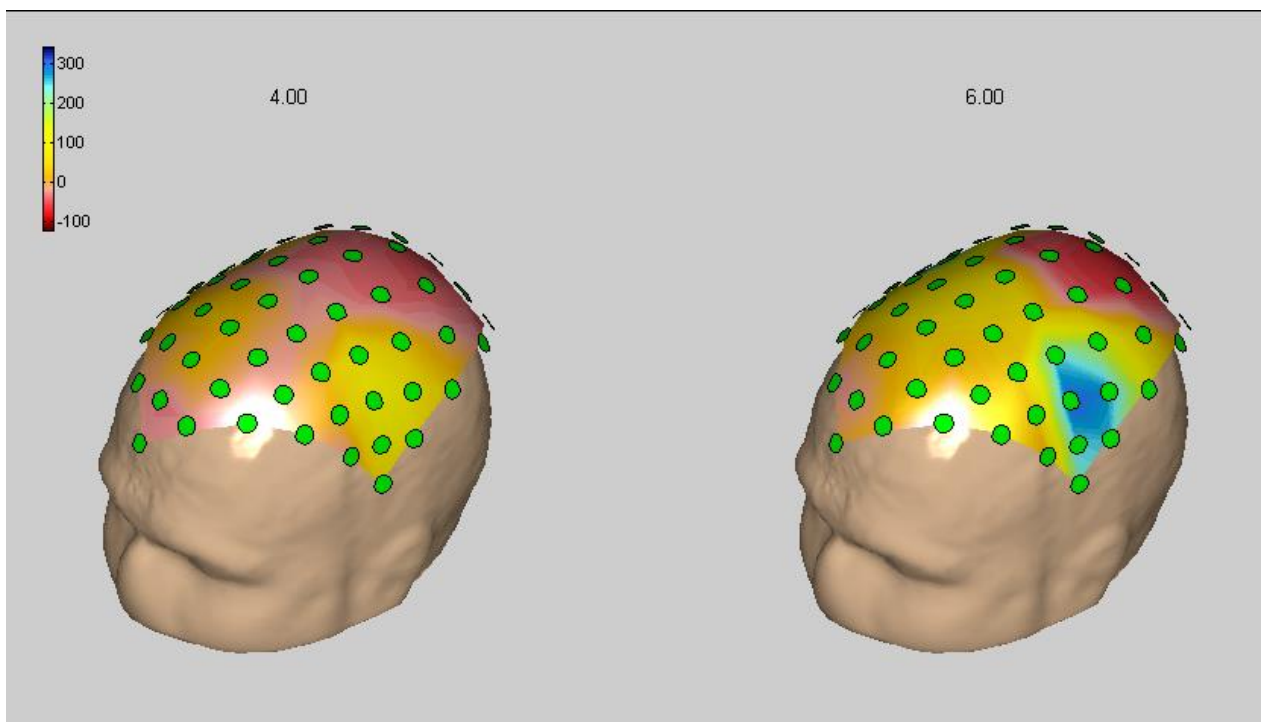
5. Open the **Interpolate Data** window from the **Data** menu

The window has the following entries:

Select channels … – select the channels that should be used for the calculation. This function is useful if a channel contains artefacts and should be removed from processing.

Read refined positions – load a boundary file (scalp or brain). The data map is interpolated onto this boundary.

Refine electrode positions – check to interpolate the existing electrodes. The algorithm sets additional electrodes between existing electrodes and interpolates the colormap.

Smoothing factor – set the smoothing factor to a value between 0 (no smoothing) and 100 (maximum smoothing)

6. Check the **Refine electrode positions** box and enter a **Smoothing factor** of 50

7. Press **Start !** to interpolate the electrode positions

g.HReeg shows the interpolated data map. The status information field of g.HReeg shows that the data map has now 218 channels. Note that the electrode channels of a montage file must match the data channels exactly if the montage should be loaded.

8. Open the **Display Settings** window and set the **Size of electrodes [mm]** to 2
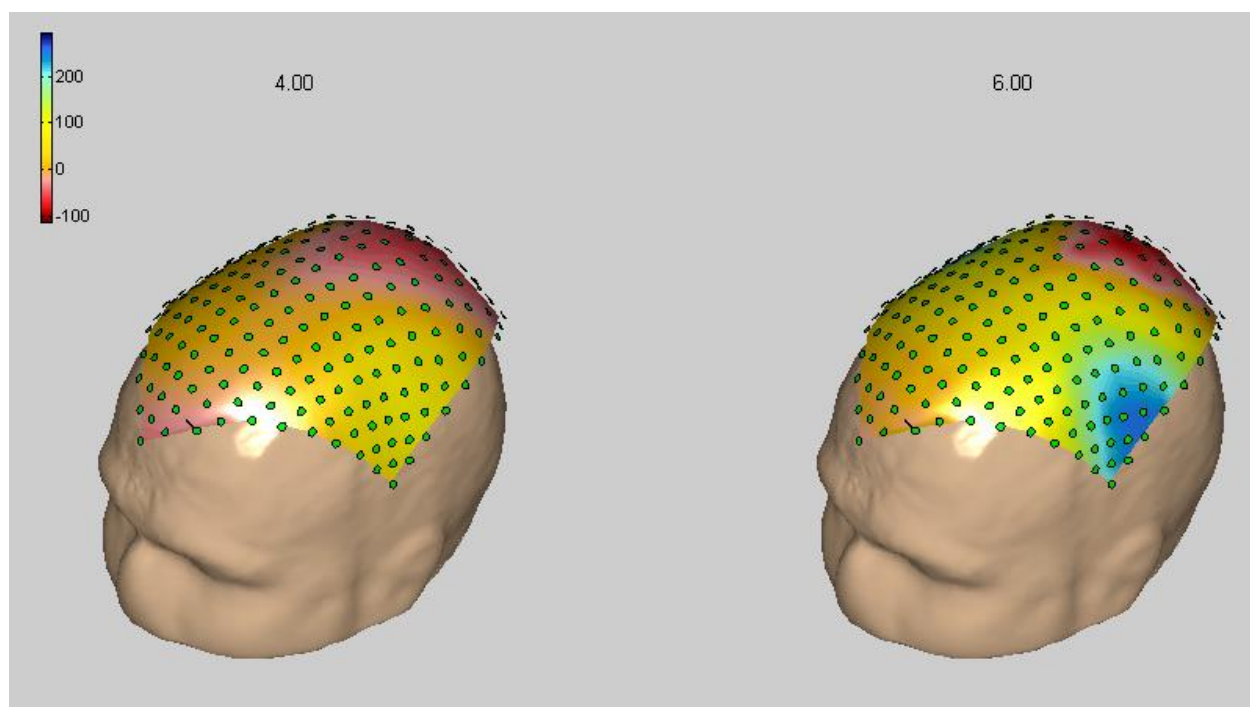
Read Refined Positions

1. Load the data file `SSLerd.mat` with **Load** from the **Data** menu from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\erd`

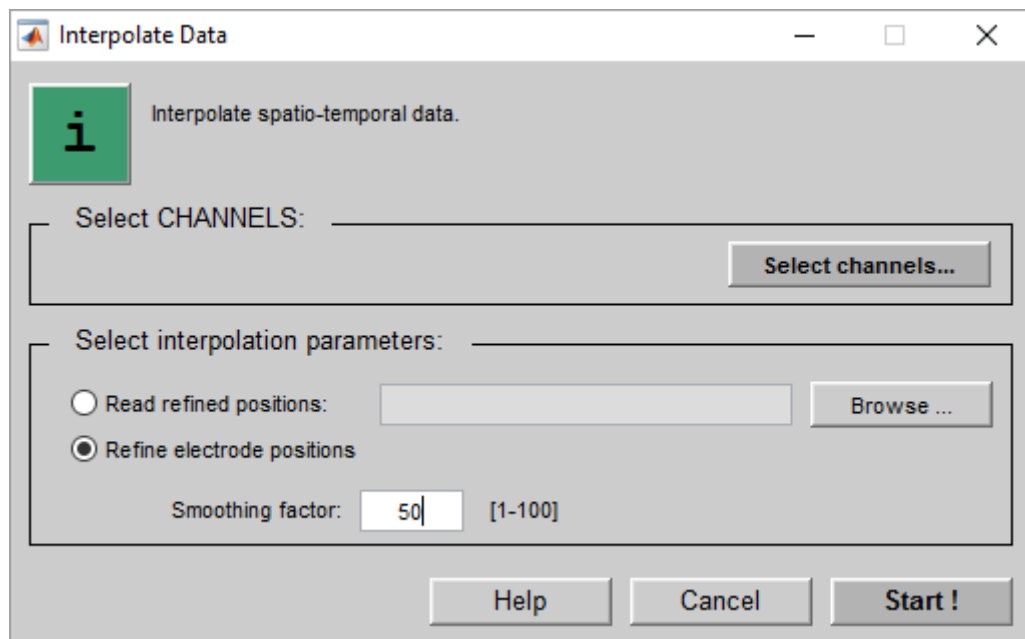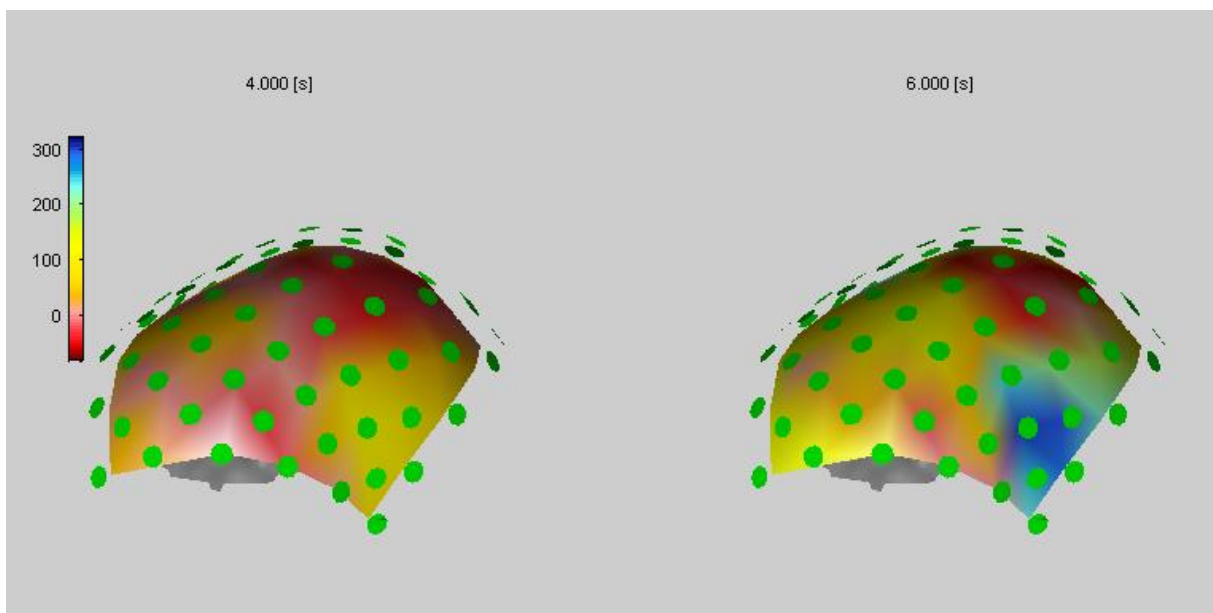2. From the **Brain** menu load the brain boundary file `brain30mm.bnd` with **Load** from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`

3. In the **Electrode** menu click **Load** to add the electrode file `electrode60.mat` from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\Electrodes`

Open **Display Setting** under the **Visualization** menu and show second 4 and 6 of the data file, invert the colormap and select **Confine to** to set the optimal scaling (**min**: `-120`; **max**: `346`).

4. Open the **Interpolate Data** window from the **Data** menu
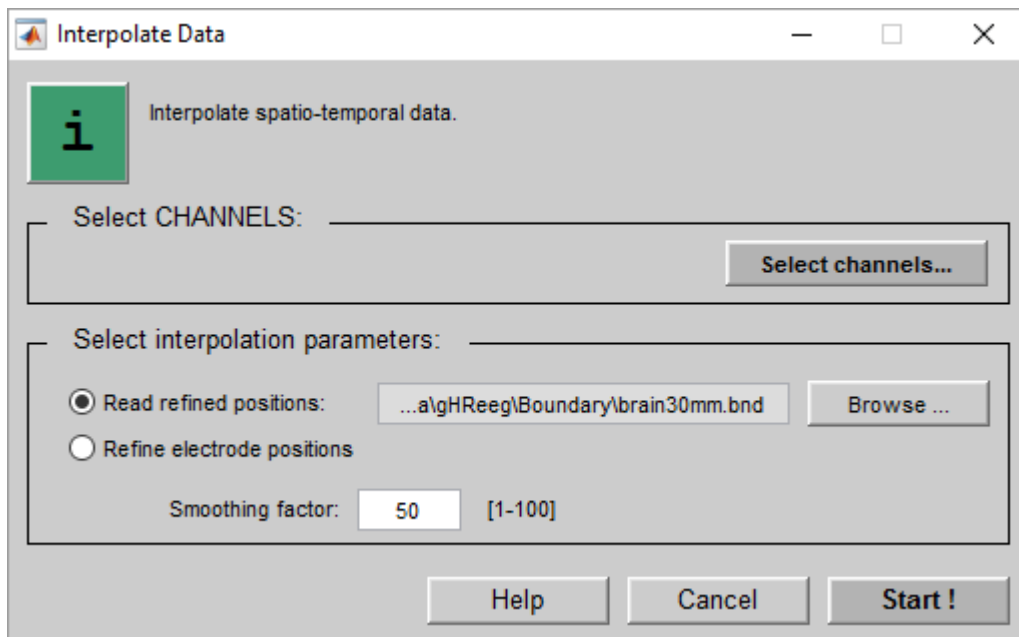
5. Check the **Read refine positions** box and **Browse** for the file `brain30mm.bnd` under

   `Documents\gtec\gBSanalyze\testdata\gHReeg\Boundary`

6. Enter a **Smoothing factor** of 50

7. Press **Start !** to perform the operation

Note that small brain boundaries should be used for a fast calculation. The whole brain boundary would need a long computation time and a lot of memory.

8. Open the **Display Settings** window. In the **Set BRAIN parameters:** section set **Transperency [%]:** to `100` and in the section **Set ELECTRODE parameters:** set the **Size of electrodes [mm]:** to `1`

g.HReeg shows the data map interpolated onto the brain boundary.
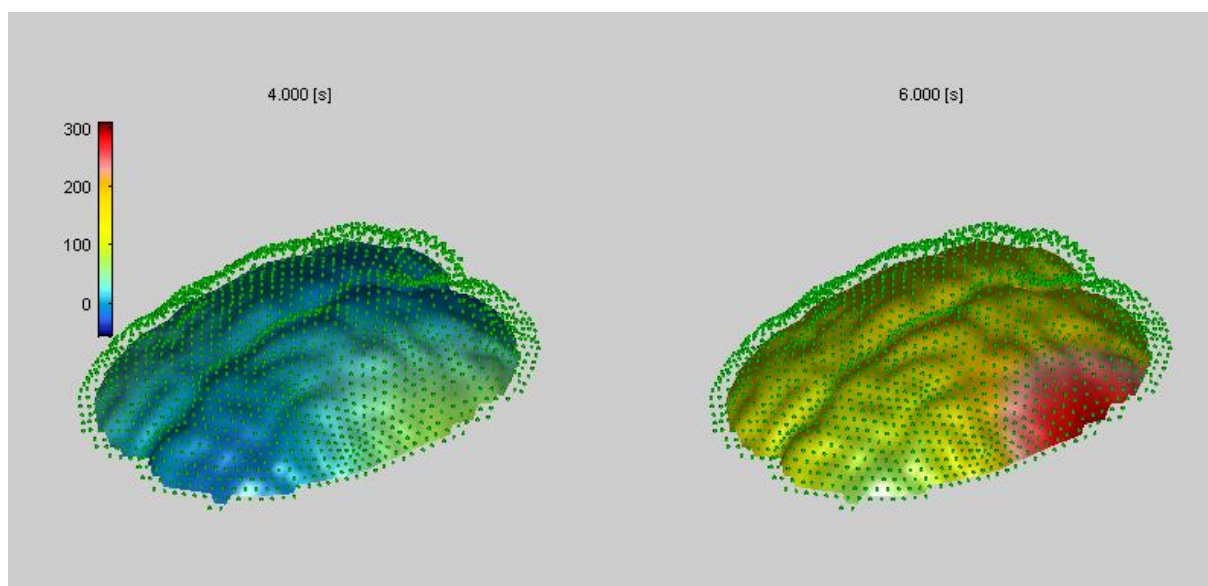
Calculate Laplace

The Spline Surface Laplacian derivation can be calculated from e.g. evoked potential (EP) signals generated with the **Average** function of g.BSanalyze.

Perform the following steps:

1. Open **gMONcreator** and load the file `44ch_sep.mat` from

   `Documents\gtec\gBSanalyze\testdata\montage`

   The Montage Creator opens an extended 10/20 electrode system montage with 44 electrodes.

2. Click on Cz to inspect the coordinates. The coorindates are defined for a sphere with 1 mm radius.

3. Press the **Fit to sphere** button and enter a radius of `100` mm to convert the coordinates

4. Save the montage file under `44ch_sep_100mm.mat` under

   `Documents\gtec\gBSanalyze\testdata\montage`

5. Open g.HReeg from the g.BSanalyze menu **Run!** with **gHReeg** and load the electrode montage file `44ch_sep_100mm.mat` previously stored with **Load** from the **Electrode** menu.

6. With **Load** from the **Data** menu add the EP data file `EP.mat` from

   `Documents\gtec\gBSanalyze\testdata\gHReeg\average`

7. g.HReeg shows the electrodes and the EP maps. Open **Display Settings** and in the **Select ARRANGEMENT and TIME frame** set in **Rows / Cols Nr. Rows:** to `2` and **Nr. Cols:** to `6` and for **Time steps [s]:** set **from:** to `0.001`, **to:** to `0.22`, **step** is `0.019`.

8. Open the window **Calculate Laplacian** from the **Data** menu:
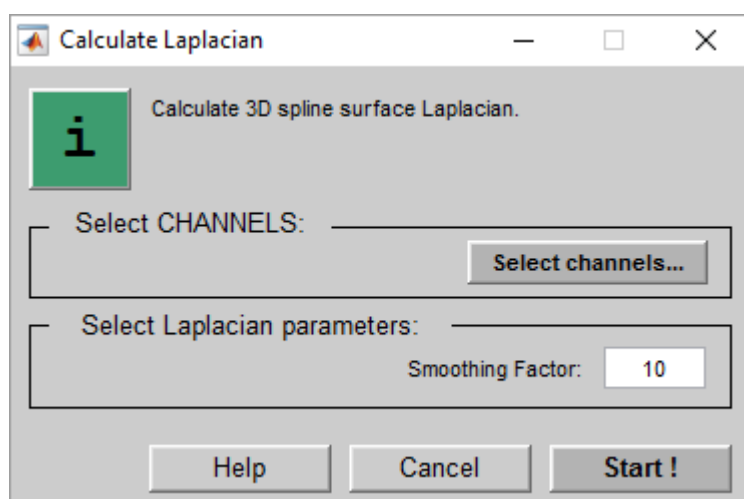
The window has the following entries:

Select channels … - define the electrodes that should be used for the calculation
Smoothing Factor – specify the smoothing value between 0 (no smoothing) and 100 (maximum smoothing)

9. Enter a **Smoothing Factor** of `10` and press the **Start !** button.

g.HReeg opens with the maps. Time point 0.172 (rounded to 0.18) is shown as example:
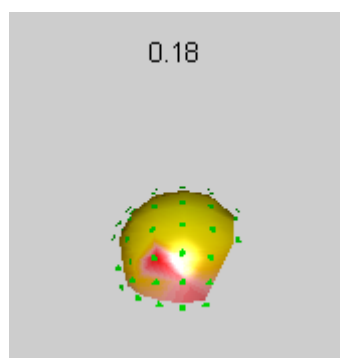
Help

g.HReeg provides a printable documentation and a function help.

The printable documentation is stored under

`C:\Program Files\gtec\gBSanalyze\Help`

as `gHReeg.pdf`. Use Acrobat Reader to view the documentation.

To view the function help type

`help gBSfunctionname`

under the MATLAB command window.

To view all functions that are available in batch mode type

`gBSfunctions`

Product Page

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g.tec medical engineering GmbH
Sierningstrasse 14
4521 Schiedlberg
Austria

tel. +43 7251 22240
fax. +43 7251 22240 39
web: www.gtec.at
e-mail: office@gtec.at