



BESA Research Tutorial

BESA®

Research 7.1

Tutorial

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Introduction

This Tutorial is created to guide you through a complete data analysis from preprocessing of individual datasets to cross-subject statistics of source analysis, time-frequency analysis or source coherence results. We will work with simulated datasets that help to understand basic mechanisms. Further we will be working with a real dataset of an auditory intensity experiment located in the BESA Examples folder

C:\Users\Public\Documents\BESA\Research_7_1\Examples\ERP-Auditory-Intensity. In this experiment 10 subjects listened to tones (1000 Hz) of different intensity (60, 70, 80, 90, and 100 dB).

Tutorial 1 – Preprocessing

What does BESA Research provide?

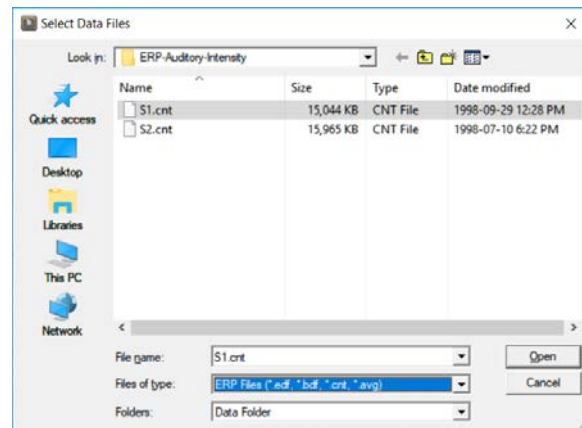
- ✓ Paging through your data screen by screen or jumping to selected time-points / events
- ✓ Adjusting signal amplitude and time-scale
- ✓ Interpolation of bad channels, changing the channel status
- ✓ Marking of Artifacts
- ✓ 3-D mapping of the topography at the selected cursor position
- ✓ Remontaging in sensor and source space
- ✓ Fast-Fourier-Transform (FFT) of the selected data block
- ✓ Density Spectral Array (DSA) view of the whole data set
- ✓ Filtering

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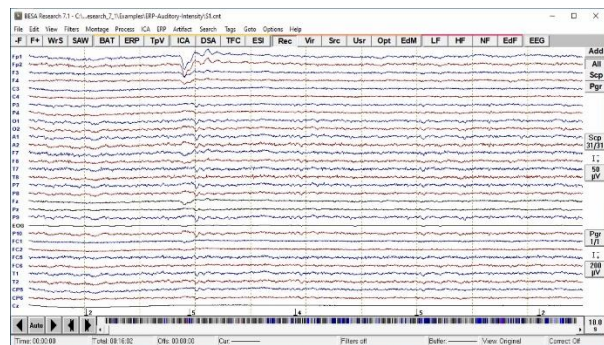
Tutorial 1 – Preprocessing

A. Data Review

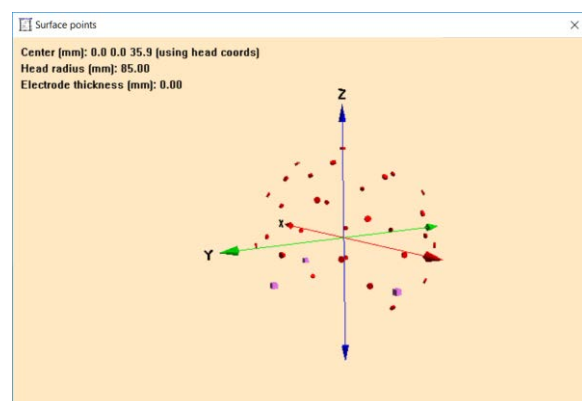
1. **Start BESA Research.** From the **File** menu, choose **Open**. In the Select Data Files box, select folder **ERP-Auditory-Intensity** in the **Examples** folder. Change the file type to **ERP files** (*.edf, *.bdf, *.cnt, *.avg) and open file **S1.cnt**.



2. This is a dataset recorded from a 32-channel electrode cap with Cz as reference and one EOG channel. Blue electrodes are over the left side of the head, red electrodes over the right side, black electrodes are over the midline. Triggers are coded as vertical black bars at the bottom of the screen.



3. To see the 3D-coordinates of the electrodes and additional head surface points, select **File / Head Surface Points and Sensors / View** (or press **V** on the keyboard). Fiducials are displayed as pink cubicles, electrodes as red discs. If you click on an electrode its label will be displayed. If you select an electrode in the main window, it will be highlighted in the surface points view. Close the surface points window.



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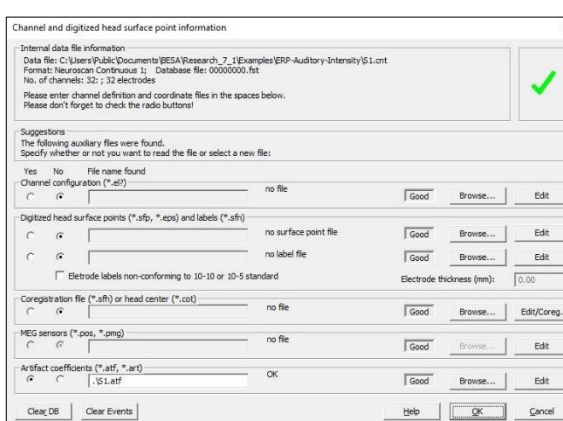
Tutorial 1 – Preprocessing

4. Select **File / Head Surface Points and Sensors / Load Coordinate Files...**

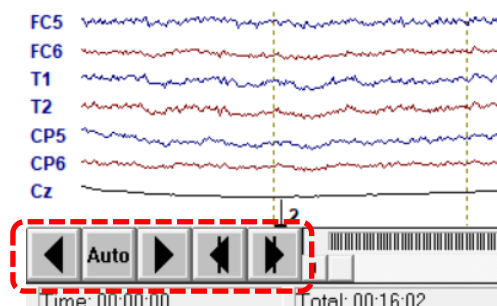
(alternatively: **ctrl-L**) A window opens showing all auxiliary information that is associated with the data file.



5. This dialog window allows to specify additional information on channel configuration (*.ela), digitized head surface points (*.sfp, *.eps) and labels (*.sfn) and more. Here, no additional files need to be loaded as all the relevant information is stored within the data file. If BESA finds auxiliary files with the same basename as the data file, they will be automatically loaded. Close the window.



6. In order to page through your data, you can either hit the space bar or use the arrows in the bottom left corner of the main window. The arrows with the vertical bar allow you to move half a page forward or backward.

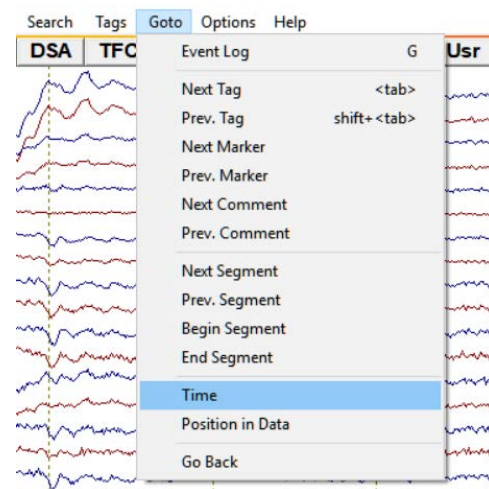


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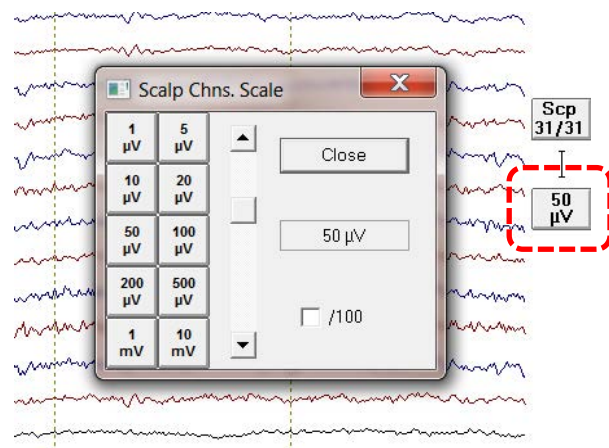
Tutorial 1 – Preprocessing

- You can also jump directly to a certain time-point by pressing **Goto / Time...**

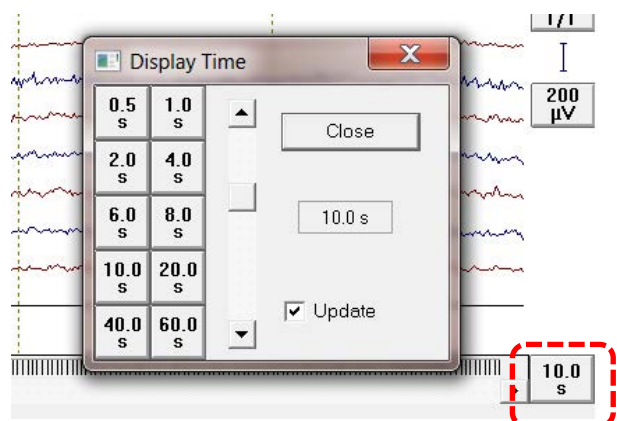
You might also add markers or comments to your data by right-clicking into the data and selecting Marker or Comment. You can then jump directly to these events via the Goto menu as well.



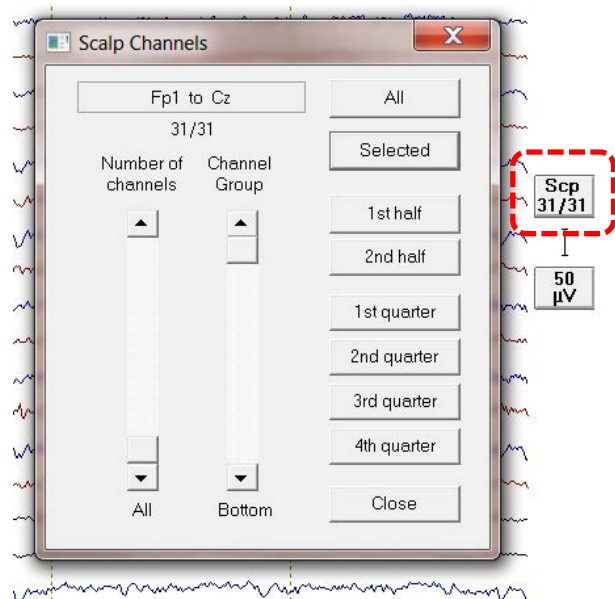
- To rescale your data, use the **amplitude scaling button** on the right side of the main window (just below the button Scp). In the present case, the scaling of 50 μV is appropriate.



- In order to change the length of the data window that is displayed at a time use the **time-scaling button** at the bottom right of the main window. In the present case 10.0 s is an appropriate viewing window.

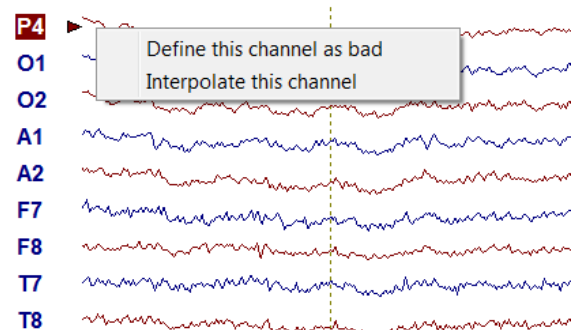


- If you only want to view a sub-set of your electrodes use the button **Scp** on the right of the main window. You can either choose the first / second half or the 1st to 4th quarter of the recorded channels. You may also adjust the number of electrodes you want to have displayed by using the sliders. In the current case, change to the all-channel view.

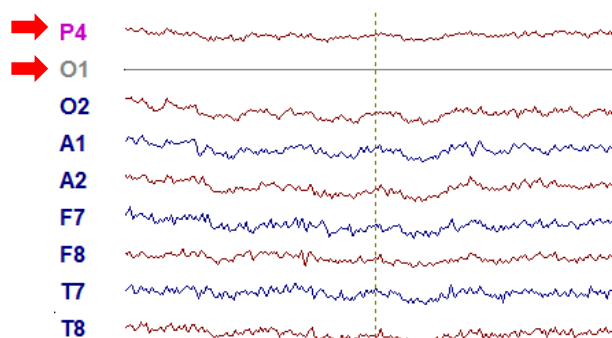


B. Interpolation, Marking of Artifacts, 3-D Mapping, Remontaging

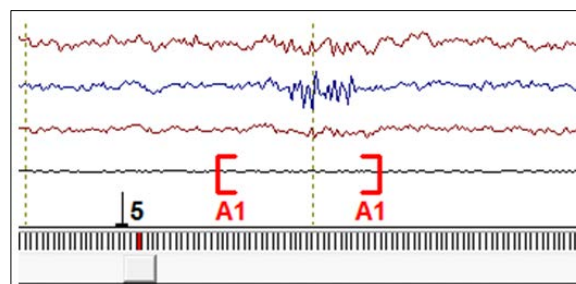
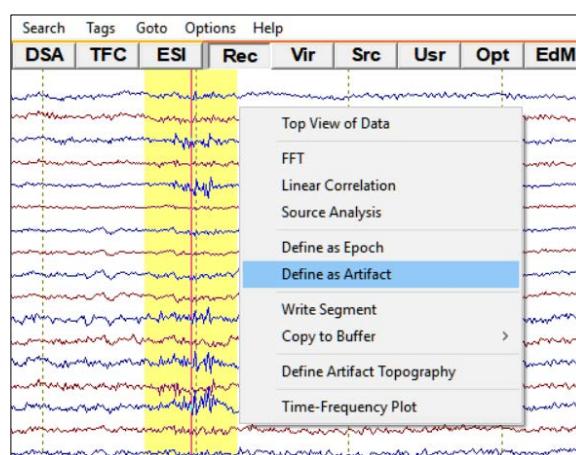
- Electrodes that display a faulty recording can either interpolate or set as bad. Interpolation is based on spherical splines, i.e. the information of all other electrodes is used to compute the interpolated signal. If a channel is set as bad it will be ignored. To interpolate or set a channel as bad **right-click onto the according channel label** and select Define this channel as bad or Interpolate this channel¹. Interpolated channels will be displayed in pink, bad channels in grey. In the current dataset, *there are no bad channels and no interpolation is needed.*



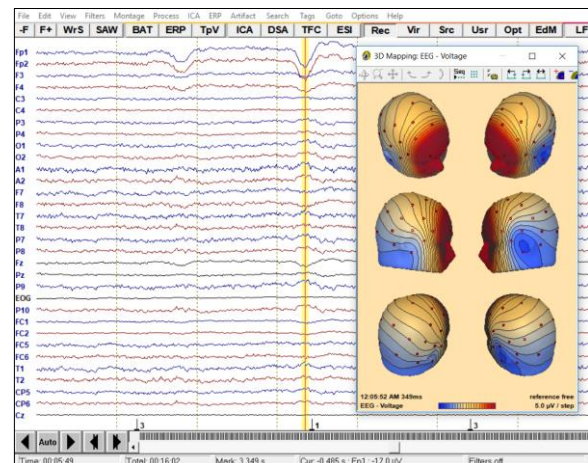
¹ Important note: in case a channel is at located at the rim of the electrode cap it is recommended to set it as bad rather than interpolate it as interpolation might be inaccurate. The position of an electrode can be checked following step A3 of this tutorial.



2. BESA uses amplitude, gradient and low-signal thresholds when scanning for artifacts (see Tutorial 2). Still, you might want to specify artifacts in your data by hand. This can be useful for e.g. muscle artifacts that are high-frequent and small in amplitude. In the current dataset **Goto Time 00:04:28**. You will see a muscle artifact. **Left-drag** a window across it, **right-click** into it and select **Define as Artifact**. A red bracket will appear at the bottom of the main window marking the artifact. It will be ignored for further analysis. The artifact marker can be deleted by right-clicking on a bracket and choosing Delete. Please delete the artifact marker in the current dataset.



3. **Goto Time 00:05:49.** You will see an eyeblink that is mainly picked up by electrodes Fp1 and Fp2. **Double-click** on it to open the **3D-Mapping** window. You will see a strong frontal positivity that is typical for eye-blinks in EEG data. We will not deal with eyeblinks at this stage.



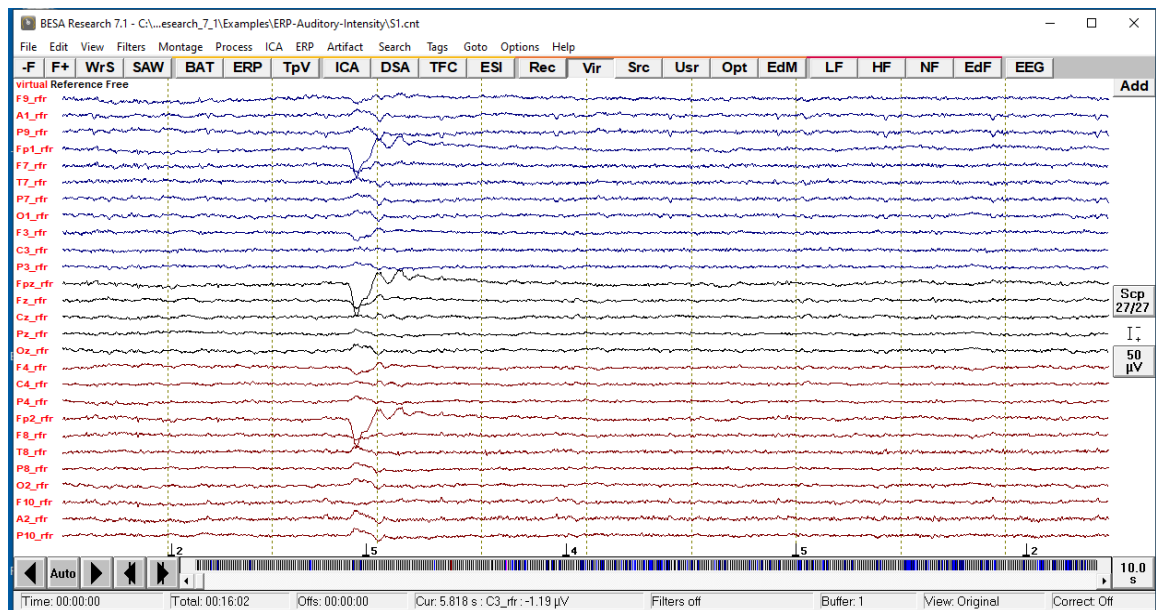
4. It is possible in BESA Research to remontage the recorded data using virtual standard electrode caps (**Vir-Button**) (international 10-10-system) or source montages. In the former case, you can view the data as if they had been recorded using a standard electrode cap. In the latter case, data are translated into source space using source montages provided by BESA (**Src-Button**) or created by the user (**Usr-Button**, see Tutorial 9) so that you can get an immediate display of activity in the respective sources in the continuous recording.



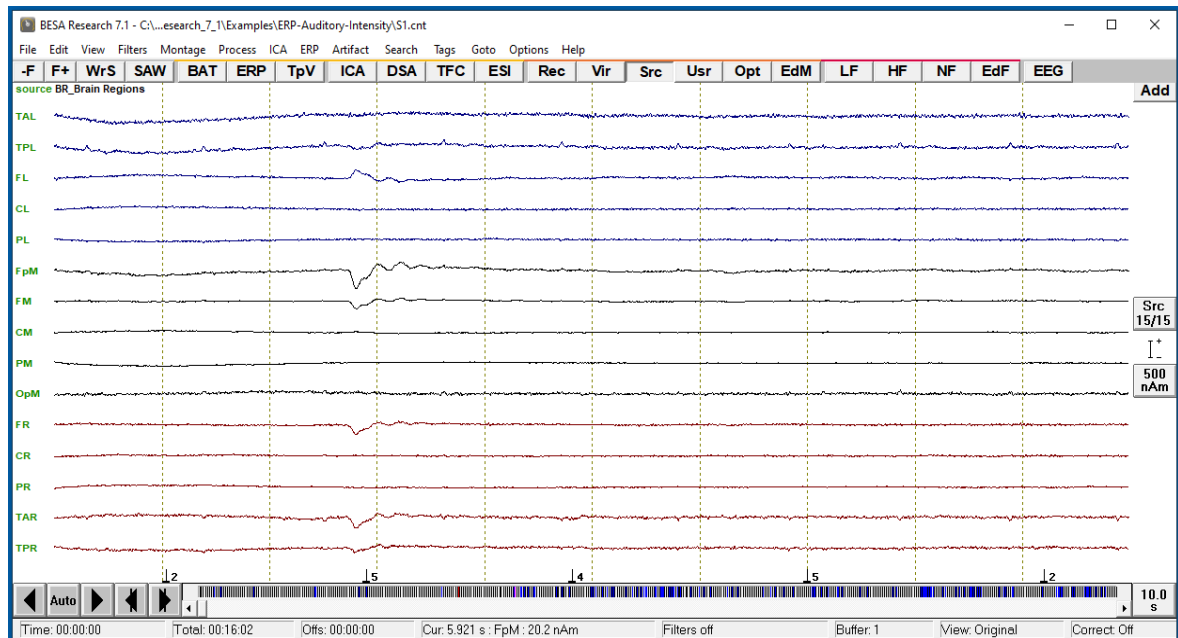
- a) Select **Vir / Reference Free**. This virtual montage consists of 27 standard EEG channels. The reference was computed as the average signal of an interpolation over the complete head surface (approximated by a sphere). Since the physical head model assumes a zero integral over the head surface, this type of referencing removes the bias of the reference electrode. Note that the Cz electrode carries signal in this montage. Also note that the signal becomes cleaner as the noise that is common to all electrodes gets subtracted by average referencing.



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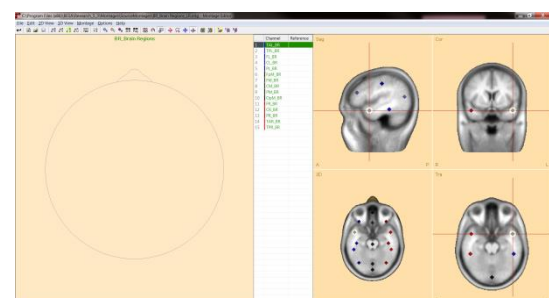
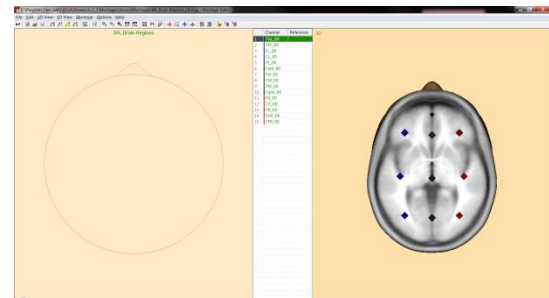
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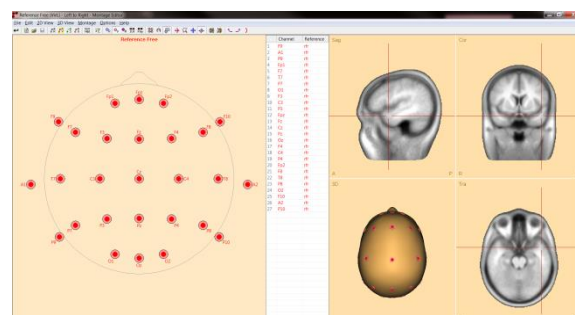
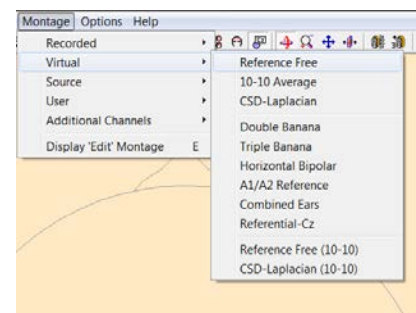
b) Select **Src / BR_Brain Regions**. Paging through the data you can immediately see that the left and right temporal sources carry more signal than the other sources.



- It is possible to view the current montage by pressing the **EdM button** (alternatively you can press **Edit / Montage**). In the current case we see a source montage that consists of 15 sources covering the whole brain. If you click on a source label in the middle panel BESA will slice the standard MRI to the position of the source. You may change to a coronal or sagittal view by pressing the according buttons . To see different views at the same time, press the button .



- In the montage editor press **Montage / Virtual / Reference Free** to change back to sensor level. Now you see the position of the 27 standard electrodes. Note that you can create your own montages or re-reference your electrodes in the montage editor as well. Return to the raw data using  the current montage by pressing the button located in the top left corner of the montage window.

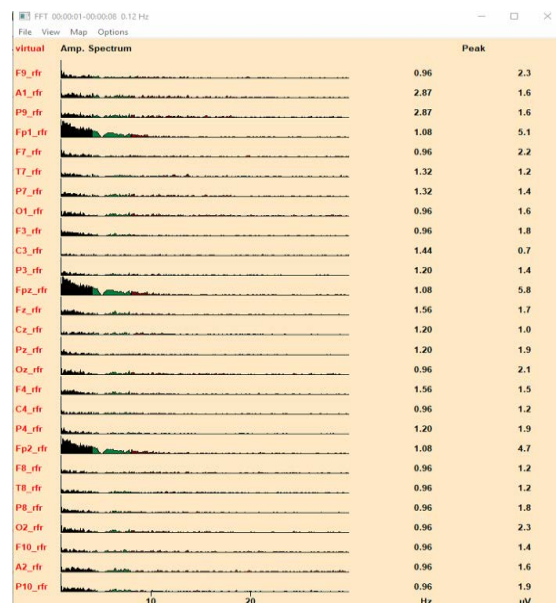
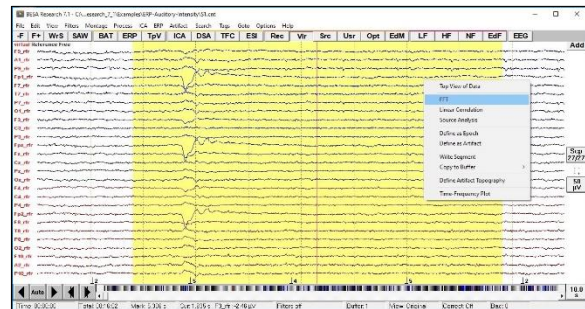


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C. FFT and DSA


1. BESA allows you to calculate an FFT on a marked datablock² to get a quick idea of the amplitude or power in different frequency ranges. Start the FFT by **left-dragging a window** in your raw data, **right-clicking** into it and selecting **FFT**. Please mark a block in the first data window that covers the eyeblink.
2. In the FFT window the electrodes of the current montage are listed along with their amplitude spectrum from 1 to 30 Hz (default). Beside every electrode the frequency is displayed that carries the peak amplitude in the specified time-range. The current view shoes that the frontal electrodes are characterised by high-amplitude low frequencies. Click into the low-frequent activity to open the 3-D Mapping window.

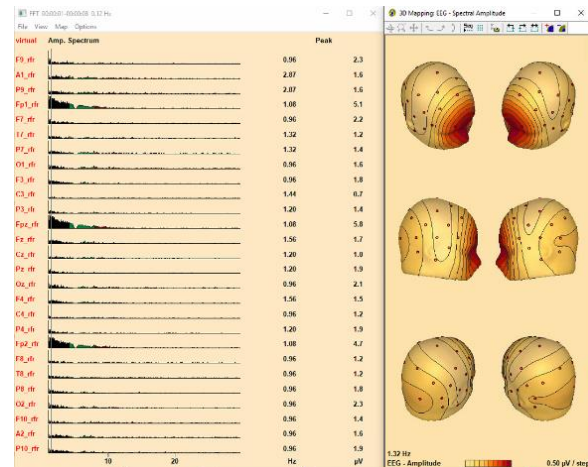


² In case you want to look at longer data periods or the whole dataset it is recommended you use the option **Process / Mean FFT-Spectrum**

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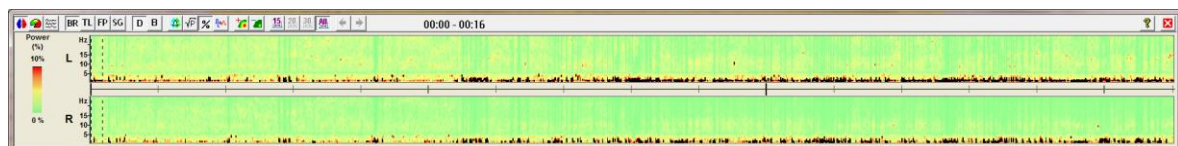
- Scale up the the voltage map by using the **upper arrow-key** on your keyboard or using the button . It becomes clear that the high low-frequent amplitudes are caused by an eye-blink in the current example. Note that you can change the frequency-range you want to view or change from amplitude to power spectrum in the View menu. In the Map menu you can choose the frequency band you want see a voltage topography of in the 3D-Mapping window. Close both the FFT and Mapping window.




- The DSA view is also based on an FFT and allows you to quickly get a feeling for the whole dataset. To start it press the **DSA** button in the main window.

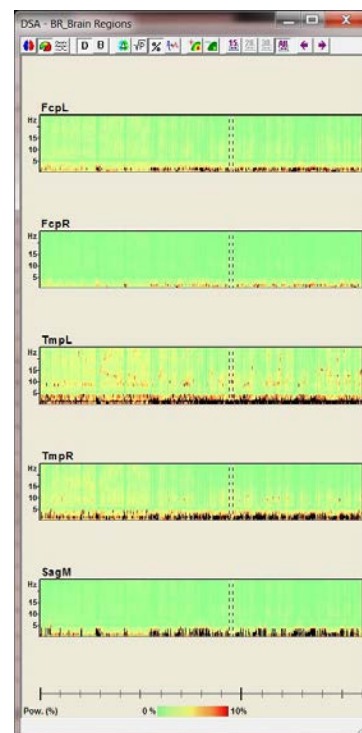


- The default DSA window is divided into left and right hemisphere. It shows a condensed FFT view of the whole dataset subdivided into blocks of 2 seconds. If you click into an event in the DSA window, BESA Research will jump to the according timepoint in the data in the main window.



- Change the view of the DSA window to multiple brain regions by pressing the button  in the top left corner of the DSA window. In this view it is possible to see that the left and right temporal regions show activity in the alpha / low beta band that is not present in the other brain regions.

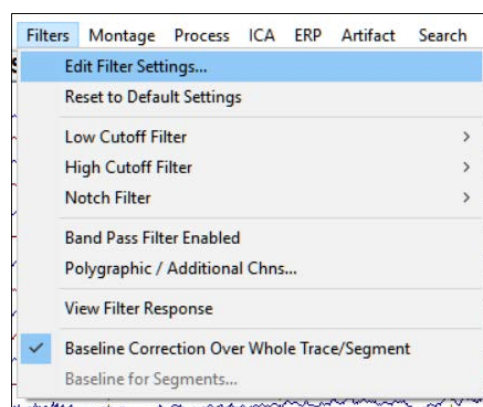
The DSA view is valuable to quickly identify time-windows in the dataset that are characterised by high signal power. This can be very useful for e.g. epilepsy research to identify seizure periods and get a rough idea of the origin of the seizure. Close the DSA view.



D. Filtering

Important note: You will need the program “BESA Simulator” for the further steps. BESA Simulator is a free program written by Dr. Patrick Berg for the simulation of EEG or MEG activity generated by model sources. Please download it from <https://www.besa.de/home/downloads/besa-simulator/>, and install it on your computer (administrator rights are required).

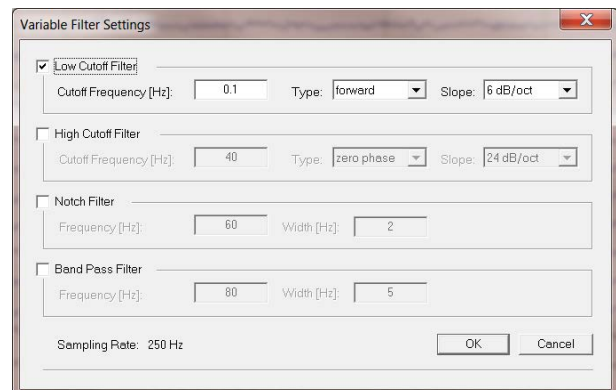
- It is possible to specify Low Cutoff, High Cutoff Notch and Bandpass filters in BESA. This can be done via **Filters / Edit Filter Settings** (also: **EdF button**) or the buttons LF, HF and NF.



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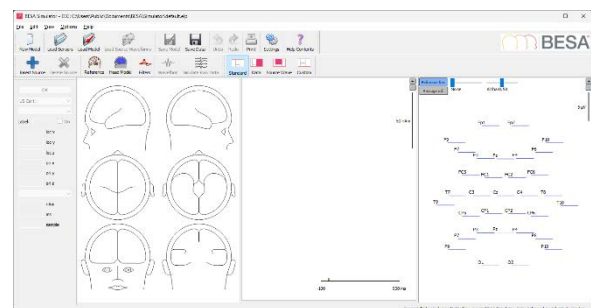
- For Low and High Cutoff filters the filter type can be set to forward, zero-phase, or backward. The slope of the filter can also be edited. In order to understand the properties of filters better we will now switch to the program “BESA Simulator”. *Please close the filter menu without setting any filters.*



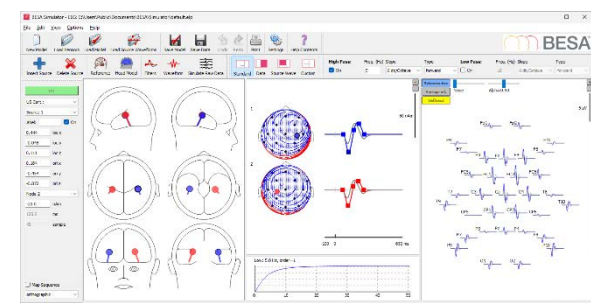
- Open the program **BESA Simulator** (that you have installed, as mentioned in the note at the beginning of this topic).



On the left of the window you see the BESA head schemes, on the right you see an electrode layout.

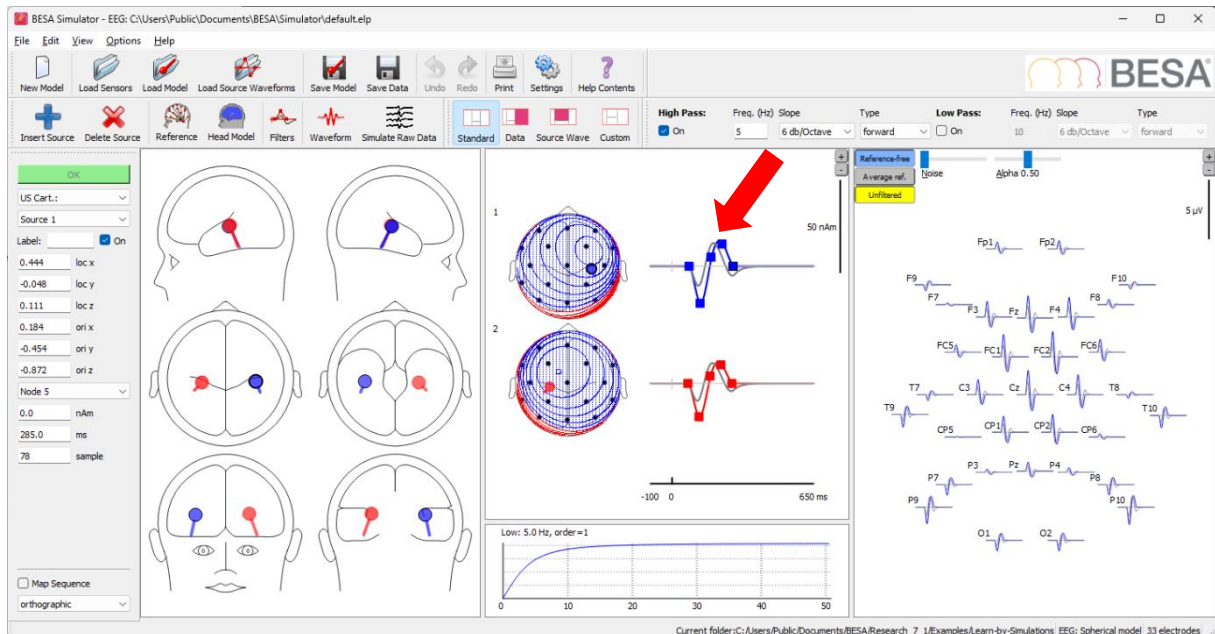


- Press **File / Load Model** and select the model **AC-2D-biphasic-synchronous.mod** located in the Examples Folder **Learn by Simulations** (**C:\Users\Public\Documents\BESA\Research_7_1\Examples\Learn-by-Simulations**). You will see two dipoles representing activity in the left and right hemisphere along with their source waveforms, i.e. their activity over time in the middle panel. Press the button **Filters** to show the filter settings. Specify a **High Pass (Low Cutoff) filter of 5 Hz, 6 dB/Octave, forward** and make sure that the box **On** is only ticked for the **High Pass** filter.

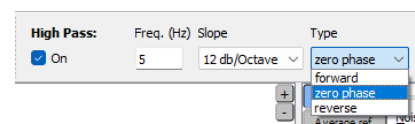


High Pass:	Freq. (Hz)	Slope	Type	Low Pass:	Freq. (Hz)	Slope	Type
<input checked="" type="checkbox"/> On	5	6 dB/Octave	forward	<input type="checkbox"/> On	10	6 dB/Octave	forward

- The grey waveforms show the effect of the filter. In the below of the topographic maps, the filter response is displayed. You can see that the High Pass (Low Cutoff) filter as specified in the previous step has an effect on both the amplitude and the shape of the waveforms. Amplitudes become smaller and the peaks get shifted forward.

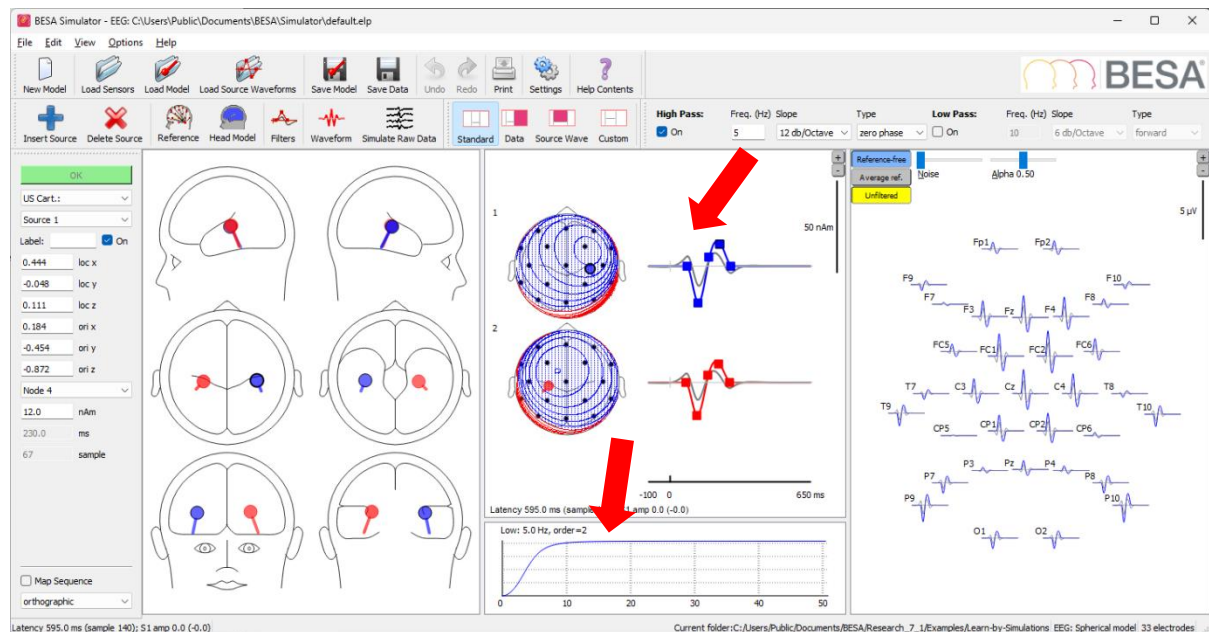


- Change the filter type to **zero-phase**. Note that the filter response changed as well as the filtered waveforms. While the amplitude of the filtered waveform is still diminished, the peaks of the filtered waveforms are closer to the ones in the unfiltered data. However, a small new “component” was caused by the filter at waveform onset and another one at the waveform offset.

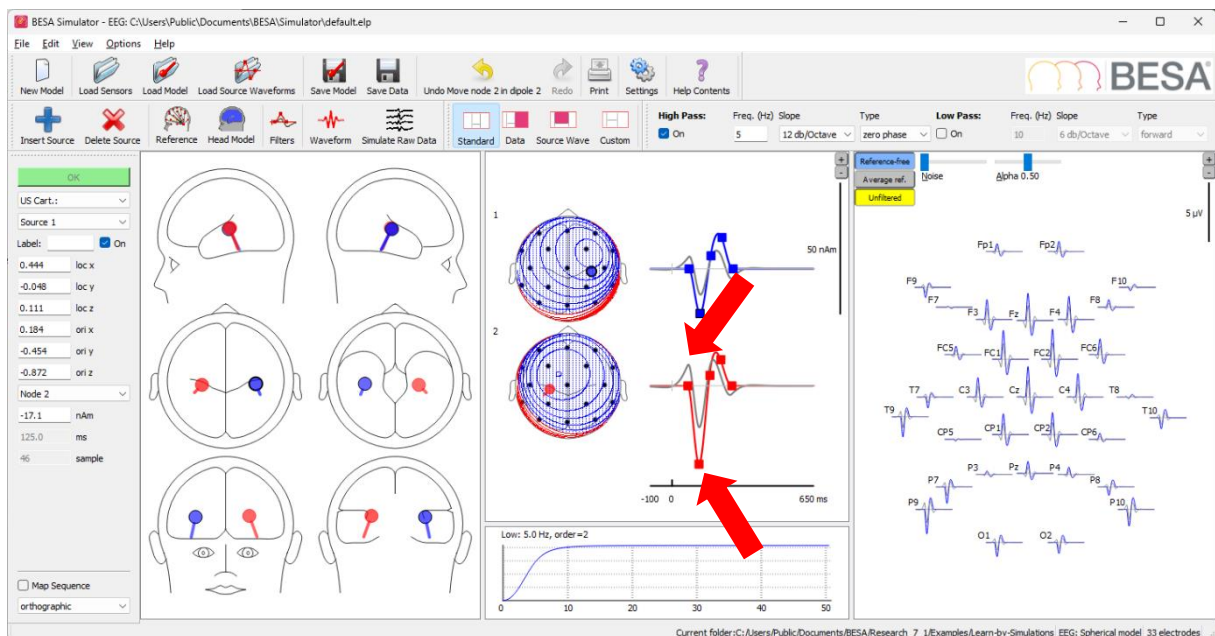


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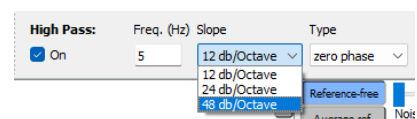
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7. Increase the amplitude of the red source waveform by dragging up the second node with the mouse. Note how the “component” at waveform onset also increases.



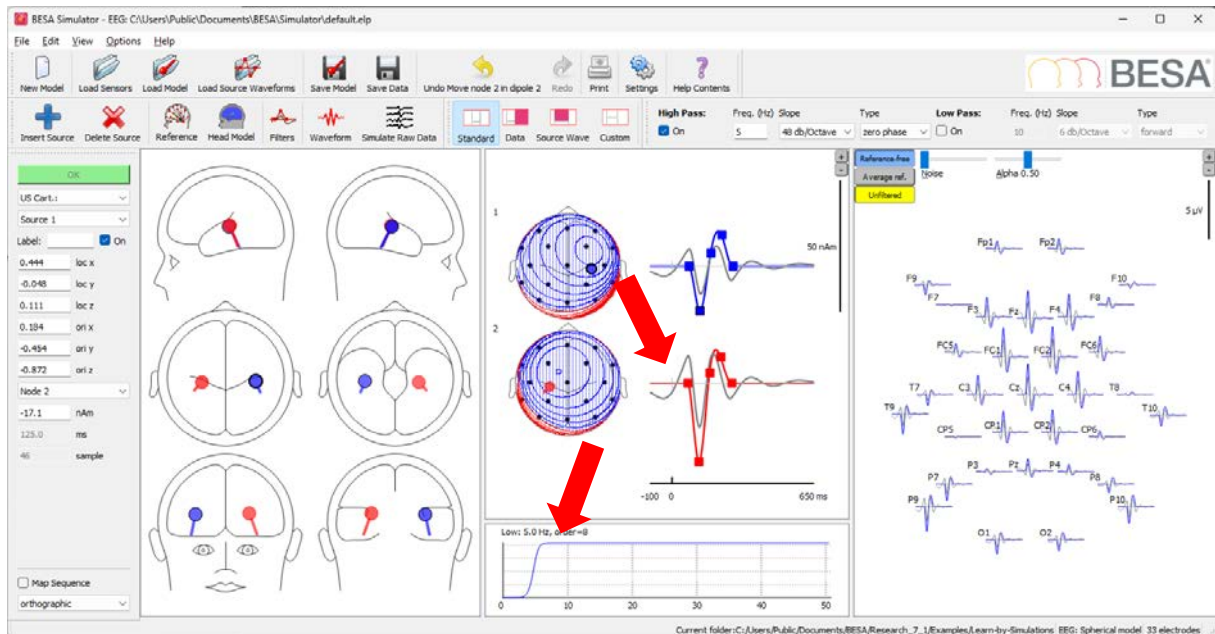
8. Change the filter slope to **48 dB/Octave**. Note that the filter response suggests better filtering properties, i.e. it filters out frequencies below 5 Hz more effectively. The



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downside is that this creates greater artifacts, distorting the waveform even further.

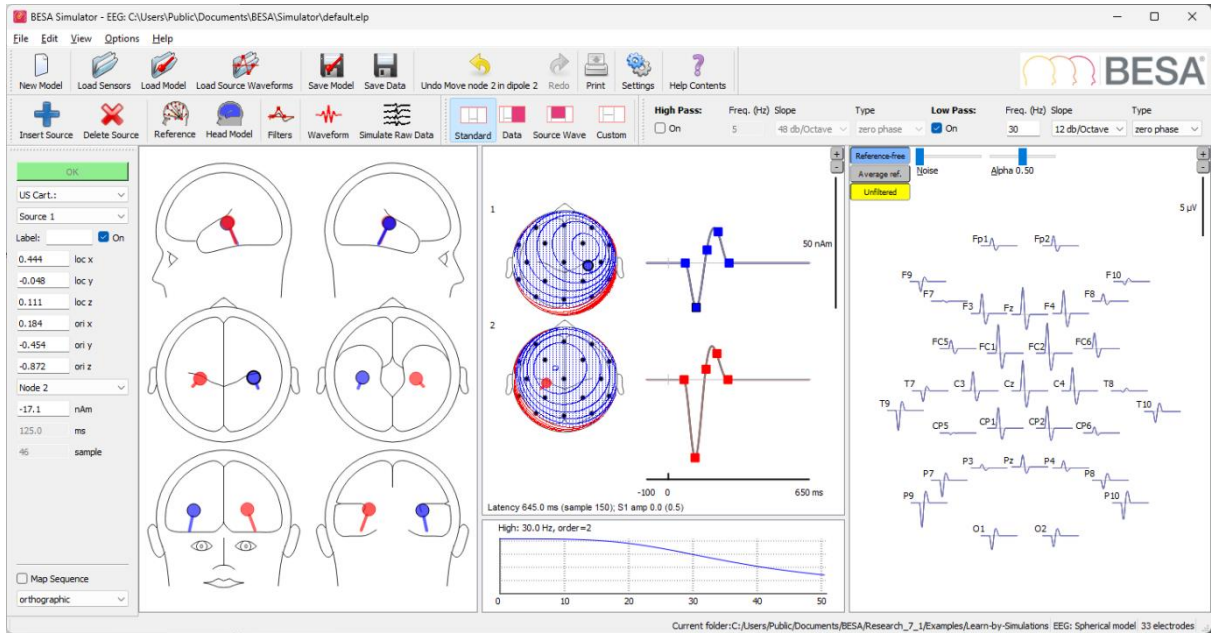


- Disable the High Pass (Low Cutoff) filter and enable a Low Pass (High Cutoff) filter of 30 Hz, 12 dB/Octave, zero phase. Note that the original waveform was not changed by the filter. This is the case because evoked potentials are generally lower in frequency.

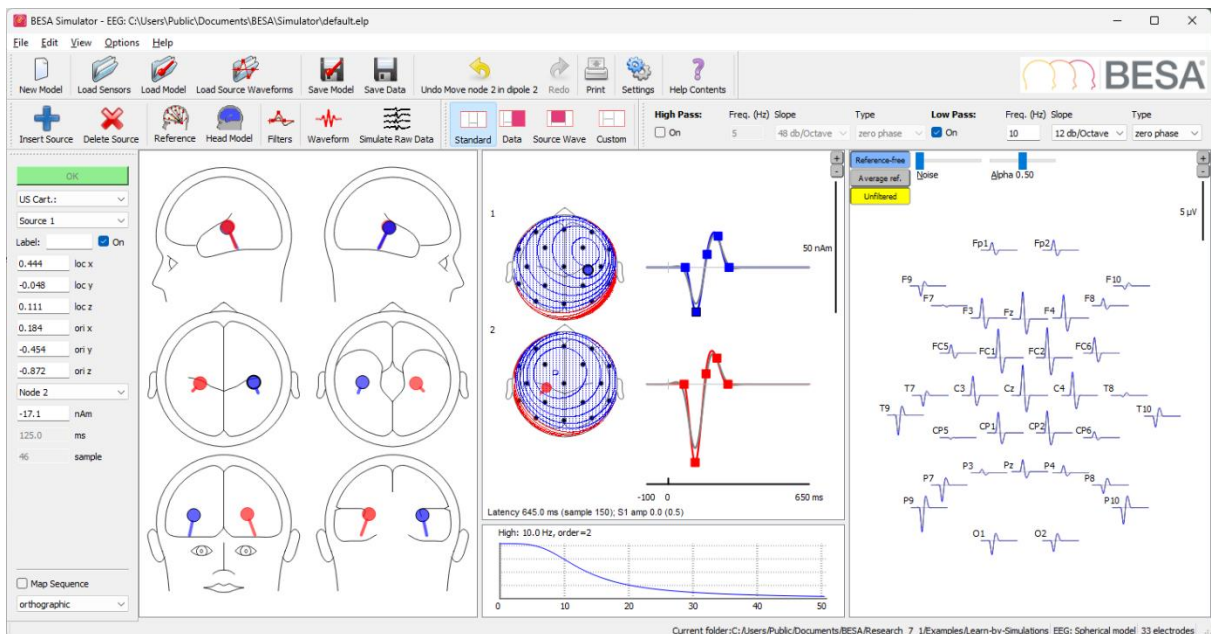
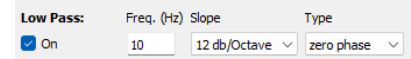
High Pass:	Freq. (Hz)	Slope	Type
<input type="checkbox"/> On	5	48 db/Octave	zero phase

Low Pass:	Freq. (Hz)	Slope	Type
<input checked="" type="checkbox"/> On	30	12 db/Octave	zero phase

Tutorial 1 – Preprocessing



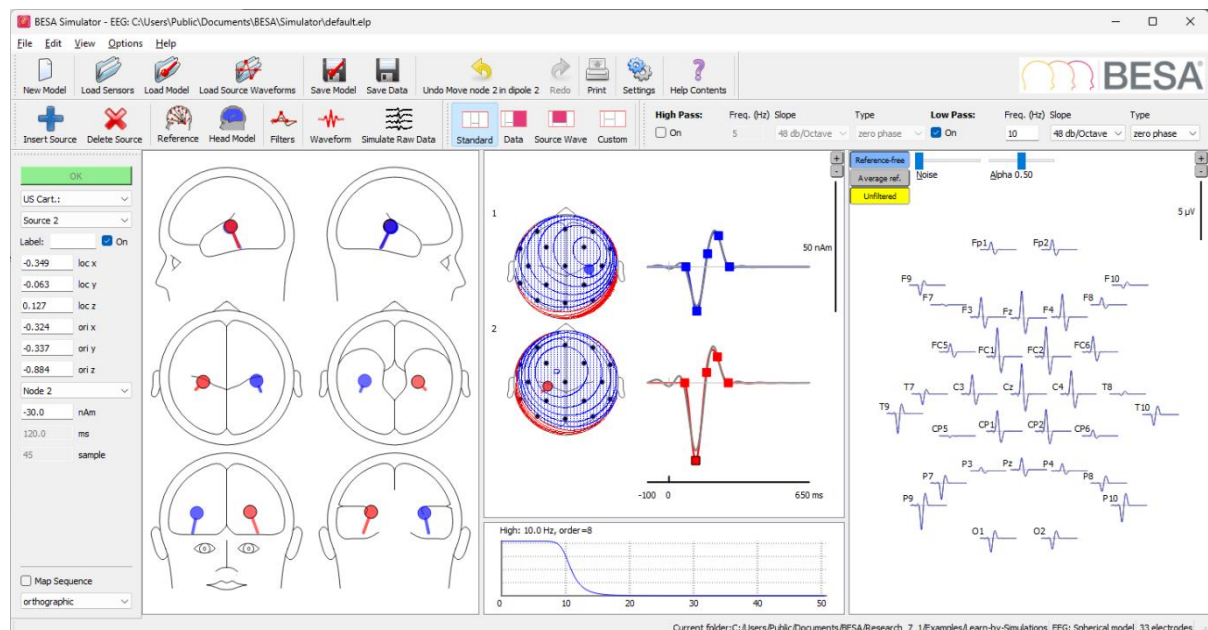
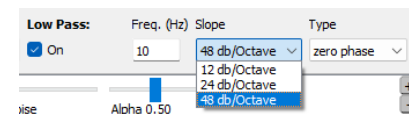
10. Change the Low Pass (High Cutoff) filter to 10 Hz, 12 dB/Octave, zero phase. The amplitude of the waveforms get decreased, while the shape of the waveform is not as distorted as in the example of the High Pass (Low Cutoff) filter.



BESA® Research 7.1

Tutorial 1 – Preprocessing

11. Increase the slope to **48 dB/Octave**. Note that the filter response again suggests better filtering properties suppressing activity > 10 Hz more effectively. The consequence is a slightly distorted waveform. Still, the effect is not as extreme as in the High Pass (Low Cutoff) examples.



Things to keep in mind when filtering

- The closer the frequency of the filters to your signal of interest, the greater the effect of the filter on your signal of interest.
- Filters affect both amplitude and shape of your waveforms.
- High Pass (Low Cutoff) filters usually have a greater impact on evoked potentials than Low Pass (High Cutoff) filters as evoked potentials are relatively low in frequency.
- The application of a filter can lead to the introduction of false “components”, the effect being the greater, the greater the signal amplitude of your waveforms.
- If you are interested in early components (< 100 ms) you should not use High Pass (Low Cutoff) filters that are zero-phase, as the signal of later components will be projected onto the earlier components.

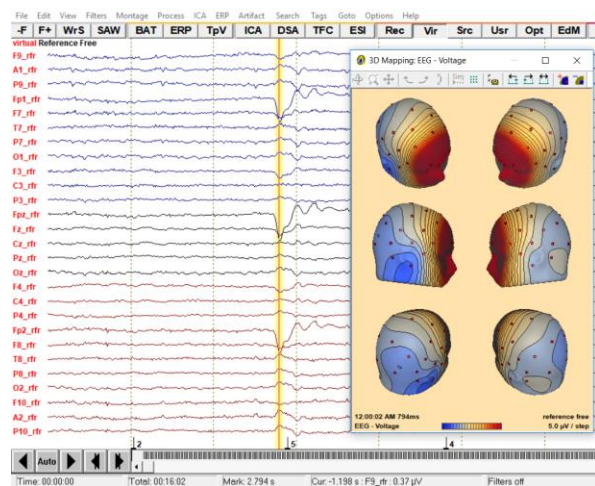
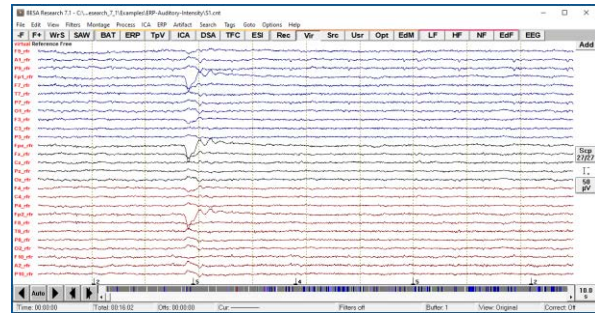
Tutorial 2 – Basic Artifact Correction, Triggers, Averaging

What does BESA Research provide?

- ✓ Automatic and user-defined artifact correction
- ✓ Definition of conditions based on trigger values, names and attributes
- ✓ Artifact rejection based on amplitude, gradient and low-signal criteria
- ✓ Averaging
- ✓ Classic ERP analysis

A. Basic Artifact Correction

1. In case you have closed the data file as used in Tutorial 1, reopen file **S1.cnt** located in the **Examples folder ERP-Auditory-Intensity** and switch on the virtual Reference-Free view (**Vir** button → **Reference Free**).
2. On the first screen, an eye-blink dominates the data. **Double click** on it to open the 3D Mapping window and view the associated typical strong frontal positivity.
3. Close the mapping window and select **Artifact / Automatic**. In the dialog box make sure that only the option **EOG** is ticked and leave the settings at default. After pressing **OK**, BESA will now automatically scan the data for eye movements using an internal model of artifact topographies.



Automatic Artifact Correction

Artifact

☒ EOG

HEOG Amplitude 150.0 μV

VEOG/Blink Threshold 250.0 μV

☐ EKG

EKG (+) (-)

EKG Amplitude Threshold 100.0 μV

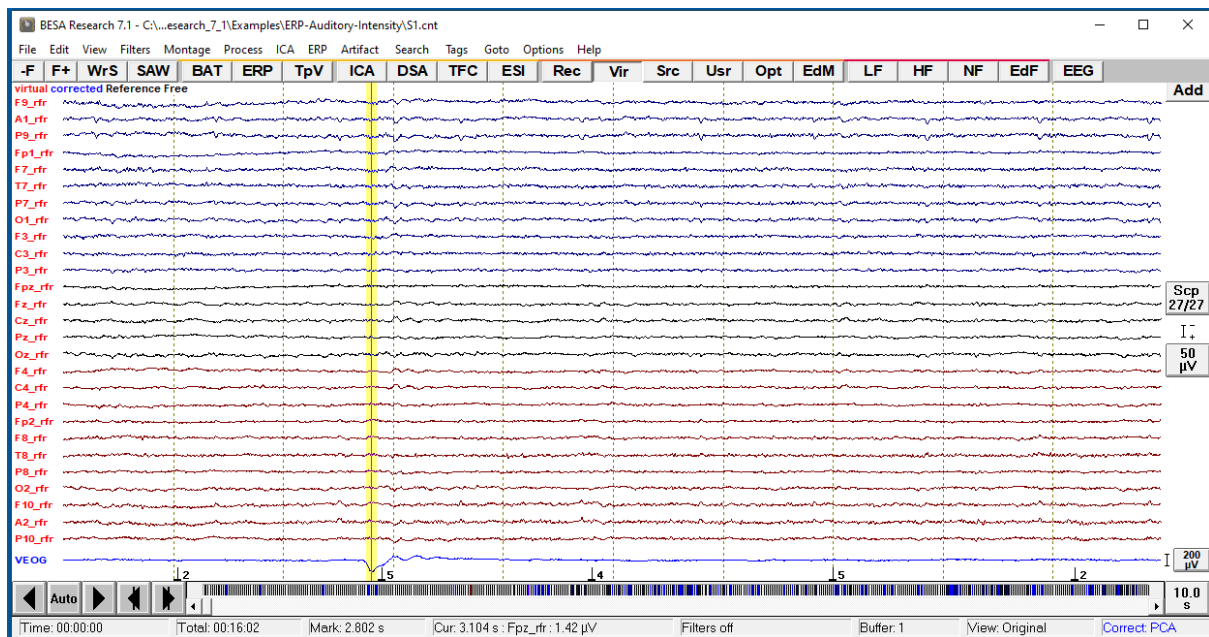
Range

☒ Whole EEG

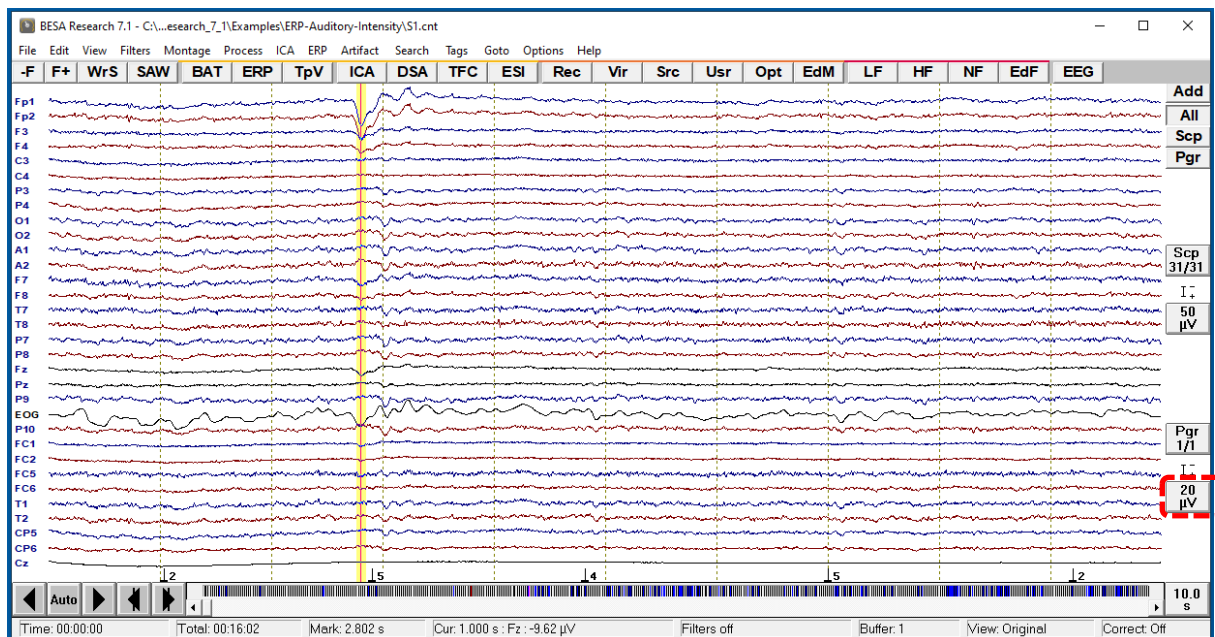
☐ Between Markers

OK Cancel

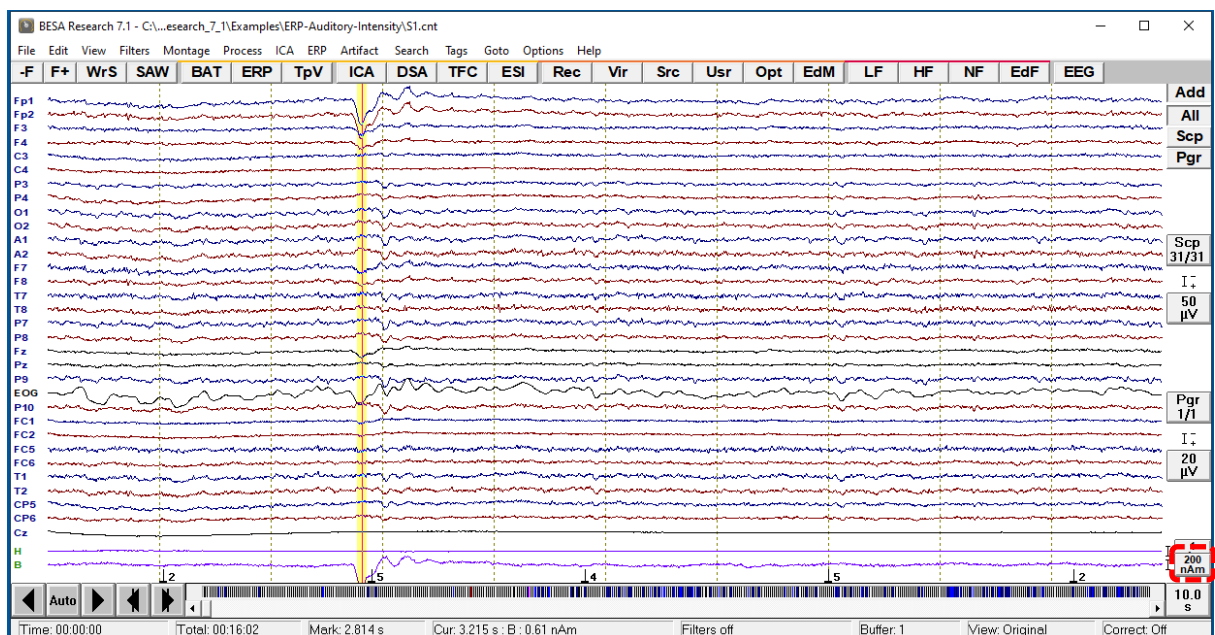
- No horizontal eye movements were found so only a virtual VEOG channel was created by BESA Research. The eyeblink that was clearly visible in the data before correction is prepresented in the virtual VEOG channel. Note that “corrected” is displayed in the top left corner of the main window when artifact correction is switched on. You may switch artifact correction on and off by pressing **ctrl+E** or by pressing **Artifact / Correct**.



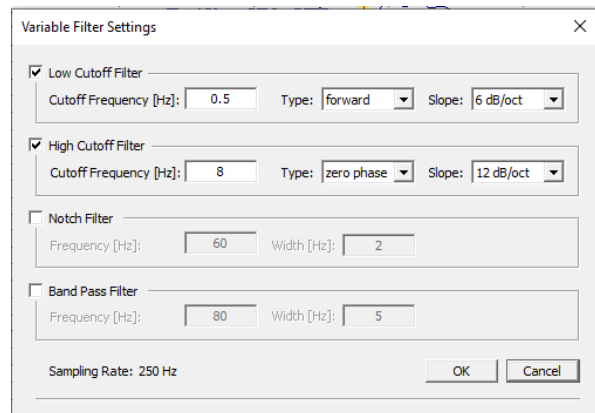
- Next we will do the eyeblink correction by hand. For this purpose, switch off the automatic artifact correction and hide the virtual VEOG channel by pressing **Artifact / View**. Switch back to the original data by pressing the **Rec** button and selecting **Original Recording**. You can see that an EOG electrode was used in this experiment. Scale it up to **20 µV** using the according amplitude scaling button.



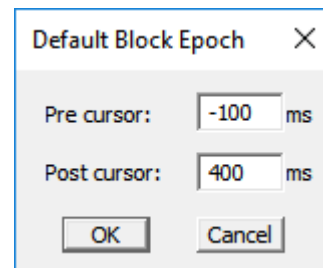
- Use the button **Add** in the top right corner of the main window and select **EOG-HB**. This will add virtual electrodes for picking up horizontal eye movements (H_EOG) and eyeblinks (B_EOG). Scale up the **B_EOG** channel to **200 nAM** by using the according amplitude scaling button. Note that the eyeblink is reflected in the EOG electrode as well as the virtual B_EOG electrode. Thus, virtual electrodes can be very useful for the identification of eyeblinks if an EOG was not specifically recorded.



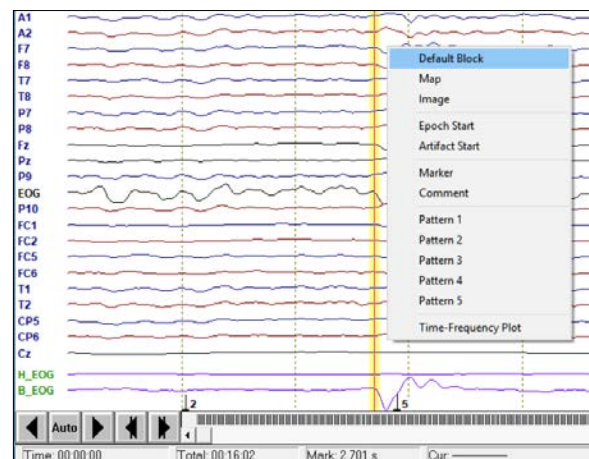
- Now we will apply filter settings that are optimal for the identification of blinks. Press the **EdF** button to open the filtering dialog. Choose a **Low Cutoff** filter of **0.5 Hz, forward, 6 dB** and a **High Cutoff** filter of **8 Hz, zero-phase, 12 dB**.



- Before marking an eyeblink, we need to define a default block epoch that will later be used for the pattern search. To do so press **Edit / Default Block Epoch** and choose the settings **Pre cursor: -100 ms** and **Post Cursor: 400 ms**. This time window is usually sufficient to cover the whole extension of the blink signal.



- Right-click** on the onset of the blink (you may use the virtual B_EOG channel as a reference) and select **Default Block**.

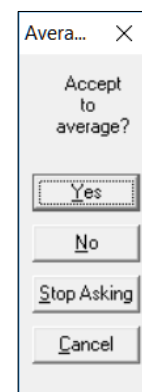
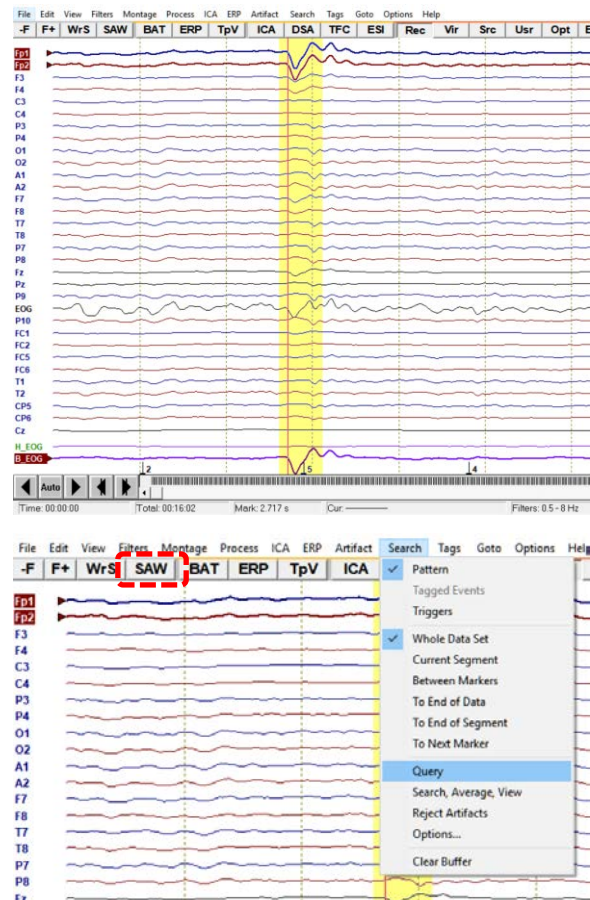


10. You may select the channels that pick up the eyeblink most clearly by holding down the ctrl-key and left-clicking on the according electrode labels. **Select Fp1, Fp2** and the virtual **B_EOG** channel. BESA Research will only use the selected channels for the pattern search. However, when data are filtered it is often not necessary to specify channels, the search algorithm may be run using all channels.

11. Before we start the pattern search, we will tell BESA Research to stop everytime a pattern is classified as a blink. To do so press **Search / Query**.

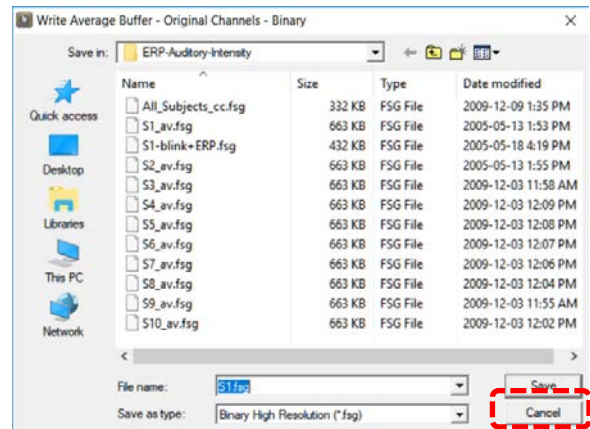
Next press the button **SAW** (Search – Average – Write) to start the pattern search.

12. Whenever BESA Research finds a pattern that correlates high with the blink we have just defined, it will ask you if you want to accept it to average. Click **Yes** to move on to the next pattern. If you are confident that the pattern search works well you may select **Stop Asking**. BESA Research will now automatically scan through the rest of the data.³



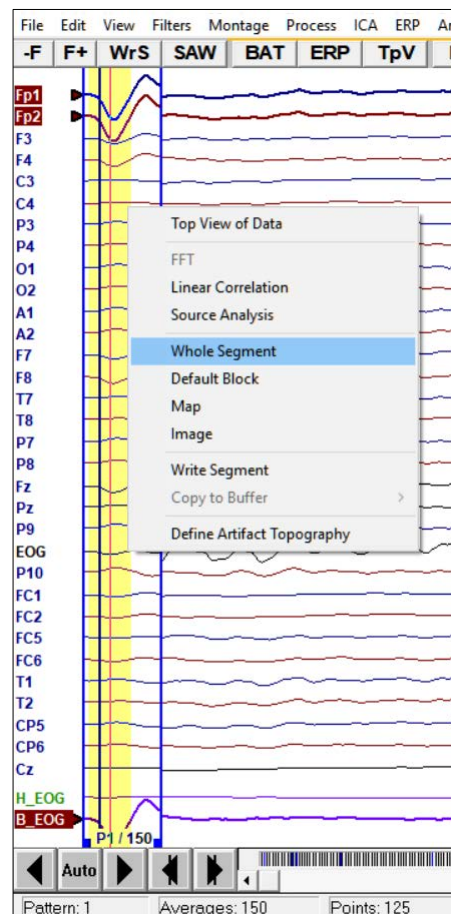
³ If your data are contaminated by many other artifacts, it is recommended to only accept blinks that do not coincide with another artifact event in order to receive a clean eyeblink topography.

13. When prompted whether to save the average buffer, choose **cancel**.

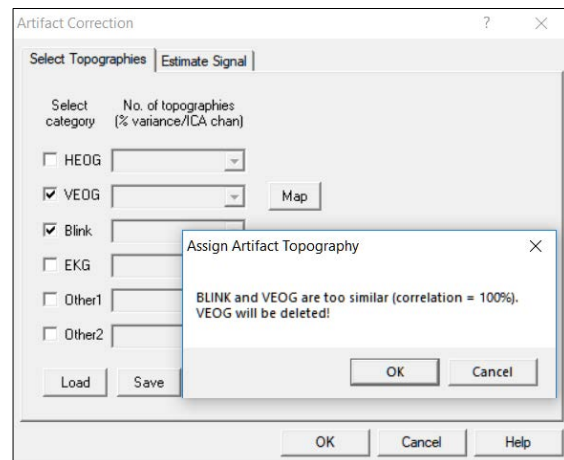


14. On the left of the main window, an average segment consisting of all blink events that were accepted during the pattern search is displayed with a baseline of -100 ms and a window length of 400 ms as specified by the default block epoch. **Left-drag** a window in it, **right-click** and select **Whole Segment**.

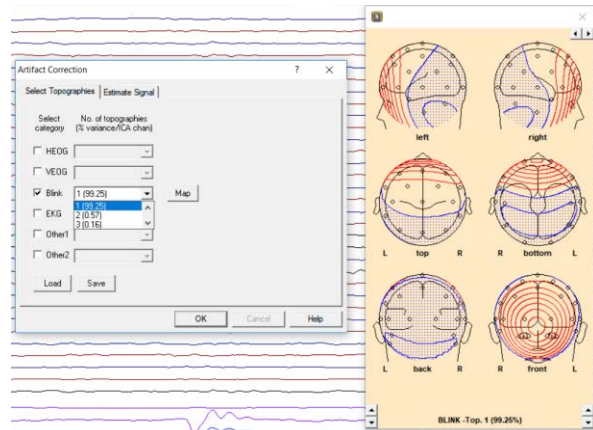
Right click again and specify **Define Artifact Topography**. (If you click next to the buffer window, it disappears. It can be displayed again by pressing View / Average Buffers.)



15. Note that VEOG is already ticked in the artifact correction window. The reason is that BESA Research still remembered the automatic artifact correction from before. Select **Blink**. An error message will appear notifying you that the blink and VEOG topographies are too similar and that VEOG will be deleted. Confirm with **OK**.

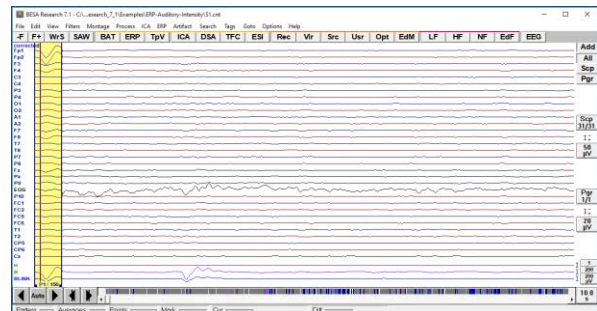


16. A 2D-mapping window opens that displays the topography of the first PCA component (principal component analysis) that was computed on the average blink signal. The PCA decomposes the blink signal into independent topographies. Generally the first component explains > 99% of the variance, so it is sufficient to only subtract the first component from the data⁴. Open the drop-down menu to view the other PCA components. Make sure that only the first component is selected and press **OK**.



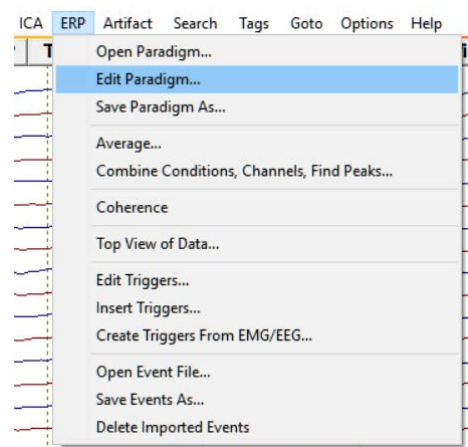
⁴ It is recommended to only select the first PCA component for artifact correction in order to prevent distortion of the data.

17. Note that another virtual blink channel was created. If you scale it up to **100 μ V** using the its amplitude scaling button you will see that it is almost identical to the virtual blink channel that was created automatically using the Add button. Switch off H_EOG and B_EOG by pressing **Add** and selecting **Switch off**. Also make sure to **switch off artifact correction** for now by pressing **ctrl+E**.

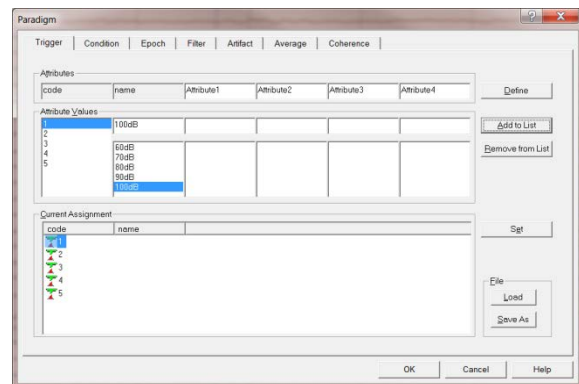


B. Definition of conditions based on trigger values, names and attributes

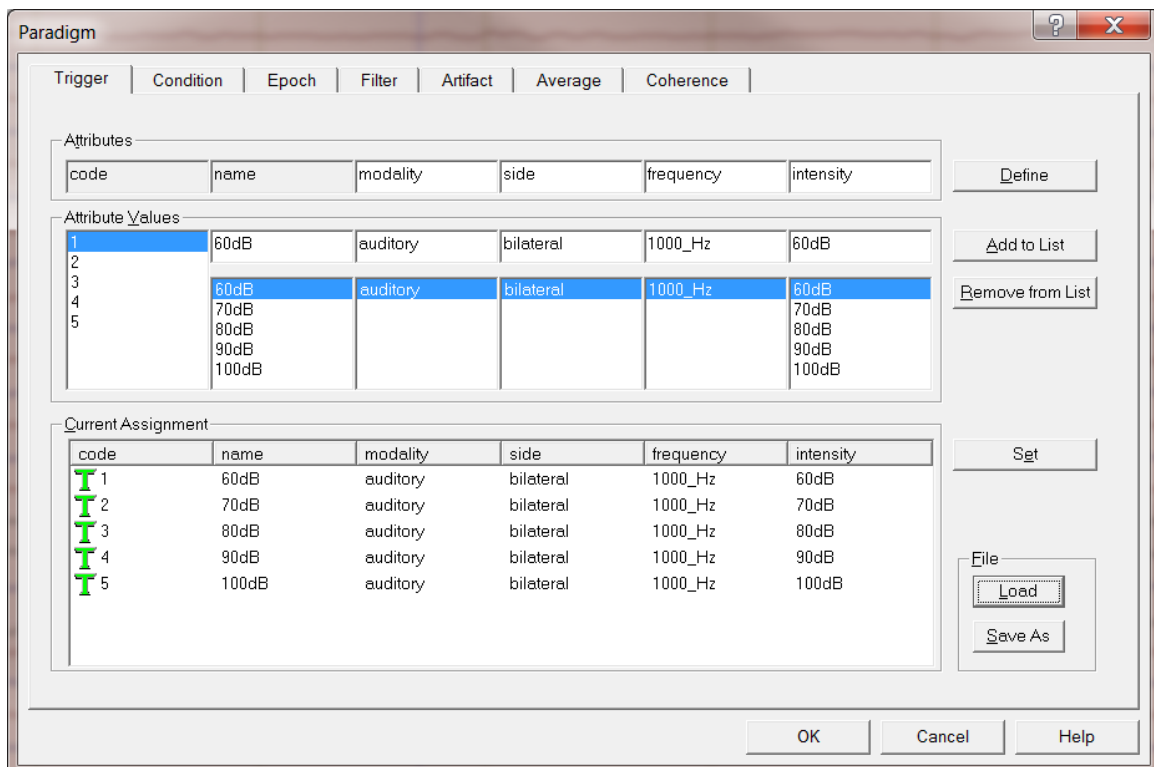
1. We will now use the trigger information in the file to specify conditions that will later be used for averaging. Press **ERP / Edit Paradigm**.



- Switch to the **Trigger** tab. 5 triggers are detected in the dataset. They correspond to stimuli that were presented at 60dB, 70dB, 80dB, 90dB and 100dB. **Enter** 60dB in the field under name and press **Add to List**. Do the same with the rest of the labels.



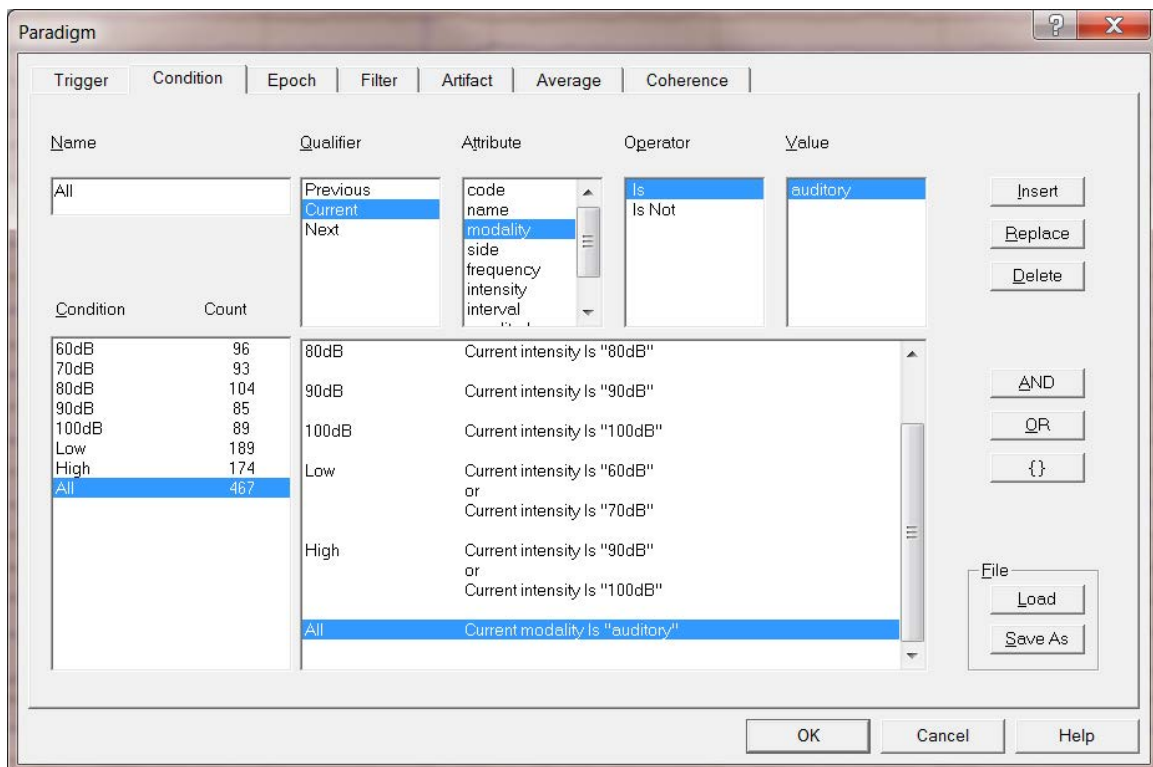
- We will add further attributes as they will make the definition of conditions easier later on. Change the name Attribute1 to modality and press **Define**. In the field below write auditory and **Add to List**. Change the name Attribute2 to side and press Define. In the field below write bilateral and Add to List. Change the name Attribute3 to frequency and press Define. In the field below write 1000_Hz and Add to List. Change the name Attribute4 to intensity and press Define. In the field below again add 60dB, 70dB, 80dB, 90dB and 100dB to the list. Finally, select Attribute Values/1, name/60dB, modality/auditory, side/bilateral, frequency/1000_Hz, intensity/60dB ad press **Set**. Proceed with Attribute value/2, name/70dB, modality/auditory, ...



- Switch to the **Condition** tab. First we want to specify our individual conditions. Enter the Name 60dB. Then select Qualifier **Current**, Attribute **intensity**, Operator **Is**, Value **60dB** and press **Insert**. Do the same for Names 60dB to 100dB.

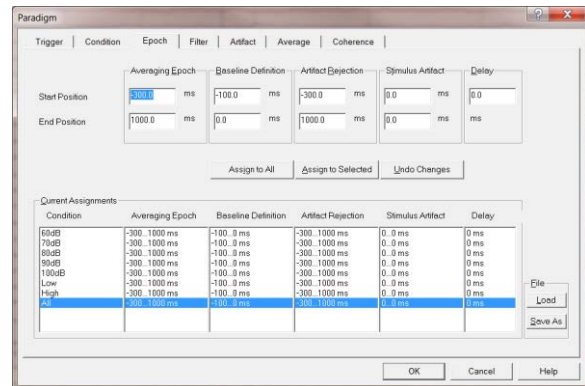
Next we want to specify the condition **Low**. Enter the name Low and again select **Current intensity Is 60dB** and press **Insert**. We want the Low condition to also contain 70dB stimuli. Thus, additionally specify the condition Low to be **Current intensity Is 70dB** and press **OR** instead of Insert. Now, the Low condition contains 60dB and 70dB stimuli. Specify condition **High** to contain 90dB and 100dB stimuli.

Finally we will specify the condition **All** by specifying **Current modality Is auditory**. (Make sure your condition definition looks like in the screenshot below.)

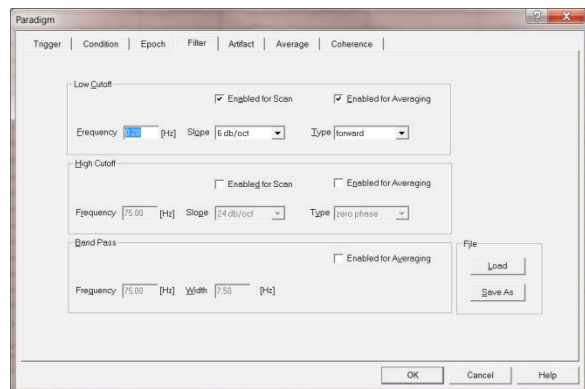


Note that it is also possible to specify other logic combinations using the Qualifier Previous and Next as well as the Operator Is Not. It is also possible to define an interval during which a previous or next event can occur under Attribute.

5. Move to the **Epoch** tab. Set Averaging Epoch to **-300 : 1000**, Baseline Definition to **-100 : 0**, Artifact Rejection to **-300 : 1000** and choose **Assign to All**. **Important note:** We recommend using long pre- and post-stimulus times to allow for optimum Low Cutoff filtering.



6. Move to the **Filter** tab. Specify a Low Cutoff filter of **0.2 Hz, 6 dB/Octave, forward**. Enable it for Scan and Averaging (i.e. the Low Cutoff filter will be switched on for the artifact scan and averaging). This prevents us from having to filter the averaged data later on and we can avoid the negative effect Low Cutoff filters can have on relatively short data epochs. We will not use a High Cutoff filter here as we can apply it later without distorting the data.

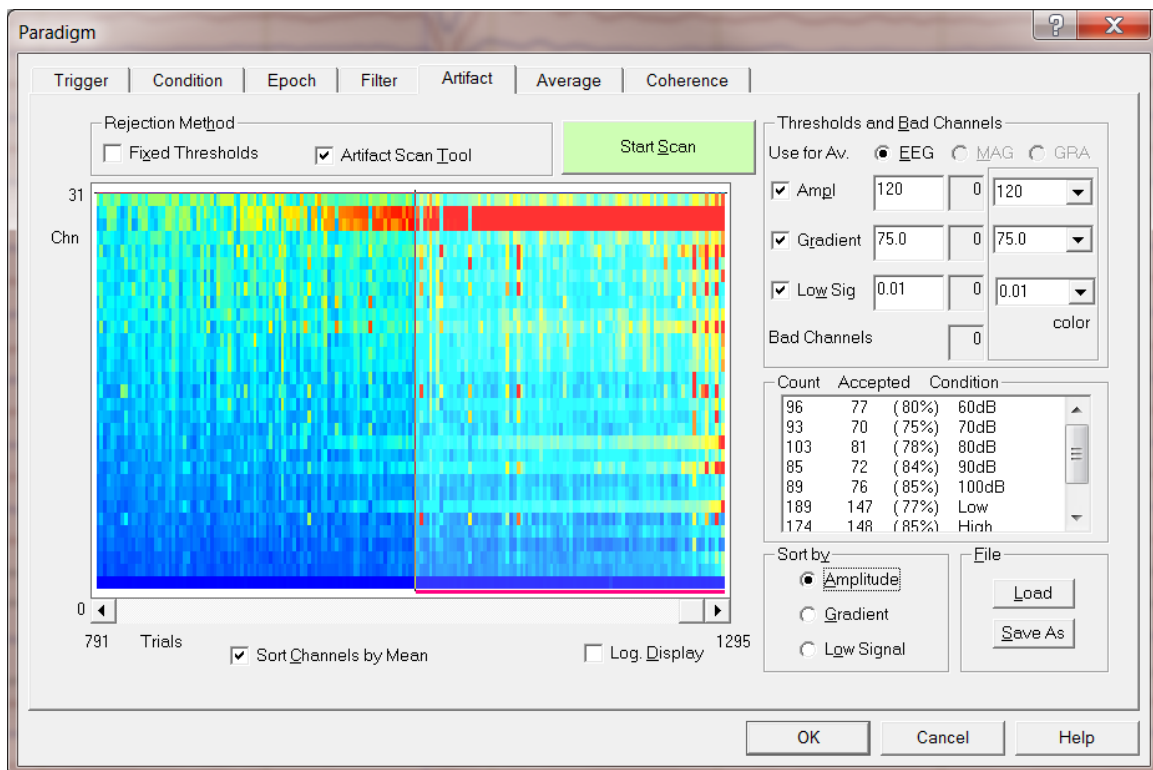


You can now save the paradigm definition by pressing **Save As**. Choose any name and add **-test** to it in order to not over-write any predefined files.

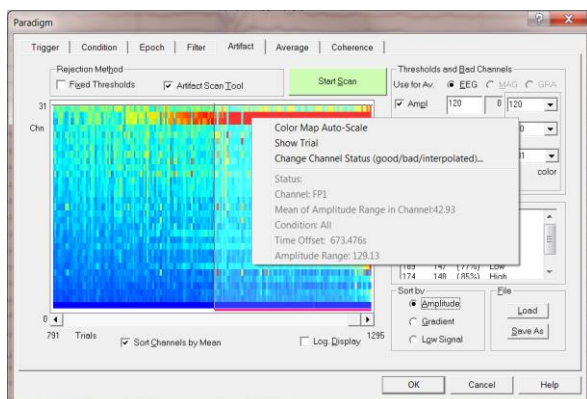
C. Artifact rejection based on amplitude, gradient and low-signal criteria

1. To make sure you have the identical paradigm settings as described here, please load the pre-defined Paradigm-file **AEP_Intensity.PDG** located in the **Paradigm directory** under **Auditory**. Move to the Artifact tab and press **Start Scan**. You will see a 2-dimensional diagram showing the channels (rows) and trials (columns) having the most noise. By default, values based on maximum amplitudes within the predefined artifact

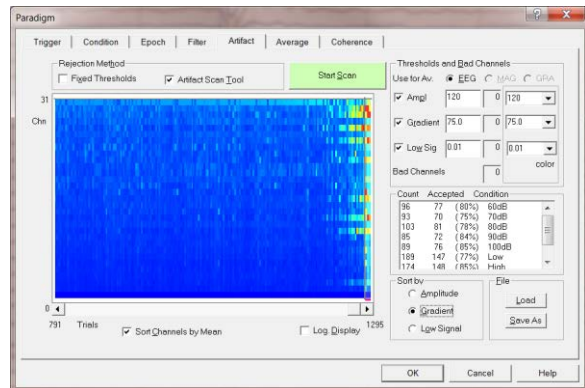
epochs are shown. Epochs that exceed the amplitude threshold (default: 120 μ V) will be excluded from further processing. You can view the number of accepted trials per condition in the Count box. As artifact correction is switched off at the moment, a substantial number of trials will be rejected.



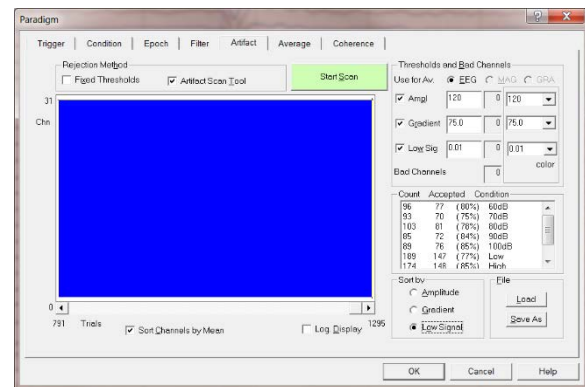
2. **Right-click** on the red channels to see their labels. The two channels that contain most bad epochs are FP1 and FP2, two frontal electrodes that pick up eyeblinks most strongly. Note that it is also possible at this stage to change a channel status to good, bad or interpolated by choosing the according option in the dialog box or by dragging the horizontal bar up or down. We will not do this at the moment, however.



3. It is also possible to view the result of sorting the data after a Gradient criterion (default: 75 μ V), i.e. epochs will be marked as bad that contain amplitude jumps of $> 75 \mu$ V between two sampling points. Choose **Sort by Gradient** to view this.

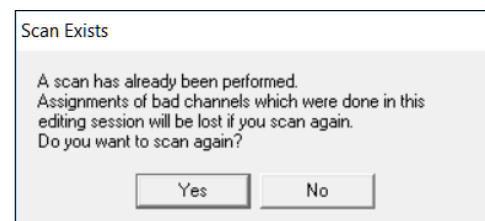


4. The Low Signal criterion can be useful to identify data periods where an electrode drops off during recording. Epochs will be marked as bad during which the signal is smaller than the threshold criterion (default: 0.01 μ V). Choose **Sort by Low Signal** to view this. In the present case, no epochs fall under this criterion. Change back to the Amplitude sorting criterion and press **OK** to close the Paradigm window.

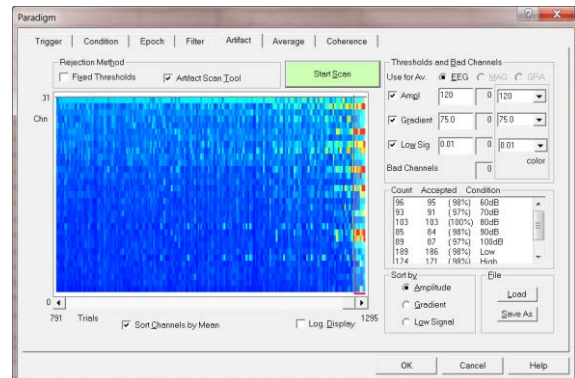


5. Switch on Artifact correction by pressing **ctrl+E**. Open the paradigm window again by pressing **ERP / Edit Paradigm** and move to the **Artifact** tab. Start the artifact scan again (now with switched on artifact correction) by pressing **Start Scan**.

A warning message will appear that a scan has already been performed. Confirm with **Yes** that you want to scan anyway.

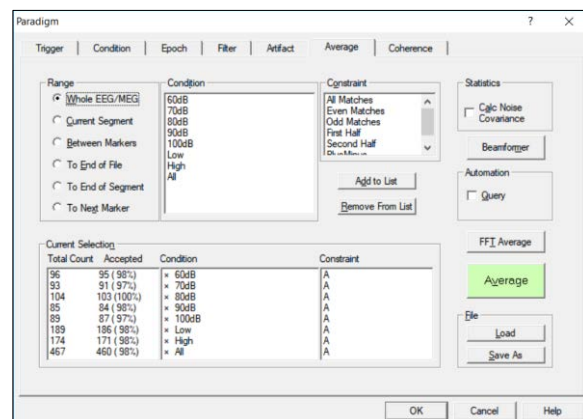


- Note that a greater number of epochs got accepted and that the two bad electrodes (FP1 and FP2) that were contaminated with eyeblinks are not conspicuous any longer. Some epochs still will be rejected as they exceed the threshold criteria. These epochs are contaminated by other, non-eyeblink related artifacts. It is possible to view the corresponding epoch in the main window by right-clicking into a red pixel and selecting **Show Trial**.

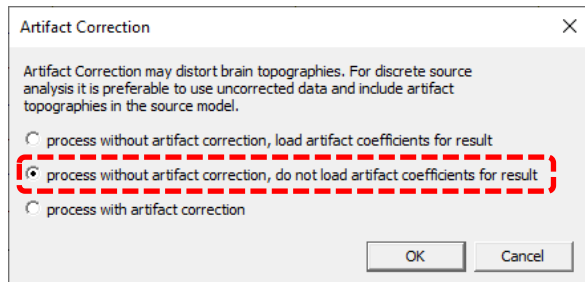


D. Averaging and Classic ERP Analysis

- Move to the **Average** tab. It is possible to restrict the number of conditions for averaging by removing unwanted conditions from the condition list. Additionally, it is possible to use constraints, e.g. to only average epochs of the first or second half of the experiment. This can be useful to make a split-half comparison. We will now average all conditions by not changing any settings and pressing **Average**.

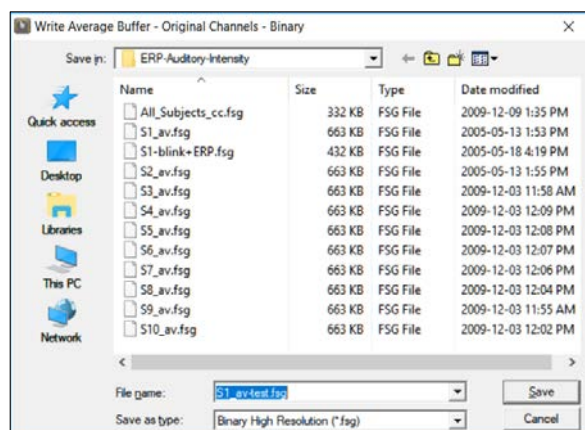


2. A warning message will appear that artifact correction is switched on, which can be problematic for later source analysis⁵. We recommend switching off artifact correction for averaging and loading the artifact topographies again at later stages. The artifact topographies can be loaded automatically (default option) by BESA Research, or it can be loaded manually later (second radio button). For teaching purposes select the **second option** and press **OK** to confirm artifact correction to be turned off during averaging, and to not load artifact topographies automatically for the result file.



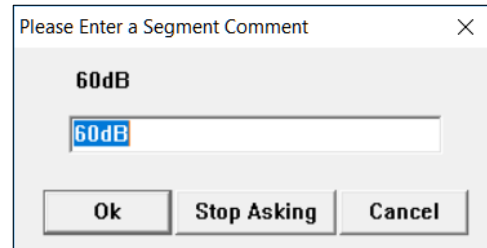
Note that artifact rejection-based epoch selection that was already performed is still valid, regardless of the choice made in this dialog.

3. When prompted to save the *.fsg file containing averaged epochs of the conditions defined in the paradigm, add a **-test** to the suggested filename in order to not over-write any predefined files (i.e. choose the name **S1_av-test.fsg**).



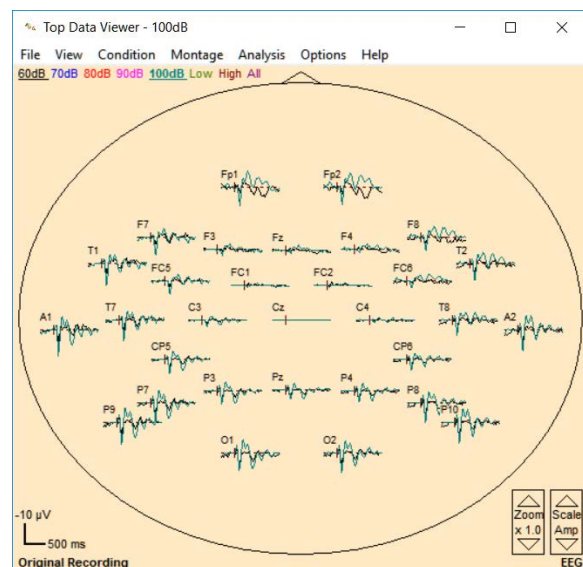
⁵ See the effect of switched on artifact correction during averaging in Tutorial 9: Source Montages.

- You will be prompted to specify names for the averaged epochs. By default, BESA will suggest the names as defined in the paradigm. Unless you want to alter them, choose **Stop Asking** and the original names will be maintained.

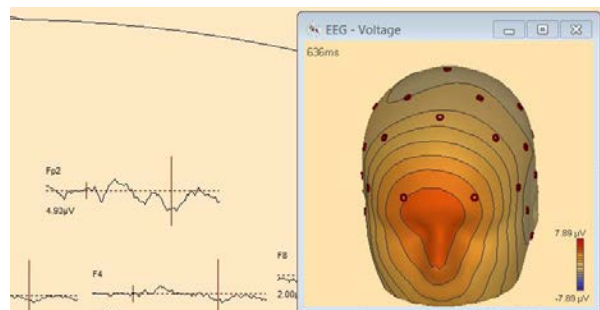


- The Top Data Viewer will automatically open displaying the averaging results. You may choose two conditions at once to be overlaid by holding down the **ctrl-key** and **left-clicking** on the conditions of interest.

It is possible to change the viewing properties (color of waveforms, labels, etc.) by selecting **Options / Preferences** or right-clicking in the background and pressing **Viewing Preferences**. The viewing epoch may be changed by selecting **View / Epoch** or right-clicking in the background and selecting **Viewing Epoch**.



- Select condition 60 dB and double click in the waveforms at 636 ms. At this time, strong activity in electrodes Fp1 and Fp2 can be seen. The 3-D mapping window will open. Again, we clearly see the frontal positivity that is typical for eyeblinks.



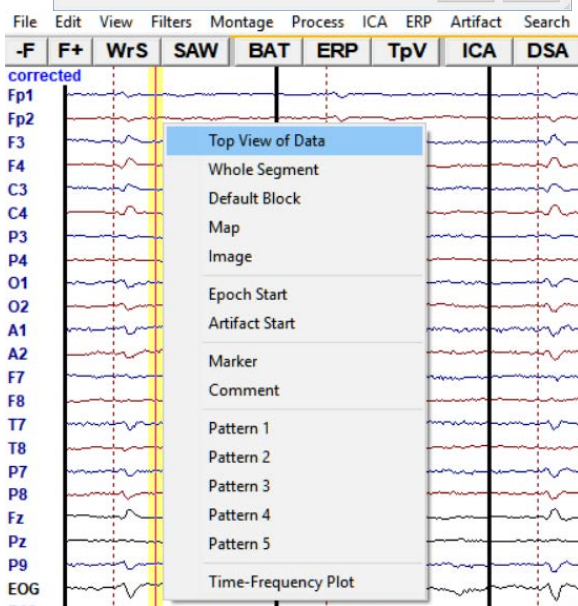
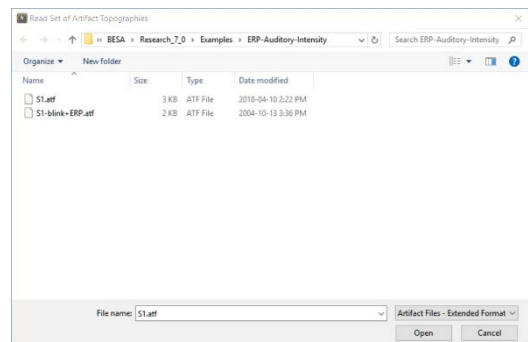
- Close the TopViewer to return to the main window. After averaging, BESA Research automatically opens the newly created average file. Therefore, we see a segmented file containing segments of the conditions as defined in the paradigm. We are now going to

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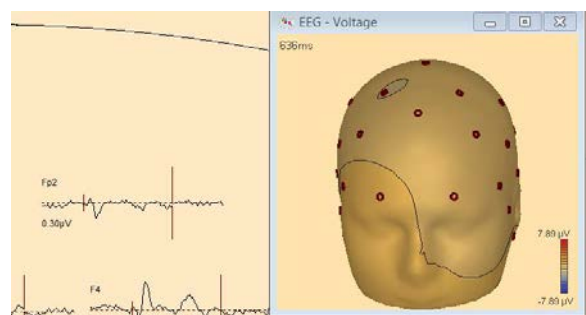
Tutorial 2 – Basic Artifact Correction, Triggers, Averaging

load the artifact topographies we defined earlier. To do so press **Artifact / Load...** and select file **S1.atf**. This file was automatically written by BESA when we defined the blink topography. Press **Open**.

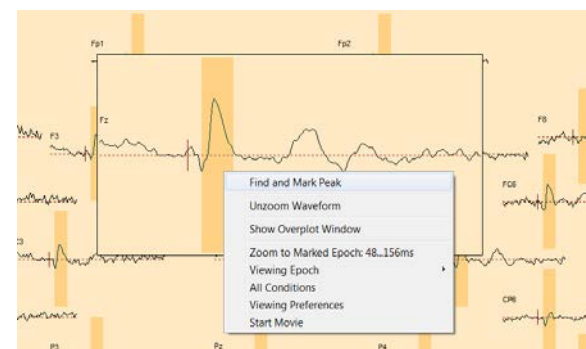
8. Loading the *.atf file will lead to BESA Research subtracting the eyeblink topography. Note that **corrected** appears in the top-left corner and a virtual EOG channel is displayed at the bottom. Switch off the filters by pressing the **EdF button** and deselecting all filters. Open the TopViewer again by **right-clicking** in the data and choosing **Top View of Data**.



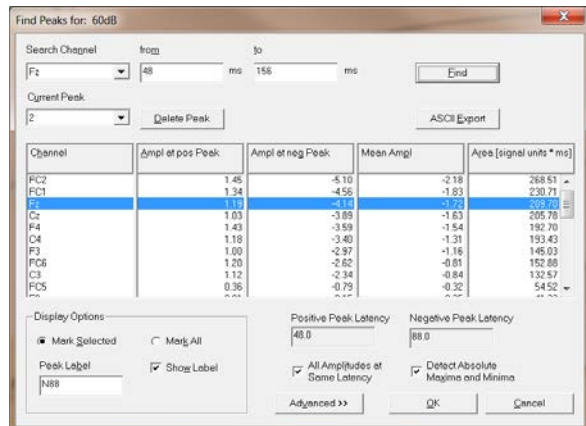
9. Return to the 60 dB condition and note that the large activity around 636 ms has disappeared. If you now **double-click** to bring up the 3D-mapping window you will see that the blink topography is gone.



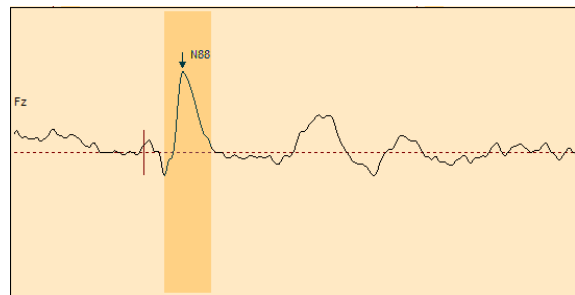
10. Zoom electrode Fz by **right-clicking** on it and selecting **Zoom Waveform**. **Left-drag** a window over the most prominent peak. **Right-click** again and select **Find and Mark Peak**.



11. The Find Peaks window will open and automatically display the search results for the marked data-block in the specified electrode as well as all other electrodes. A time of the large negative peak is 88 ms. BESA also outputs the mean amplitude in the specified time-range as well as the Area under the signal. These results can be saved using the ASCII Export option. Press **OK**.



12. Back in the TopViewer an arrow will now mark the peak position.



Tutorial 3 – Batch Processing, Combine Conditions

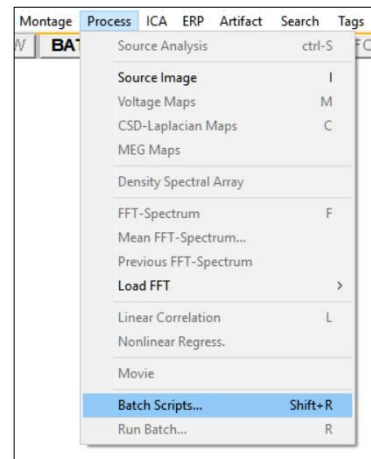
What does BESA Research provide?

- ✓ Batch processing
- ✓ Creating grand averages
- ✓ Creating new conditions from combinations of existing conditions
- ✓ Averaging of channels

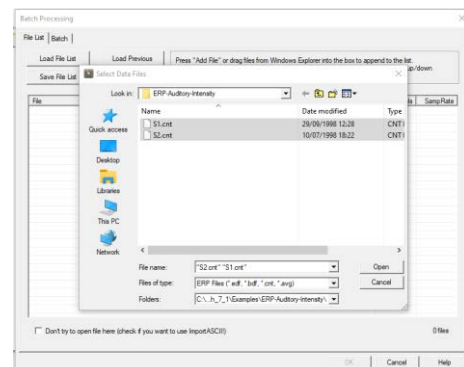
A. Batch Processing

In the following we will create a batch script that performs the same preprocessing, artifact treatment and averaging in all individual datasets.

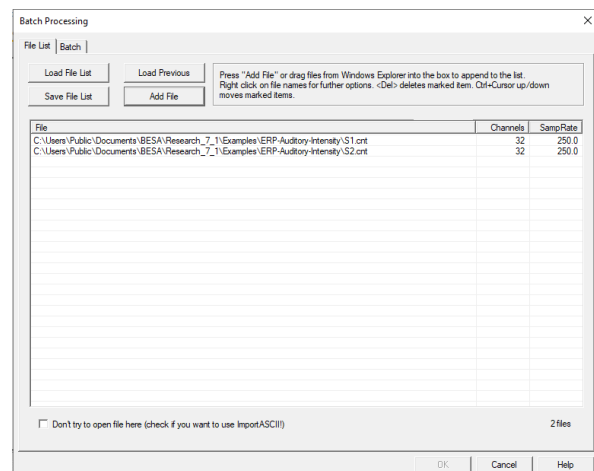
1. In BESA Research, select **File / Close All**. Now select **Process / Batch Scripts**. This will bring up the Batch Processing dialog.



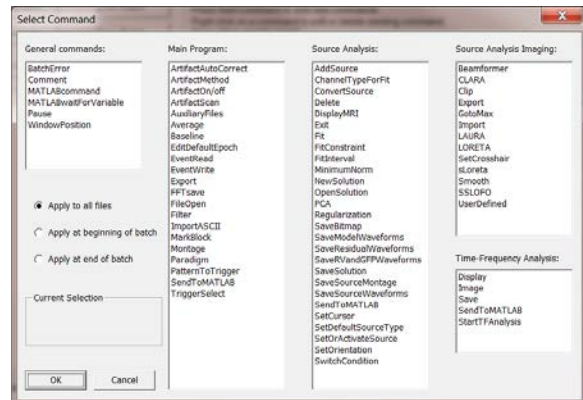
2. Press **Add File** and select both available ***.cnt files** (S1.cnt and S2.cnt). Press **Open**.



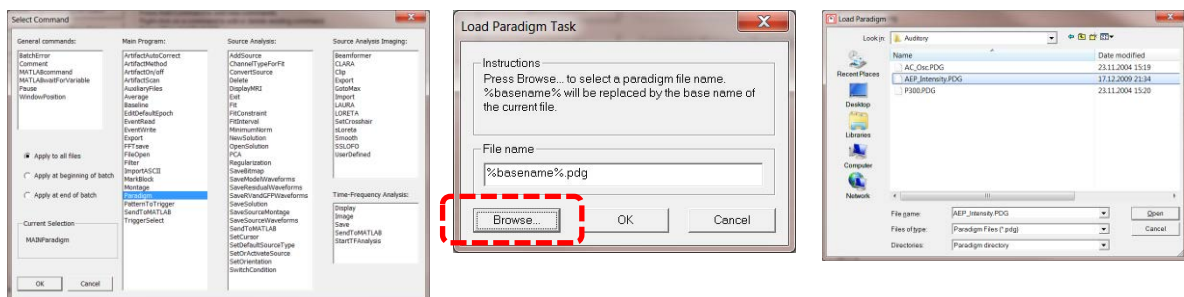
3. The file-list now contains the raw data of subjects S1 and S2. For display purposes only two datasets were selected, in principle, an arbitrary number of files can be selected. We can see that both files contain data of 32 electrodes sampled at 250 Hz. It is possible to save or reload a file list at this stage by pressing the according buttons.



- Move to the **Batch** tab and press **Add command**. This will bring up the Select Command window that is sub-divided into 4 command sections corresponding to the main program, source analysis, imaging, time-frequency analysis and general commands.

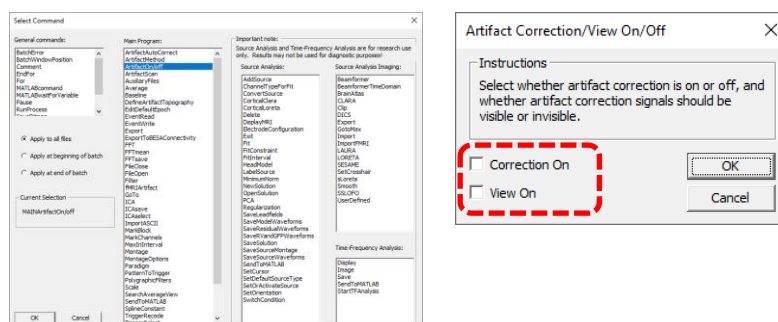


- First, we want to apply the predefined paradigm file (cf. Chapter 2 B) to each data set, therefore select **Paradigm** from the list of commands in the Main Program group to load a defined paradigm file to each data set. Hit **OK**. The **Load Paradigm** window opens. Select **Auditory / AEP_Intensity.PDG**, press **Open** and confirm by pressing **OK**.

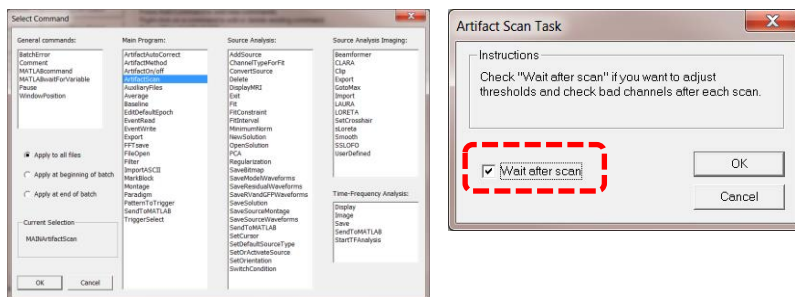


- We would like to also make sure that artifact correction is disabled. Press **Add Command**, select **ArtifactOn/Off** from the list of commands in the Main Program group and hit **OK**. Make sure that all checkboxes are unchecked and then press **OK**.

Note that if data is artifact corrected, the Artifact Scan is performed on artifact corrected data, the averaging is done without correction (to not distort source analysis), and artifact topographies are automatically loaded for the averaged file.

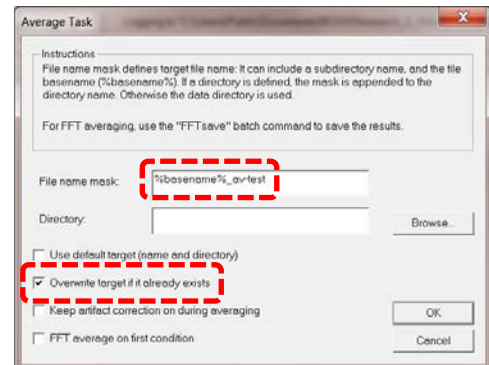
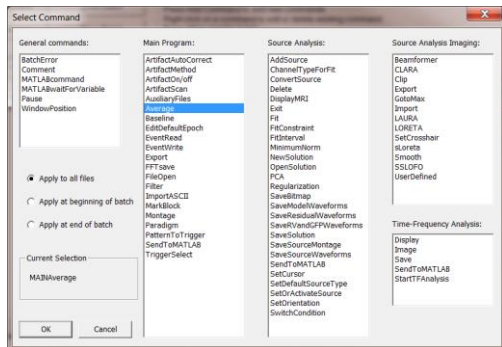


- Next, instruct BESA Research to perform an artifact scan on each data set. Press **Add Command**, select **Artifact Scan** from the list of commands in the Main Program group and hit **OK**. The **Artifact Scan Task** window opens. You may have artifact rejection run fully automatically. However, it is recommendable to visually inspect the results of the artifact scan in each subject, because e.g. in some data sets it might be necessary to exclude a bad channel manually. Therefore, make sure the option **Wait after scan** is selected, which will prompt for an OK after each artifact scan and allows making manual corrections. Press **OK**.

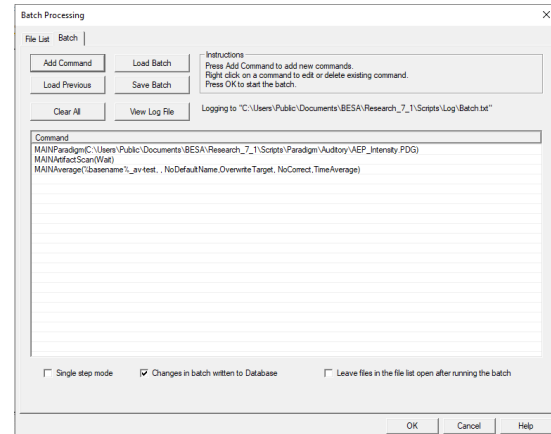


- Finally, press **Add Command** again, select **Average** from the Main Program group and press **OK**. In the **Average Task** window, BESA Research allows to specify a file name for the averaged individual data. Uncheck the option **Use default target** and change the File name mask to **%basename%_av-test**. This will create BESA binary files (*.fsg) with a base name derived from the corresponding raw data set. The averaged segments of file S2.cnt will be written to file S2_av-test.fsg, for example.
Make sure **Overwrite target if it already exists** is checked. You can also specify whether artifact correction should be performed during averaging. This is relevant only if one is working with artifact corrected data (using either the semi-automatic artifact correction options described in the Tutorial on Artifact Correction or the automatic artifact correction that can be executed using the **ArtifactCorrect** command in the command list). Here, however, for the sake of simplicity, we will reject all artifacts from further processing rather than performing an individual blink correction. For the grand averaged data, enough artifact-free epochs will be available even after artifact rejection. Press **OK**.

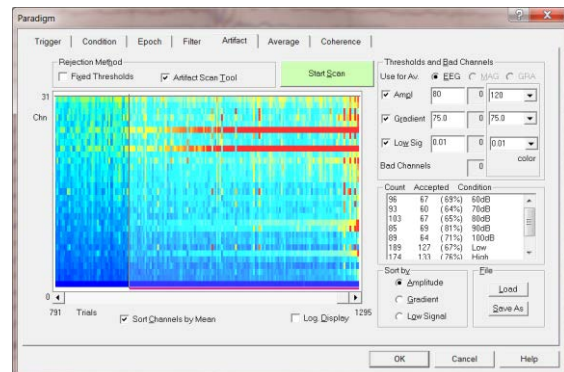
Tutorial 3 – Batch Processing, Combine Conditions



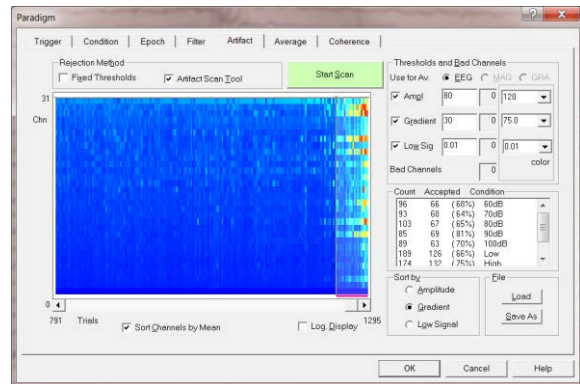
9. The three commands have been added to the command list with all specified options. You may save this batch and reload it for further analyses using the Save Batch and Load Batch buttons. Press **OK** to start the batch processing with the first file (S1.cnt).



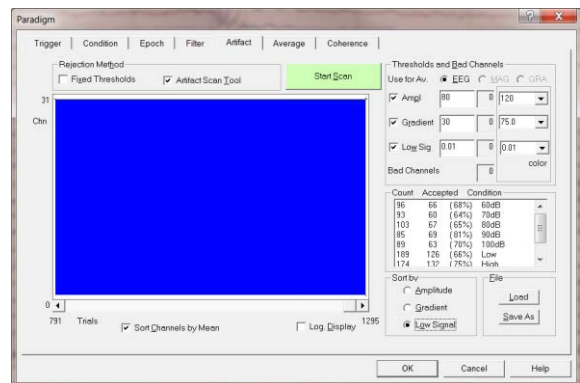
10. BESA Research stops after the artifact scan has been performed. You can now manually adjust the number of rejected trials and channels. In file S1.cnt, many blinks can be observed, primarily in channels Fp1 and Fp2. The preset amplitude threshold is not low enough to exclude all blink-contaminated trials. Drag the vertical red bar to the left to exclude more trials or **set the amplitude threshold manually to 80 μ V**. This will reject more epochs but we can be certain that no artifacts are retained in the data.



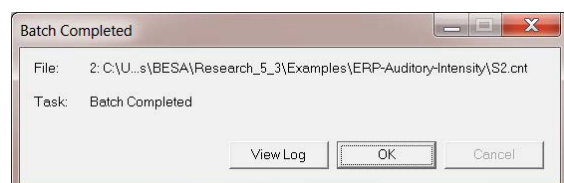
11. Select **Sort by Gradient**. Place the scrollbar to the right end of the display to see the trials with large gradient artifacts. The gradient threshold should be lowered (i.e. the vertical red bar in the 2D display should be moved to the left) to exclude all artifact-contaminated trials. **Set the gradient threshold to 30 μ V**.



12. Select **Sort by Low Signal** to see whether there are any channels that dropped out during the measurement. This is not the case.



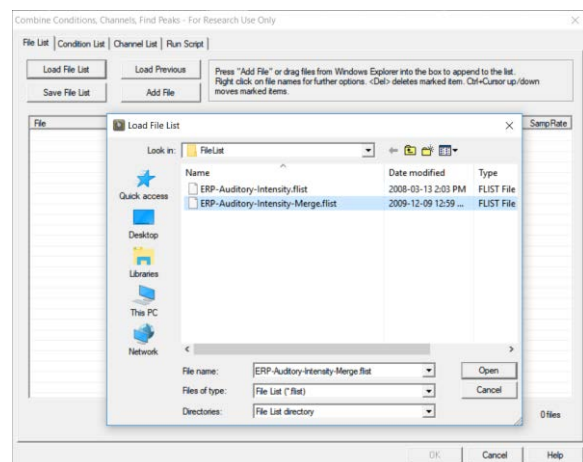
13. Press **OK** to finish artifact rejection in the first data file. BESA Research now averages all specified conditions and proceeds with the next data file. In file **S2.cnt**, adjust the artifact thresholds to **100 μ V** (amplitude criterion) and **50 μ V** (gradient criterion). After processing the batch on all data files, BESA Research gives a notification and offers to view the automatically generated log file (**View Log** button). Press **OK**.



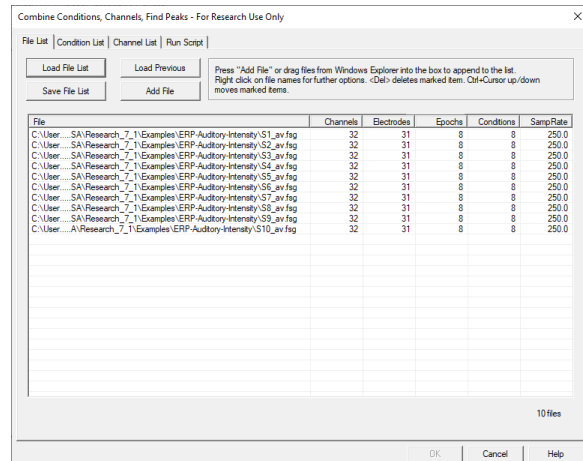
B. Creating Grand Averages

As a next step we will create a grand average across subjects using individual average files. Grand averages are useful for later source analysis and also for documenting differences between conditions across all subjects in classic ERP analysis. Individual average files (*.fsg) of 10 subjects (S1 to S10) are provided in the BESA Research examples folder **Auditory Intensity**.

1. In the BESA Research main window, select **ERP / Combine Conditions** to open the according dialog window. Press **Load File List** and select the pre-defined file **ERP-Auditory-Intensity-Merge.flist** and press **Open**. This will load *.fsg-files containing average data of subjects S1 to S10.

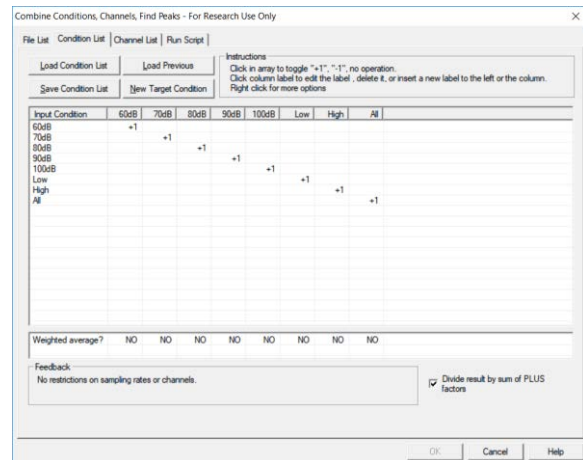


2. The number of channels, electrodes, epochs, conditions, and the sampling rate is displayed for each file. You may increase or reduce the width of the columns in the table by dragging the column border in the title bar.

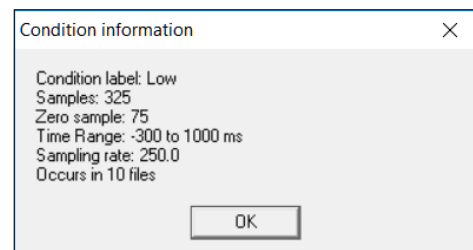


3. Switch to the **Condition List** tab.

Here it can be specified how the input conditions (the conditions available in the loaded data files) are to be combined to new target conditions. In the left column, the available input conditions are listed - in our case the eight conditions that were defined in the paradigm file (Tutorial 2, step B) and averaged using the batch script used in the present tutorial under step A. Conditions having the same segment comment in the different files are grouped into one entry.



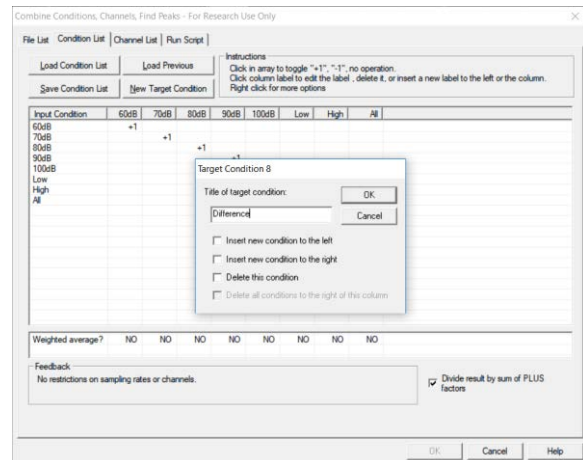
4. **Right-click** onto the input condition **low** in the left column. A window opens displaying information about the condition. The bottom line indicates that a low condition with the specified parameters is present in all ten input files. Press **OK** to close this window.



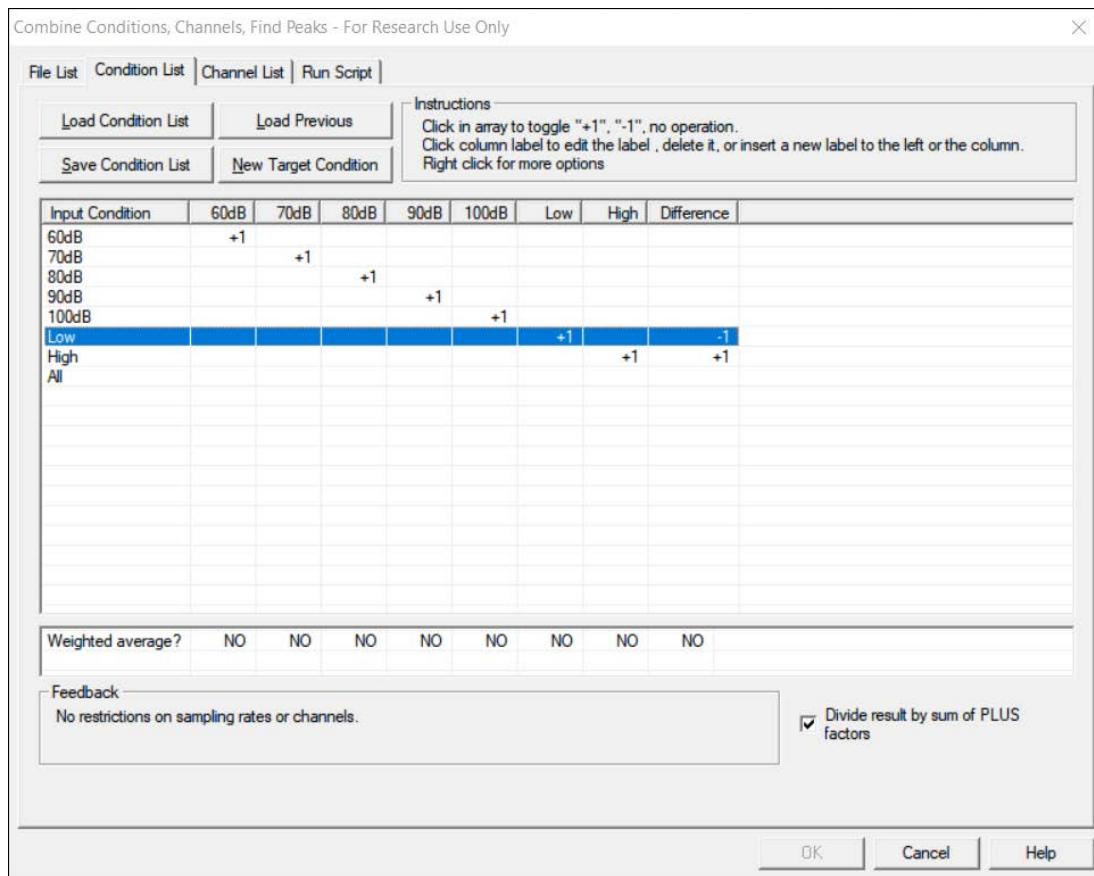
5. BESA Research automatically defined new target conditions (columns 2 – 9) with the same name as the input conditions. The numbers in the table indicate how the input conditions are to be combined to form the new target conditions. The default entry +1 in the column of the 60dB condition, for example, will generate an average of all input conditions labeled 60dB. Hence, the default definitions define grand averages of all input conditions.

6. We will modify the default definitions.

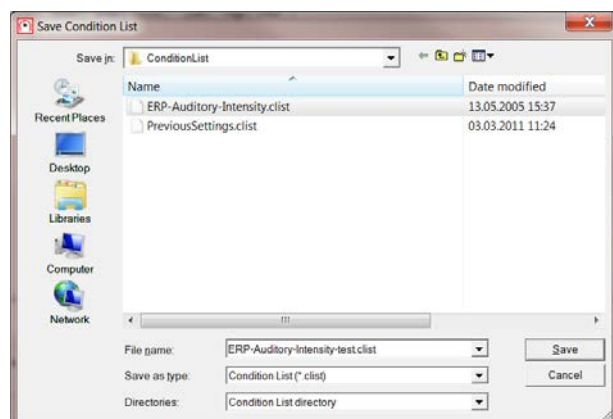
Instead of creating a grand average of the **All** condition over subjects, we will create a new condition that contains the grand averaged *difference* between the High and the Low condition. **Left-click** onto the label of the target condition **All** in the title bar of the table. This allows to create new target conditions by inserting new columns, or to rename an existing target condition. **Change the label** of target condition All to **Difference** and press **OK**.



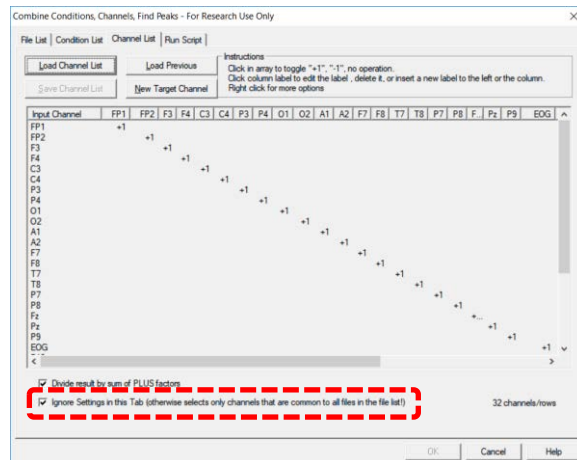
7. The target condition has been renamed to Difference. **Left-click twice** onto the +1 entry that links this condition to the All input condition. This will remove the link and leave the field blank. To define the Difference condition as the average of *High minus Low* over subjects, **left-click once** into the field linking input **High** with target **Difference** to generate an entry **+1** in this field. **Left-click twice** into the field linking input **Low** with target **Difference** to generate an entry **-1**. Note that arbitrary weights of conditions apart from +1 and -1 can be assigned by a right-click into the corresponding field. This is not necessary in our case. The bottom line (Weighted average?) allows to weigh each input condition with the number of averages it contains. We will leave the default settings to create non-weighted grand averages. Un-ticking the option Divide result by PLUS factors allows creating a target file containing the sum rather than the average of input conditions. We want to create a grand average, so we will not remove the tick-mark for Divide result by PLUS factors.



- Press **Save Condition List** to store the defined conditions to disk. Enter **ERP-Auditory-Intensity-test.clist** as file name and press **Save**. You may press **Load Condition List** to load the predefined condition list **ERP-Auditory-Intensity.clist**.

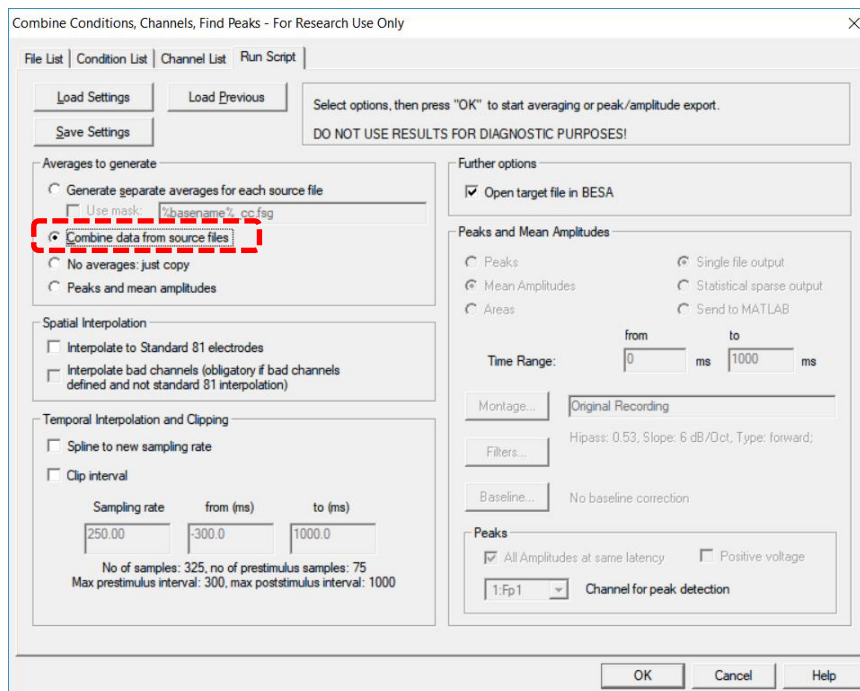


- Proceed to tab **Channel List**. By default, settings in this tab are ignored (checkmark at the bottom left). It allows combining data of different channels. To create our grand average, this is not necessary, therefore we leave the settings in this tab unchanged.

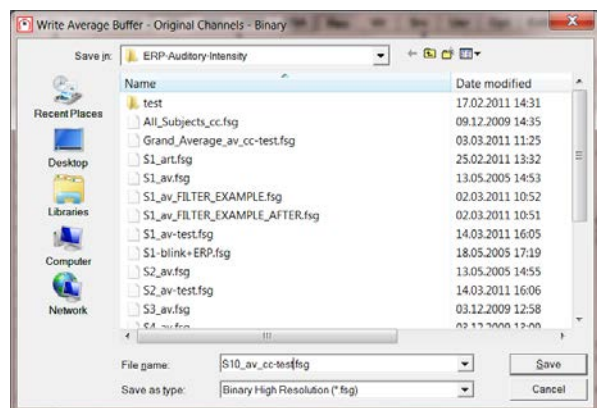


- Switch to the **Run Script** tab. Global output options can be specified here. Make sure **Combine data from source files** is selected in the box Averages to generate, as we want to create a file containing averages over subjects. The options under Spatial Interpolation allow to handle differences in the electrode configurations of the different source files. In our example, all subjects have the same electrode configuration and no bad channels have been defined. Therefore, no spatial interpolation is required. The same is true for Temporal Interpolation and Clipping: All input conditions have the same latency range and sampling rate, therefore no temporal interpolation of the data is necessary.

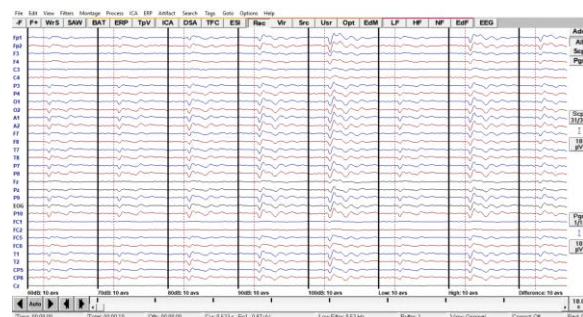
Note that the Run Scripts tab also allows analyzing peaks and mean **amplitudes** in multiple data files. This is achieved by selecting Peaks and mean amplitudes, which activates the bottom right segment of the window. Traditional peak analysis can be performed quickly in an automated fashion, producing ASCII output files containing the selected peak parameters (latency, amplitude, area).



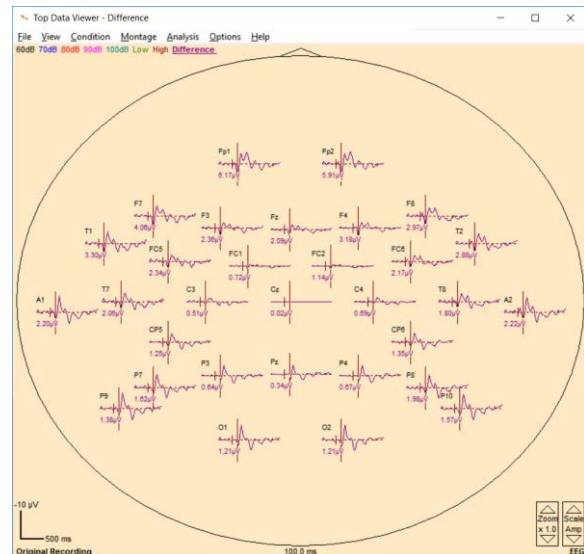
11. Click **OK** to start the batch. BESA Research computes the specified grand averages and prompts for a file name. Enter **All_Subjects_cc-Test.fsg** and press **Save**.



12. The generated grand average file contains the specified target conditions 60dB to 100dB, Low, High and the Difference condition. The number of source conditions is shown at the bottom next to the condition label, in our case 10, one for each subject.



13. **Right-click** into the data and select **Top View of Data**. Let's have a look at the condition Low, High and Difference. It becomes very clear that there is a difference in brain activity when listening to low and high-frequent tones. On the one hand, we can see an amplitude modulation; on the other hand, we can see a change of waveform morphology from low to high. Close the TopViewer.



Tutorial 4 – Discrete Source Analysis

What does BESA Research provide?

- ✓ Fitting of single dipoles and regional sources
- ✓ Using PCA
- ✓ Using regularization

This tutorial is designed to teach the basic concepts of multiple source analysis. At the same time, it can be used to get familiar with the user interface of the source analysis window in BESA Research.

The first chapter provides the basic theoretical foundation of the concept of discrete source analysis. The following hands-on examples introduce the source analysis interface of BESA Research and apply the provided principles to simulated EEG data sets. A concluding chapter summarizes the obtained results and lists some guidelines for source analysis.

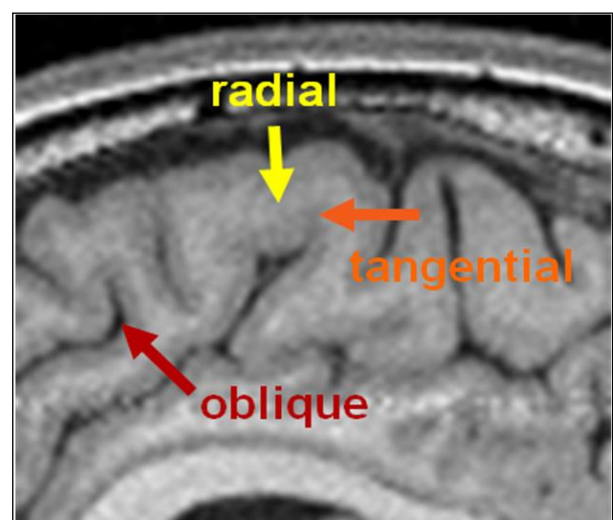
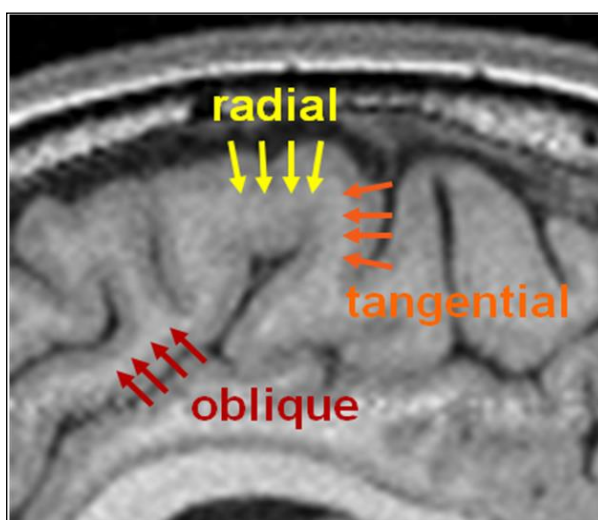
A. Theoretical introduction

Equivalent current dipoles

Neuronal current in the cortex flows predominantly perpendicular to the cortical surface for two reasons: First, the pyramidal cells in the cortical columns are aligned perpendicular to the cortical surface. Second, the dendritic trees that are parallel to the cortical surface have near-rotational symmetry and the electric fields of the related intracellular currents cancel to a large degree.

Activity in multiple brain regions = postsynaptic current flow in pyramidal cells

Discrete equivalent current dipoles as model for the activity in each brain region



The intracellular postsynaptic current vectors of nearby cortical columns sum linearly and can be represented very accurately by an equivalent, compound dipole current vector. Areas with up to 3 cm in diameter can be very accurately (> 99%) modeled by a single equivalent dipole.

Currents at the cortical convexity have a predominantly radial orientation; currents in cortical fissures have predominantly tangential orientation. Generally, a patch of activated cortex in a sensory, motor or spiking area will have an oblique orientation depending on the net orientation of the activated cortex.

Thus, an equivalent current dipole is specified by its location (the equivalent center of the modeled gray matter patch) and its orientation (the net direction of the modeled postsynaptic neuronal current, perpendicular to the surface of the modeled gray matter patch). The orientation of a dipole therefore indicates the local orientation of the pyramidal cells in the gray matter – it is not to be confused with a direction of signal propagation across the brain! The orientation of a dipole is usually symbolized by an arrow or a short line.

The third parameter of an equivalent current dipole is its strength or amplitude, reflecting the modeled net postsynaptic current flow. Its units are that of a dipole moment, i.e. nAm (nano-Ampere × meter). It can be thought of as the product of the total postsynaptic current flow (in nA) and the length over which this current is flowing (on the order of the length of a pyramidal cell in meters). The temporal evolution of the dipole moment is called the source waveform and is in many respects the most important outcome of source analysis.

Volume conduction and the principle of linear superposition

An ideal patch of superficial cortex creates a net radial current flow that can be very accurately modeled by an equivalent dipole near its center.

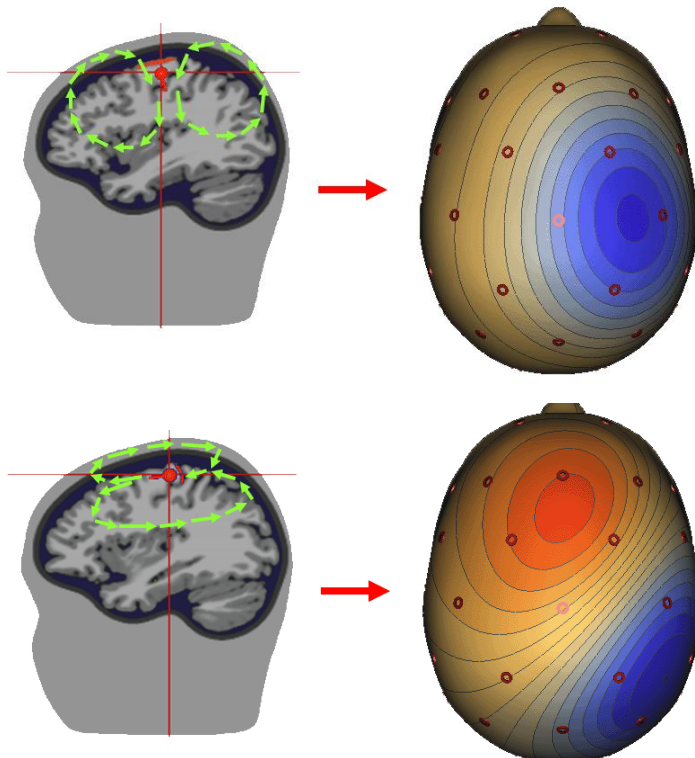
Current loops in a conductive medium like the head are closed. Therefore, the intracellular currents resulting from action and post-synaptic potentials are accompanied by secondary return currents in the head volume. Since the brain and scalp have a higher electrical conductivity as compared to the cranium, most currents return within the extracellular brain space. Only a very small fraction flows out through the poorly conducting cranium and along the scalp before returning to the brain.

Inside the head:

Primary (postsynaptic, neuronal) current in red, secondary (volume) in green

Signal on the head surface:

Generated potential changes (= EEG maps / topographies). Blue: negativity, Red: positivity



Top: Radial primary current flow at the cortical convexity in the right central cortex.

Bottom: Tangential primary current flow in a cortical fissure.

Although the location of the active brain region is nearly the same, the different orientation of the patch surfaces and the associated different flow of the secondary volume currents lead to a completely different potential distribution. Maximum EEG activity is not necessarily generated directly on top of the active brain region.

The propagation of the volume currents to the scalp is described by the so-called head model. The head model, or forward model, predicts the voltage at any electrode due to an equivalent dipole with a given location and orientation within the brain.

The volume conduction results in a widespread, smeared voltage topography over the whole scalp with a maximum over the activated cortical sheet. A corresponding activity of opposite polarity appears on the other side of the head. By the laws of physics, the integral of the potential over the whole head is zero. Therefore, any negativity has a corresponding positivity somewhere else over the head. The voltage map (topography) displayed on the top right of the figure above is typical for focal radial activities at the cortical surface. The shown maps illustrate the limited spatial resolution of the EEG. The precise orientation of the map, and the underlying equivalent dipole, can only be determined if inferior electrodes are present to help define the location of the positivity on the other side of the head.

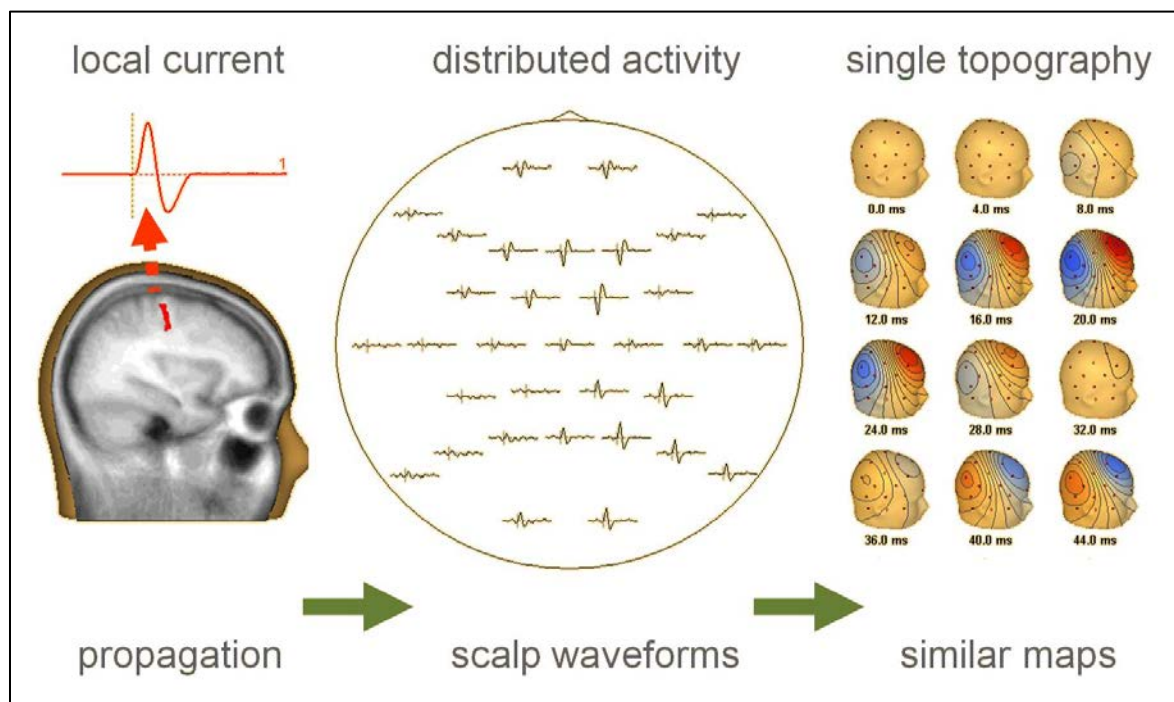
BESA® Research 7.1

Tutorial 4 – Discrete Source Analysis

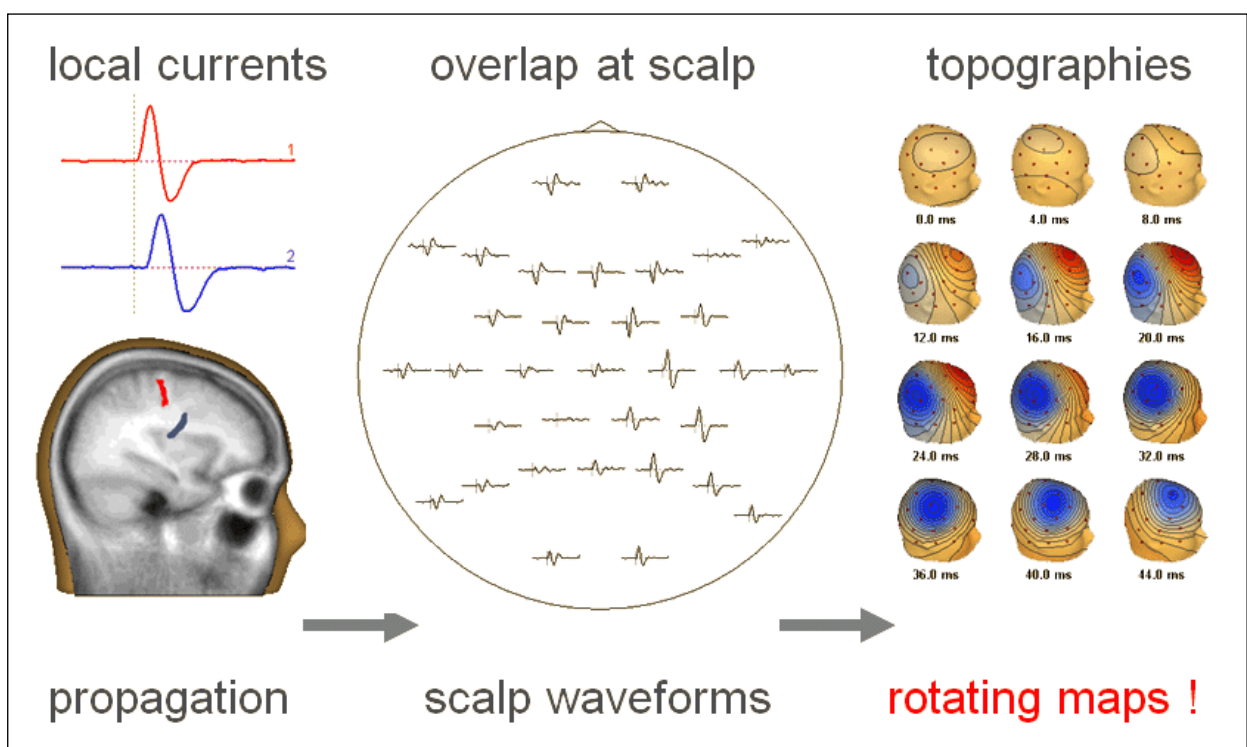
A cortical patch in a fissure generates a tangentially oriented dipole field (bottom of the figure above). The return currents in the scalp create a dipole map with symmetric positive and negative poles aligned in the direction of the dipole. The potential change directly over the source is zero, but the gradients are maximal. The source is below the site of the densest equipotential lines. These lines and the whole shape of the topography carry more information on the location of the underlying generators than the colorful peaks.

An EEG electrode does not record the potential at a certain location on the head surface. Rather, it records a voltage (= potential difference), i.e. an EEG signal is always the difference between the potential at a certain electrode location on the head surface and the potential at another electrode - the reference electrode - or the average of several electrodes. Thus, the choice of the reference electrode(s) determines the recorded signals, but the underlying potential distribution (the potential map) is independent of this and solely determined by the underlying brain processes.

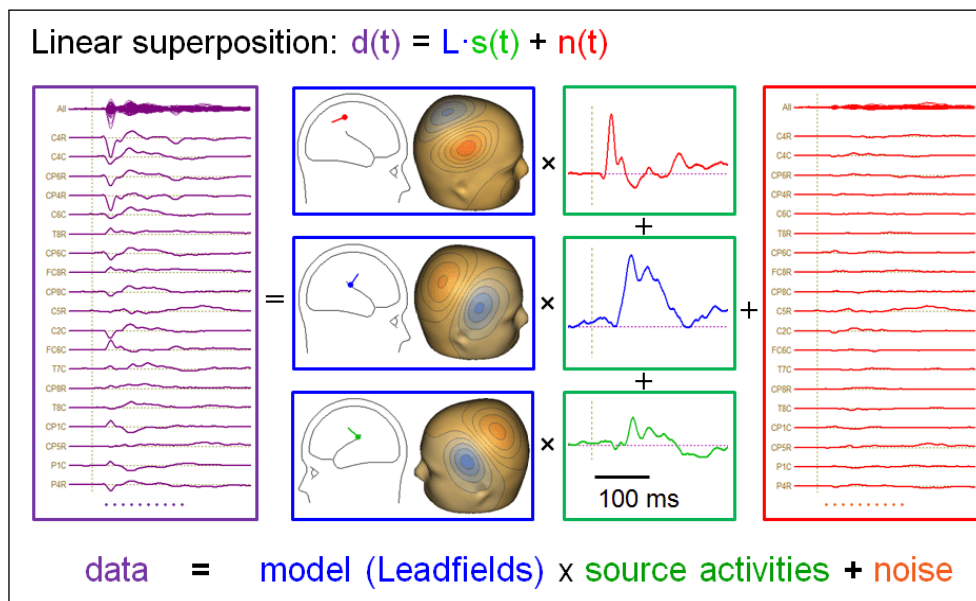
Using a simulated example, we will now learn how to discriminate the scalp waveforms and topographies due to a focal activity of one brain region and temporally overlapping activity of two brain regions.



An assumed activity in the right central sulcus produces a near-tangential dipole field with a positive peak (shown downwards in the EEG top view in the middle) over the mid-frontal region (Fz and FC2) and a negative more widespread peak over the right inferior parietal regions (max. at P4). The patch is synchronously activated and there is no propagation. Accordingly, the net orientation remains the same. The waveforms at the different electrodes have different magnitudes but the same evolution over time. The topographic maps change only in magnitude but not in shape. Map polarity simply reverses in the second phase following the initial activity.



Now consider the situation of two brain regions separated by about 3 cm and activated within a few milliseconds. Each of the areas has a biphasic pattern with onset, peak, and polarity reversal. The two patches have different orientations. This is the main cause for their very different scalp topographies. Due to the time difference in activation their maps overlap with continuously changing magnitudes according to the instantaneous strength of the 2 compound currents. This results in an apparent rotation of the maps over time, and it becomes difficult to identify and separate the two sources by mere visual inspection.

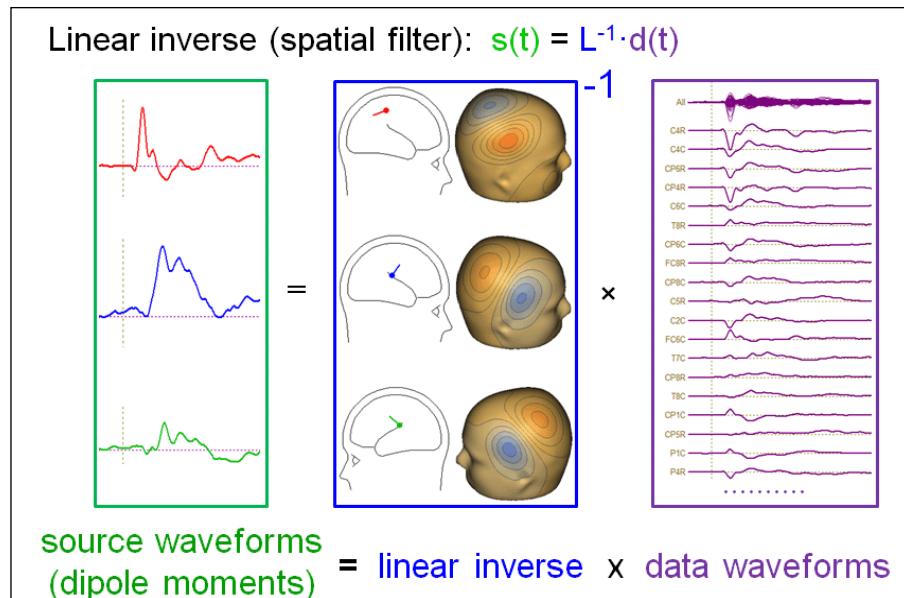


Using the laws of basic physics, we can now formulate the principle of linear superposition. This is illustrated here for 3 equivalent dipoles, but it would be the same for 10000 cortical current elements: The measured data (in this example MEG sensor signals, left, generated by tactile stimulation of the left index finger) are the sum over the contributions of all sources. In source analysis, each active brain region is modeled by one equivalent dipole source. Each source is fixed to the cortical patch or region it represents, and changes its total current strength over time according to the local physiology. In 1986, this was named a source waveform (Scherg and von Cramon, *Electroenceph. Clin. Neurophysiol.* 65:344). With a given volume conductor model, e.g. a spherical head model, a boundary element model (BEM), or a finite element model (FEM), it is now possible to predict the leadfields, i.e. the magnitude of the signal each source will contribute to each sensor. Because the model is an approximation, both in terms of the volume conductor and the simplification of using equivalent dipoles at the centers of activity, there is a residual. Ideally, if we have a good model, this residue should be small and consist only of sensor noise and brain background activity not related to the tactile stimulus.

BESA® Research 7.1

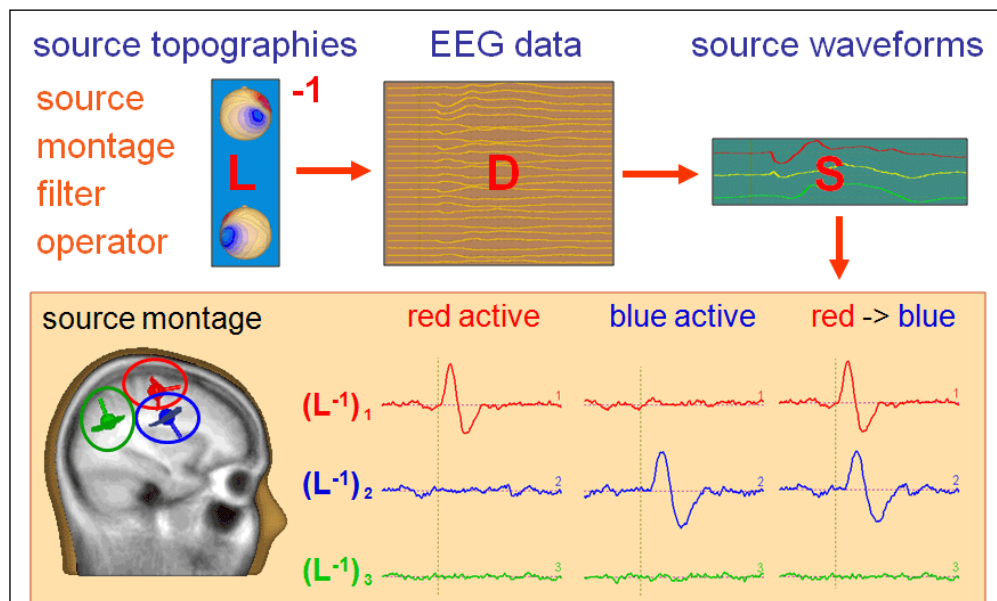
Tutorial 4 – Discrete Source Analysis

The inverse operator: Reconstructing brain activities



In our superposition, equation the source waveforms are the unknown, given we know the centers (and orientations) of source activity in the brain. In this case, the source activities can be calculated directly by inverting the leadfield matrix and multiplying from the left onto the superposition equation. In the illustrated case, the leadfield matrix consists of the three sensor topographies which have to be inverted. The noise contribution is neglected in this process. Accordingly, unmodeled noise will be projected onto the calculated source waveforms.

The linear inverse operator acts like a spatial filter that deblurs the measured waveform to unfold and separate the underlying source waveforms (Scherg and Picton, EEG Suppl. 42, 1991). In other words, source waveforms are calculated by combining the temporal information in all channels giving specific weights to each signal. Each row in the matrix L^{-1} is a linear operator reconstructing one source waveform.



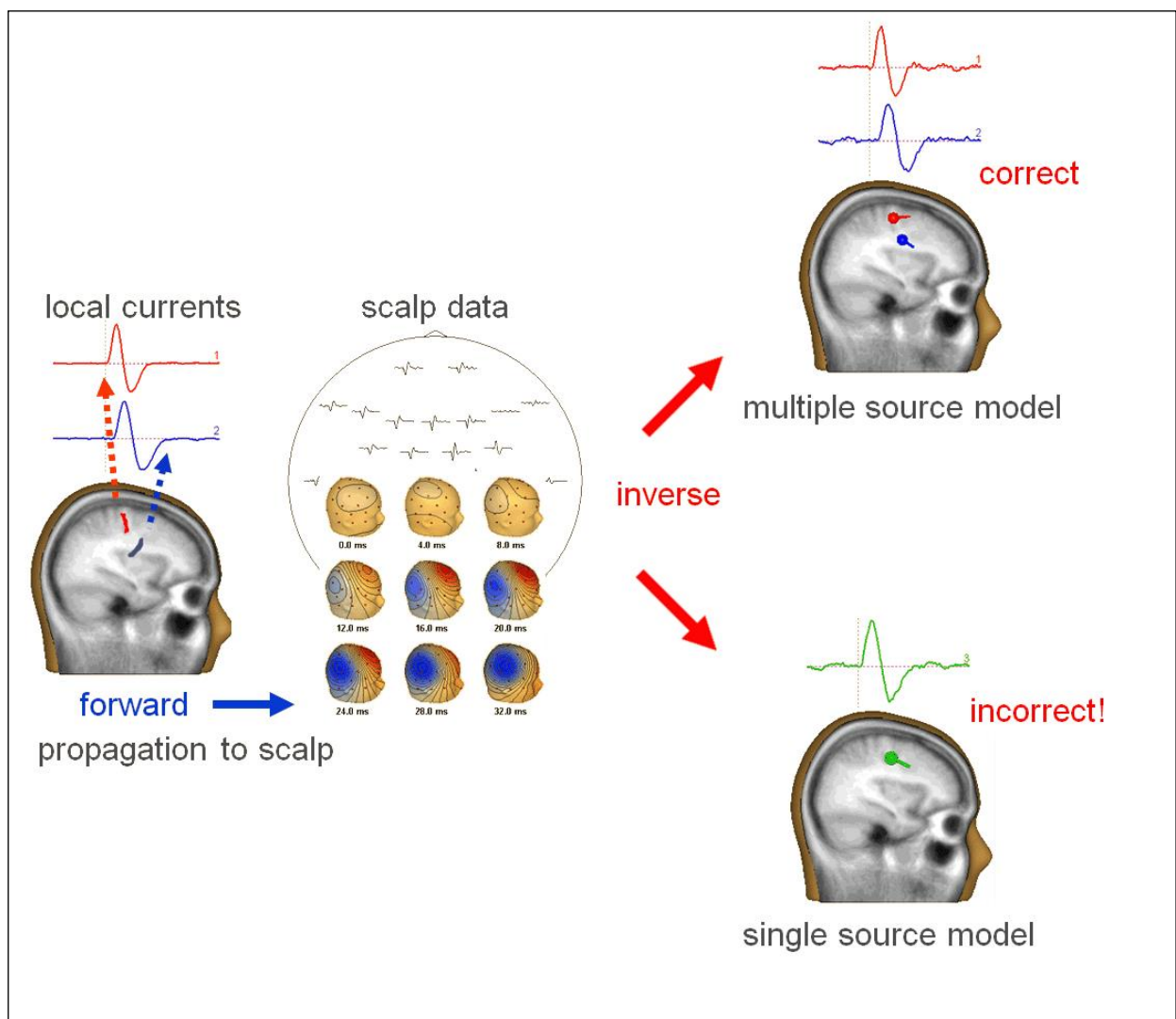
The above example demonstrates the full separation of the source activities 1 & 2 in three simulated cases and illustrates the absence of activity in source area 3 since its source waveform shows only EEG background signal.

Thus, multiple sources can mutually contrast and separate the activities of the brain areas that they represent.

The displayed circles on the left illustrate that separation of the activity from several brain areas is principally possible, if they are sufficiently remote from each other (> 3 cm). However, precise localization within each region is not possible in typical data because of the EEG background noise.

In the overdetermined case, i.e. if there are less sources than measured channels, the linear inverse operator L^{-1} is constructed to fully separate the different source activities. The vector operator for source 1 will fully recover source activity 1, but will not be sensitive to any activity at sources 2, 3... and vice versa. This sharp separation has a drawback, if some of the sources have a high spatial correlation in the sensor space. Then the inverse operator will have large entries and the noise will be amplified accordingly. However, this problem is easily handled by modest regularization (default in BESA Research is 1%) when calculating the inverse of the topography matrix. How regularization effects the source waveforms will be demonstrated in Chapter B (Step 16).

If we apply a two-dipole model to our simulated data set, they separate the two activities in their source waveforms provided that appropriate equivalent locations and orientations had been selected. If we try to model the data with a single dipole only, we obtain an incorrect localization intermediate between both sources. The source waveform combines both underlying activities into a broader pattern which has a latency intermediate between the original activities. Therefore, care must be taken to create a multiple source model that is appropriate for the current data set. In the following we will see how this can be achieved. The following section shows how a source model can be created by fitting discrete sources to the EEG or MEG data.

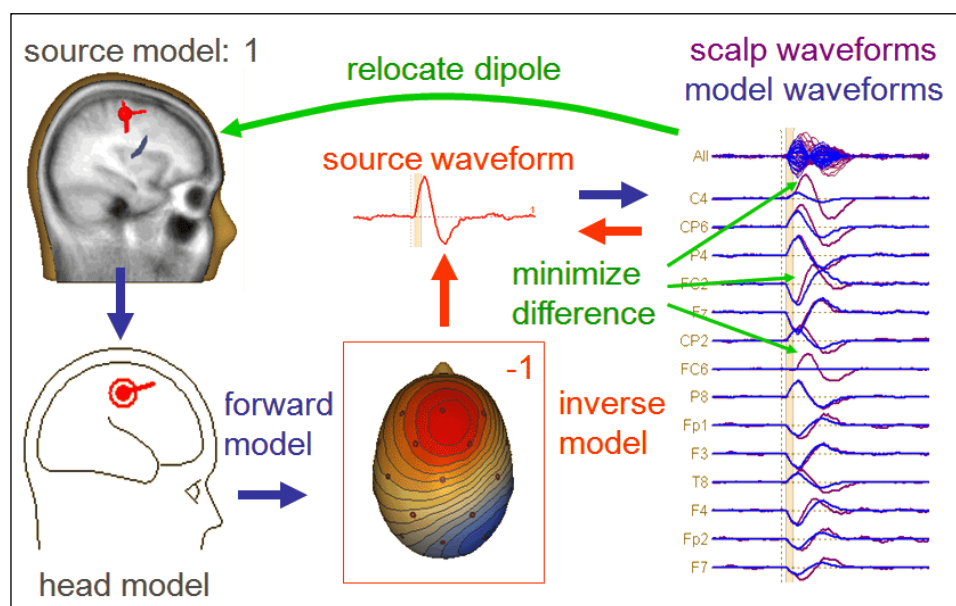


BESA® Research 7.1

Tutorial 4 – Discrete Source Analysis

The fit procedure

We assume that a single dipole will explain the early onset phase (i.e. initial source model hypothesis is a single equivalent dipole). Using the head model, the forward model topography (= leadfield) is estimated. The inverse of this leadfield matrix is applied to the data to estimate the source waveform. The source waveform is projected back to the scalp using the forward coefficients of the map to estimate the model signals (blue curves in the figure below). Measured and modeled data are subtracted to estimate the residual waves. In an interactive process, dipole location and orientation is adjusted and the calculation process is repeated until the residual difference between scalp and model waveforms is minimized. The equivalent dipole locates in or near the active cortex if the hypothesis, head model, and data are sufficiently accurate.

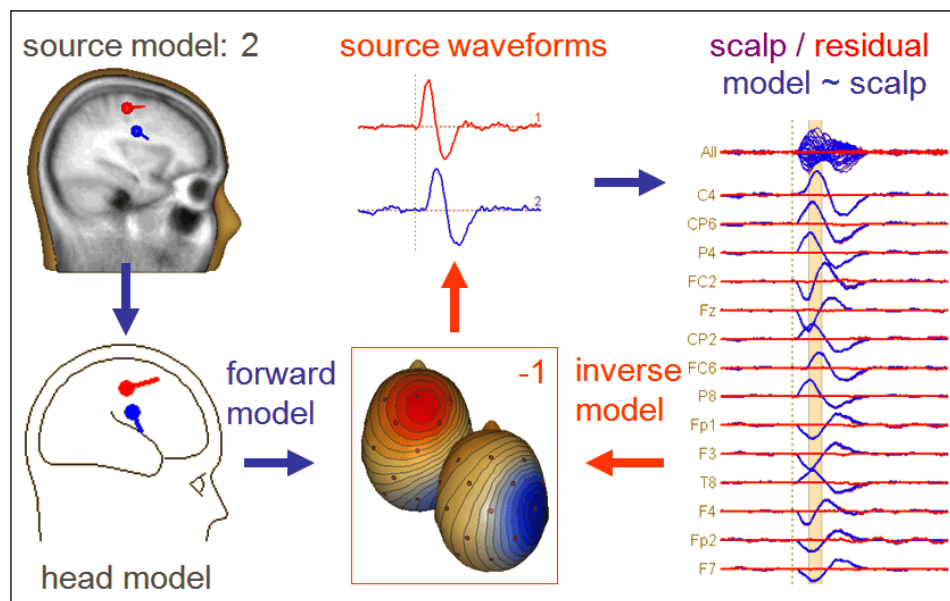


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Tutorial 4 – Discrete Source Analysis

Fitting strategy for multiple activities – step 1:

Use the 3D maps to define the fit interval from the time when a clear dipole field emerges until it starts changing. Perform a principal components analysis (PCA) over this interval: The PCA decomposition should show one dominant component. The percentage of variance it explains should decrease, if the interval is extended further. Fit the first dipole over this interval.



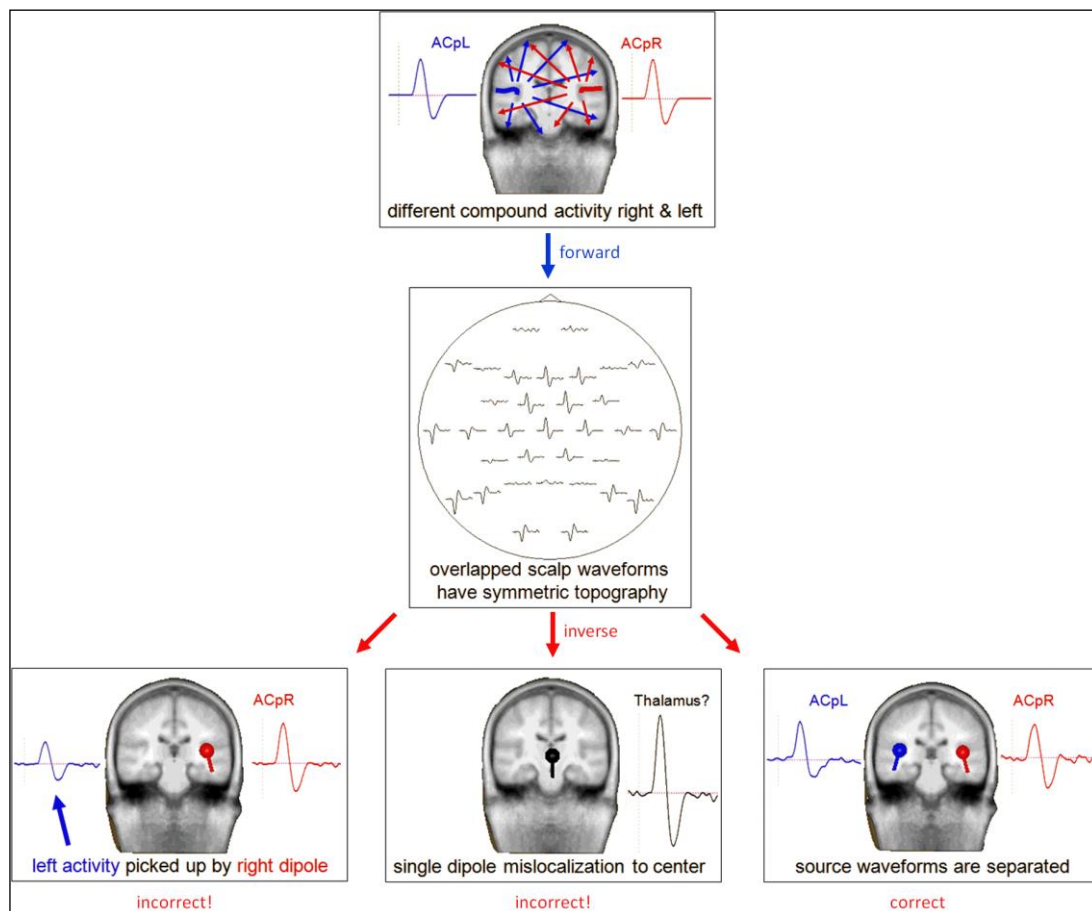
Fitting strategy for multiple sources – step 2:

Display the residual waves and maps. Perform a PCA on the residual waves and repeat the same procedure to mark the next onset interval in the residual data. Fit a second dipole to this interval while keeping the first dipole fixed in location and orientation. In the simulated example with good signal-to-noise, this results in the separation of the underlying active areas and their source waveforms.

Finally, we should check the homologous brain region in the other hemisphere for a potential spread of activity using a probe source at the mirror location of dipoles 1 and 2.

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The above figure shows a simulated example that illustrates the need to create an appropriate source model in order to obtain correct source waveforms. We assume a situation where both auditory cortices are active. Their topographies on the scalp surface overlap, and the recorded signal at each electrode is a superposition of the contributions of the two sources. If we apply a source model with one dipole in the right auditory cortex only, its source waveform will not only pick up the right hemispheric activity. It will rather contain some contribution from the left hemisphere as well, which is not properly modeled. An attempt to fit a single equivalent dipole to this data results in a mislocalization in the head center close to the thalamus. The reason is that the ACpL and ACpR sources generate a symmetric topography on the scalp surface with largest signals over the scalp midline. The obtained source waveform is a linear superposition of the activities of both brain regions. The correct source activities are reconstructed only when two equivalent current dipoles are used to model the data. Only with this two-dipolar model, the spatial filter can separate the activities of the two brain regions.

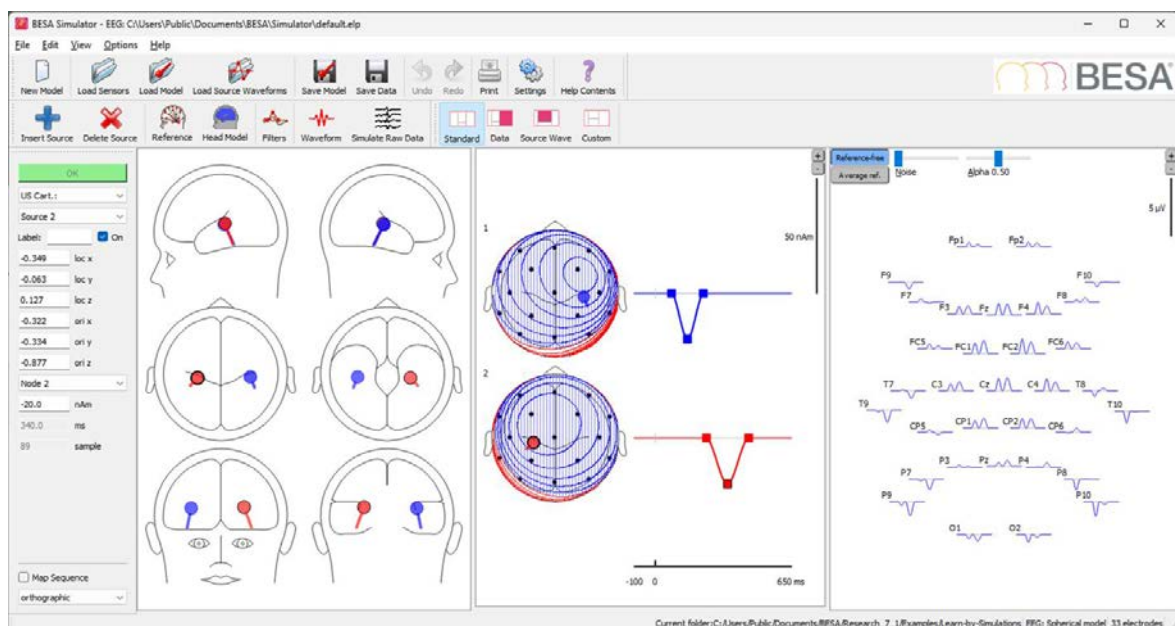
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Tutorial 4 – Discrete Source Analysis

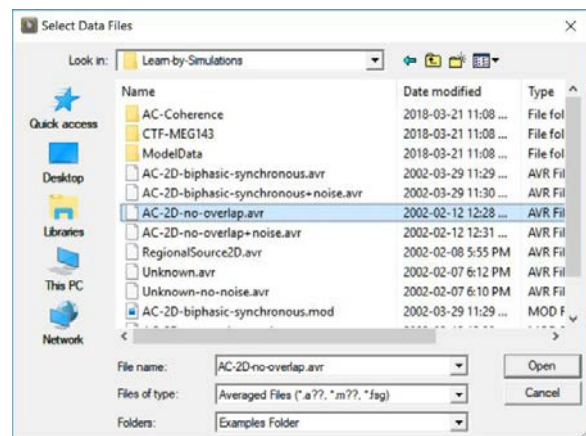
B. Single Dipole Fitting with Simulated Data

Before we will create a source model for the auditory intensity data we have been working on so far, we will work with three simulated datasets to understand the principles of dipole fitting.

1st simulated data set: In the first example, non-overlapping (asynchronous) activity in both auditory cortices is simulated. Current flowing in the depth of the Sylvian fissure is oriented orthogonal to the temporal plane, because pyramidal cells are perpendicular to the cortical surface. Therefore, the net effective dipole is oriented vertically and orthogonal to the fissure. This source is nearly tangential to the scalp surface. Because the current flows into the cortex, the dipole is pointing downward. The resulting voltage topography shows a fronto-central negativity and an associated positivity over the right infero-temporal posterior scalp.



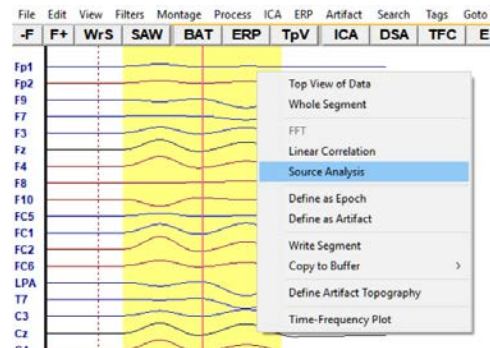
1. In the main window, select **File / Open** and browse to the **Learn-by-Simulations** subfolder of the Examples folder to load the simulated data set **AC-2D-no-overlap.avr**. You might need to change the file-type to Averaged Files (*.a??, *.m??, *.fsg) to see it. Press **Open**.



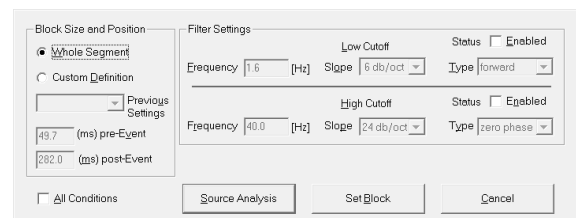
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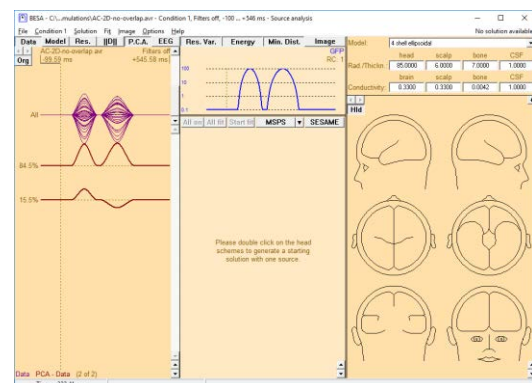
- We want to perform source analysis on this data now to see if we can recover the brain activity that is underlying the recorded signals. Source analysis is performed in a separate window of BESA Research. To start source analysis, **left-drag over the data** to mark a block. Then **right-click** into the block. From the popup menu select **Source Analysis**.



- A dialog window appears which allows specifying the time range of the data to be sent into the source analysis window. Select **Whole Segment**. It is also possible to specify temporal filters to be applied before source analysis to remove slow drifts and noise from the data. For our simulated data sets we don't need to apply filters. Press **Source Analysis** to open the source analysis window with the specified data segment.



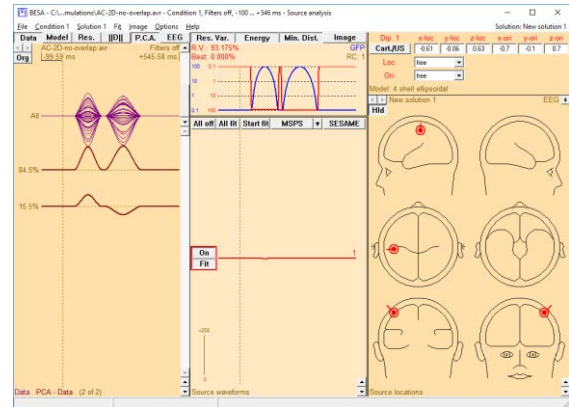
- On the left of the source analysis window, the recorded channels are displayed in average reference: The top row shows a butterfly plot of all channels; below that, the PCA decomposition is shown by default, indicating the number of components that can be expected in the data. In the top middle box, the global field power (GFP; the sum of squares of all channels, normalized to 100%) is displayed in a logarithmic scale. The central and right-most sections of the window are dedicated to the model that describes the data; as there is currently no model defined yet, they are empty at this point. On the right, the head sketches are shown analogously to the BESA Simulator program (<https://www.besa.de/home/downloads/besa-simulator/>). The parameters of the applied head model are shown at the upper right. **Double-click** into any of the 6 heads to insert a first dipole.



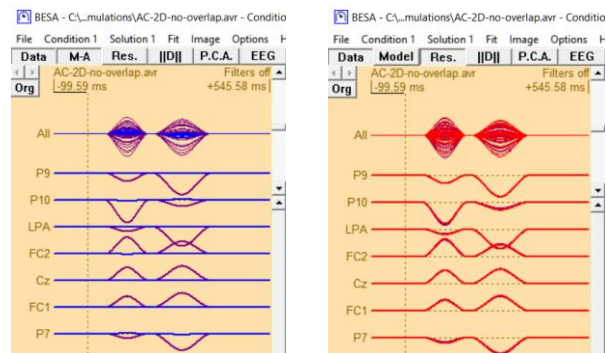
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5. This defines a first (still inappropriate) source model. The source waveform in the middle box is calculated from the recorded data using the head model (= model for the distribution of the electrical conductivity inside the head) and the source model on the right as a hypothesis. Source waveforms are dependent variables. Source locations and orientation are independent variables.



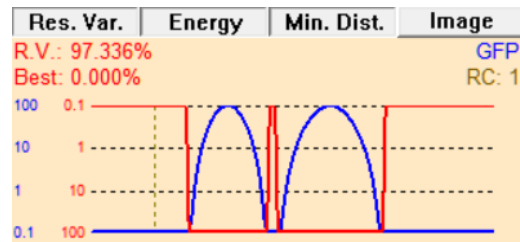
6. Based on the source waveforms and the source leadfields (as defined by source location, orientation, and head model), the model waveforms can be computed, i.e. the data that would be generated by the current source model. First of all, by un-checking the **P.C.A.** button above the waveform display, you can visualize the measured data for each channel (sorted by variance). Now you can visualize the model waveforms (blue) by hitting the **Model** button in the upper left corner. The difference between recorded (purple) and modeled (blue) waveforms is the *residual*. It can be displayed in red by hitting the **Res.** button.



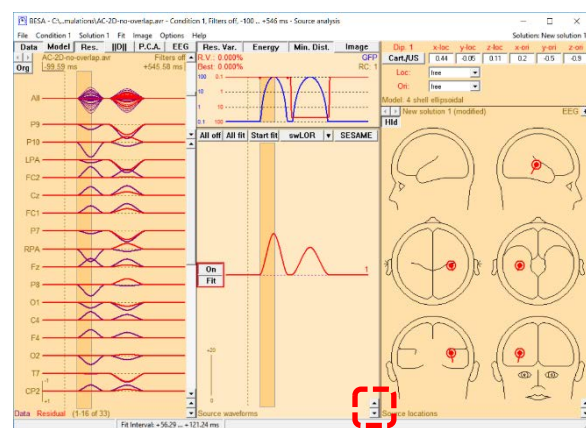
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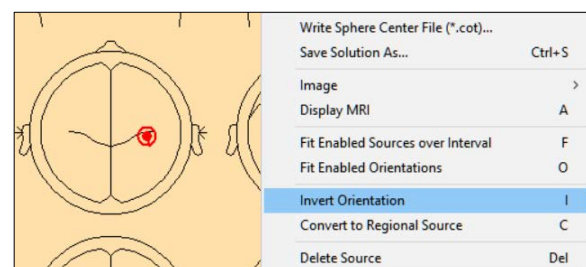
- The normalized sum of squares over channels of this residual activity is the *residual variance* (RV), i.e. the unexplained fraction of the data variance. It is displayed in the top middle box (red) together with the GFP. Note the inverted logarithmic scale for the RV. The goal of the source fitting process is to find a source model that minimizes this residual variance.



- Left-drag** over the data approximately from the onset of the first EEG activity to the first peak. Then hit the **Start Fit** button in the waveform box to determine the optimum location and orientation for our first dipole in order to explain the data in the marked fit interval. The result is independent of the initial dipole position and confirms the simulated generator of the brain activity in this time range in the right auditory cortex. Use the scaling buttons at the bottom right of the middle panel to increase the source waveform scaling.



- Note that it is arbitrary if the dipole is represented with its flag pointing in one direction or in the opposite direction. If you wish, you can invert the source orientation by **right-clicking** onto the **source** and selecting **Invert Orientation**.



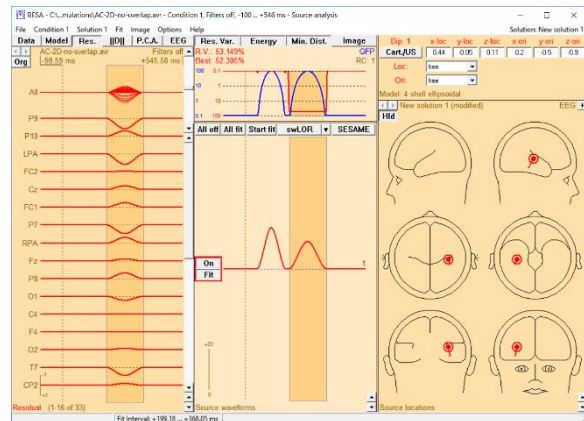
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Tutorial 4 – Discrete Source Analysis

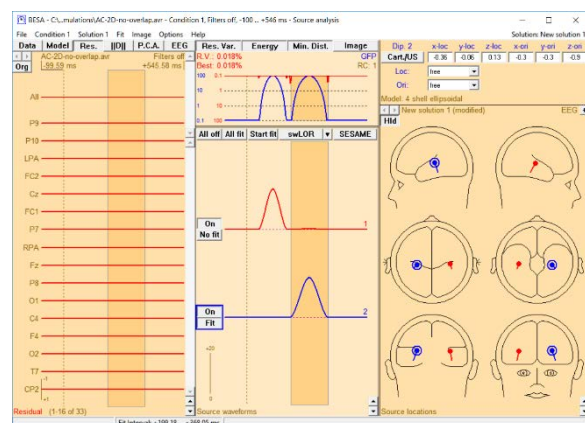
10. Release the **Data** button in the upper left corner to show the residual activity only.

In our marked initial fit interval, the dipole in the right auditory cortex explains the recorded data without any remaining residual. However, its source waveform is not correct – it shows activity also during the later time range of simulated activity in the left hemisphere. This is so because

the required source accounting for this activity is not included in our source model. This is also reflected in the high residual variance in this latency range. Therefore, left-drag to mark a second fit interval across this later time range.



11. **Double-click** into the head to **insert a second dipole**. The button next to its source waveform will automatically show **Fit** to indicate that its location and orientation will be optimized in the next fitting step; in contrast, the button of the first dipole says **No Fit**, because it will be held fixed – its location and orientation has already been determined by the first fitting step. Press **Start Fit** to start the fitting process. As expected from our simulation, the second dipole localizes in the left auditory cortex. The flat residuum indicates that this two-source model perfectly explains variance in the data.



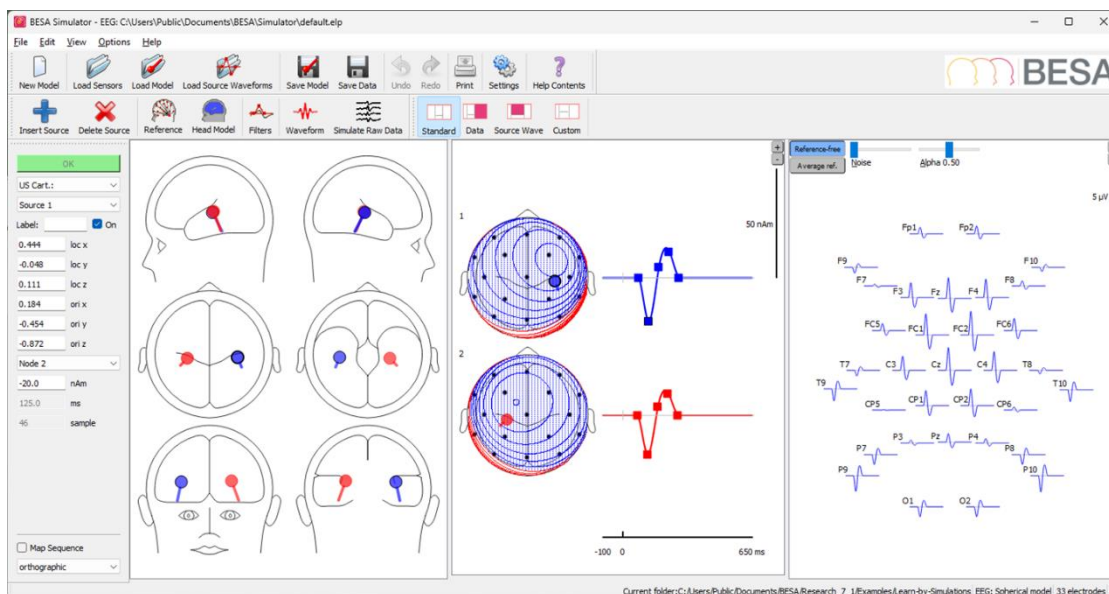
step. Press **Start Fit** to start the fitting process. As expected from our simulation, the second dipole localizes in the left auditory cortex. The flat residuum indicates that this two-source model perfectly explains variance in the data.

The fit results in a complete separation of the activities of the right and left AC. The addition of the left dipole has changed the calculation of the right source waveform. It is now blind to activity from the left source, and does not show any activity in the later interval when the left source is active. The analogous statement is true for the source in left AC. Therefore, an appropriate source model that should reconstruct the correct source activities must contain dipoles representing at least all active brain areas. Otherwise, activity in unmodeled brain areas will be projected onto the source waveform of the modeled sources.

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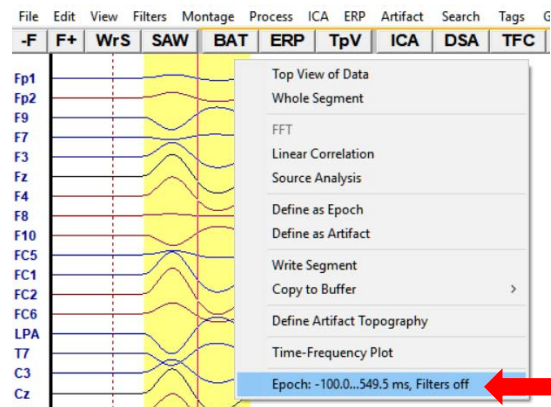
2nd simulated data set: Severe overlap and high synchrony between hemispheres is what we must expect in auditory evoked potentials. Furthermore, cortical source activities are more complex and often biphasic. Therefore, the next simulated data set, **AC-2D-biphasic-synchronous.avr**, contains biphasic source waveforms which are synchronous in both auditory cortices. Negative source waveforms represent postsynaptic current flow into the direction of the flag of the dipole symbol; positive source waveforms reflect current flow in the opposite direction. Remember that the source waveforms reflect the local current flow within the modeled gray matter patch – it does not represent the direction of signal propagation within the brain!



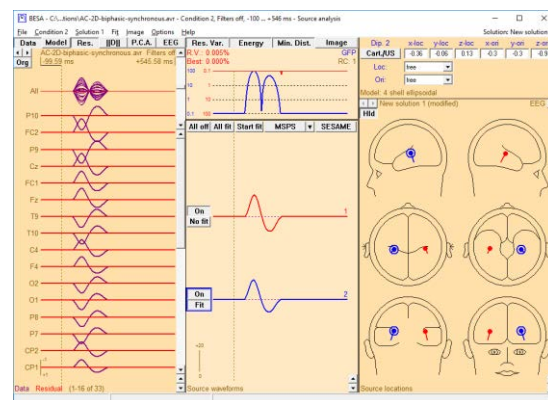
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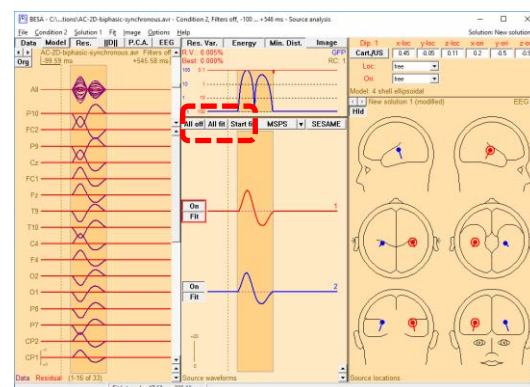
12. Minimize the source analysis window and select **File / Open** in the main window to load the second simulated data set **AC-2D-biphasic-synchronous.avr**. **Left-drag** to mark a block and **right-click** into it. BESA Research remembers the previous settings used for source analysis that you can quickly re-apply by selecting it at the bottom of the popup menu.



13. The source analysis window appears with the new data set, the previous dipole model still applied. Press the **Data** button to show the biphasic EEG signals of this data set. Since the data set has been simulated with the same active brain regions, the source model is correct for this data, the residual variance being nearly zero. The source waveforms are now computed from the new data and therefore reflect the synchronous bilateral biphasic activity.



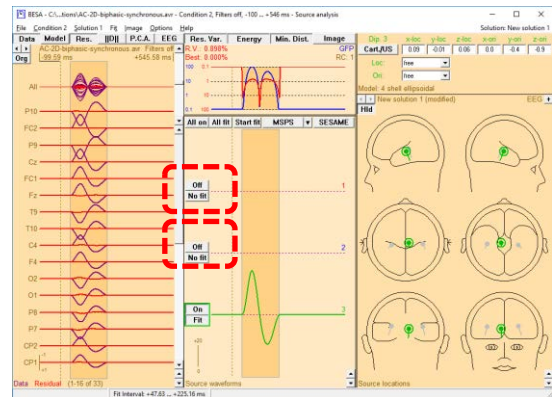
14. We could have obtained this source model by fitting both dipoles simultaneously to the data. To see that, **left-drag** to mark a fit interval over the time range of EEG activity. Then hit the **All fit** button – this turns both sources into the *Fit* state. When pressing the **Start Fit** button now, location and orientation of both sources will be optimized. The result does not differ from the previous model.



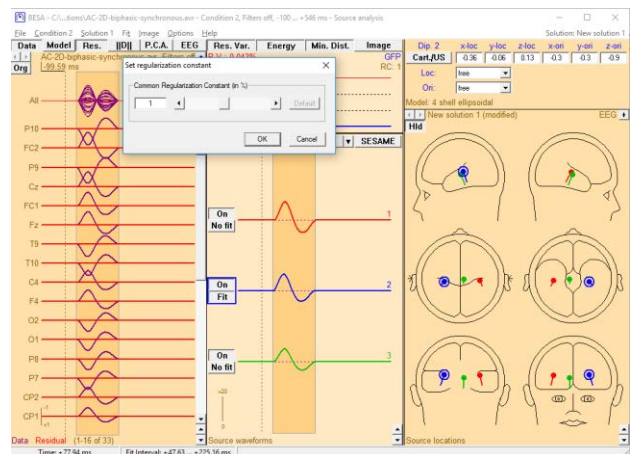
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15. Let's see what happens if we had tried to model this data (incorrectly) with a single dipole only. Deactivate the two dipoles by hitting their **On** buttons. This effectively removes them from the source model. **Double-click** to add a new dipole and press **Start Fit**. This results in a dipole in the middle of the head, compromising to explain the left- and right-hemispheric activities. Although the result is incorrect, the residual variance is less than 1% (as displayed as *R.V.* at the top)!



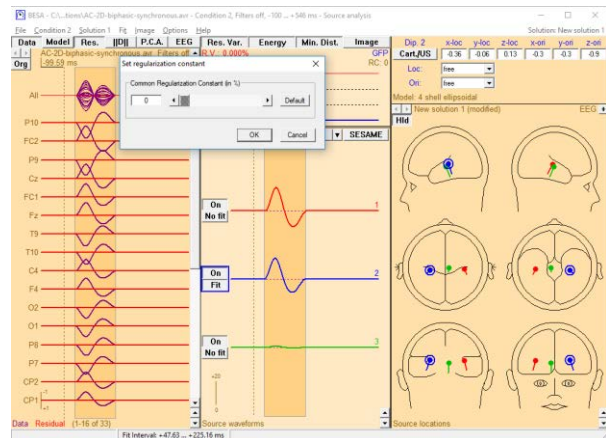
16. How can one decide whether the one-source or the two-source model is correct? This can be done by contrasting the two source models. **Switch back On** the two first dipoles. Now the three source waveforms should be able to contrast and mutually separate the activities in the three modeled brain regions. The reason for the still non-vanishing source activity of the third dipole is a parameter called **regularization constant**. Select the corresponding entry from the **Options** menu.



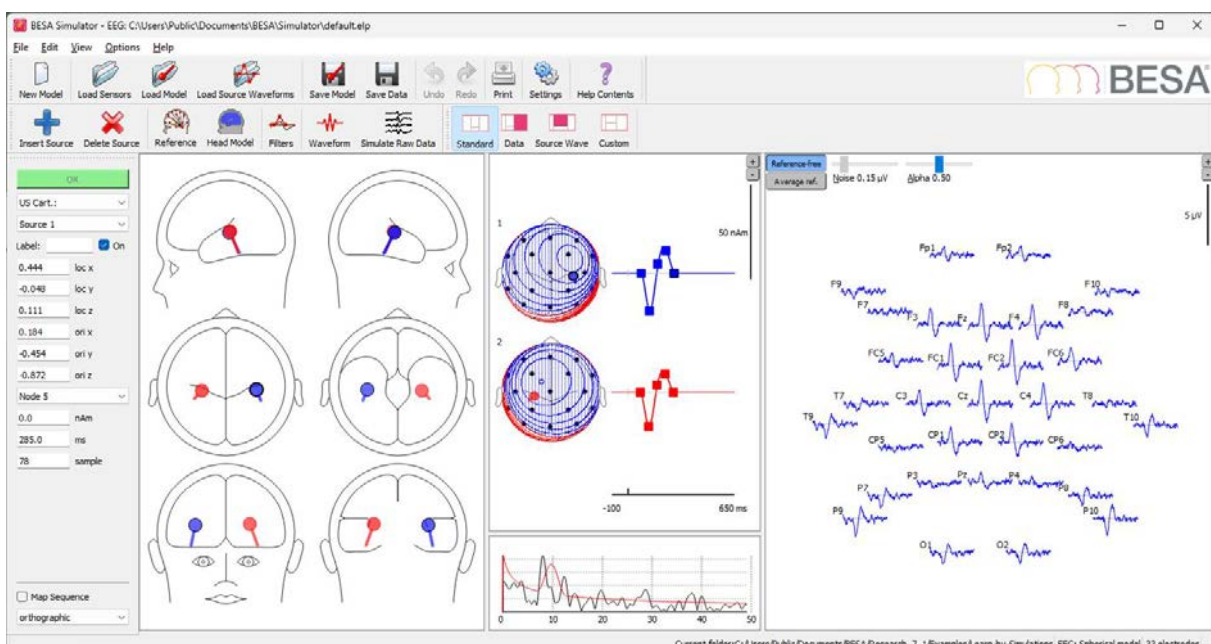
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17. Reduce the regularization constant to **zero**. With this setting, the separation capability of the source waveforms is optimal, and the flat source waveform of the third dipole indicates that there is no brain activity in the middle of the head. Rather, the two-dipoles in the bilateral auditory cortices correctly represent the truly active brain regions. So if regularization blurs the spatial filter and increases crosstalk between sources, what are the benefits of it? We will see the answer in the next simulation. Click **OK** to close the regularization dialog.



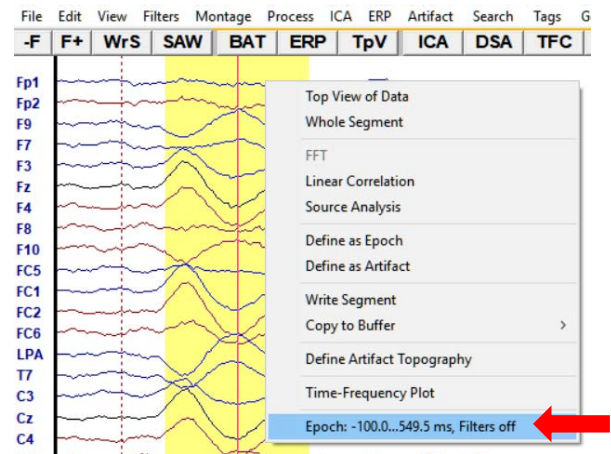
3rd simulated data set: Finally, the third simulated data set has been designed to be even more realistic by adding background noise to the same simulated brain activity as before (**AC-2D-biphasic-synchronous+noise.avr**).



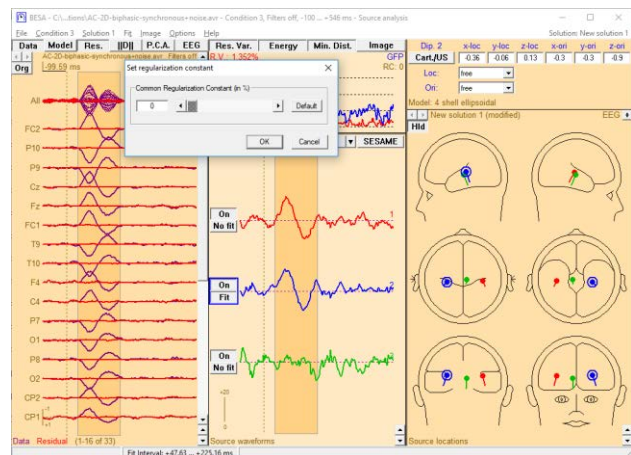
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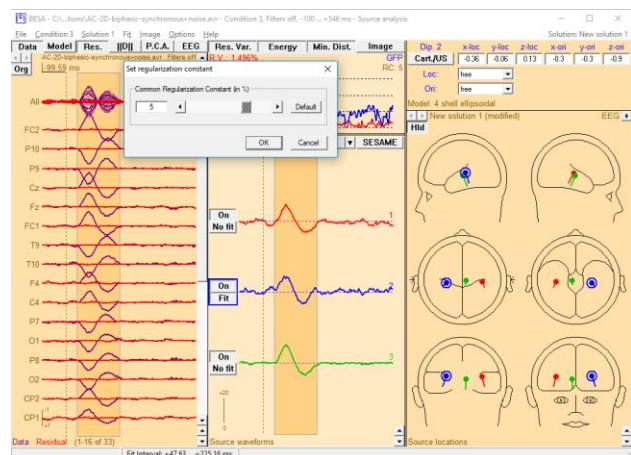
18. Minimize the source analysis window. In the main window select **File / Open** to load the file **AC-2D-biphasic-synchronous+noise.avr**, the same simulation as the previous one, but with some small background noise added to the data. Again, send the data into the source analysis window: **left-drag** to mark a block, **right-click** into it and **select the bottom-most entry**.



19. The previous solution is now applied to the noisy data. The channel noise is strongly projected onto the source waveforms when the regularization is set to zero. Select **Options / Regularization constant** again and see how increasing the regularization constant affects the reconstructed source waveforms.



20. As regularization is increased, crosstalk increases as in the previous example, i.e. the third source waveform reflects activity that is truly generated in the brain regions represented by the other two sources. However, as a positive effect, the source waveforms are substantially cleaned from noise. This positive effect in noisy data implicitly stabilizes source fitting results in

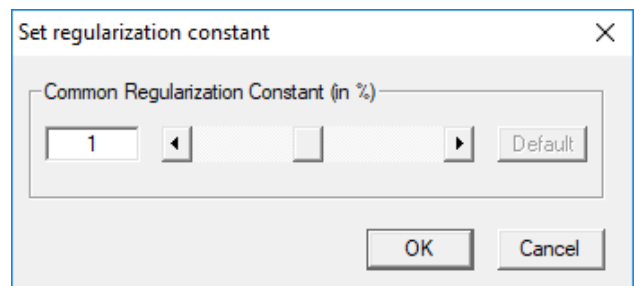
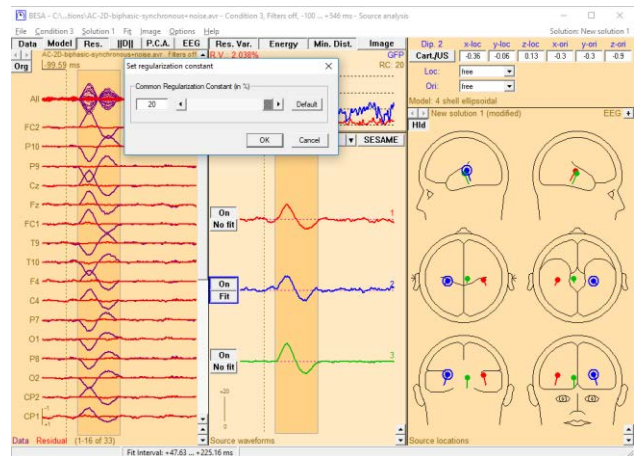


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the presence of noise. Therefore, a modest regularization is recommended in real data sets. The default regularization of 1% is usually an appropriate compromise and does not need to be changed. Crosstalk between source waveforms is usually smaller than in the current simulation, in which the correlation between the leadfields of the modeled sources is especially high.

21. Set back the regularization to 1% and hit OK. Then **close the source analysis window** (confirm with **OK** that the developed source model does not need to be saved to disk).



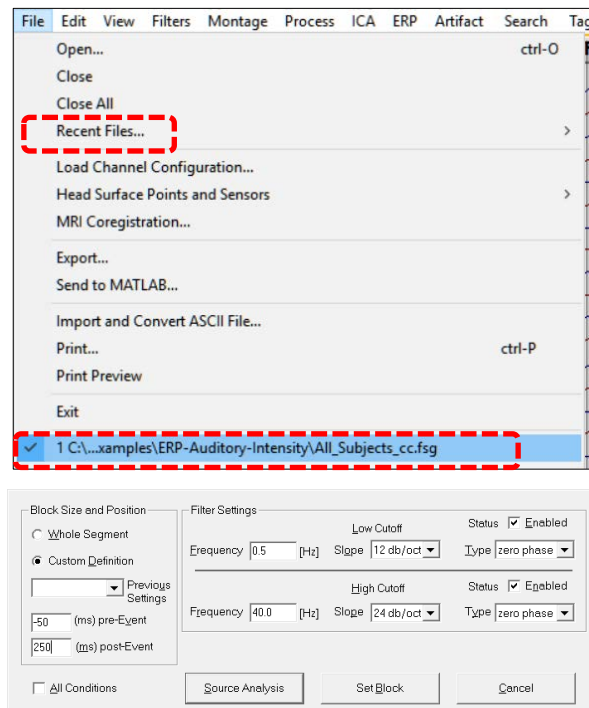
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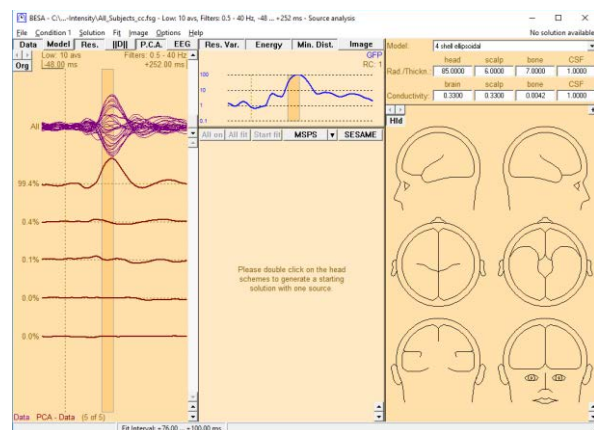
C. Single Dipole Fitting in Real Data

1. Back in the main BESA window the file **All_Subjects_cc-Test.fsg** should still be available at the bottom of the File menu. If it is not, please select it pressing **File / Recent Files /**

Left-drag a block in condition **Low**, **right-click** to send it into **Source Analysis** with custom definition settings **-50 to 250 ms**, a **Low Cutoff filter of 0.5 Hz, 12 dB/oct**, **zero-phase shift**, and a **High Cutoff filter of 40 Hz** (keep the default parameters **24 dB/oct, zero-phase**). The low cutoff filter will create an improved baseline and reduce the overlapping slow activity.



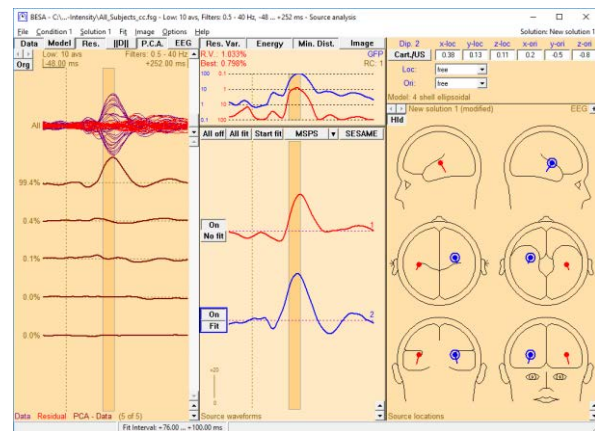
2. It is not possible to fit a good source model for the P50 as its signal-to-noise ratio is poor. Therefore, we will focus on the N100, which has the largest amplitude in our signal. Mark a time-window from the beginning to the maximum of the auditory N100 (76 to 100 ms). As we are dealing with auditory data, we know that we need to fit at least 2 dipoles to obtain a correct source model. **Double-click** in the heads twice to **place 2 initial dipoles**. Press **All fit** and **Start fit**.



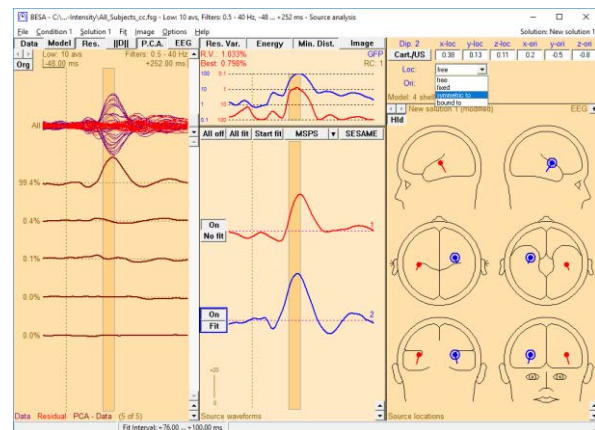
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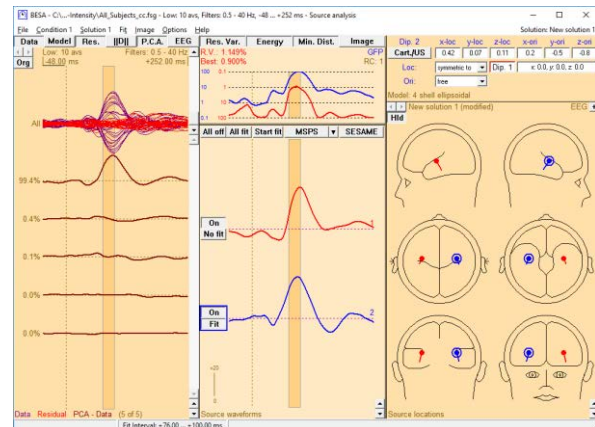
3. Both sources will fit in auditory areas, the right source being located further anterior than the left source. The right source seems located slightly too medial.



4. The fit can be improved by introducing a symmetry constraint. This can be very useful for stabilizing a fit, particularly when data are noisy. To do so click on one of the sources and select **symmetric to** in the **Loc.:** drop-down menu. Press **All fit** and **Start fit** again.



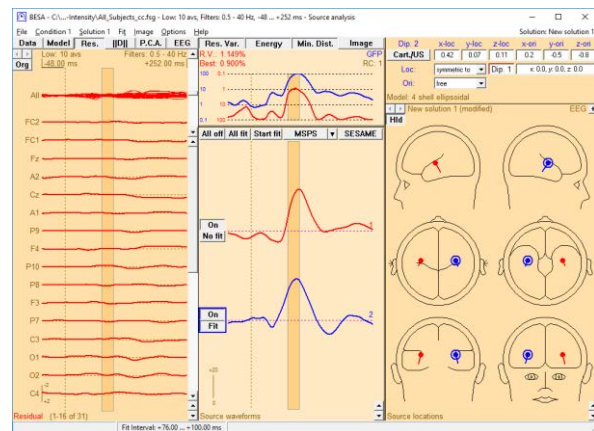
5. Both dipoles are located symmetrically in the auditory cortex. Note that the residual variance is slightly bigger using the symmetry constraint. However, the solution with the smallest residual variance is not always the correct anatomical solution. You should keep in mind that deeper dipoles explain more variance. Therefore, in noisy data dipoles will have a bias to localize deeper to explain more variance.



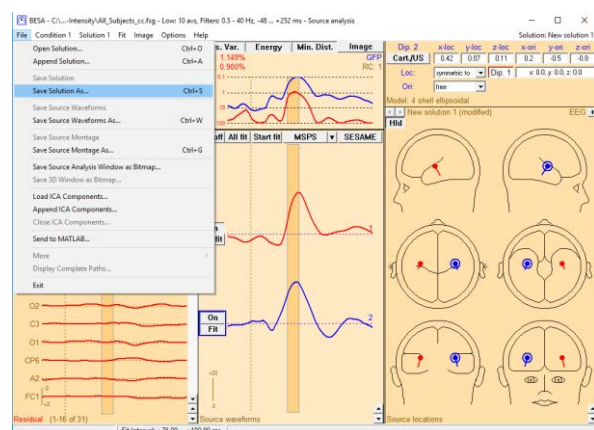
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6. Release the **Data** button and the **PCA** button to only display the residual variance (if it is not activated, click on the **Res.** Button). Note that our source model explains the data very well for the given time-range. Keep in mind for later that the source model does not explain the P50 or the N150 sufficiently. This can be seen by the higher residual variance in the according time-ranges. You may click on the **||D||** button to change channel sorting.



7. Save the current source solution for later by pressing **File / Save Solution As...** under the name **LowIntensity_2SD-test.bsa**. Close the source analysis window.



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D. Fitting Regional Sources in Simulated Data

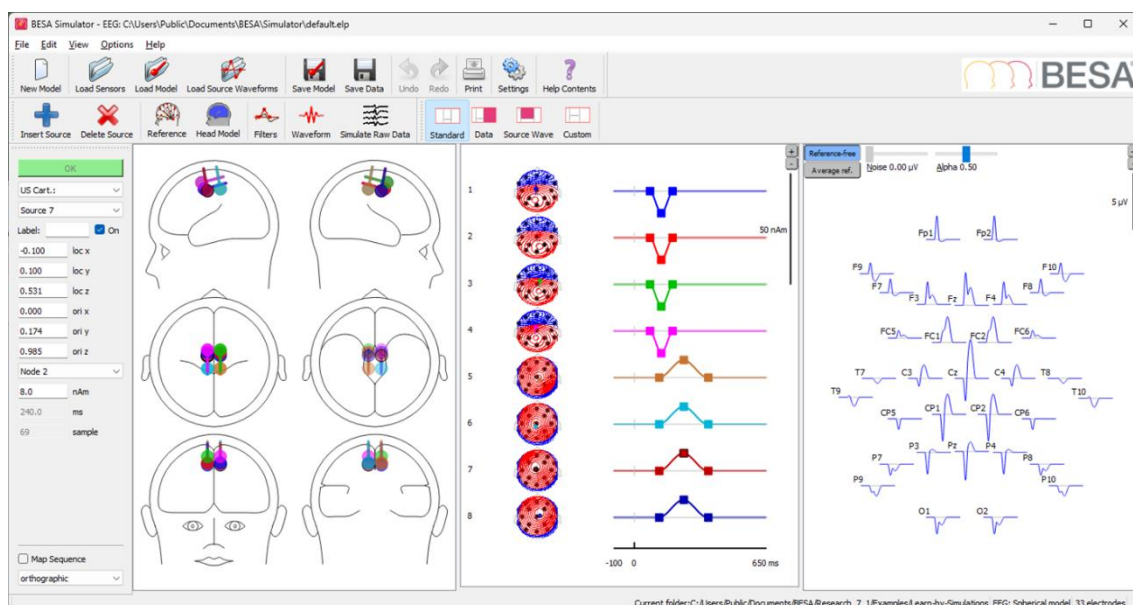
In order to understand the concept and advantages of regional sources we will again work with a simulated dataset.

Simulated dataset: Two extended square surfaces ($\sim 10\text{-}15\text{ cm}^2$) of planar cortex are modeled, each represented by four equivalent dipoles. The dipoles are approximately 2 cm apart. Each dipole can be thought to represent a smaller square surface ($2 \times 2\text{ cm}$).

The first simulated brain region is thought to represent **supplementary motor area (SMA)**. The four dipoles are located symmetrical to the interhemispheric cleft with **nearly tangential orientation**, reflecting a planar fissure to both sides of the interhemispheric cleft. The modeled time-course is the same in each dipole, representing synchronous monophasic activity in the SMA (dipoles 1-4 in the above figure).

Similarly, four **nearly radially oriented** dipoles are simulated, representing **cingulate gyrus** activity (dipoles 5-8).

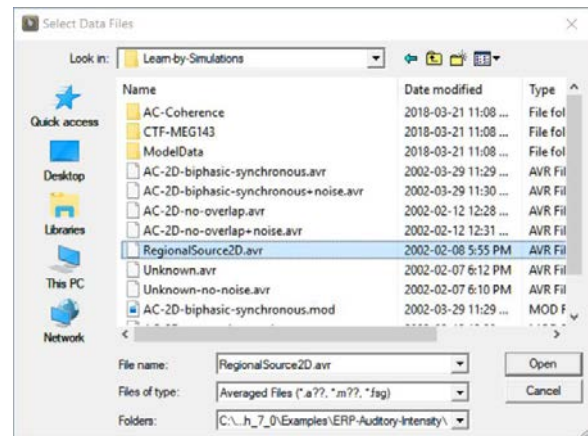
Thus, the two modeled extended brain regions are in **close proximity to each other**, but **differ from each other by the direction of the neuronal current flow** (i.e. the orientation of the active gray matter surfaces). The time courses of the two activities are simulated to be partly overlapping, with the activity of the SMA starting earlier than that of the cingulate gyrus.



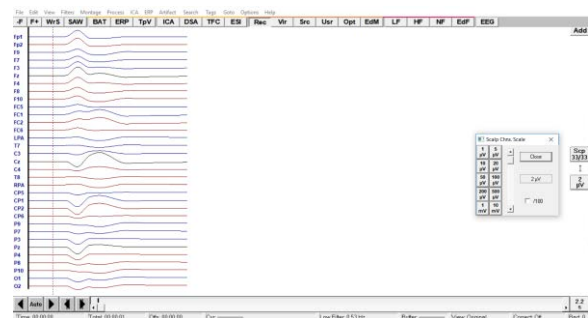
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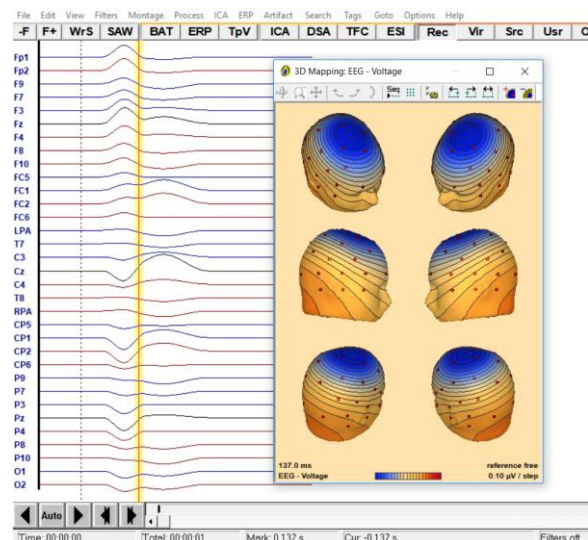
1. Load this data set in BESA Research:
Select **File / Open** and open **RegionalSource2D.avr**.



2. You may increase the amplitude scaling by pressing the **amplitude scaling button** at the right of the window. Change the scaling to **2 μ V**. It is evident that due to the effect of volume conduction, each electrode records signals from both modeled brain regions to some extent.



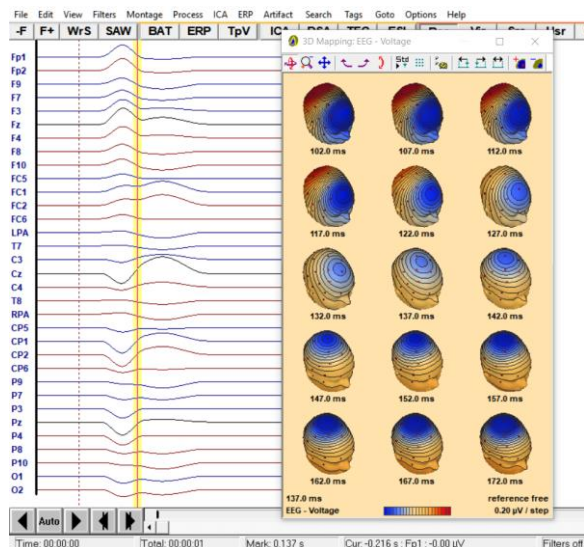
3. The overall distribution of the EEG activity at the scalp surface can best be observed by viewing a 3D whole-head map. Open the **map window** by **double-clicking** into the data approximately where a polarity reversal is observed in electrode Cz. A cursor is set and the map window appears.



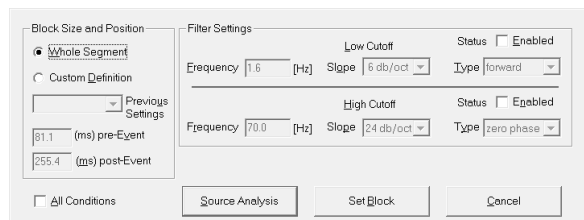
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Tutorial 4 – Discrete Source Analysis

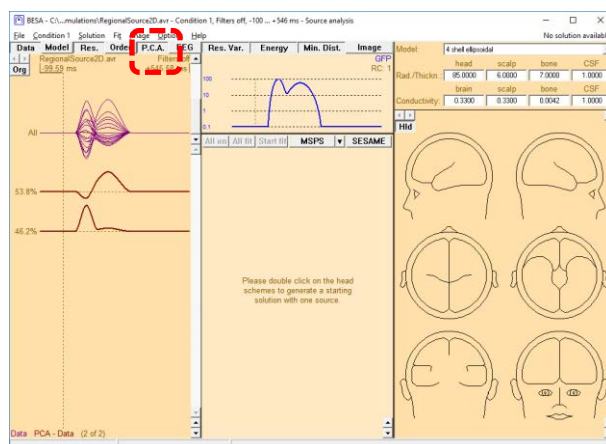
- To obtain a **time sequence** of maps, **click** onto one of the heads, e.g. the view of the right side (left head in the middle row). The display changes, and maps from 35 ms before to 35 ms after the cursor are shown in steps of 5 ms. The map seems to rotate from an early tangential map (activity of the tangentially oriented SMA) to a later nearly radial map (cingulate gyrus activity). Note that this apparent rotation is not generated by the rotation of one active brain region, but by the differential activity of multiple fixed gray matter patches with different orientations.



- In order to model the underlying activity, we will perform source analysis again: **Left-drag** to mark a block, **right-click** into it and send the whole segment into the source analysis window.



- The **PCA** button should already be pressed. This means that a principle component analysis of the data is computed. A PCA decomposes the data into contributions of mutually orthogonal topographies (i.e. topographies that are maximally dissimilar to each other in a mathematical sense). In this process, the first PCA topography is selected to explain the most data variance, the second topography the largest part of the



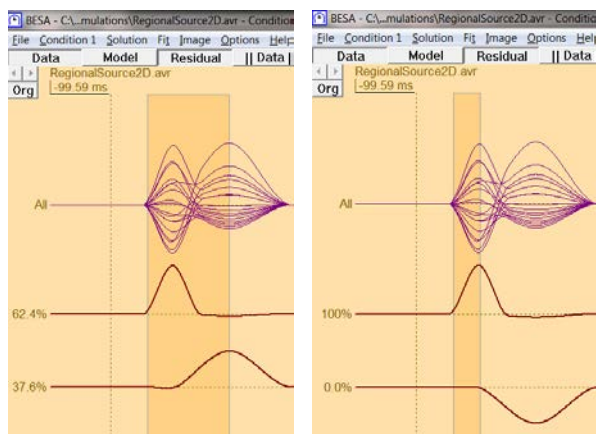
remaining variance etc. The curves at the left indicate the associated time courses.

The variance explained by the corresponding component is displayed next to it. It becomes obvious from the time courses, that a **PCA does not provide a separation of the multiple brain activities** (they were simulated to be monophasic, but the PCA time courses show two peaks each). However, the PCA provides a good estimate for the **minimum number of brain regions** that are contributing to the EEG data: A single brain region cannot generate EEG data that contains contributions of two mutually orthogonal topographies. We can therefore immediately conclude that we are dealing at least with two active brain regions in the current data set. Since **synchronously active brain regions cannot be separated by a PCA**, we only obtain a lower, but no upper bound on the number of sources required to model the data.

Note that in real data, there are as many PCA components as there are recording channels, most of them solely representing noise activity. The ones relevant for our considerations are those with a substantial contribution to the data variance and a time-course that indicates activity that clearly emerges from the background noise.

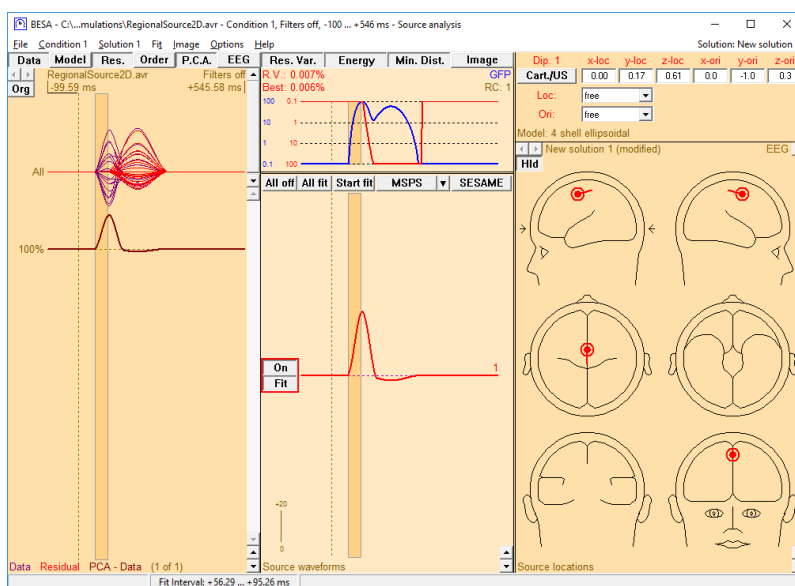
Next, we will see how we can also employ the PCA to estimate the appropriate duration of a fit interval.

7. If a fit interval is marked, the PCA decomposition is computed for the marked data segment only. **Mark a fit interval** that starts at the onset of observable EEG activity and vary its duration. Note that every time you change the length or position of the fit interval, the PCA waveforms and explained variances change.



8. We want to apply a *sequential fitting strategy*, i.e. first fit a dipole to represent the earliest brain activity. For that purpose, we should make the fit interval short enough not to include any brain activity from other brain regions that starts at higher latencies. Therefore, the fit interval should be chosen such that **one topography dominates the data**, i.e. one PCA

topography should explain the majority of the variance. If this is not the case, this would indicate that at least two brain regions contribute to its generation. We would get incorrect fitting results if we tried to fit a single dipole to the data. On the other hand, the fit interval should not be shorter than necessary either, so that the effect of channel noise on the fit result gets reduced. In our example, an appropriate first fit interval is e.g. approximately **from the onset of EEG activity to the first peak** – in that time range, the SMA region is active, whereas there is no cingulate gyrus activity yet (PCA topographies show 100% and 0% contribution, respectively). Then **double-click** into the heads to create one dipole and hit **Start Fit**. The dipole localizes in the center of the simulated SMA activity. Note that the SMA region was modeled with 4 dipoles to represent activity of a relatively large cortical patch. Still it is possible to reconstruct its activity with only 1 dipole with near perfect explanation of the variance.

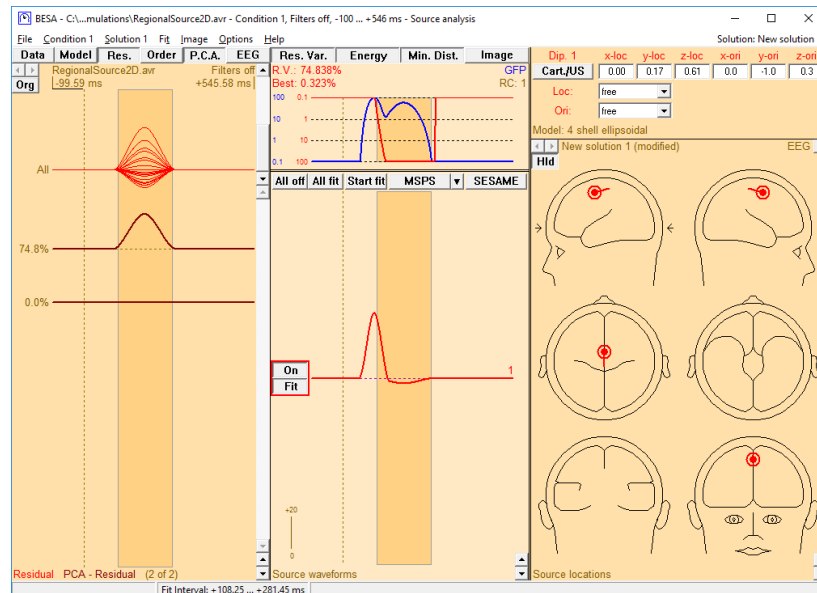


- Release the **Data** button in the upper left corner to display the residual (i.e. unexplained) activity only. Now **mark a second fit interval** to include the left-over residual variance. Because the data is not displayed anymore, the PCA is computed for the residual activity only. For the second and all additional fitting steps, this is our criterion for the selection of the fit intervals. In this simulated example, there is only one additional brain activity, i.e.

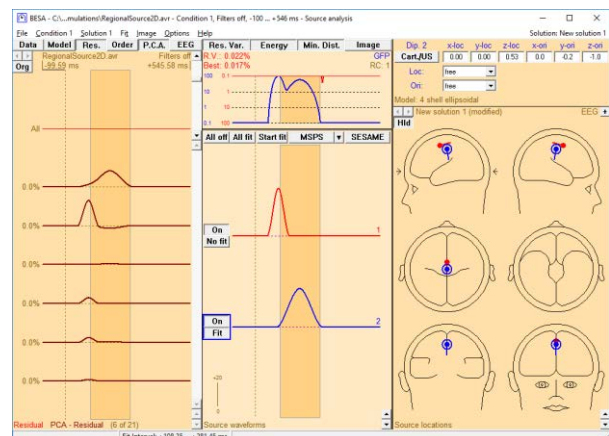
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no matter how long you choose the fit interval, it will result in one additional PCA component with substantial contribution⁶.



- After deciding on a fit interval, add a second dipole by **double-clicking** into the heads. Hit **Start Fit** to localize it into the cingulate gyrus area. Note the vertical orientation of this source, in agreement with our simulation. The two-dipole model now separates the activities of the two brain regions. The source waveforms reconstruct the correct time courses, indicating the earlier activation of the SMA as compared to the cingulate gyrus.

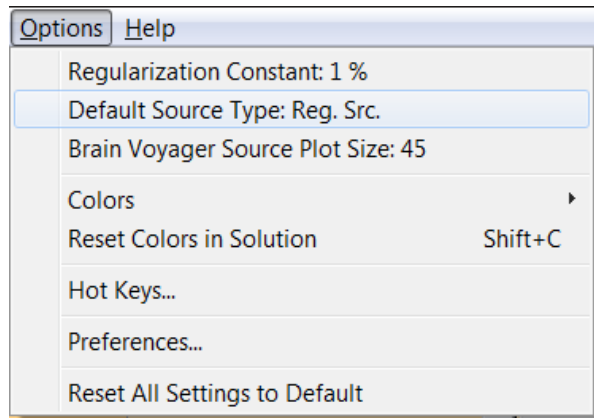


⁶ The PCA variances computed for the residual do not sum up to 100%, but rather to the total residual variance in the marked block

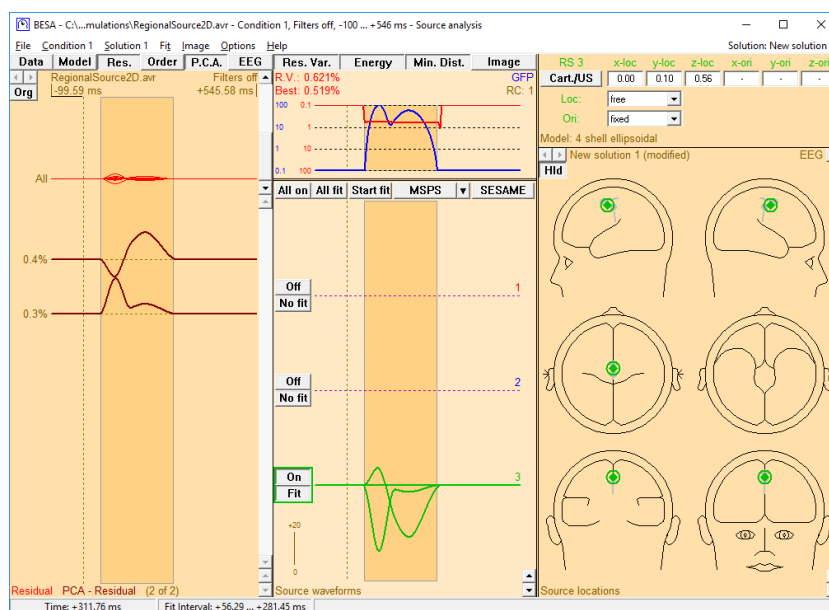
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11. Open the **Options** menu. Currently the default source type is set to Dipole (2nd row). Please **click** onto this entry. When you open the Options menu again, the default source type has been set to **Regional Source**. With this setting, a double-click into the heads will automatically add a regional source as opposed to a dipole.



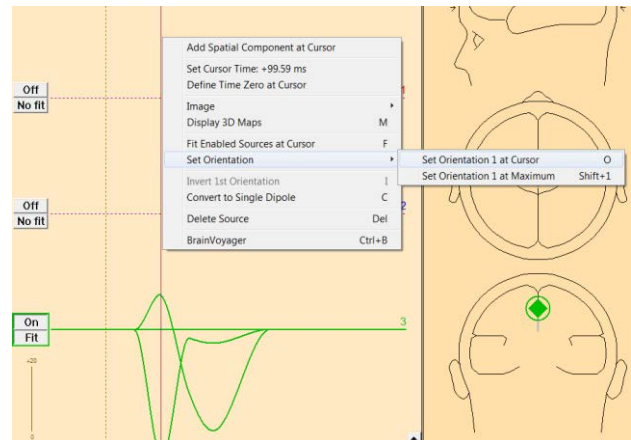
12. A regional source has a location and three (MEG: two) orthogonal orientations, in order to model all activity that stems from a particular brain region, no matter in what direction the current flows. To model the two simulated brain regions with a single regional source, **switch off** the two single dipoles in the model. **Double-click** into the heads to insert a regional source. Because it consists of three orthogonal dipoles, the corresponding source waveform consists of three curves, each representing the source waveform of one underlying dipole. **Mark a fit interval over the whole time range** of activity and hit **Start Fit**. The fitted source location compromises between explaining the SMA and the cingulate gyrus activity. The obtained residual variance is less than 1%, indicating that this source models the data very accurately.



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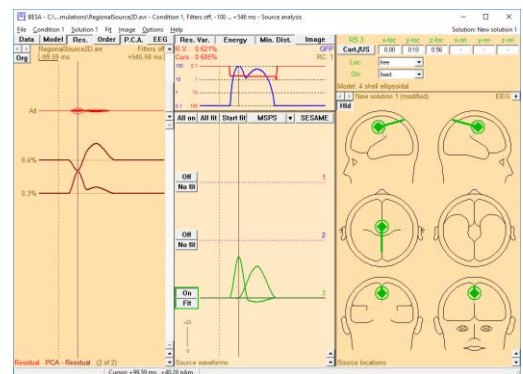
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13. The three mutually orthogonal dipoles of a regional source models current flow in any arbitrary direction in a certain brain region. Mathematically speaking, we will get exactly the same representation of activity if we rotate the axes from the initial x-, y- and z-direction to new orientations such that the 1st dipole of the regional source represents the initial peak of activity. To do that,



double-click onto the source waveform to set a cursor at the first peak (around 100ms). **Right-click** and select **Set Orientation / Set Orientation 1 at Cursor**.

14. This rotates the regional source so that the first of its dipoles points into the direction of current flow at the cursor latency. Note that as a consequence its source waveform picks up all activity at the cursor latency; the other two source waveforms show zero activity at the cursor. The second and third dipole components are rotated with it so that they remain mutually orthogonal. The second dipolar component is automatically set to model the largest current flow perpendicular to the first source. As a consequence, the source waveform of the third component is flat in this simulated example.

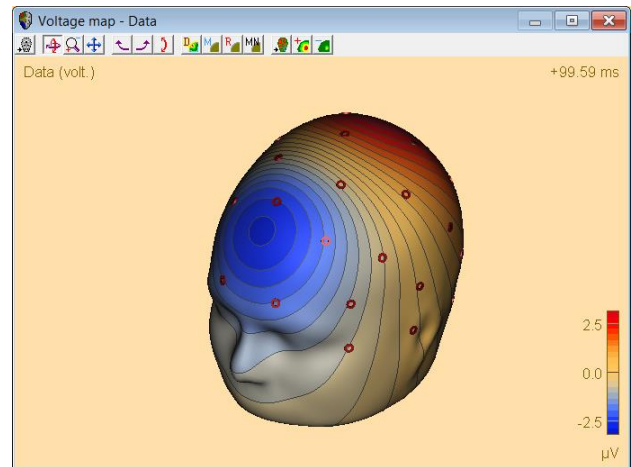


This means that we can apply regional sources for the purpose of modelling the activity of a specific brain region, and, by orienting the components, also for the purpose of separating activities with different orientations of cortical patches. Note, however, that a full separation of differently oriented components is only possible if their orientations are indeed orthogonal to each other, like in this simulated example. We will see the strengths and drawbacks of regional sources again shortly when we apply them to real data sets.

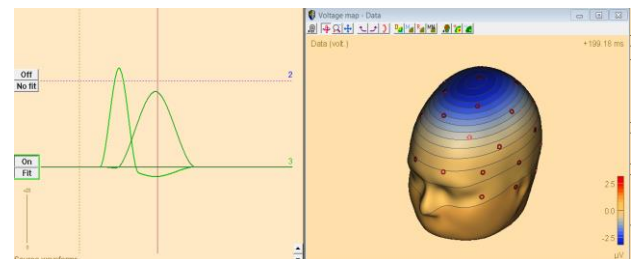
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- With the cursor still set at the first peak, you can hit the **M** key on the keyboard (or **right-click** and select **Display 3D Maps**) to view the voltage topography at that latency. It reflects the tangential dipolar topography of the SMA region.



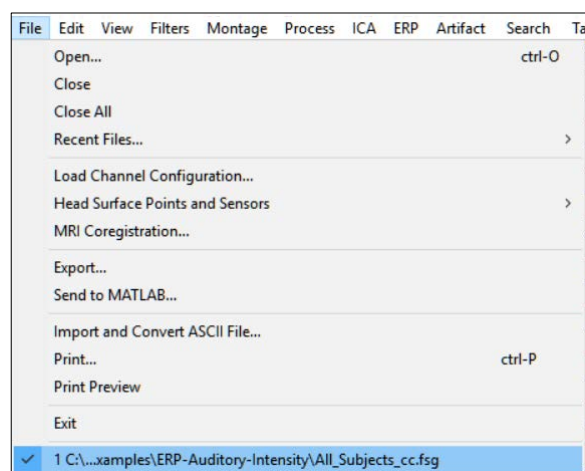
- Use the **arrow keys** or the mouse to **drag the cursor to the second peak** and observe the radial EEG map generated by the cingulate gyrus with the large central negativity. **Close** the source analysis window without saving the solution.



E. Fitting Regional Sources in Real Data

We will now use regional sources instead of single dipoles to reconstruct activity in our real auditory intensity dataset.

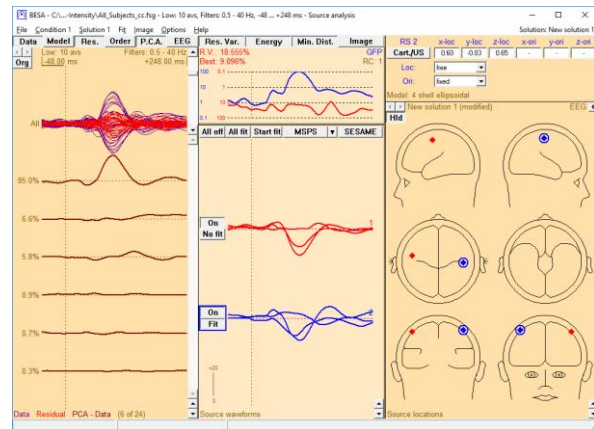
- We will now return to the dataset **All_Subjects_cc-Test.fsg**, which should still be available at the bottom of the File menu. If it is not, please select it pressing **File / Recent Files / ...**. **Left-drag** a block in condition **Low**, **right-click** to send it into **Source Analysis** with settings **–50 to 250 ms**, a **Low Cutoff filter of 0.5 Hz**, **12 dB/oct**, **zero-phase shift**, and a **High Cutoff filter of 40 Hz**, **24 dB/oct**, **zero-phase**.



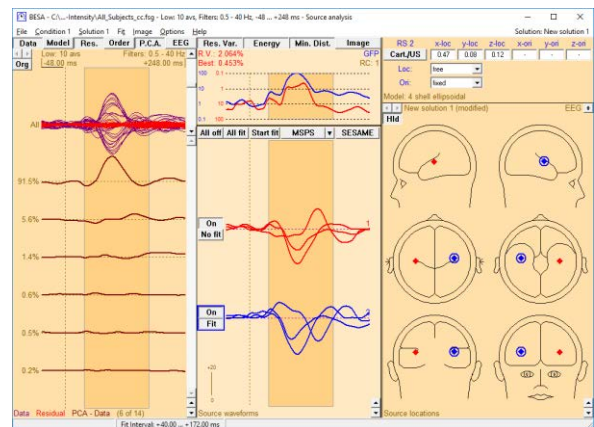
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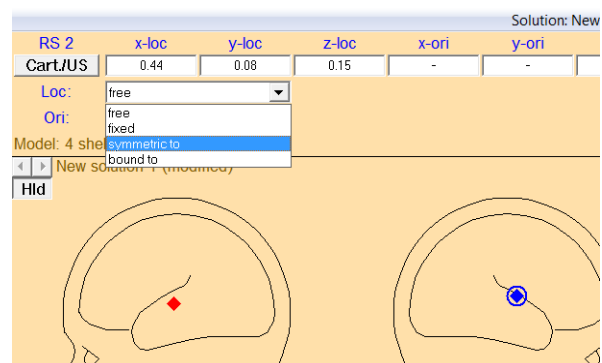
- With pressed **P.C.A.** button, a principal component decomposition of the data is displayed. Condition **Low** is dominated by one large PCA topography, mainly representing the N100 activity. Create an initial source configuration with two sources by **double clicking** onto the right and left head scheme.



- As regional sources can explain activity with up to three brain orientations at the same time we can expect the two sources to model the three main components in the auditory cortex area (P50, N100 and N150). Therefore, we will not set a short fit interval comprising only one component, but rather mark a fit interval over the activity range of these three AEP components. **Drag** the cursor over the source waveforms to mark the interval from **40 ms to 172 ms**. You may set the interval by **right-clicking** and selecting **Set fit interval**. Press **All Fit** and **Start fit** to fit both sources simultaneously. Use the arrow buttons in the source waveform box to **adjust waveform scaling**.



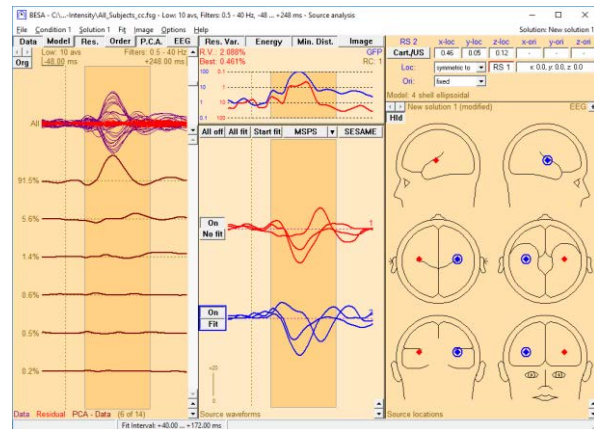
- The sources are quite symmetric with a slightly more anterior source in the right hemisphere. As stability might be much worse in individual data, we will impose a symmetry constraint on the source location again. Activate the second source by clicking onto its waveform. In the upper right box, select **symmetric to** from the drop-down menu next to **Loc**.



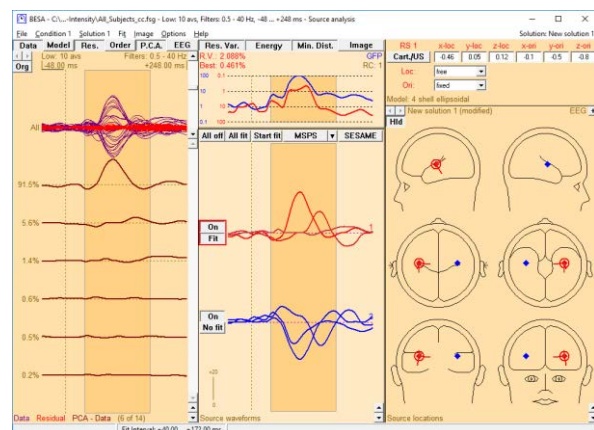
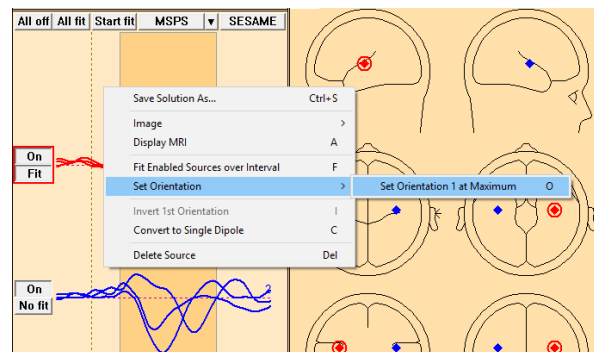
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5. Press **All Fit** and **Start fit** again. Note that the residual variance (**Res.** button needs to be pressed to view this) and the source waveforms only change marginally.



6. We want to identify the direction of current flow of the N100 component. To do so, activate source one by clicking onto the source. **Right-click** and select **Set orientation / Set orientation 1 at Maximum**. This rotates the source such that the peak around 100 ms is now fully accounted for by the first component (source waveforms for orientations 2 and 3 are now zero at this latency).

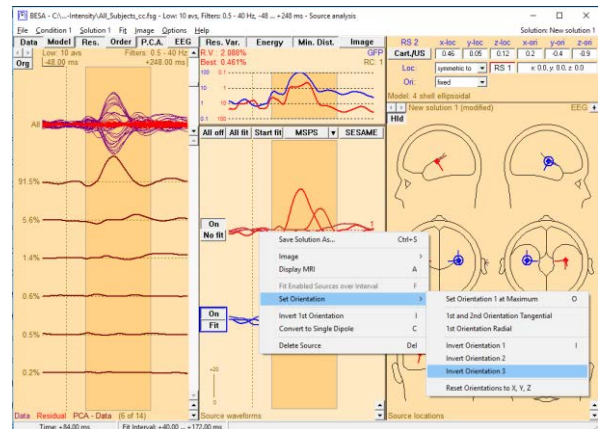


BESA Research not only sets the first orientation, but also automatically adjusts the second orientation of the regional source to explain the maximum activity perpendicular to orientation 1 in the whole time interval. Thus, the second orientation accounts for the N150 component (second largest component). The orientation of N150 is close to radial and reflects current flow at the lateral surface of the supratemporal gyrus. Alternatively, the second component of a regional source could be set at a specified latency by double-clicking to set a cursor, right-clicking and selecting **Set orientation / Set orientation 2 at Cursor**.

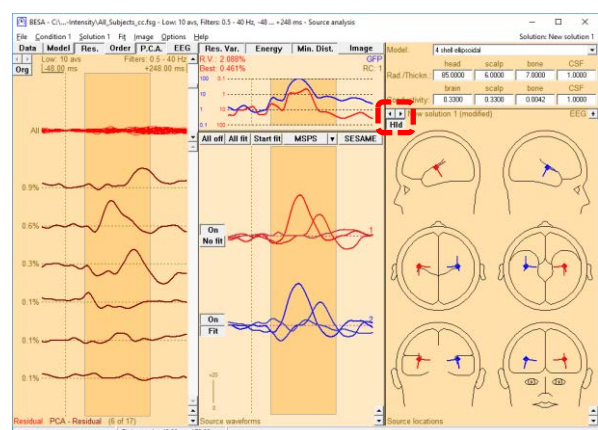
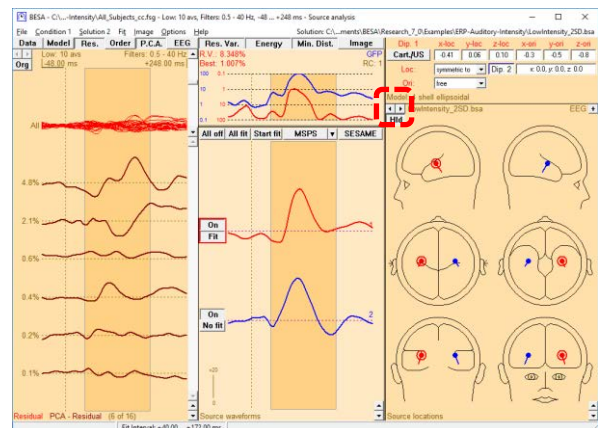
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7. Next, we will orient the second source as described in step D6. If necessary, **Right-click** onto its waveform and select **Set Orientation / Invert Orientation 3** to make orientations of source one and two consistent. (This 2-source model has been saved in file LowIntensity_2RS.bsa. You may load this file from the menu entry **File / Open Solution.**)



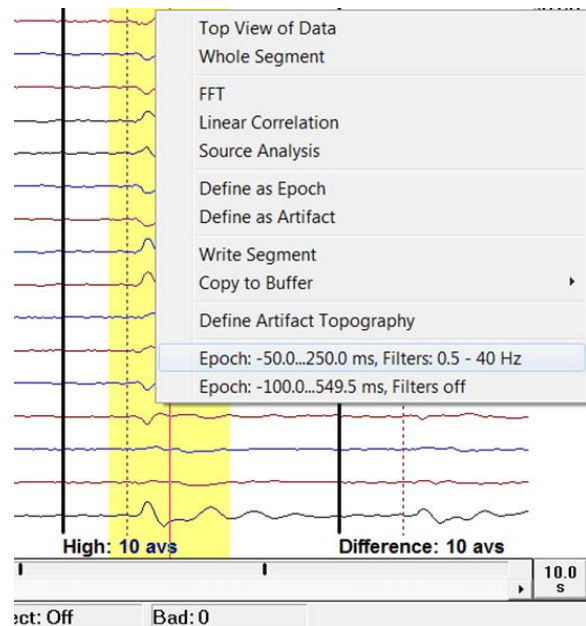
8. Let us compare the solution using regional sources with the solution using single dipoles we saved earlier on. Please press **File / Open Solution** and select **LowIntensity_2SD-test.bsa**. Release the **Data** button to only display the residual variance. You can toggle between the two solutions using the arrow buttons in the top left corner of the head scheme field. Note again that the single dipole solution does not explain the P50 and N150 components, while the regional source solution explains all activity from the temporal region very well.



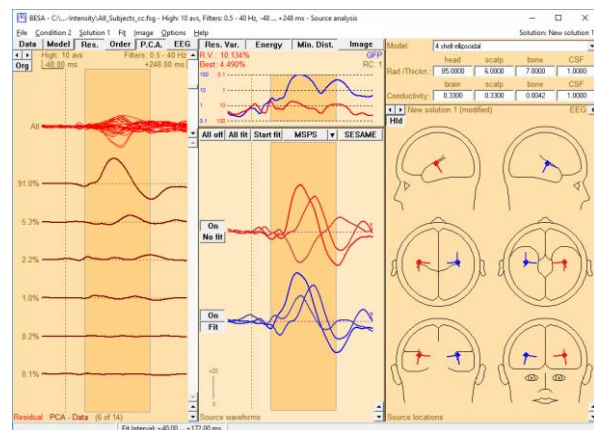
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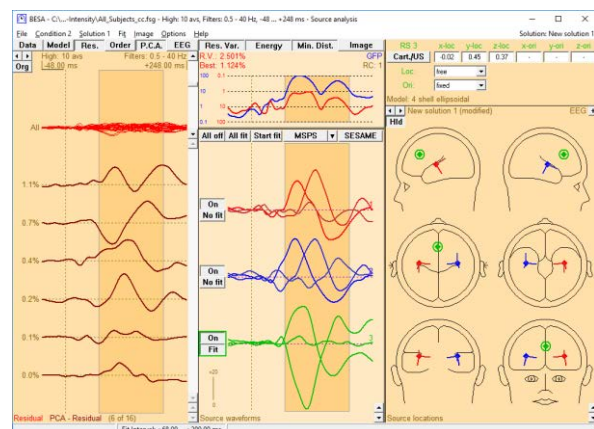
9. Make sure you switch back to the regional source solution and minimize the source analysis window (don't close it) to return to the average data in the main window. Select condition **High** and send it to source analysis with the same settings as the Low condition by **left-dragging a block**, **right-clicking** and selecting the according entry at the bottom of the dialog.



10. If the **Data** button is still released and the **Residual** button is pressed we can immediately see that the source solution that explained the data in the Low condition very well is not satisfactory in the High condition.




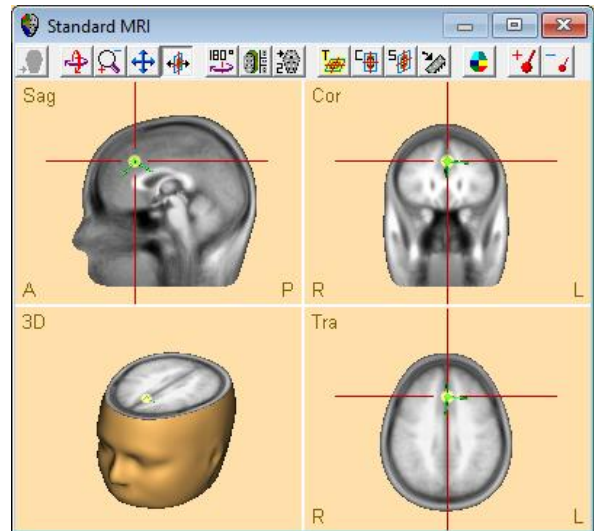
11. Mark a fit interval from 68 to 200 ms that covers the unexplained activity. **Double-click** into the head schemes to place a third regional source. Press **Start Fit**.



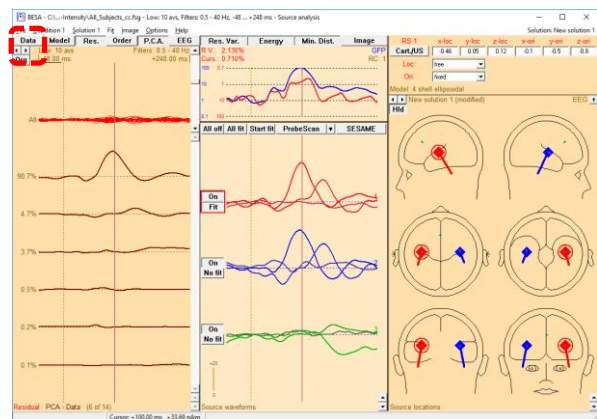
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12. **Right-click** on source waveform 3 to set orientation 1 at the maximum or hit the **O** key, the short cut for this action. Scale down the source waveforms if necessary by using the arrow buttons in the bottom right corner of the source waveform field. **Right-click** on the source waveform and select Display MRI (or press the **A** key). **Press** the  button to change to multiple view. The third source localizes frontally, representing activation in the cingulate gyrus or frontal cortex. **Close** the standard MRI window.



13. Switch back to condition **Low** by using the arrow buttons in the top left corner of the channel field. Note that the ACC/frontal source is silent in the Low condition. Its presence does not alter the source waveforms of the auditory sources. You can probe this by switching the frontal source on and off. Close the source analysis window and save the current solution as **HighIntensity_3RS-test.bsa**. (This source solution has already been saved as HighIntensity_3RS.bsa.)



F. Conclusions

General guidelines for source analysis

We can conclude this tutorial with the following general results and guidelines:

1. The idea behind source analysis is to place or fit sources into the brain at all regions contributing to the data. Localization/fitting is hypothesis testing: The computed source waveforms separate the modeled brain activities and answer the question if and when activity takes place in the modeled brain region. Thus, BESA Research reconstructs the brain activity with high temporal resolution.
2. Synchronous activity over several square cm can be modeled by a single equivalent source.
3. Sources that are close together, have the same orientation and synchronous activity are indistinguishable.
4. Sources that are close together but have different orientations and non-synchronous activity can well be separated by a discrete source model.
5. Source waveforms are relatively insensitive to variations in dipole location. Therefore, a single regional source can accurately model activity of multiple gray matter patches in its vicinity. Regional sources should have a mutual distance of approximately 3 cm or more between each other to prevent crosstalk of their source waveforms.
6. Regional sources tend to provide more reliable solutions in noisy data as compared to single dipoles, because during a fit of a regional source only its location needs to be determined (no orientation has to be fitted).
7. Very often the brain responds to a stimulus with bilateral symmetrical activation. Therefore, a pair of symmetrical regional sources is often a good initial source configuration. The resulting source waveforms will then indicate if the activity is really bilateral.
8. The criterion for a good source model is not solely the residual variance. Rather, the following criteria should be met:
 - The source model should be in agreement with proven knowledge about the underlying brain activity (e.g. bilateral activation of the auditory cortex after an auditory stimulus as opposed to a single central brain area).

- The source waveforms are an important indicator for the quality of a source model: When the time course of the obtained source waveforms for a (pair of) source(s) are distinctly different from those of other sources, this indicates that the corresponding source correctly models distinct brain activity. On the contrary, when two source waveforms show nearly the same time course, it should be checked if they pick up activity of a brain region that is not part of the model, rather than truly modeling brain activity generated at their source locations.
- PCA can be helpful in determining the minimum number of sources required to adequately model the data.

What does BESA Research provide?

Although source analysis is the core of the program, BESA Research provides comprehensive and excellent tools for complete data analysis. This includes among others:

- Data review and mapping
- Preprocessing: Paradigm definition, artifact detection and correction
- Averaging
- Traditional ERP analysis
- Interactive source analysis and source imaging
- Coregistration with MRI/fMRI
- Time-Frequency and coherence analysis

It is recommended to perform preprocessing of your raw data with BESA Research, to secure that your averaged files match the quality requirements for source analysis. This is not guaranteed if you import averages from other systems.

What should you provide?

Independent of the analysis capability of the software, good analysis results also depend on the experimenter. Make sure to:

- Define the goals of your experiment/measurement
- Acquire data of appropriate quality
- Understand the basic principles of source imaging
- Utilize knowledge on brain anatomy and function
- Appreciate the limits of source localization. For example, in data with low signal-to-noise ratio, source fitting might not provide reliable results. In that case, it is preferable not to fit dipoles at all. Rather, the source model can be created by seeding dipoles or regional sources into the brain based on knowledge e.g. from anatomy or fMRI.
- Do not try to determine parameters if they cannot be estimated reliably (e.g. dipole localization in depth)

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Tutorial 5 – Source Montages

Tutorial 5 – Source Montages

What does BESA Research provide?

- ✓ Pre-defined source montages
- ✓ Resting state montages
- ✓ User-defined source montages

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Tutorial 5 – Source Montages

The present chapter will introduce the concept of source montages. In BESA Research, source montages can be created by the user, e.g. by a fitting process or by placing sources in regions of interest. Alternatively, it is possible to use pre-defined source montages.

Source montages (Scherg et al., 2002) are especially useful for reviewing high density data. They are provided to facilitate the detection of focal source processes in the brain by reversing the overlap from different brain regions seen at the scalp. If brain activity is focal, i.e. represented predominantly in one source waveform, a large amount of the recorded scalp activity reflected in this trace will originate in the related brain region. If source activity is distributed over several traces, the origin is likely to be more widespread or in areas not precisely modeled by the combination of sources in the selected source montage. Each channel in a brain source montage can be viewed as a 'gross virtual electrode' placed onto a particular brain region. Using either pre-defined or user defined source montages allows to evaluate data at the source level, rather than sensor level. This transition allows for in example allows for faster and more precise epilepsy assessment (Beniczky et al., 2016; Rodin et al., 2004). It may allow for observation of brain physiology that is not clearly visible with the traditional approach and might be helpful to monitor activity in deep brain structures where it is not possible to use classical montages (Scherg et al., 2002). Source montages are highly beneficial for connectivity studies as well (see Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming).

The resting state montages are a special case of pre-defined source montages. Resting state network nodes are well-established in fMRI studies (Damoiseaux et al., 2006) and have been related to functional patterns in many publications over the last years. In BESA Research the resting state montages contain regional sources in brain regions associated with the Default Mode Network – DMN (Raichle et al., 2001), fronto-parietal task control system as well as the dorsal attention system and the ventral attention system (Power et al., 2011). They allow investigating resting state EEG and MEG data in a swift and straight-forward manner. They can be also used to compare EEG data directly with fMRI results (Rusiniak et al., 2018).

More details about how these pre-defined montages were created can be found in the BESA Research help documentation.

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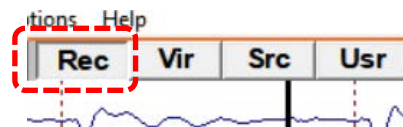
Tutorial 5 – Source Montages

A. Pre-defined Source Montages

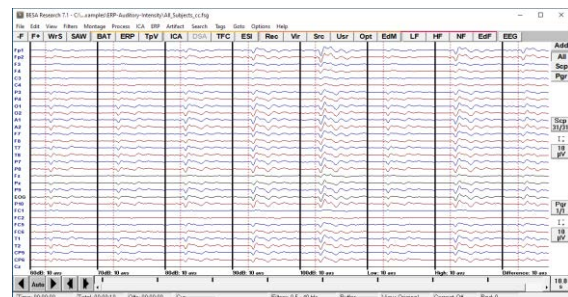
1. The file **All_Subjects_cc.fsg** should still be open. If it isn't, open it from your recent file list: **File / Recent Files...**



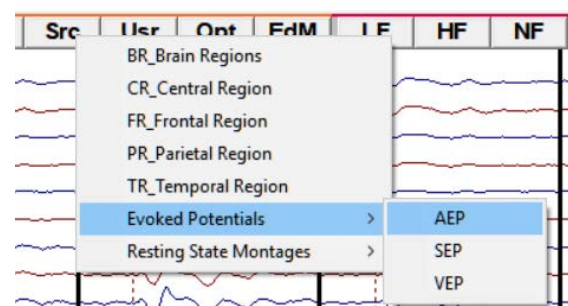
2. Make sure the button **Rec** is pressed to display the original recorded data.



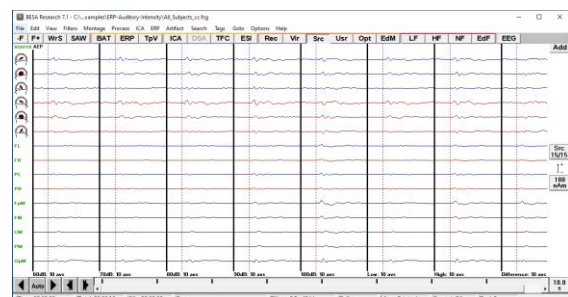
3. From what we see on the screen at the moment, we cannot infer which brain regions might be responsible for creating the evoked potentials that can be seen across all electrodes.



4. We will now load a source montage that is part of the BESA installation and was created for auditory evoked potentials. Press the **Src** button and select **Evoked Potentials / AEP**.



5. Now the sensor-space data are automatically translated on the sources in the source montage. As discrete sources have good separation properties we can immediately see that activation is not distributed over all channels any longer but mainly reflected by the temporal sources. You might notice that some sources are displayed with a head scheme, while others only

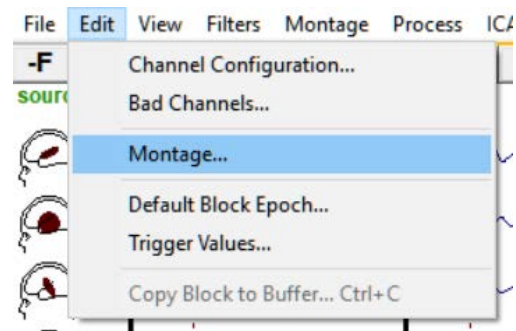



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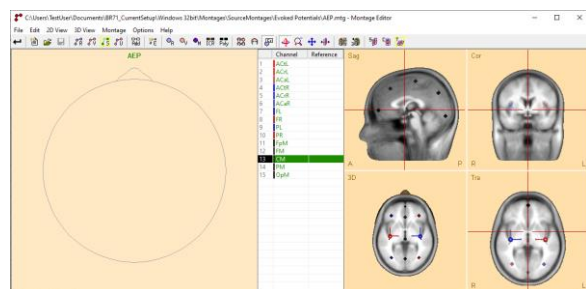
Tutorial 5 – Source Montages

have a label. We want to look at the montage in more detail to find out why.

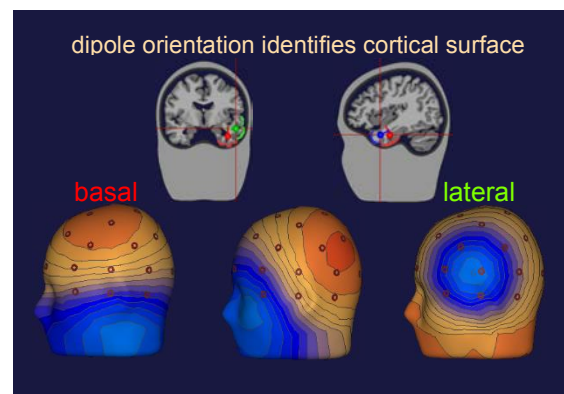
- Press **Edit / Montage** to open the montage editor window. The current montage will automatically be loaded.



- In the montage editor window press the **button**  to display a multiple head view. The sources are listed in the middle panel. Have a look at the different sources by clicking on the label.



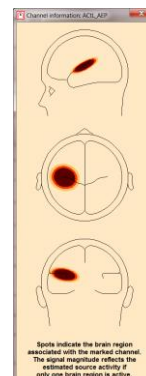
- You will note that the first 6 sources are single dipoles with an orientation while the other sources are regional sources that have not been oriented. The idea behind this montage is that it was optimized to model auditory data. Therefore, the auditory cortex sources have an orientation to reflect activity in the different major temporal lobe surfaces (see graphic), while the regional sources were placed to increase the sensitivity of the auditory cortex sources. Thus, any activity that does not originate in the temporal lobe will be projected on the regional sources.



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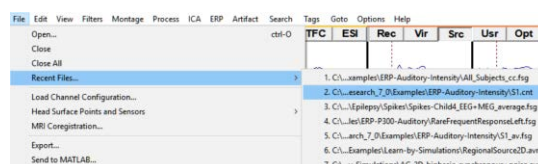
Tutorial 5 – Source Montages

9. Close the montage editor window and **right-click** on the first of the head schemes on the left of the main window. A window will pop up that displays the cortical area that is covered by the according source. You can view the associated brain regions of all sources displayed on the left of the main window.

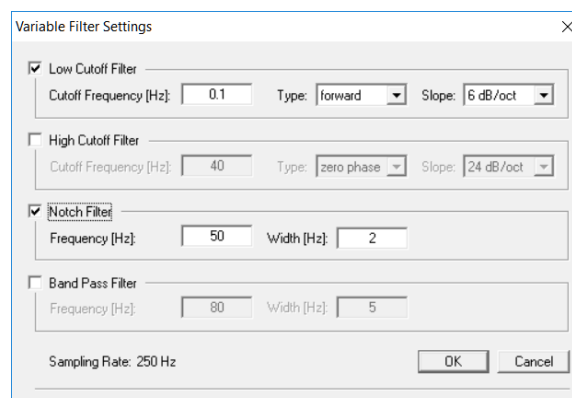


10. Note that BESA Research provides predefined source montages for auditory, somatosensory and visually evoked potentials as well as montages for central, frontal, parietal and temporal brain regions. The according brain regions are modeled by oriented dipoles, while the regions that are not of interest are modeled by un-oriented regional sources. The source montage BR_Brain Regions does not contain any oriented dipoles and was designed to get a quick overview about activity in the whole brain. Note that source montages can not only be applied on average data to get a quick impression about the active sources. Their particular strength is that they can be applied on raw data. We will do this in the next step.

11. We will return to the dataset **S1.cnt** of the auditory intensity experiment that should still be available in your recent file list: **File / Recent Files...**



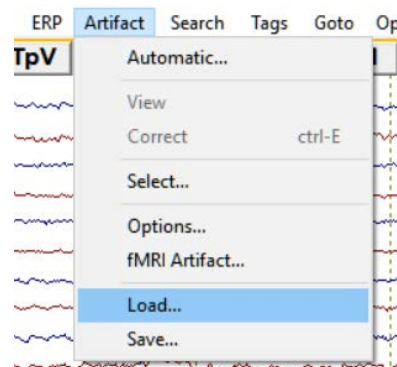
12. Next, we will filter to the data by pressing the **EdF** button or (**Filter / Edit Filter Settings**). Define a Low Cutoff filter of **0.1 Hz, forward, 6 dB/oct** and a notch filter of **50 Hz, Width: 2**.



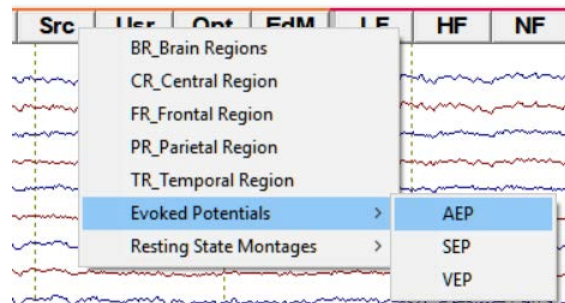
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Tutorial 5 – Source Montages

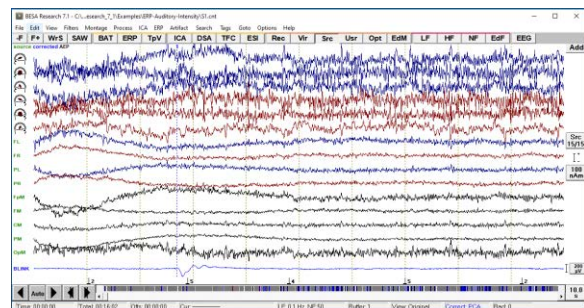
13. Now we will load the artifact definition file that contains the blink information we created earlier. Press **Artifact / Load** and select the file **S1.atf**. Make sure the artifact correction is switched on (a blue corrected should be displayed in the top left corner of the main window).



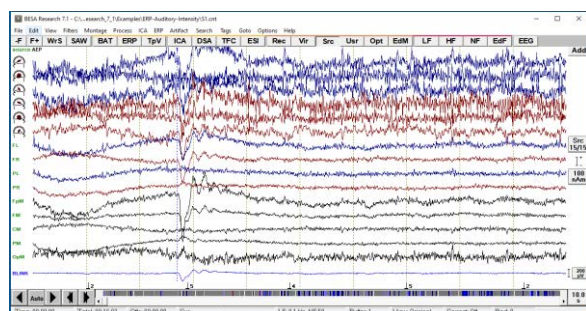
14. We will now apply the source montage **AEP** again by pressing the button **Src** and selecting **Evoked Potentials / AEP**.



15. Again, we immediately see – even in the raw data! – that the majority of variance in the data is produced by temporal lobe sources.



16. Make sure you are in the first screen and switch off artifact correction by pressing **ctrl-E**. Note that a large signal now appears in the frontal sources (mainly FpM). Also note, how the eyeblink has an effect on auditory cortex sources. This demonstrates the necessity to control eye artifacts by either rejecting them or correcting them. Switch



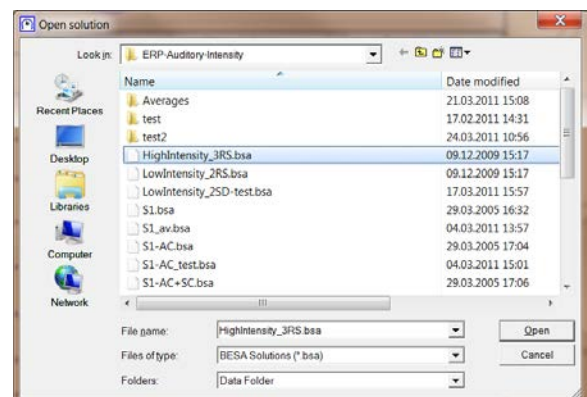
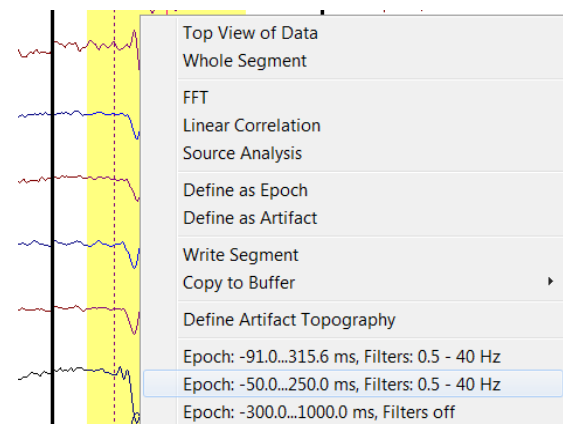
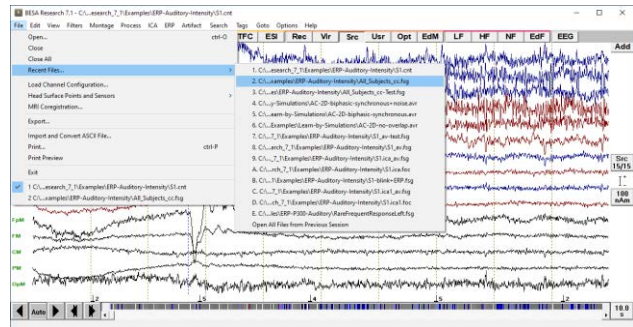
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Tutorial 5 – Source Montages

correction back on by pressing **ctrl-E** again.

B. Creating a source montage

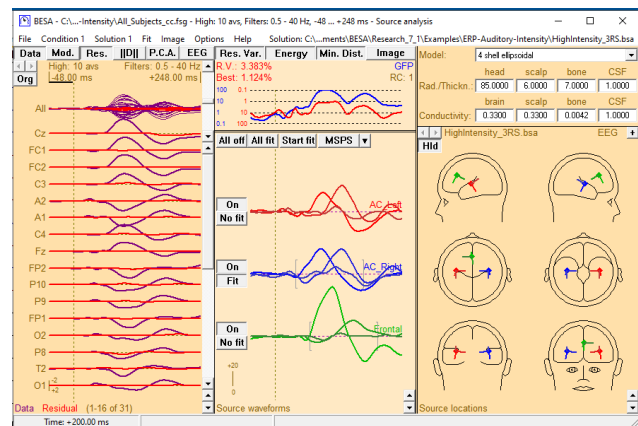
1. We will now create our own source montage based on the source model we created using the grand average data of the auditory intensity experiment. Return to the dataset **All_Subjects_cc.fsg** that should be available in the file menu. If it isn't, open it from your recent file list: **File / Recent Files...**
2. Select condition High, **right-click** and send it to **source analysis** with settings **-50 to 250 ms**, a Low Cutoff filter of **0.5 Hz**, **forward**, **zero-phase**, **12 dB/oct.** and a High Cutoff filter of **40 Hz**, **zero-phase**, **24 dB/oct.**
3. Open the source solution we created earlier on in step D of Tutorial 4. Press **File / Open Solution** and select the file **HighIntensity_3RS.bsa**.



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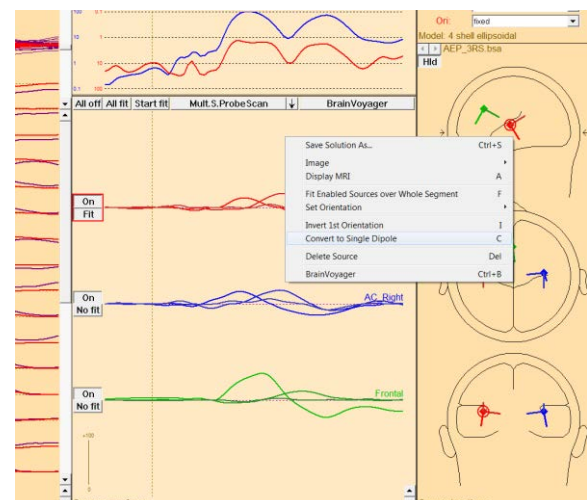
Tutorial 5 – Source Montages

- We will use this source model as a source montage for our raw data. In the present case, this source model is sufficient, but when data are very noisy, it is advisable to add probe sources to the model.



Remember that activity in any brain region that is not modeled by a regional source will be projected on the sources of interest. I.e. any noise or unsystematic brain activity that is not related to the stimulation would be projected on our three sources.

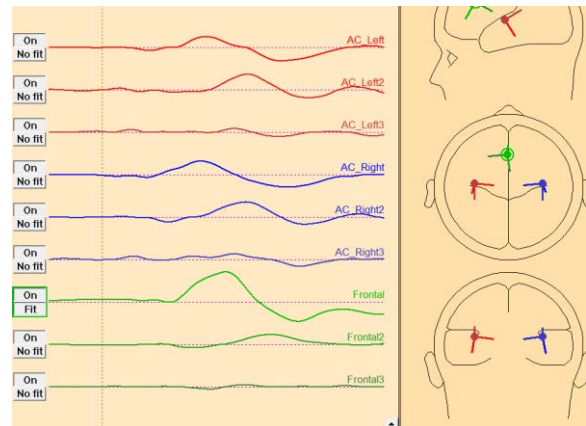
- As we are interested in auditory cortex activity and activity in the frontal area that becomes active in the high intensity condition, we need to make sure that BESA uses oriented sources in the source montage. In order to make the orientations of the auditory cortex and frontal sources available for the source montage, we need to convert the according sources to single dipoles. Select source **AC_Left** in the head schemes, **right-click** and press **Convert to Single Dipole**.



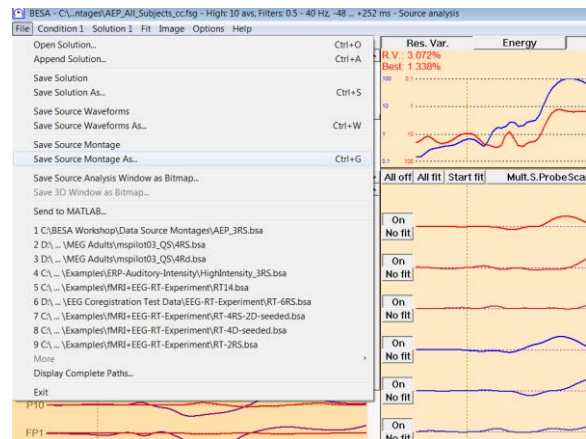
BESA® Research 7.1

Tutorial 5 – Source Montages

- You will now see three individual traces for AC_Left, AC_Left2 and AC_Left3. They correspond to orientation 1 to 3 of the regional source. **Repeat** the previous step for source **AC_Right** and **Frontal**.



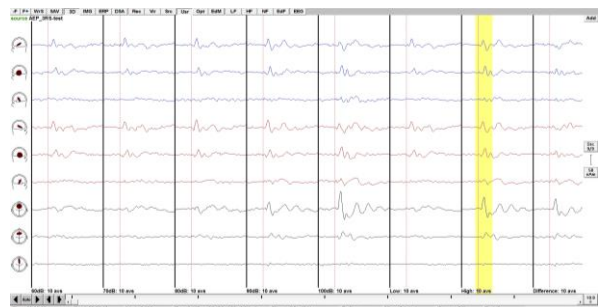
- Save the source montage by pressing **File / Save Source Montage As...** and specify the name **HighIntensity_3RS-test.mtg**. Close the source analysis window. Press **OK** to terminate without saving the source solution.



Note that the created source montage is only available for datasets located in the current folder as we saved it in the data folder. To make it globally available you may save it in folder **User Montages** which is easily accessible via the **Folders** drop down list at the bottom of the save dialog.

Now we have created our own source montage for the auditory intensity condition that includes the fitted sources along with probe sources. We will now apply this montage on our grand average data and the raw data of subject 1.

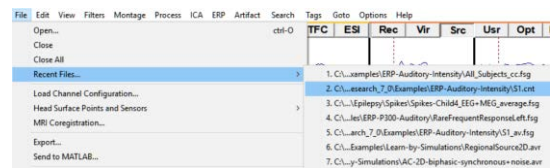
- Return to the main window. The newly generated source montage was already applied to the grand average data. Please note that the activity increase from 60 to 100 dB in the frontal source can clearly be observed using this montage.



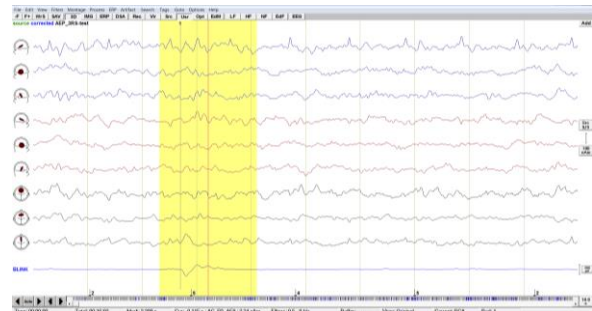
BESA® Research 7.1

Tutorial 5 – Source Montages

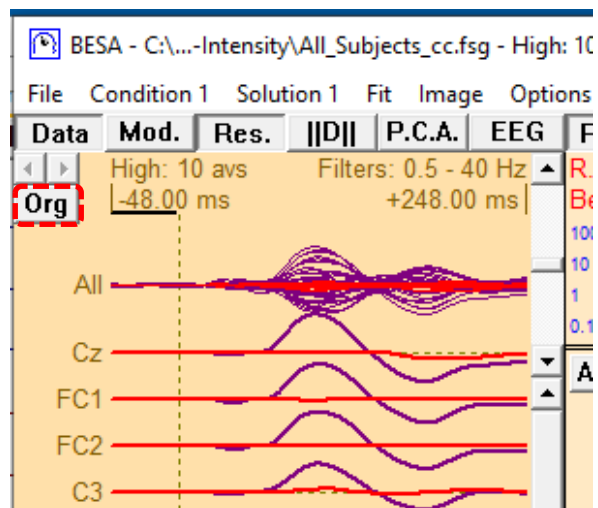
9. We will now return to the raw data of subject 1 (**S1.cnt**). It should still be available in your recent file list: **File / Recent Files...**



10. Press the **Usr** button and select our source montage **HighIntensity_3RS-test**. We will use this source montage later on for coherence analysis.



11. **Note** that the source montage was created based on the current channel configuration. BESA Research automatically checks if a source montage is matching the current data channel configuration. If not, the particular source montage will be not available. It is possible to create a source montage that can be loaded for any EEG channel configuration. To do so you need to press the **Org** button in the left top corner of the channel waveforms window to switch from original montage to Standard 81 channel montage (the button should display **Std**). When a source montage is saved now it will be available for all datasets (as long as they have EEG sensor type).



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Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

What does BESA Research provide?

- ✓ Automated MRI segmentation (in BESA MRI) using T1 and optionally T2 sequence data:
 - Loading MRIs in DICOM, NIFTI or ANALYZE format
 - Guided definition of landmarks for AC/PC and Talairach transformation
 - Automatic inhomogeneity correction
 - Automatic segmentation of skin and cortex
 - Automatic setup of 4-layer FEM model (skin, skull, CSF, and brain)
 - Automatic setup of 3-layer BEM model (skin, skull, and brain)
- ✓ Co-registration with and without individually digitized electrode positions
- ✓ Display of individual cortex and skin in source analysis window
- ✓ Source Localization with Individual Head Model (FEM/BEM)

A. Introduction

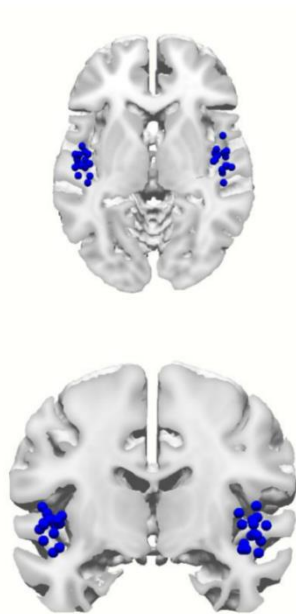
Co-registration of EEG and MRI data allows mapping a source position to an actual cortical area. Without co-registration it can only be roughly estimated, which cortical area a certain x-y-z position corresponds with. Further, individual anatomy can be used for seeding sources or verifying source localizations.

When EEG and MRI data are co-registered using BESA Research and BESA MRI, data are transformed into a coordinate system, which is based on internal landmarks of the individual subject. First, a transformation into the AC/PC (anterior / posterior commissure) coordinate system is performed. Data are then transformed into standard Talairach space. This ensures that the same standard coordinate space based on individual anatomical landmarks is used when different subjects are compared.

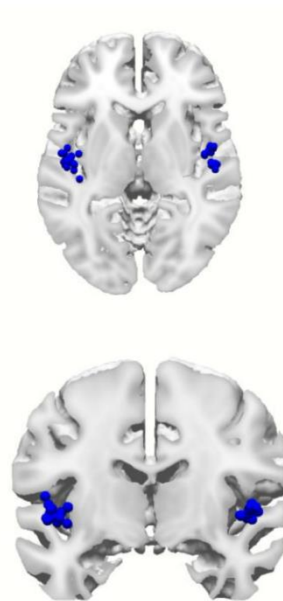
Using the same standard coordinate space based on **internal landmarks** is *essential* when source localizations are to be compared across several subjects:

- a. between two groups of subjects (e.g. patients vs. control subjects)
 - Anatomy can vary considerably between subjects and a different x-y-z localization in two people can still be in the same anatomical region. Not taking individual anatomy into account when constructing the coordinate system would disregard this fact.
- b. at two measurement time-points within the same group of subjects (e.g. pre vs. post treatment, test vs. retest)
 - If an EEG (and more so MEG) is measured at two instances in the same subject, electrodes (MEG sensors) are likely positioned slightly differently at the two instances. Here, not taking individual anatomy into account when constructing the coordinate system can lead to higher variance in source localization within the same subject.

PAN



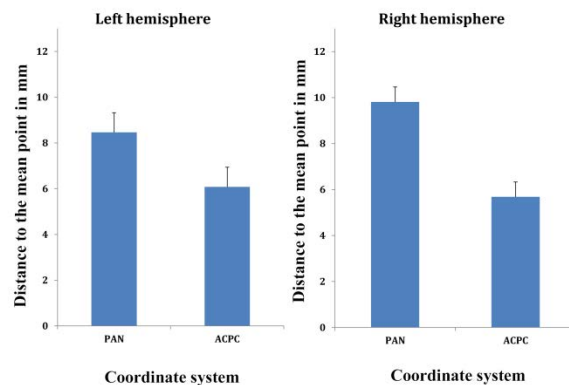
ACPC



The above image illustrates the variance of Heschl's gyrus positions across 15 subjects. The PAN (PreAuricular points + Nasion) coordinate system is based on the fiducials only without using any internal landmarks. The same positions are displayed in the AC/PC coordinate system on the right. It is apparent that the variance across subjects is greatly reduced merely by using internal landmarks when defining the coordinate system.

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

The reduction in variance using the AC/PC coordinate system compared to the PAN is statistically significant (see image on the right). The effect is particularly prominent in the right hemisphere ($p < 0.0001$), but also apparent in the left hemisphere ($p < 0.05$). This illustrates that it is important to use the individual anatomy for defining the coordinate system whenever possible.



Usually, good co-registration depends on digitized electrode positions to precisely fit the measured electrodes to the skin of the subject (as segmented from the MRI). Using BESA Research and BESA MRI it is possible to co-register EEG with MRI data even if no individual electrode positions were digitized as long as there were some electrodes that coincide with positions of the standard 10-10 system. The idea is that if some standard electrode positions are known in a subject, positions of other electrodes of the 10-10 system are also known and can be used for co-registration purposes only (not for any signal analysis). This procedure makes co-registration much more precise than only relying on fiducial positions.

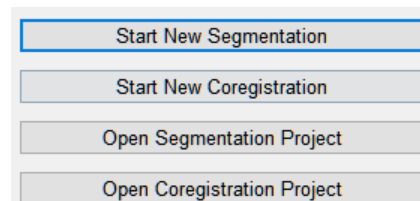
Before starting the co-registration, MRI data must be segmented. The segmentation in BESA MRI is fully automatic after setting up anatomical landmarks. Entire procedure is described below.

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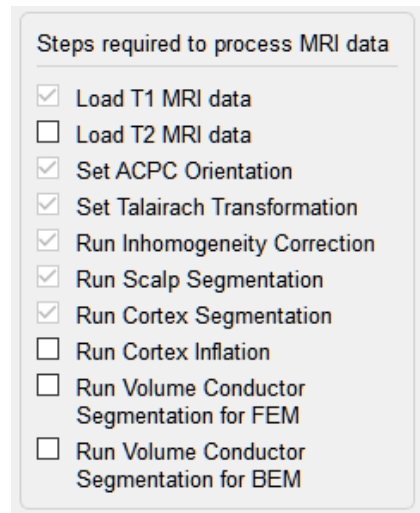
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

B. MRI segmentation

1. Start the **BESA MRI** program and press **Accept** on the welcome screen. Press the **Start New Segmentation** button in the interaction window

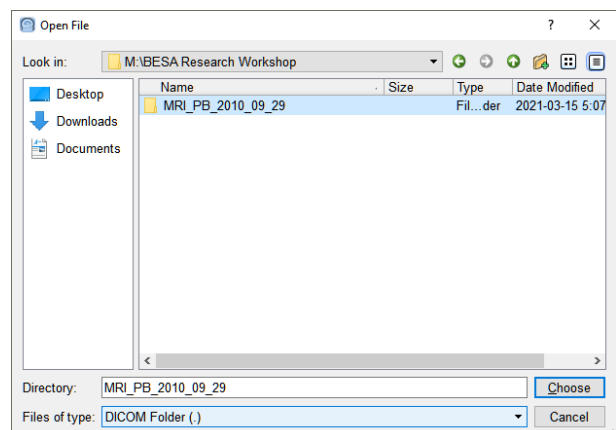


2. In the next screen additional features can be added, like Cortex Inflation or Volume Conductor Segmentation. Press **Next** button to proceed to the next screen.



Tip: A T2 sequence can be also added to improve the quality of segmentation. Please read the BESA MRI manual for further details.

3. Press **Load T1 Data** in the interaction window. A new dialog box will be opened. Navigate to folder **MRI_PB_2010_09_29**⁷ and then change the **Files of type** to **DICOM Folder (.)**. Select the **MRI_PB_2010_09_29** folder and then press **Choose**.

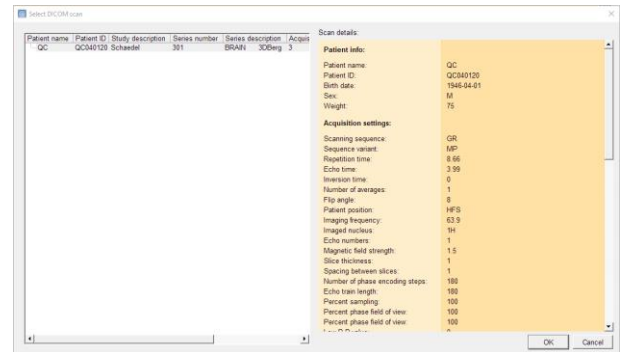


⁷ The folder will be provided by the presenter during the tutorial.

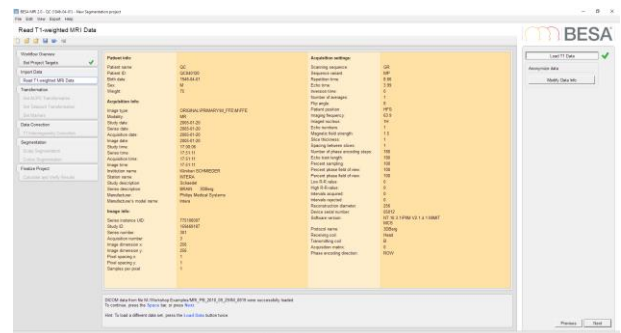
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Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

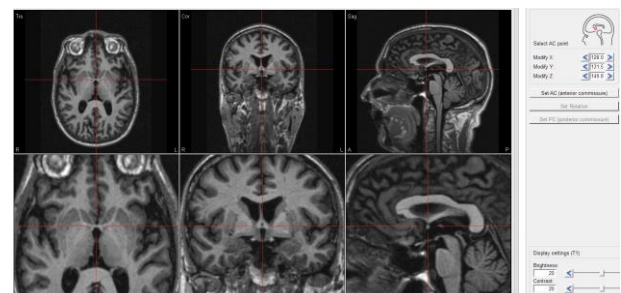
- In the next displayed window, the MRI series detected in the folder will be presented. For this particular case only, the sequence named **BRAIN 3DBerg** is available. On the right part of the screen, you will see the series details. Press the **OK** button to advance.



- Now the main window of BESA MRI is filled with MRI acquisition details that were read from the DICOM header. Note that there is a green checkmark beside the button **Load T1 Data**. Press the **Next** button to proceed to the next step.

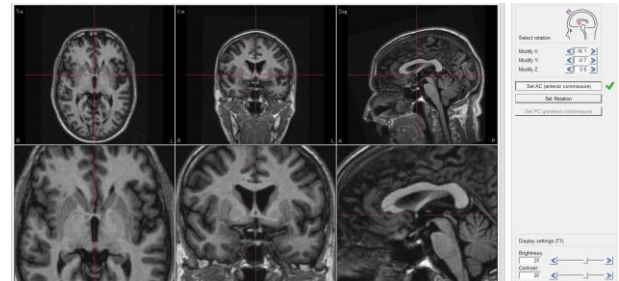


- Mark the **anterior commissure (AC)** point on the MRI slices using the crosshair. The bottom views provide higher detail for easier navigation to the correct location. Note the head schematic image in the interaction window that shows the rough location of AC. Press **Next** to continue.

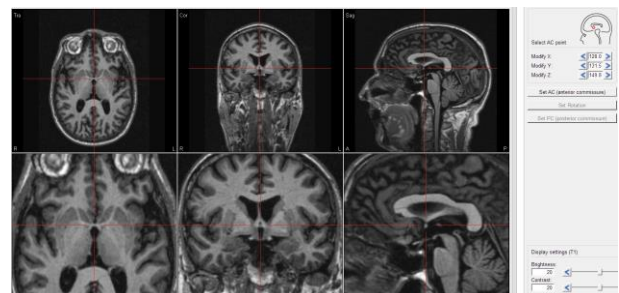


Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

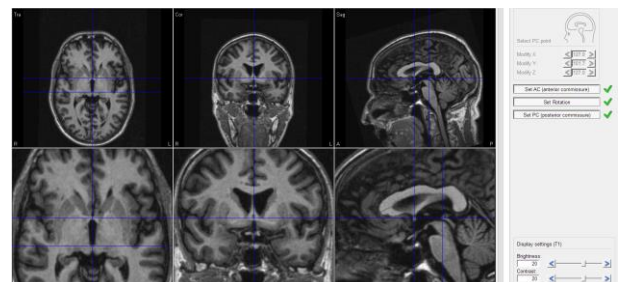
7. **Set rotation** of MRI slices by placing the mouse in the bottom views and dragging the cursor to the desired position while the left mouse button is pressed. Start with the left view (coronal) to align left and right hemisphere. The rotation should be set such that axial and coronal view are symmetric; in the sagittal view, the rotation is set such that commissures are aligned horizontally (both visible in the coronal view). Press **Next** to continue.



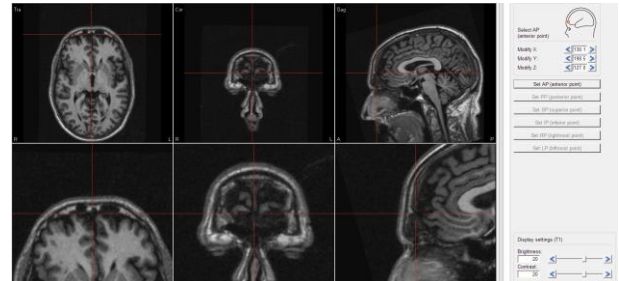
8. **Mark the posterior commissure (PC) point** on the MRI slice using the crosshair. Press **Next** to continue.



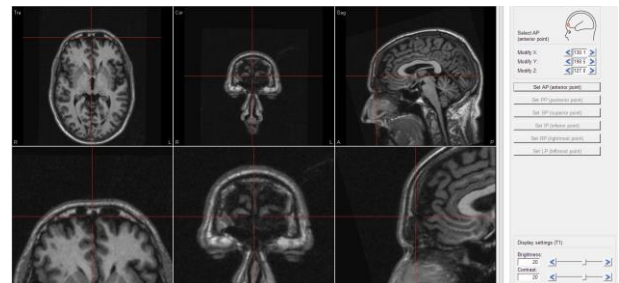
9. Review if all landmarks' definitions (shown as blue lines) are correct and press **Next** to continue if so. Press **Previous** if you need to make any adjustments.



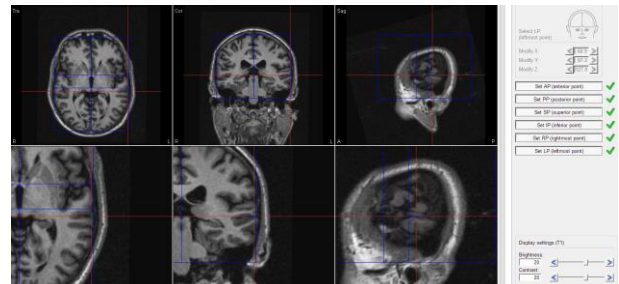
10. Mark the **anterior point (AP)** on the MRI slice using crosshair. Note the head schematic image in the interaction window that shows roughly where the AC is located. Press **Next** to continue.



11. Repeat step 10 for **posterior point (PP)**, **superior point (SP)**, **inferior point (IP)**, **rightmost point (RP)**, **left most point (LP)**. Mark **anterior point (AP)** on the MRI slice using the crosshair. Note the head schematic image in the interaction window that shows roughly where each landmark is located. Press **Next** to continue.



12. When all points are defined you can again review them (note green checkmarks beside the buttons). The brain should be inscribed in a blue box. Press **Next** to continue.

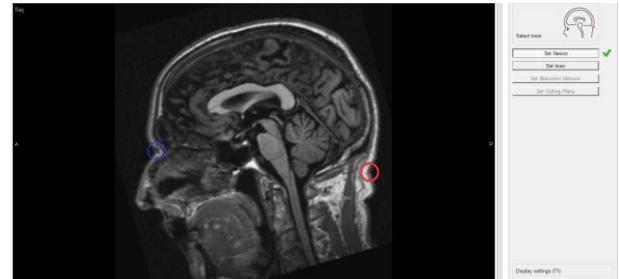


13. Mark the **nasion** on the sagittal slice as indicated in the head scheme. Press **Next** to continue.

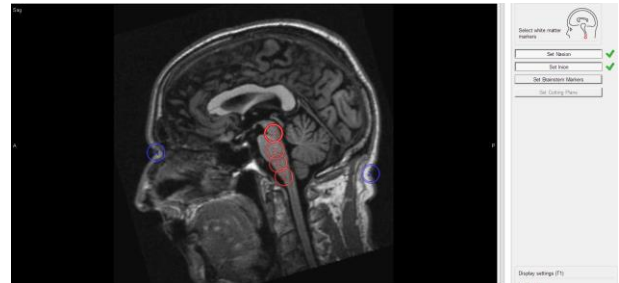


Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

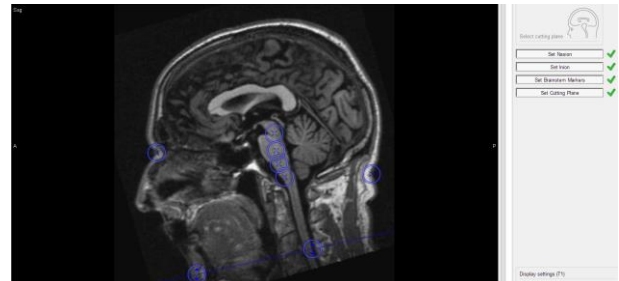
14. **Mark the inion** on sagittal slice as indicated in the head scheme. Press **Next** to continue.



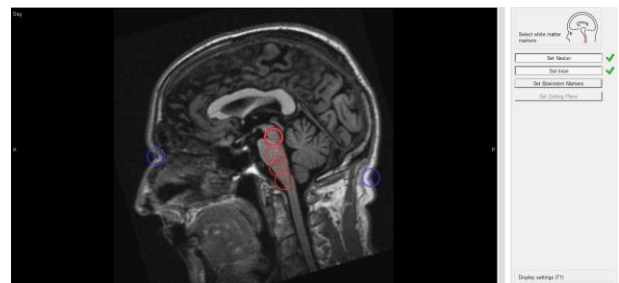
15. **Mark 3-5 Brainstem markers** on the sagittal slice as indicated in the head scheme. The markers have to be located within the brainstem, but there is no rule about exactly where to place them. Press **Next** to continue.



16. When all points are defined you can again review them (note green checkmarks beside the buttons). Press **Next** to continue.



17. Finally **set cutting plane** on the sagittal slice as indicated in the head scheme. Dragging the left arrowed circle moves the cutting plane up and down, dragging the right one changes the angle. Set the cutting plane such that it includes visible MRI data; the inion needs to be above the cutting plane. Press **Next** to continue.



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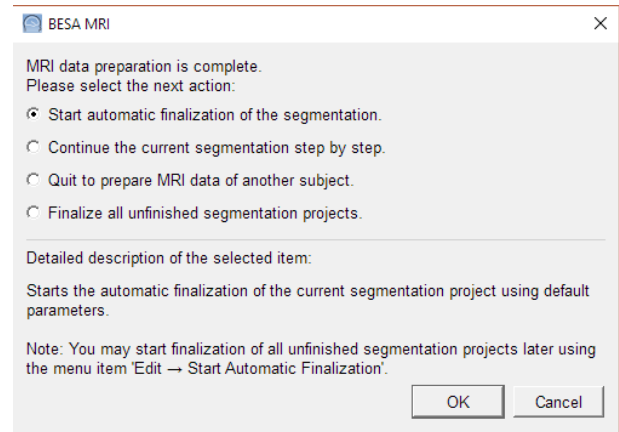
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

18. A new window will pop up. Here you can decide whether you want to:

- Start automatic segmentation
- Perform step by step segmentation
- Quit to prepare another subject
- Finalize all unfished projects

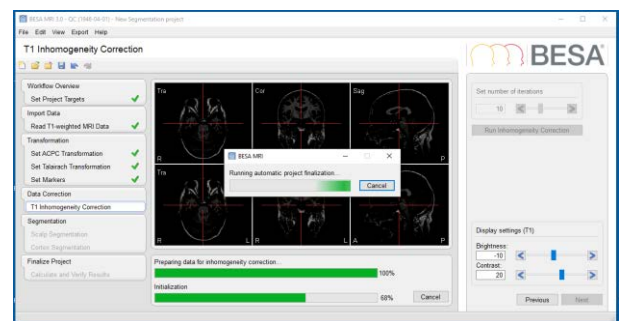
By default, the **first option** is selected.

Press **OK** to start segmentation.

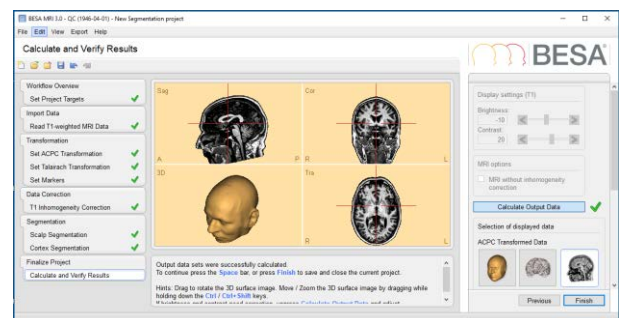


Note: This process may take a while.

During segmentation, the current step and overall progress is presented on the screen.



19. When segmentation is finished the results can be reviewed by pressing buttons in the interaction window at the right. Press the **Finish** button to save it.

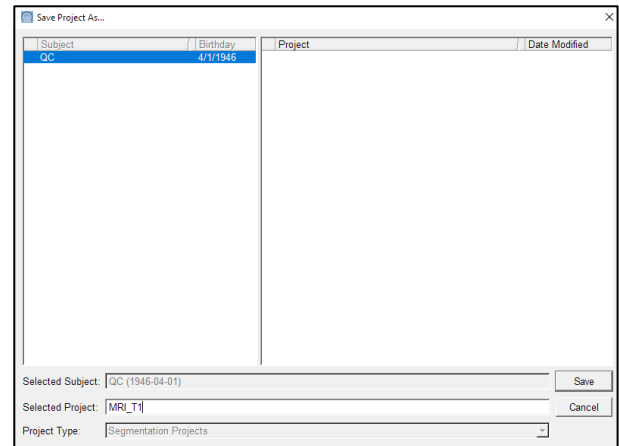


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Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

20. A popup window for saving will be displayed. Press the **Save** button to save with default settings (Project name: **MRI_T1**).

After saving the segmentation workflow will be closed. The segmentation results will now be available for co-registration.

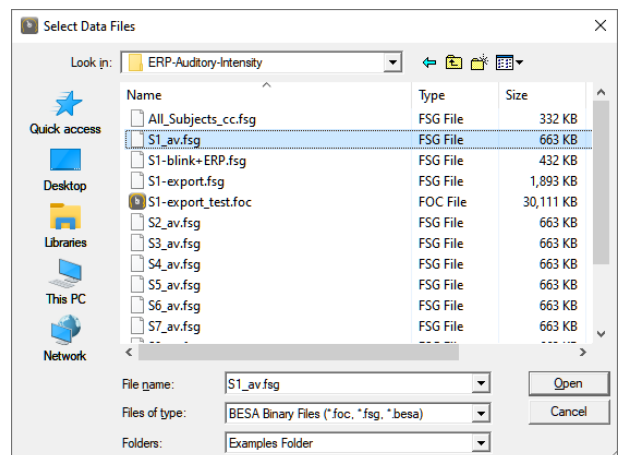


C. Co-registration of EEG and MRI data using BESA Research and BESA MRI

1. Creating electrode coordinates on the individual scalp surface by following the 10-10 EEG placement rule

In the following, we will co-register the EEG data of subject S1 (Auditory Intensity Experiment) with an MRI image by following **the 10-10 EEG placement rule**, as we do **not** have individually digitized electrodes available. Electrode coordinates can be automatically generated on the subject's scalp surface by following 10-10 placement rules in BESA MRI.

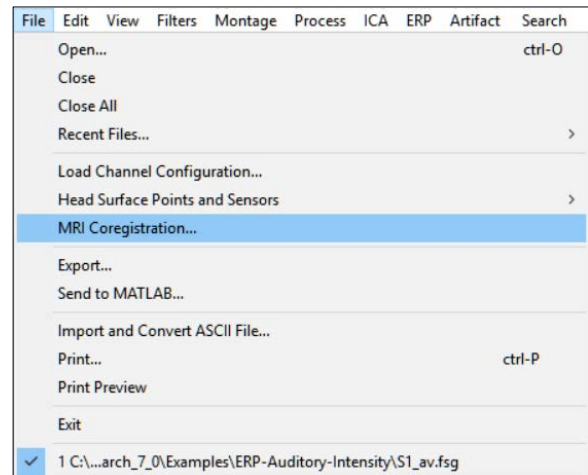
1. In BESA Research please **open** the example dataset **S1_av.fsg** (located here: **C:\Users\Public\Documents\BESA\Research_7_1\Examples\ERP-Auditory-Intensity**).



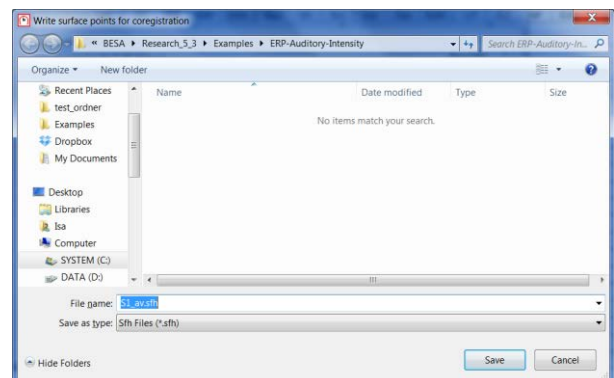
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Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

2. Press **File / MRI Coregistration**.



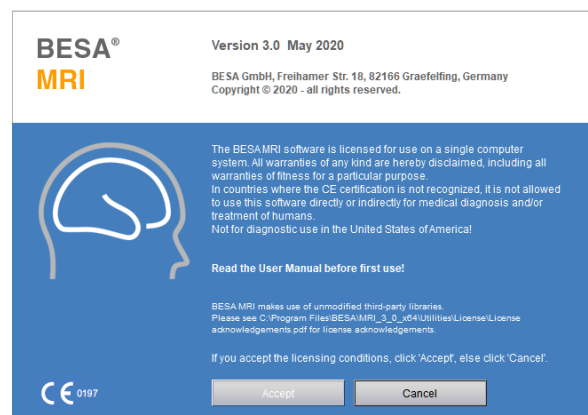
3. You will be prompted to create and save an ***.sfh** file, which will be used to store all coregistration information necessary for the interaction between BESA Research and BESA MRI. BESA Research will automatically suggest the filename of the current subject plus the extension **.sfh** (**S1_av.sfh**). Confirm the suggested name by pressing **Save**.



4. BESA MRI will open. Press **Accept** in the welcome screen.

Important: Do not close BESA Research!

Please make sure that the data folder is set to the BESA MRI Example projects folder (**File / Select Data Folder**).



BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

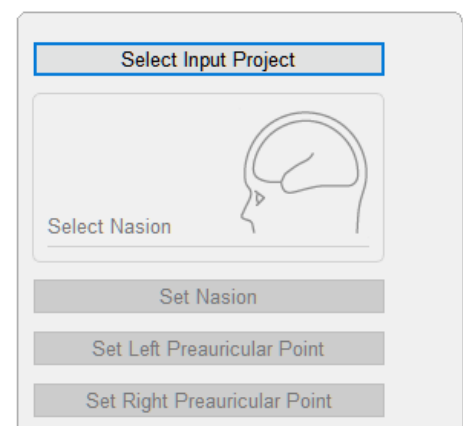
5. New coregistration project is started automatically.

Check the **Place 10-10 Electrode system** checkbox and then press **Next** on the bottom right (or hit the space bar).

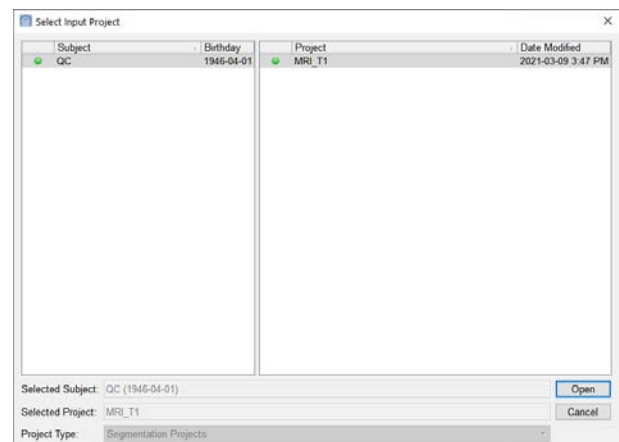
Steps for coregistration

- ☐ Skip electrode and fiducial fit
- ☒ Place 10-10 electrode system
- ☐ Generate FEM EEG leadfield
- ☐ Generate FEM MEG leadfield
- ☐ Generate BEM EEG leadfield
- ☐ Generate BEM MEG leadfield

6. Press **Select Input Project** in the interaction window.



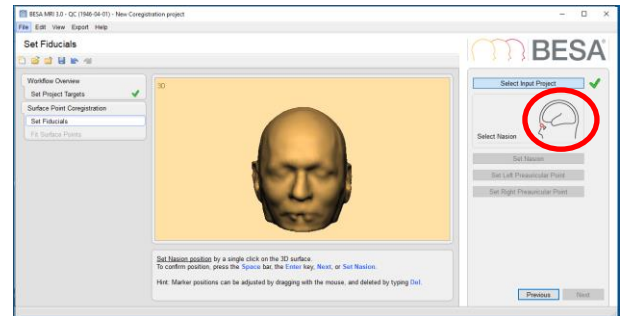
7. Choose the project **MRI_T1** of subject **QC**. Press **Open**.



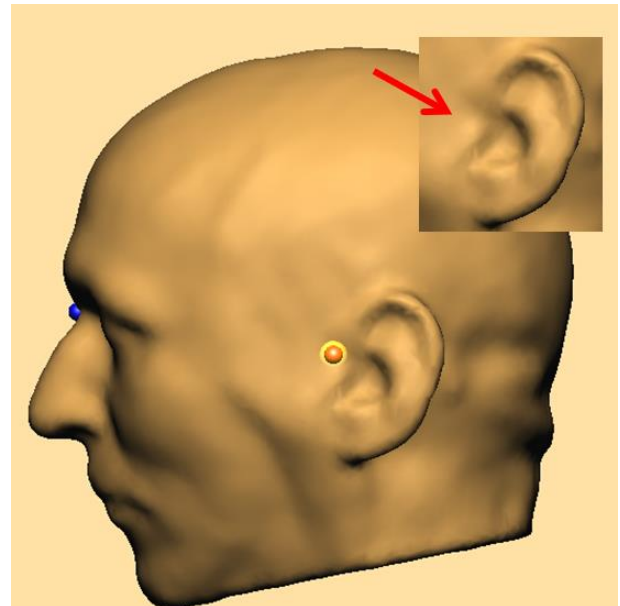
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

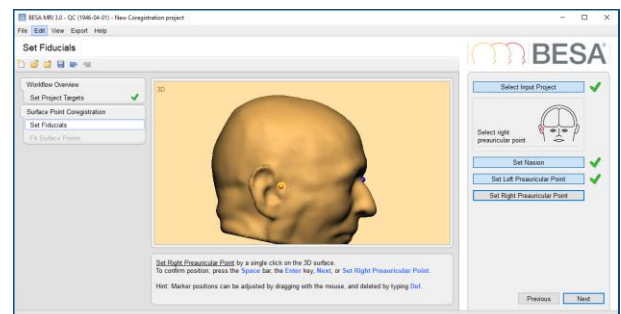
8. Mark **Nasion** on the segmented skin surfaces as indicated in the head scheme. Press **Next** to continue.



9. Mark **LPA** (Left preauricular point) as indicated in the head scheme in the interaction window. In this subject LPA position can be identified quite well by the shadow that is cast in LPA's dent. Press **Next** to continue.



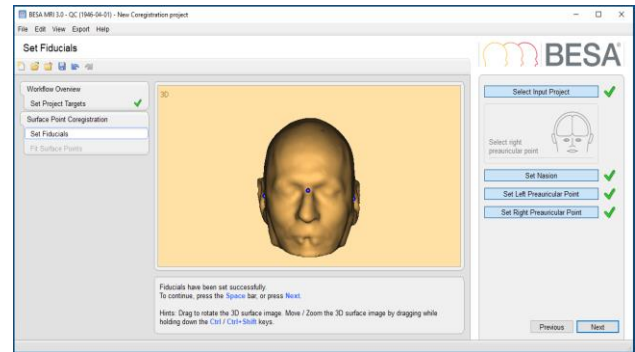
10. Mark **RPA** (Right preauricular point) and press **Next** to continue.



BESA® Research 7.1

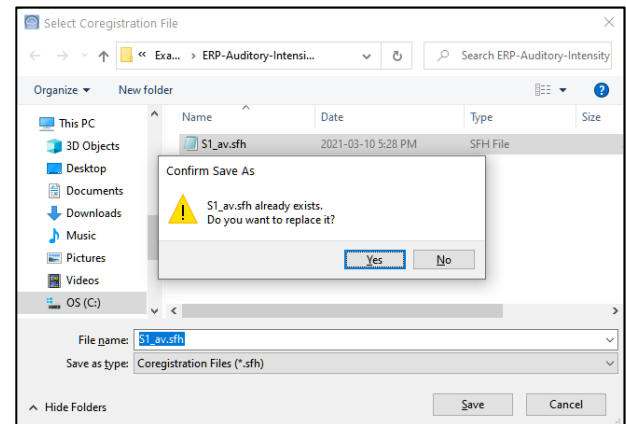
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

11. All fiducials are now positioned. Press **Next** to continue.

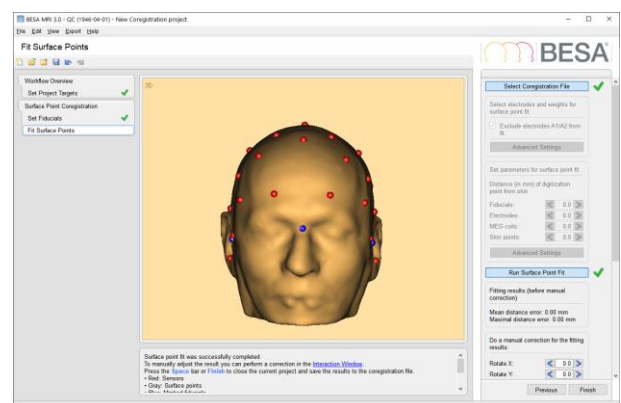


12. Press **Select Coregistration File** to load the **S1-av.fsh** file we created in the previous step. It is located in the Examples folder under Auditory Intensity. Press **Save**.

Click on the **Yes** button in the “Confirm Save As” dialog.



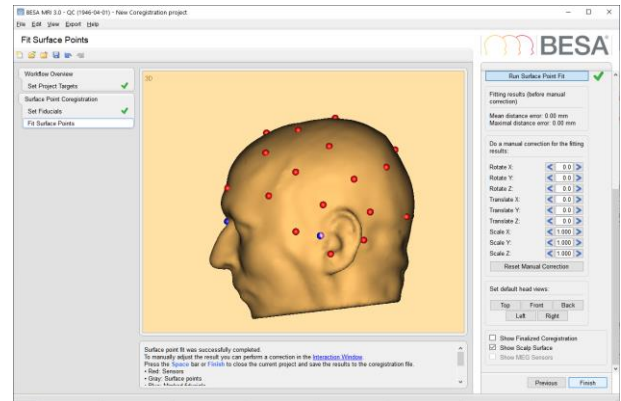
13. The electrode coordinates are automatically created on the scalp surface by following the 10-10 EEG placement rule.



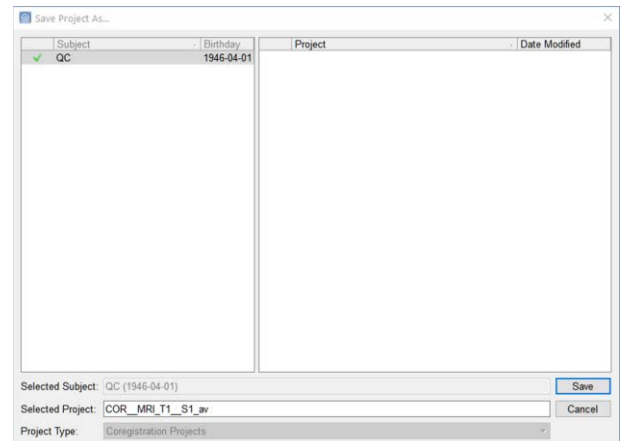
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

14. Press **Run Surface Point Fit** and then press **Finish**.



15. Please **save** the coregistration project under the suggested name.



2. (Optional section) Surface point fit using standard electrodes

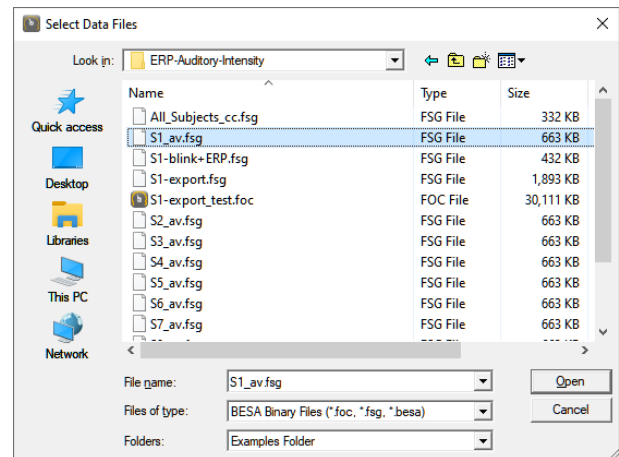
Note – this approach is recommended for EEG datasets that contains electrodes not labeled according 10-20/10-10 international system.

It is also possible to co-register the EEG data of subject S1 (Auditory Intensity Experiment) with an MRI image using **the coordinates of standard electrodes** when individually digitized electrodes information is **not** available.

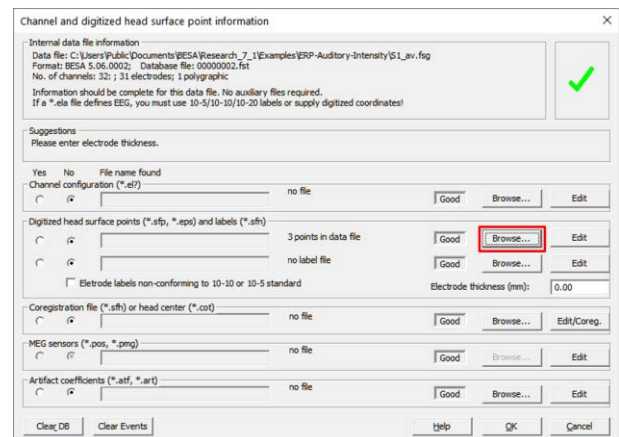
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

1. In BESA Research please **open** dataset **S1_av.fsg** (located here: **C:\Users\Public\Documents\BESA\Research_7_1\Examples\ERP-Auditory-Intensity**). Press **File / Head Surface Points and Sensors / Load Coordinate Files** (or press **ctrl-L**).

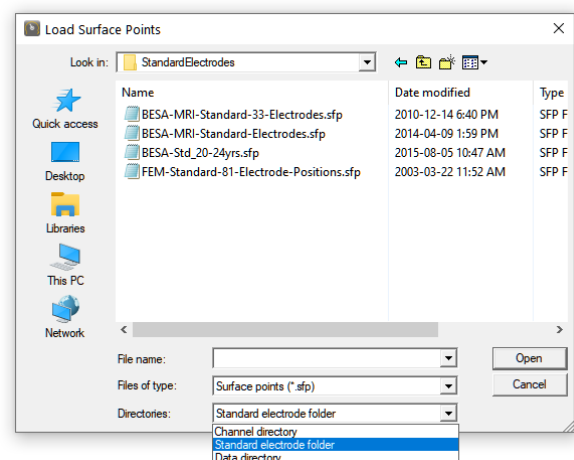


2. In the section Digitized head surface points press **Browse**.



3. Under the **Directories** drop-down list, please select the option **Standard electrode folder**.

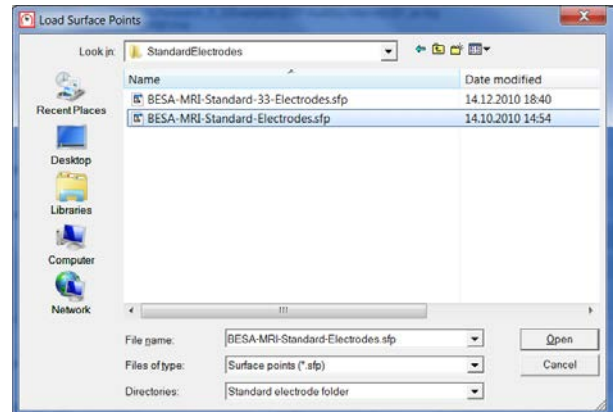
Note: In the **Channel Directory** you can find more standard channel definition for different vendors.



BESA® Research 7.1

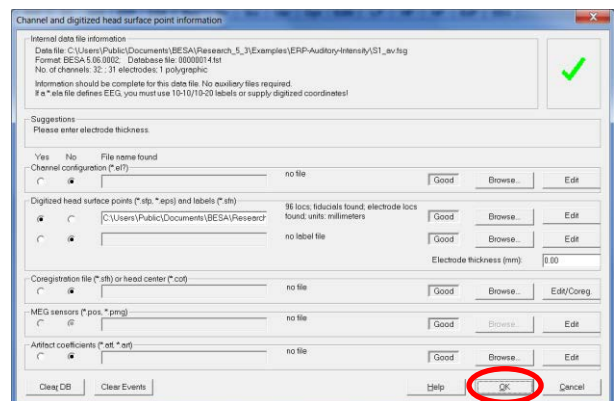
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

Select the file **BESA-MRI-Standard-Electrodes.sfp** and press **Open**. It contains 96 standard electrode positions. Some of the S1's electrode names match the labels in this standard electrode file so BESA can match them.

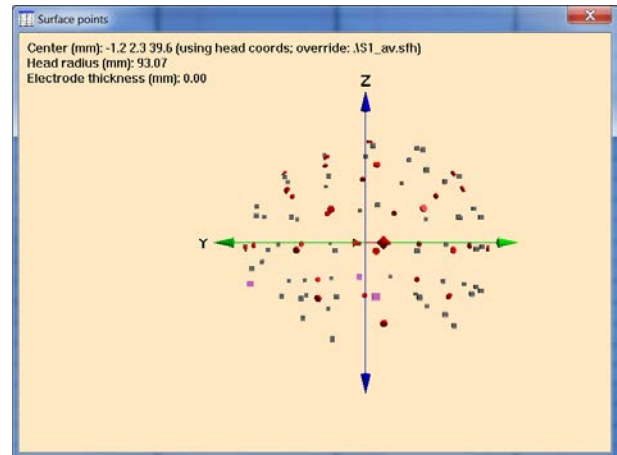


The other file (**BESA_MRI_Standard-33-Electrodes.sfp**) contains 33 standard electrode positions. It is not suitable for us as none of the electrodes that were measured in subject S1 have names that coincide with the 33 standard electrode names. Thus, BESA cannot match them.

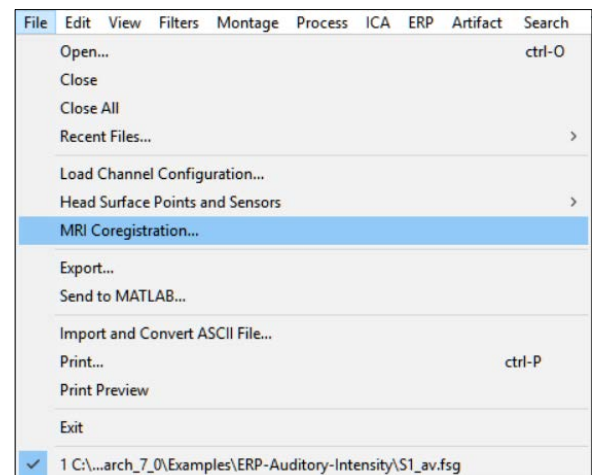
4. Press **OK** to close the dialogue.



- Press **V** on the keyboard to bring up the surface points window. The 96 standard electrodes are now displayed. Those standard electrodes whose labels coincide with S1's electrode labels are marked red. Please note that the grey standard electrode positions are merely used for better fitting the electrodes to the subject's skin. They do not carry any signal. **Close** the surface points window.

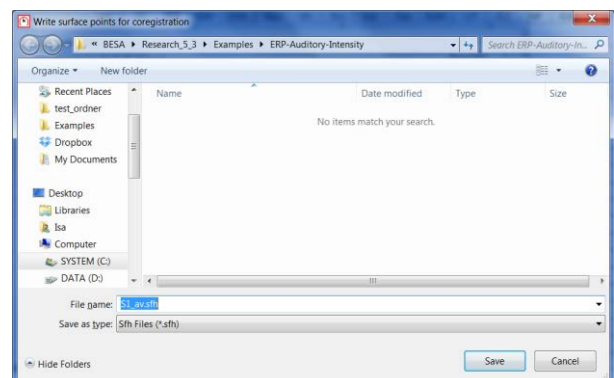


- Press **File / MRI Coregistration**.



- You will be prompted to create and save an ***.sfh** file, which will be used to store all coregistration information necessary for the interaction between BESA Research and BESA MRI. Confirm the suggested file name (**S1_av.sfh**) by pressing **Save**.

Note: If the S1_av.sfh file already exists, create new file with different file name.

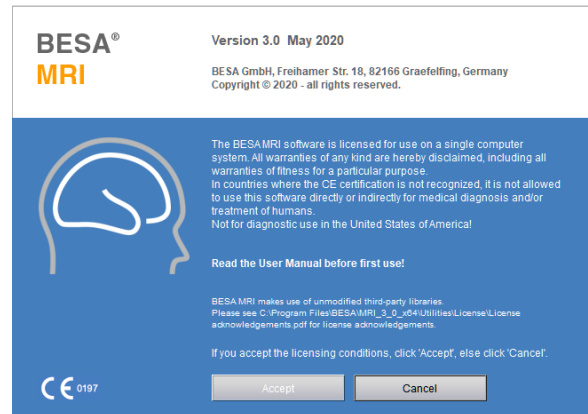


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Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

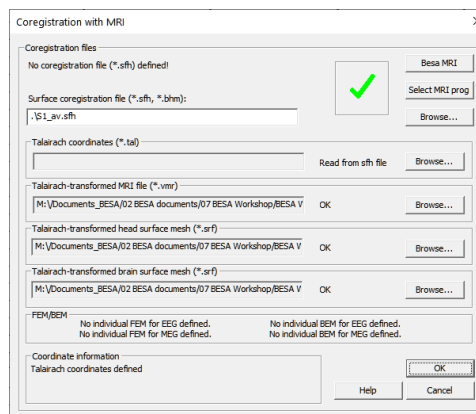
8. BESA MRI will open. Press **Accept** in the welcome screen.

The next steps are identical as described in the section C.1 of this chapter, with the difference that **Place 10-10 Electrode system** checkbox should not be checked.

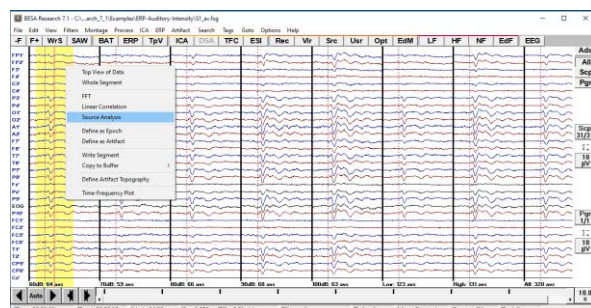


D. Utilizing the individual anatomy in BESA Research

1. Return to BESA Research. All coregistration information containing surfaces and transformations have automatically been sent to BESA Research. A green arrow indicates that all necessary information is available. Press **OK**.



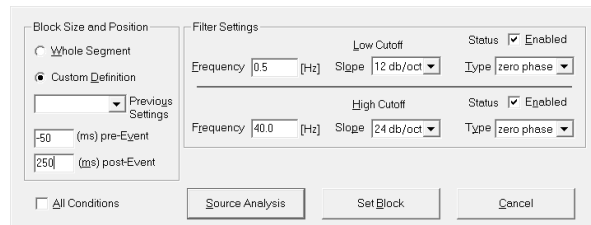
2. Send the condition **60dB** to source analysis by **left-dragging** a block, **right-clicking** and selecting **Source Analysis**.



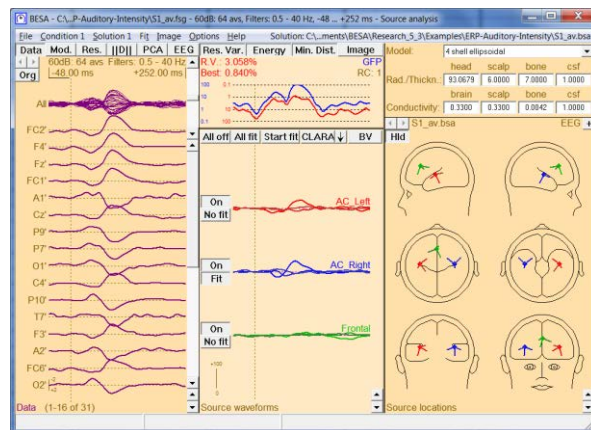
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

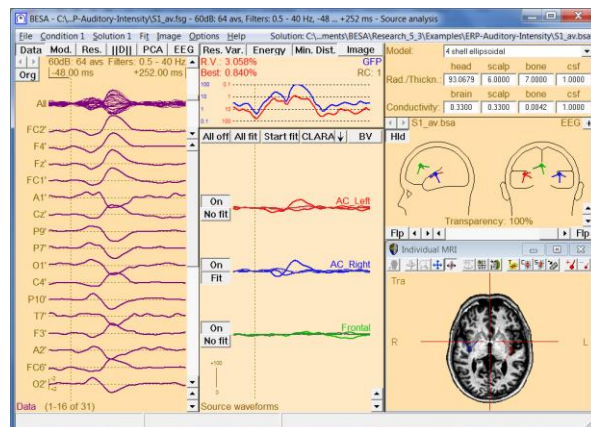
3. Select the custom definition **-50 to 250 ms**, Low Cutoff Filter **0.5 Hz**, **12 dB/Oct**, **Zero Phase**, High Cutoff Filter **40 Hz**, **24 dB/Oct**, **zero phase**. Press **Source Analysis**.



4. Our source model consisting of 3 regional sources will automatically open as we saved it per person in the batch created before.



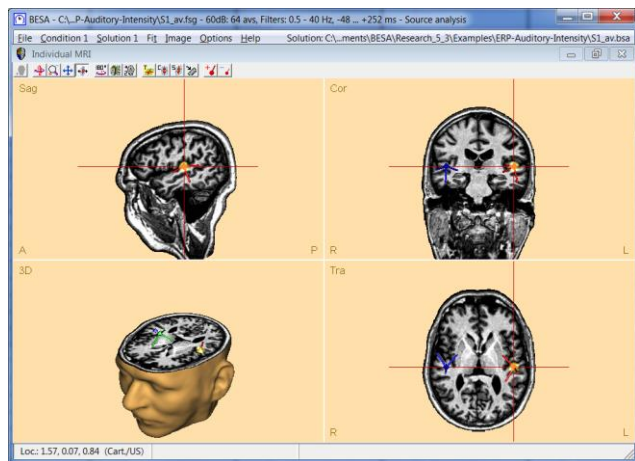
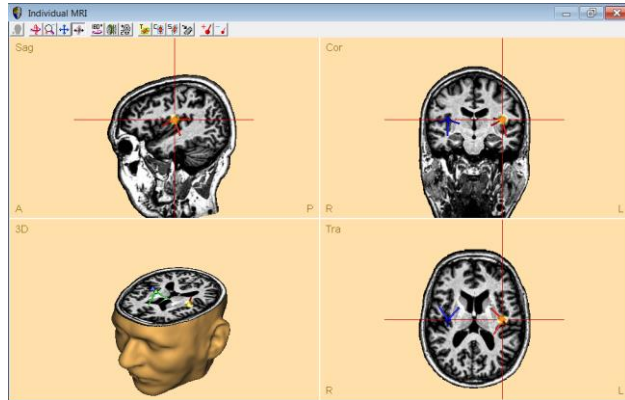
5. Press **A** on the keyboard to bring up the individual anatomy of the present subject. Since we coregistered the EEG and MRI data, the individual MRI is now available. Without coregistration, only a standard MRI can be displayed.



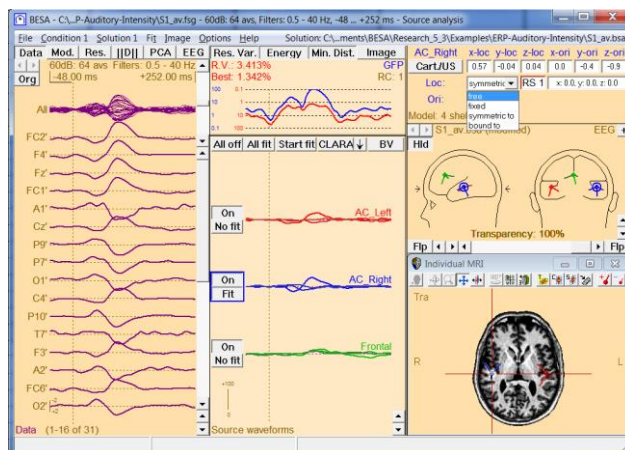
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

6. Select the first source by clicking on its source waveforms in the middle pane and enlarge the MRI window to get a better view. It can be seen that the source model we created using the grand average is located in the auditory cortex of subject S1. The model can still be optimized, however.
7. Let us first drag the red regional source to left Heschl's gyrus. You will notice that the position of the right auditory source (blue) also automatically changes position, as we imposed a symmetry constraint. We will now change this constraint back to free.



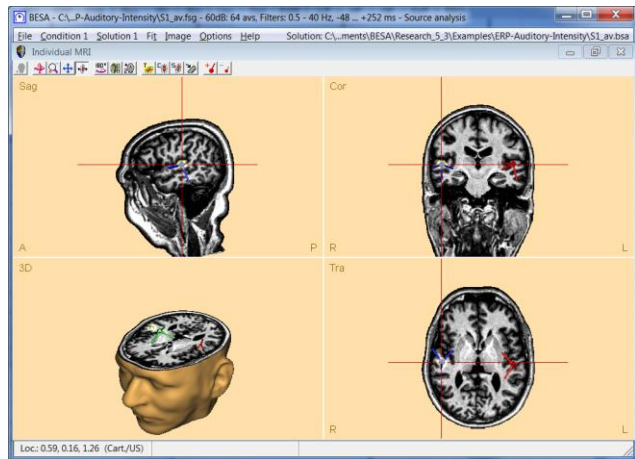
8. Minimize the MRI window and select the **blue source** by clicking on its source waveform. From the drop-down menu under **Loc** at the top right of the window please change symmetric to **free**. Maximize the MRI window again.



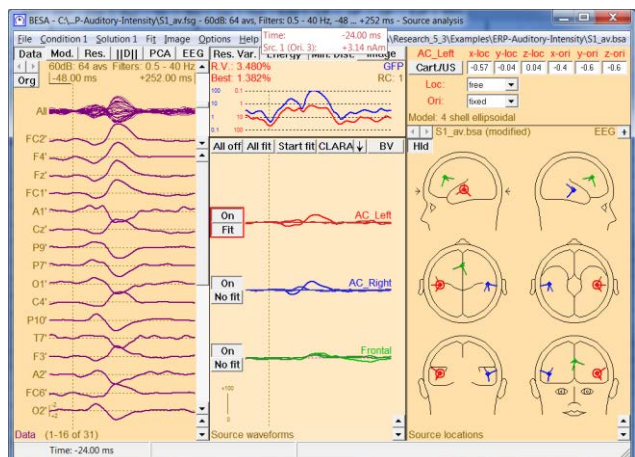
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

9. Now let us move the blue auditory cortex source to right Heschl's gyrus. We now see a slight asymmetry in this subject with the right hemispheric source (blue) located more anterior than the left-hemispheric source (red). Please close the MRI window.



10. We have now optimized the positions of the auditory cortex sources based on the subject's individual anatomy. What we still need to do is to refit the orientations of the regional sources based on the new positions. The blue source is still selected, so simply **press O** on the keyboard to set the first orientation at the maximum of the activity. **Repeat** for the red source.



We are now finished optimizing our source model based on the individual anatomy of the subject.

E. Individual Head Model (FEM/BEM) for Source Analysis - Introduction

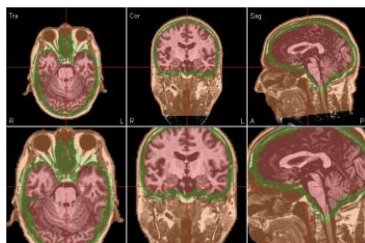
Localization precision can further be increased by using a **volume conductor** model that is also based on the individual subject's anatomy.

When is localization precision critical? For example:

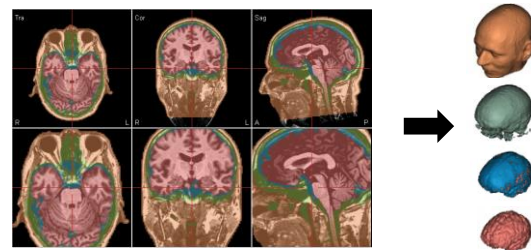
- When the precise position of a source is the leading research question
- Localization of epileptiform activity
- Comparison between patients and control subjects regarding the brain region involved in a particular cognitive task
- Investigation of treatment effects on source localization

In BESA MRI, T1 (and optionally T2) images can be used for creating individual, realistic head models using the **boundary element method (BEM)** or the **finite element method (FEM)**.

BEM



FEM



BEM modeling:

The BEM model assumes a simplified description of the head geometry on the boundaries of head tissue. A 3-layer realistic head model (scalp, skull, and brain) is created using the volume conductor segmentation in BESA MRI. To compute the BEM forward solution, BESA MRI uses the OpenMEEG (Kybic et al., 2005; Gramfort et al., 2010) which was developed within the Athena project-team at INRIA Sophia-Antipolis. The OpenMEEG is used solving forward problems in the field of EEG and MEG, and it consists of the symmetric BEM.

Individual BEM models can be used in BESA Research after coregistration has been performed in BESA MRI. In the coregistration process, BESA MRI will generate a leadfield

table, and a description of the source space. The leadfield table contains the simulated EEG potentials or MEG signals for sources in x-, y-, and z-direction distributed on a regular grid (4 mm resolution) covering the entire source space. During dipole fitting BESA Research computes the EEG potentials or MEG signals for any given dipole source employing cubic Bezier-spline interpolation.

FEM modeling:

BESA MRI creates a 4-shell FEM model (scalp, skull, brain, and CSF) also containing a CSF compartment. Each compartment is associated with a specific conductivity value: scalp 0.33 S/m; skull 0.0042 S/m; brain 0.33 S/m; CSF 1.79 S/m.

Modeling CSF is critical for source localization precision as it is yet another layer with a specific conductivity in addition to brain, skull, and scalp (Baumann et al. 1997). Ignoring CSF leads to wrong assumptions about the origin of the current (Ramon et al. 2003, Wendel et al. 2008).

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

When current flows through a volume, it will change direction whenever it passes a new layer with differing conductivity (see image on the right).

In principle, the head model can consist of even more than four layers. The skull, for example contains at least two different tissues with differing conductivities. However, this would mean that head model generation becomes more complex, less automated and more heavy on computation. Additionally, MRI data quality needs to be exceptionally good to model all the different tissue types and the combined use of T1, T2- weighted MRIs as well as CT data is vital. We will see in the following that a four-layer model leads to very good results.

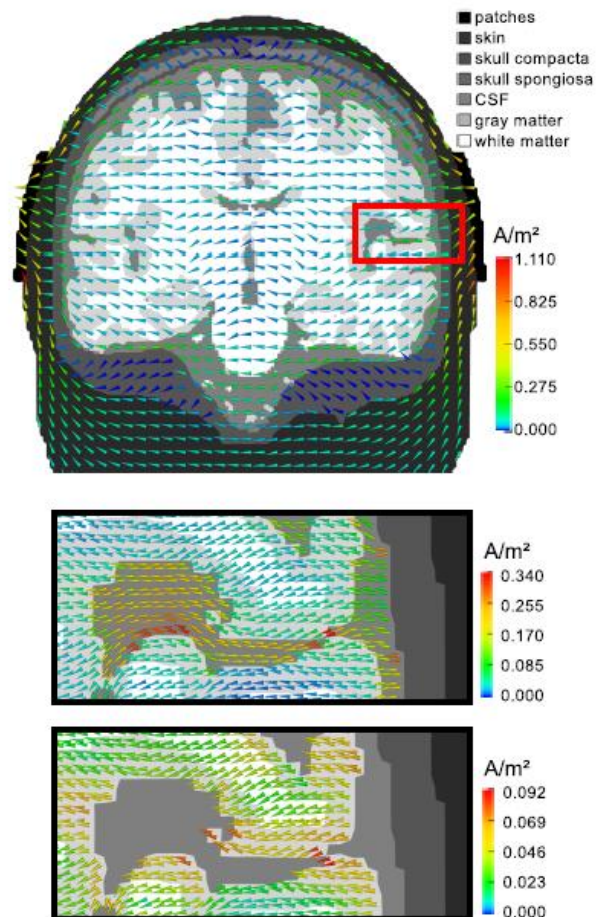
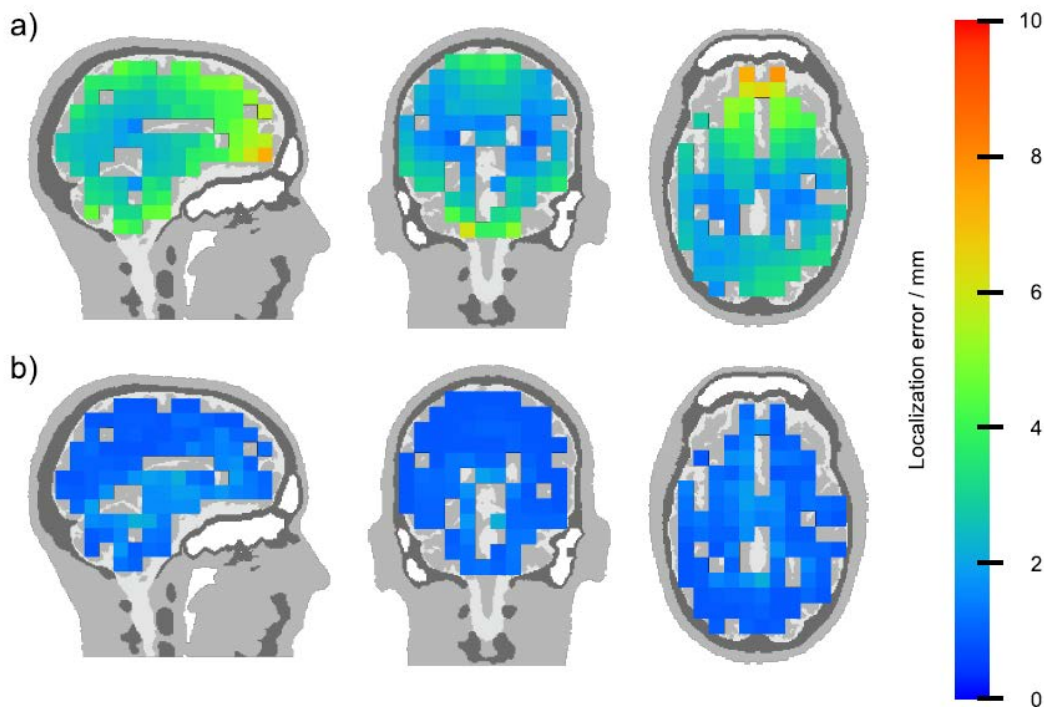


Image taken from *Neuling et al., 2012, Neuroimage*



The above image displays source localization errors when using a 3-shell model (scalp, skull, brain) **neglecting** CSF (a) and when using a 4-shell model **including** the outer CSF layer between cortex and inner skull (b). It is apparent that including CSF in the forward computation drastically reduces localization errors. Optimally, the CSF-filled ventricles should also be modeled, yet BESA Research requires a homogeneous volume without gaps for source analysis. This is why only the outermost CSF-layer is taken into account⁸. As the outer CSF layer is the most critical for source analysis precision, localization errors caused by un-modeled ventricles are negligible.

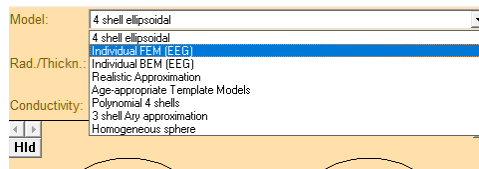
Once the FEM model is built, a new leadfield table needs to be computed for the individual forward model and the current electrode layout. This is done during the last step of the BESA MRI coregistration dialogue. This means that the magnitude of the signal any source inside the head will contribute to each sensor must be calculated anew based on the individual FEM

⁸ BESA MRI models all CSF, BESA Research only uses the CSF layer between cortex and inner skull.

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

model. The computation can take several minutes, depending on the number of electrodes in the electrode layout. A grid resolution of 2 mm is assumed.

Individual FEM models that were created in BESA MRI are available in the head model drop-down menu of the BESA Research source analysis module after coregistration.



By using a FEM model, the forward model for source analysis is tailored to the individual subject and in consequence the inverse solution can become more precise (Vanrumste et al. 2002, Roth et al. 1993, Cuffin 1996). This is especially true (a) for sources in brain regions that are not described well by a spherical head model (e.g. basal temporal lobe); (b) when individual heads show deviations from the norm (e.g. lesions). Thus, if the research target is to achieve maximal localization precision, an individual realistic head model is strongly recommended.

The segmentation algorithm and FEM model creation were developed in cooperation with the research group around Dr. Carsten Wolters (University of Münster).

References

BEM

- Gramfort A., Papadopoulos T., Olivi E., Clerc M. "OpenMEEG: opensource software for quasistatic bioelectromagnetics." BioMedical Engineering OnLine 45:9 (2010).
- Kybic J., Clerc M., Abboud T., Faugeras O., Keriven R., Papadopoulos T. "A common formalism for the integral formulations of the forward EEG problem." IEEE Transactions on Medical Imaging, 24 (2005): 12–28.

FEM

- Baumann, S.B., D.R. Wozny, S.K. Kelly, and F.M. Meno. "The Electrical Conductivity of Human Cerebrospinal Fluid at Body Temperature." IEEE Transactions on Biomedical Engineering 44 (1997): 220–223.
- Cuffin, B. N. "EEG Localization Accuracy Improvements Using Realistically Shaped Head Models." IEEE Transactions on Biomedical Engineering 43 (1996): 299–303.
- Neuling, T., Rach, S., Wagner, S., Wolters, C. H., & Herrmann, C. S. (2012). Good vibrations: Oscillatory phase shapes perception. NeuroImage, 63(2), 771–778.

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

- Ramon, Ceon, P. Schimpf, J. Haueisen, M. Holmes, and A. Ishimaru. "Role of Soft Bone, CSF and Gray Matter in EEG Simulations." *Brain Topography* 16 (2003): 245–248.
- Roth, Bradley J., Marshall Balish, Alexander Gorbach, and Susumu Sato. "How Well Does a Three-sphere Model Predict Positions of Dipoles in a Realistically Shaped Head?" *Electroencephalography and Clinical Neurophysiology* (1993): 175–184.
- Vanrumste, Bart, Gert Van Hoey, Rik Van de Walle, Michel R. P. D'Havé, Ignace A. Lemahieu, and Paul A. J. M. Boon. "Comparison of Performance of Spherical and Realistic Head Models in Dipole Localization from Noisy EEG." *Medical Engineering & Physics* (2002): 403–418.
- Wendel, K, N G Narra, M Hannula, P Kauppinen, and J Malmivuo. "The Influence of CSF on EEG Sensitivity Distributions of Multilayered Head Models." *IEEE Transactions on Bio-Medical Engineering* (2008): 1454–1456.

F. Coregistration with Individual MRI and use of FEM/BEM Model for Source Analysis

In the following, we will coregister an individual subject's MRI with their EEG data that were recorded in an auditory oddball experiment. We will see the improvements in source localization precision when using an individual FEM/BEM volume conductor in contrast to a 4-shell ellipsoidal model.

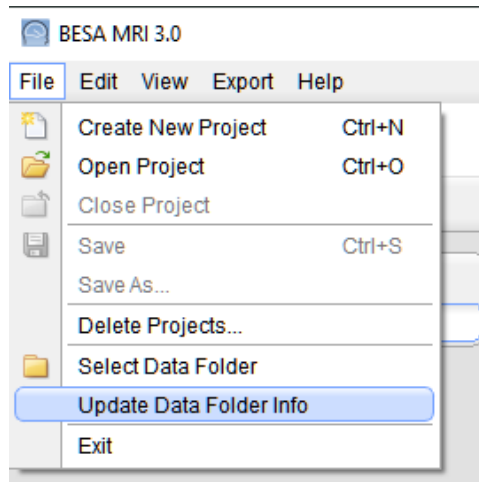
The data we will be working with are located in the BESA Research examples folder "**ERP-P300-Auditory**". During the oddball experiment, standard and rare tones were presented that differed in frequency. 160 standard tones were presented at 1200 Hz, 40 rare tones were interspersed at 800 Hz. The subject pressed a button with the left index finger whenever he heard a standard tone.

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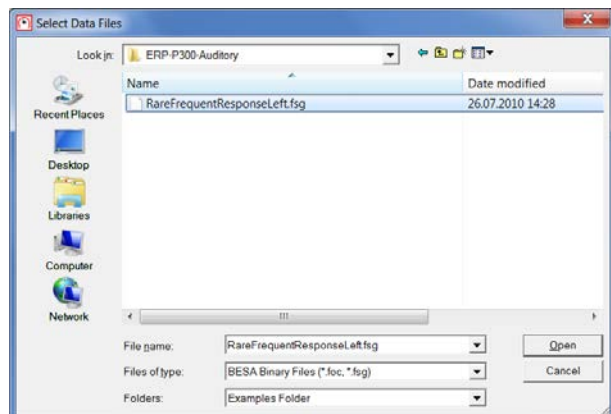
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

1. Copy the **QC_Tutorial_19460401**⁹ folder to the **BESA MRI Data Folder** and then press **File / Update Data Folder Info** in BESA MRI.

The FEM and BEM segmentations of the subject's MRI has already been performed and pre-saved in the copied folder to save time.



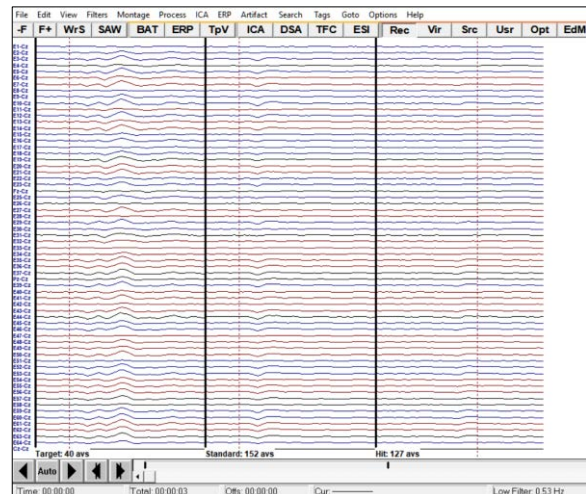
2. In BESA Research, open File **RareFrequentResponseLeft.fsg** (located here: **C:\Users\Public\Documents\BESA\Research_7_1\Examples\ERP-P300-Auditory**).



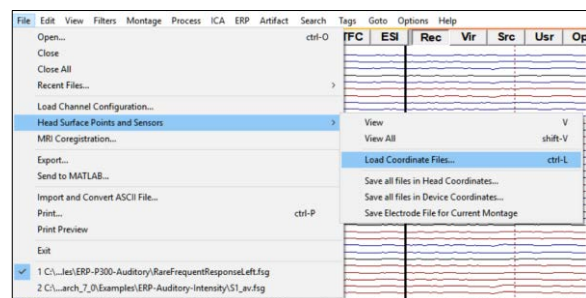
⁹ The folder will be provided by the presenter during the tutorial.

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

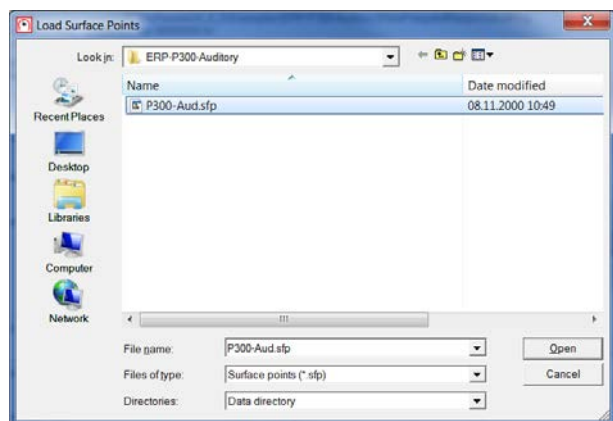
- The file contains 3 segments containing average data of conditions Target, Standard, and Hit. We will be working with condition Target, as the condition only involved listening to tones without any button pressing.



- Press **File / Head Surface Points and Sensors / Load Coordinate Files**.



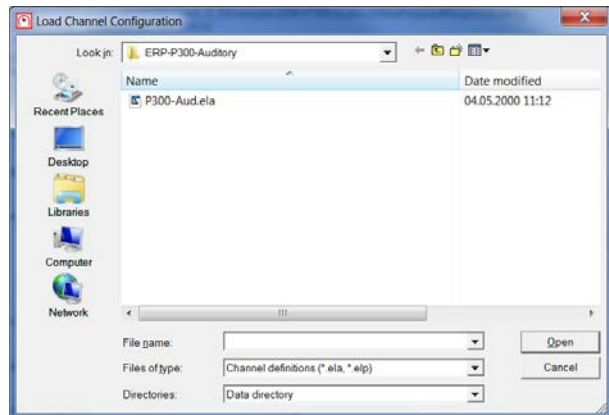
- Press the **second Browse...** button (for Digitized Head Surface Points) and choose file **P300-Aud.sfp**. This file contains individual digitization points of electrode positions. Press **Open**.



BESA® Research 7.1

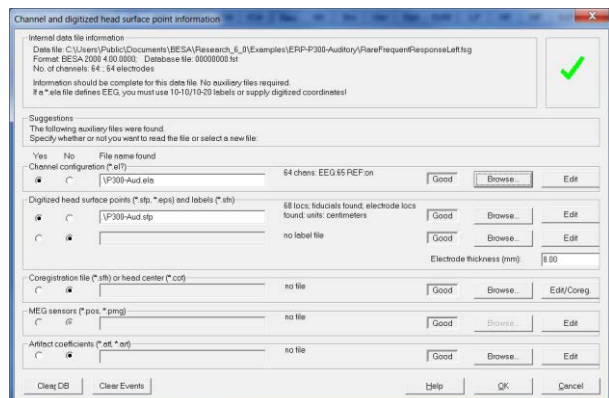
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

6. Press the first **Browse...** button (for Channel Configuration) and choose the file **P300-Aud.ela** containing the electrode labels and channel specifications. Press **Open**.



7. Instead of standard electrode positions, we are now going to use the digitized electrode positions of the subject. A green arrow should be present indicating that all necessary channel information is available.

In the same dialogue, press the **Edit/Coreg.** Button to start coregistration of the EEG data with the individual MRI.



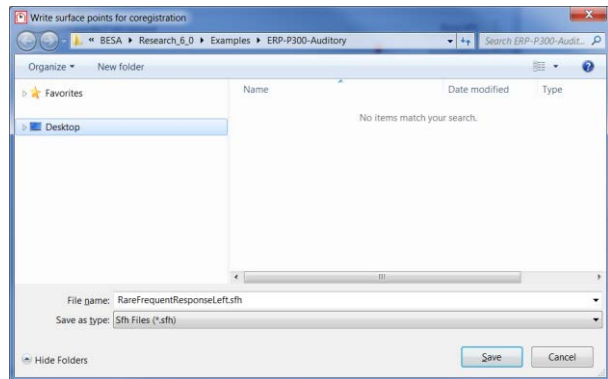
Tip: If there is not enough time for computing head models during the workshop, the precomputed FEM and BEM head model can be used by loading the **RareFrequentResponseLeft_Tutorial.sfh**¹⁰ file in the xxx folder after pressing the **Browse...** button in the “Coregistration file (*.sfh) or head center (*.cot)” section.

¹⁰ The folder will be provided by the presenter during the tutorial.

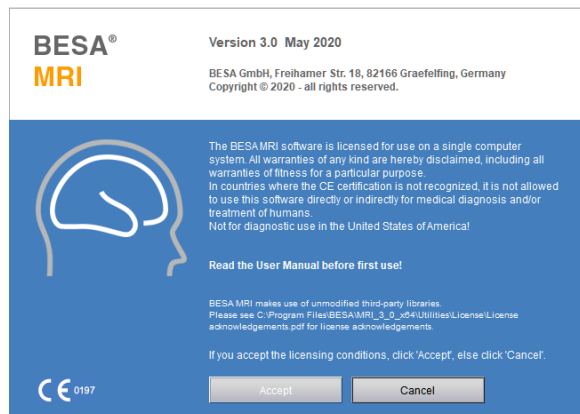
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

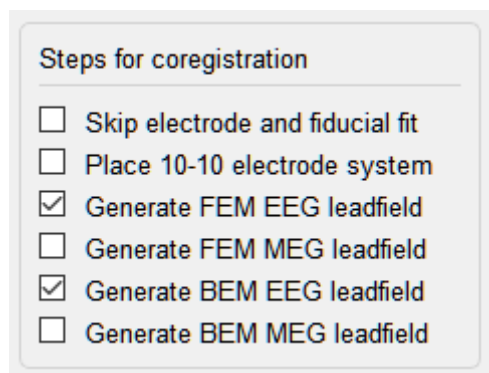
8. You will be prompted to save a sfh-file that will store information about the coregistration later. You can use the suggested name **RareFrequentResponseLeft.sfh**. Press **Save**.



9. BESA MRI will open. Press **Accept**.



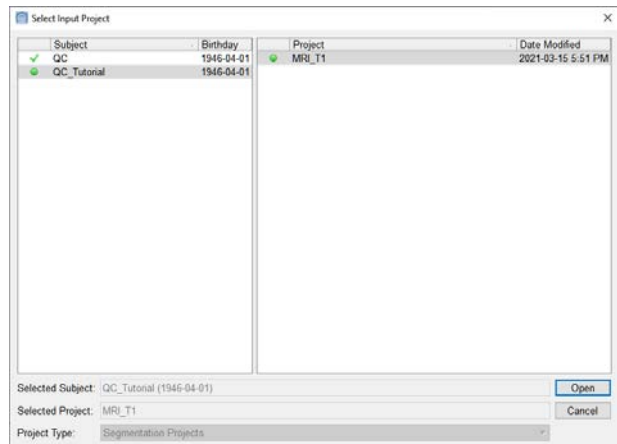
10. BESA MRI will automatically display the coregistration workflow. Make sure to select the option **Generate FEM EEG leadfield** and **Generate BEM EEG leadfield**. Press **Next** or hit the space bar to continue with the workflow.



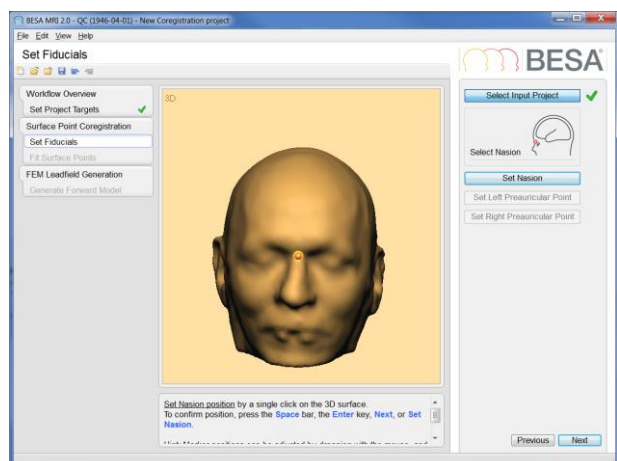
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

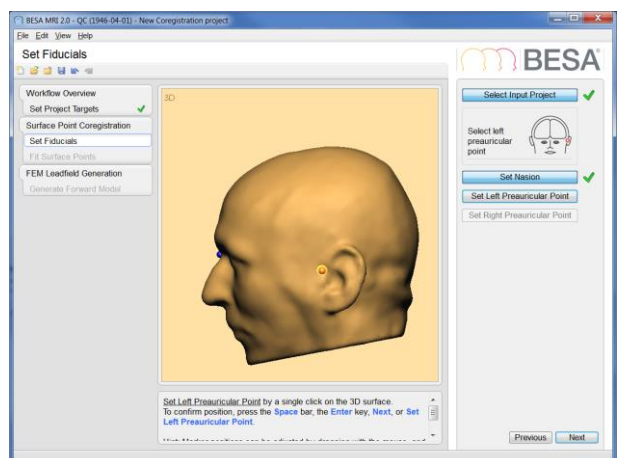
11. Press **Select Input Project** and choose project **MRI_T1** of subject **QC_Tutorial**. Press **Open**.



12. Select **Nasion** and press **Next**.



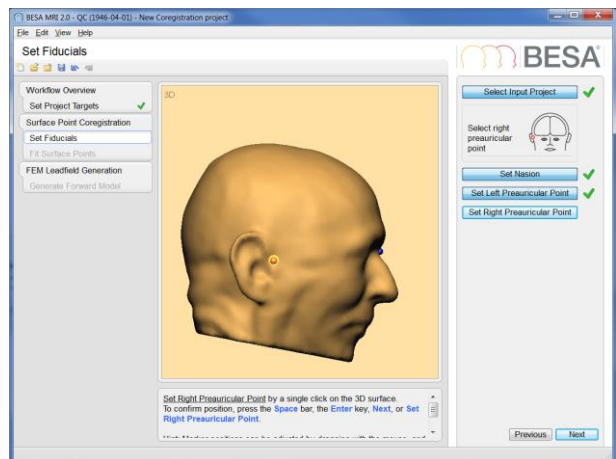
13. Select **LPA** and press **Next**.



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Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

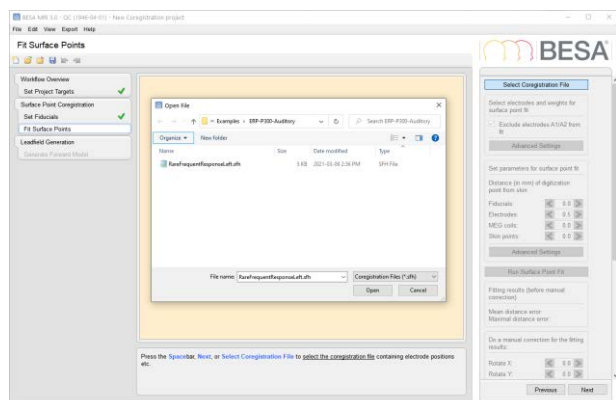
14. Select **RPA** and press **Next**.



15. The fiducial positions will be used as a first reference for a first coregistration of the electrodes with the scalp surface. Press **Next** to continue.



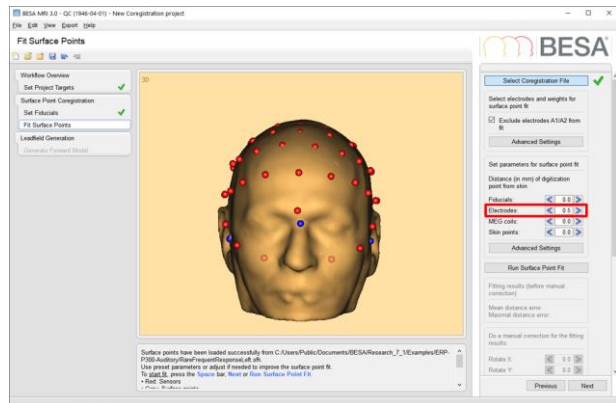
16. Press **Select Coregistration File** and choose **RareFrequentResponseLeft.sfh**. Press **Open**.



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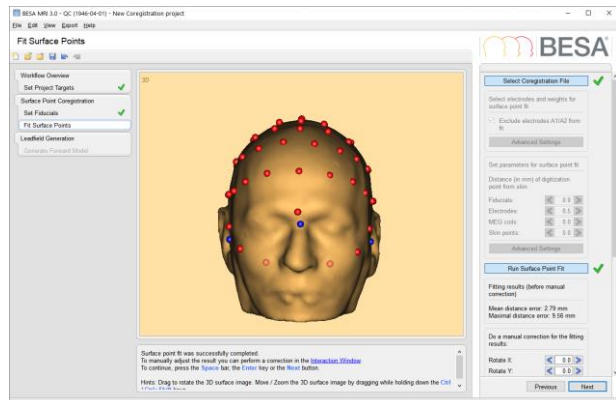
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

17. In the field **Electrodes**, enter **0.5 mm** to indicate the distance of the digitization points from the scalp. Then press **Run Surface Point Fit**.

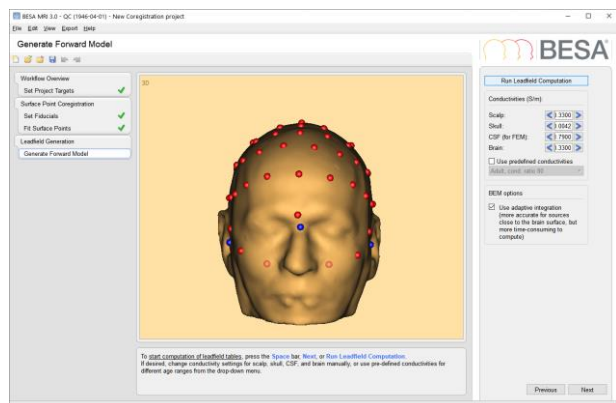


18. Once the surface point fit has run and the result is satisfactory, press **Next** to continue.

Note: In case the surface point fit appears inadequate, you might consider revisiting the definition of the fiducials.



19. Press **Run Leadfield Computation** to start leadfield calculation with the given FEM/BEM model and electrode layout. During FEM EEG leadfield computation, the electrode that is currently being processed is highlighted in orange, the electrodes that are already finished are displayed in blue.



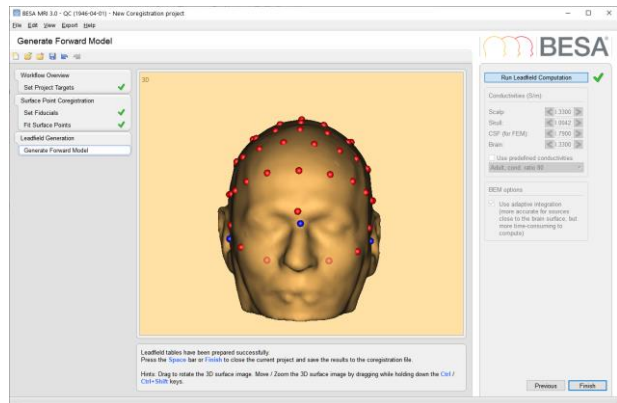
Note: The computation will take time as the forward signal for each electrode needs to be computed under the assumption of activity in each brain voxel.

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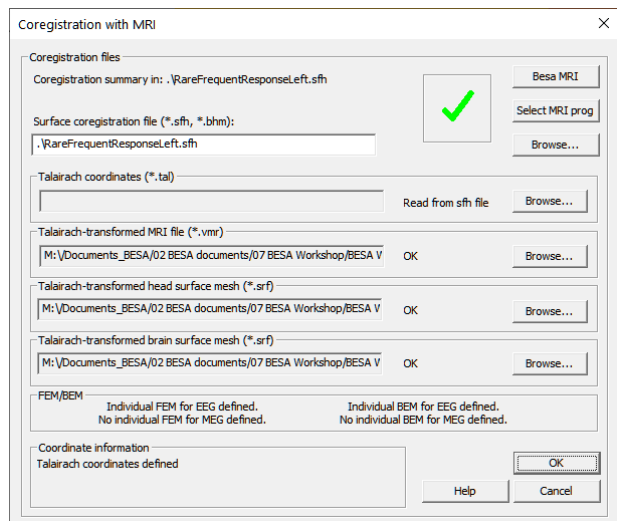
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

20. Once the FEM/BEM EEG leadfield computation is done, press **Finish** and save the project under the suggested name.

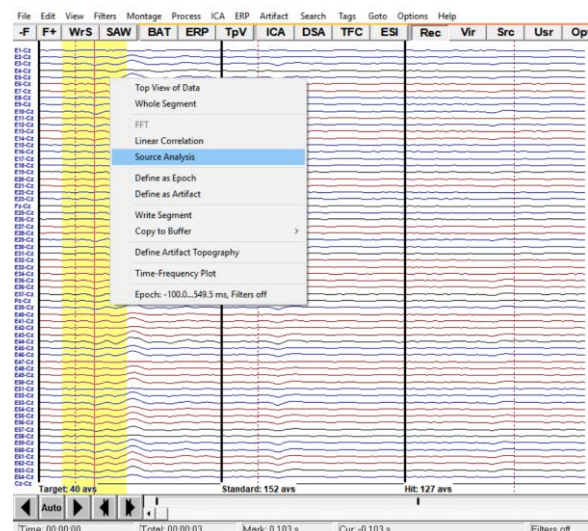
Close BESA MRI and return to BESA Research.



21. In the window **Coregistration with MRI** you should now see a green tick mark indicating that all information regarding the coregistration and FEM/BEM models are available to BESA Research. Close the window by pressing **OK**.



22. **Left-drag** a block in the condition Target, **right-click** and select **Source Analysis**.



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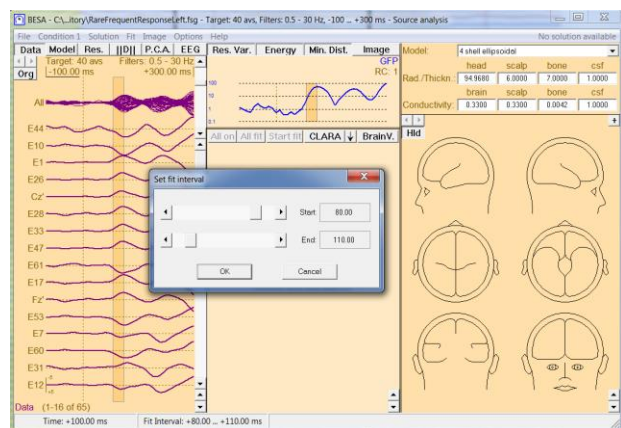
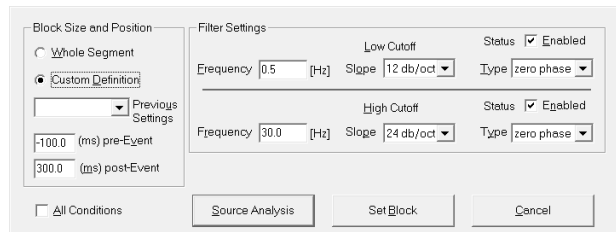
Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

23. Select:

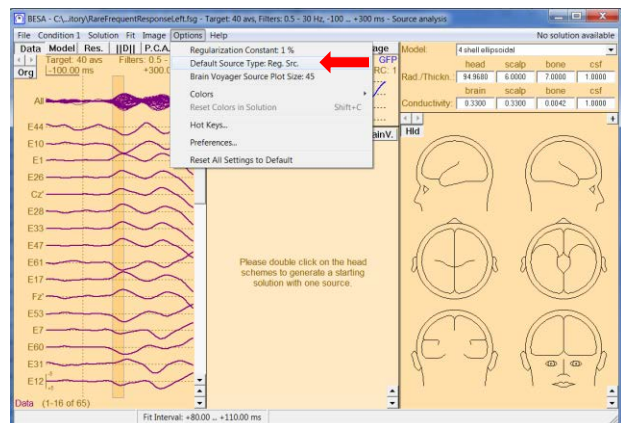
- **Custom definition** of -100 to 300 ms,
- **Low Cutoff Filter** of 0.5 Hz, 12 dB/Oct., **zero-phase** and
- **a High cutoff Filter** of 30 Hz, 24 dB/Oct., **zero-phase**.

Press **Source Analysis**.

24. In the SA-window, please **left-drag** a block from **80 to 110 ms** over the EEG signal. You can easily select the time-range by right-clicking into the marked segment and choosing **Set Fit Interval**.



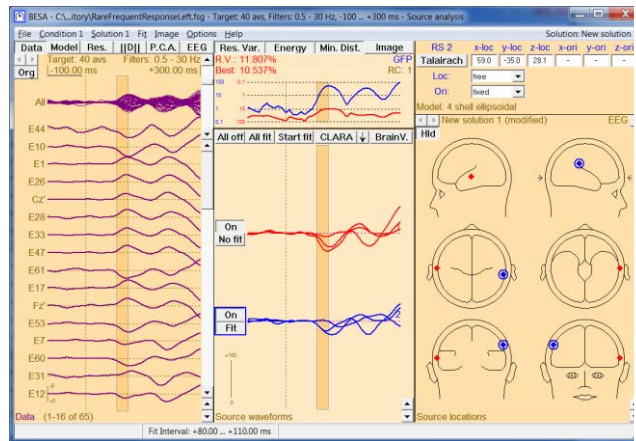
25. Make sure that the default source type is set to **Regional Source** by pressing **Options**. In case the default source type is Dipole, change it to **Reg. Src.** (Regional Source).



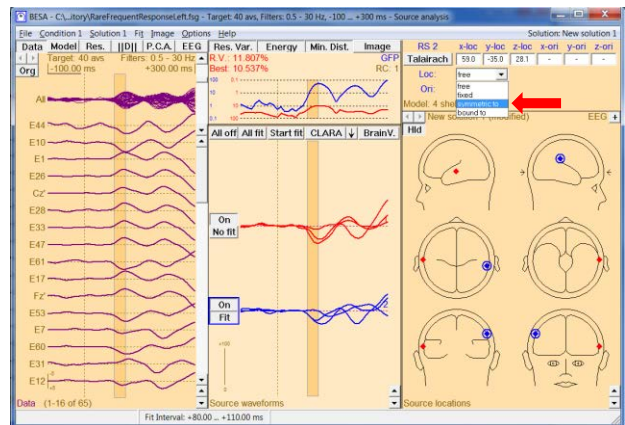
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

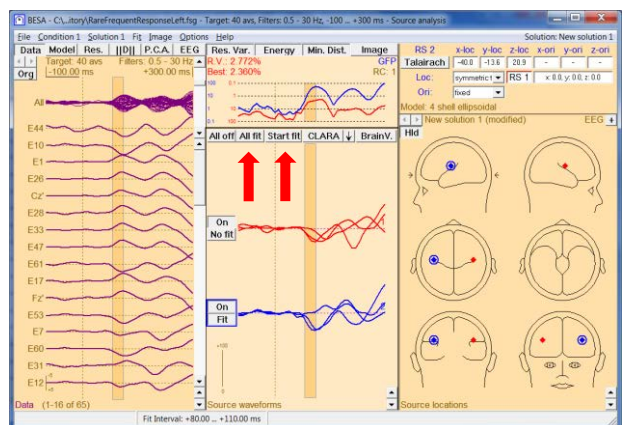
26. We will first try to fit the auditory N100 with two regional sources using the default head model **4-shell ellipsoidal**. Please **double-click** into the head schemes twice to **place two regional sources**, one in the left hemisphere, one in the right hemisphere.



27. We will add a **symmetry constraint** as we are working with bilateral individual activity that is heavily overlapping. Open the drop-down menu next to **Loc.:** and change the constraint of the second source to **Symmetric to**.



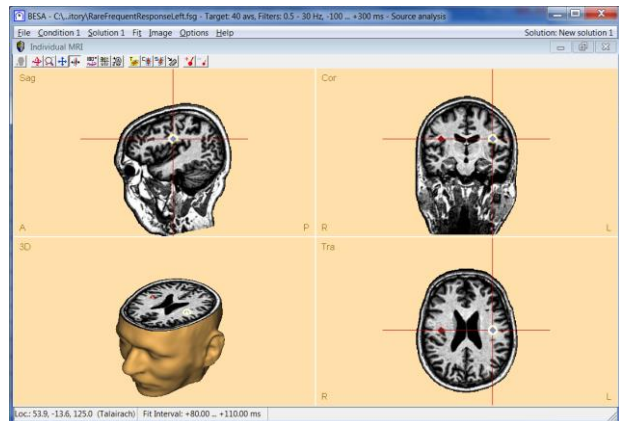
28. Press **All Fit** and **Start Fit** to start source localization.



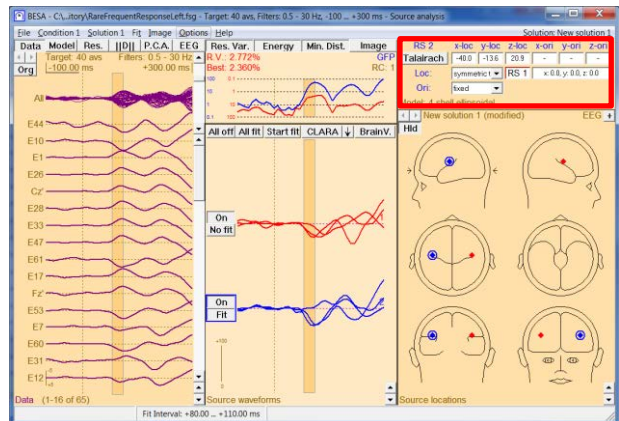
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

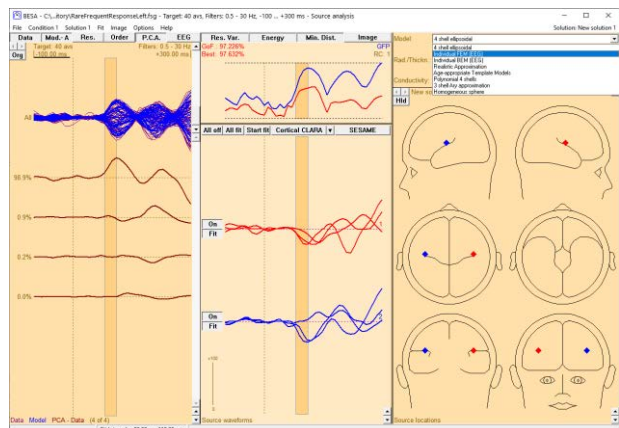
29. Press **A** on the keyboard to bring up the anatomical view. We will see that the two regional sources are located in bilateral auditory areas. We do notice, however, that the sources are not located in Heschl's gyrus as expected, but too superior.



30. **Close** the window displaying the individual MRI. **Click** into the empty **area** in the box in the upper right corner that is now displaying the source position. This will switch the contents to the head model selection.



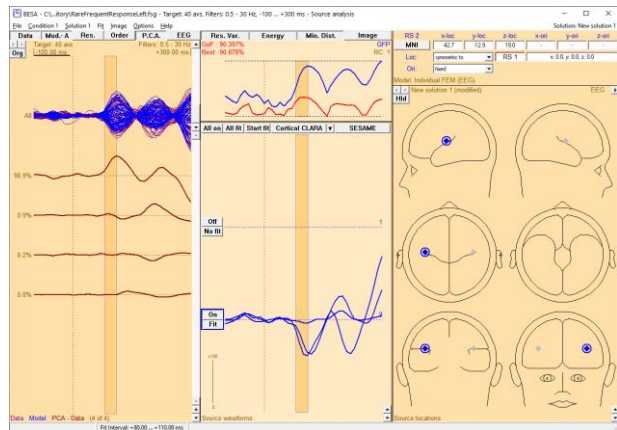
31. **Open** the head model drop-down menu and select **Individual FEM (EEG)**. It might take a couple of seconds to load the FEM model.



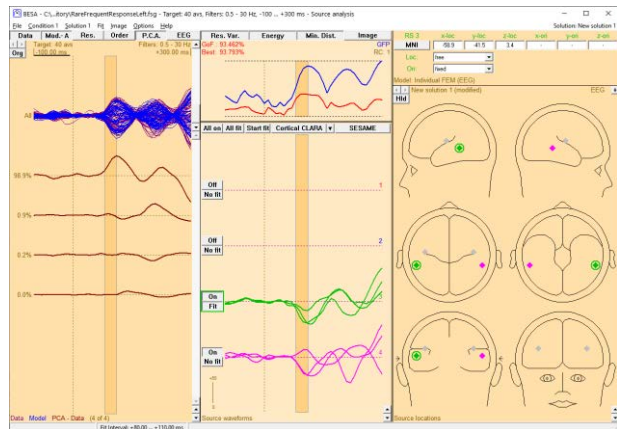
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

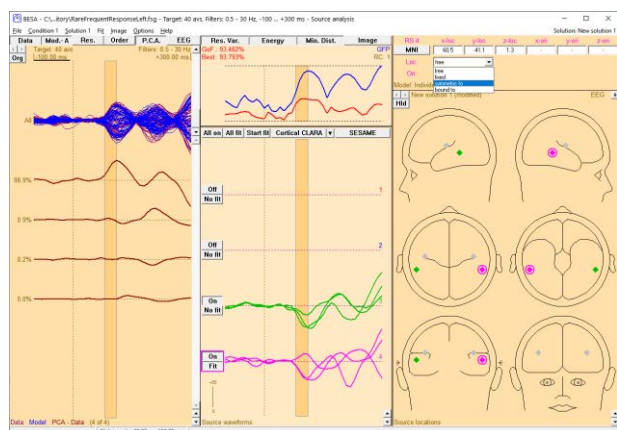
32. Switch off both regional sources off by clicking on the **On** button next to the source waveforms.



33. Insert **two new regional sources** by **double-clicking** in the head schemes, one source in the left, one source in the right hemisphere.



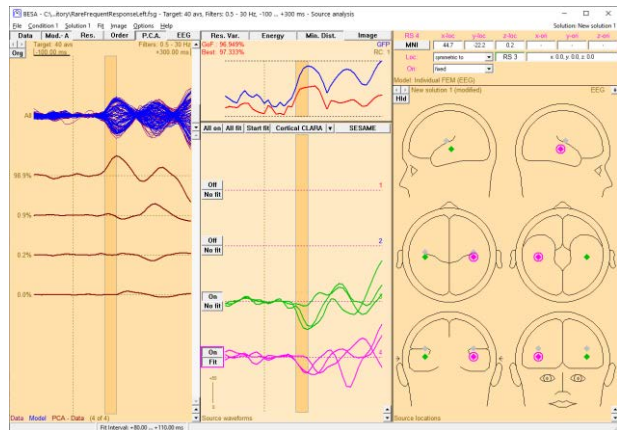
34. Add a symmetry constraint again by opening the drop-down menu next to **Loc.:** and changing the constraint of the fourth source to **Symmetric to**.



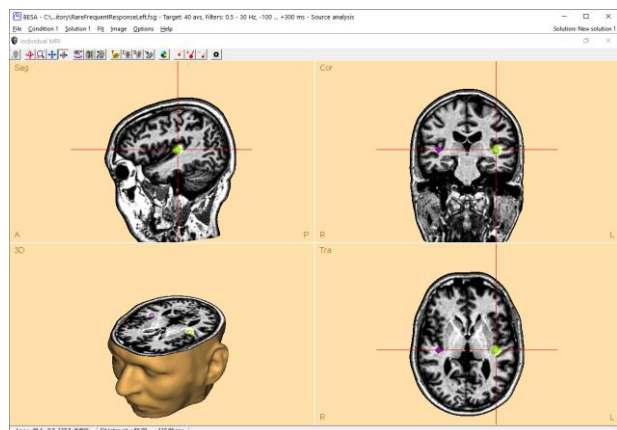
BESA® Research 7.1

Tutorial 6 – MRI Segmentation, Coregistration and Individual Head Modeling (FEM/BEM)

35. Press **All Fit** and **Start Fit** to start source localization. It becomes apparent that source localization with the individual FEM model leads to more inferior solutions compared to the 4-shell ellipsoidal model.

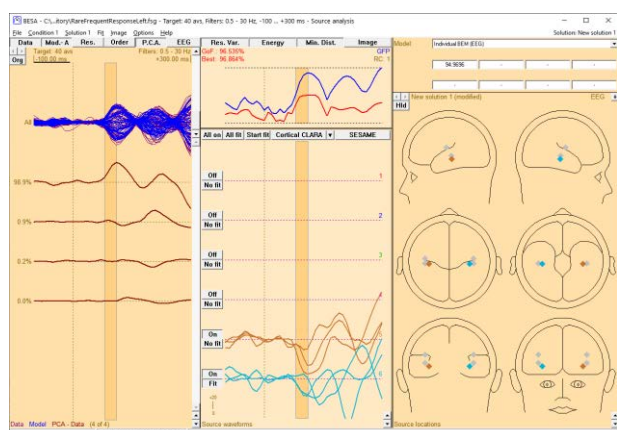


36. Bring up the individual MRI by pressing **A** on your keyboard. We now see that both sources are located in Heschl's gyrus.



37. Change the head model to **Individual BEM (EEG)** and then start source localization as the previous steps (see the step 30–35).

Source localization with the individual BEM model also leads to more inferior solutions compared to the 4-shell ellipsoidal model.



This example illustrates the superiority of an individual realistic forward model for source localization precision. The temporal lobe is a structure that is described particularly badly by a spherical model, so individual anatomical information will lead to obvious advantages.

Tutorial 7 – Distributed Sources I: Volume Methods

What does BESA Research provide?

- ✓ Volume methods
 - LAURA
 - LORETA
 - sLORETA
 - swLORETA
 - CLARA
 - sSLOFO
 - User-defined
- ✓ Brain atlases
 - Brainnetome
 - AAL
 - Brodmann
 - AAL2015
 - Talairach
 - Yeo7
 - Yeo17
- ✓ Slice view
- ✓ Atlas-based montages
- ✓ Export of images per time-point or for time-series

Distributed Source Imaging: Volume Methods

This tutorial introduces the principles of distributed source imaging. A short theoretical introduction is presented, followed by hands-on examples that demonstrate the properties of the different methods and the important effects of regularization on the obtained results.

A. Short theory of distributed source images

Discrete versus distributed source analysis

Both discrete and distributed source models use dipoles or regional sources as their basic elements to model brain activity. However, the relationship between the number of sources and the number of recording sensors differs between those two approaches. This has several consequences that are listed schematically in the table on the next page.

The following abbreviations are used:

D: The recorded EEG or MEG data. The dimension of this matrix is [Number of sensors × Number of time points].

Each row of D contains the signal of one sensor as a function of time. Each column of D contains the recorded topography at one time point.

S: The source waveforms. The dimension of this matrix is [Number of sources × Number of time points].

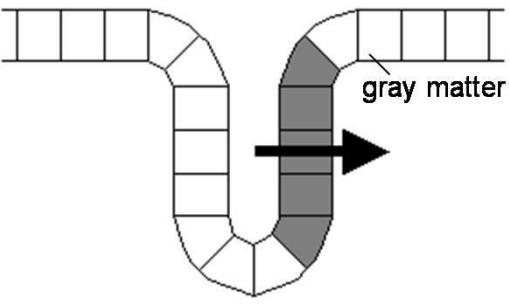
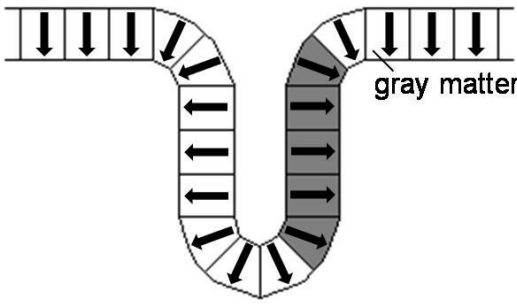
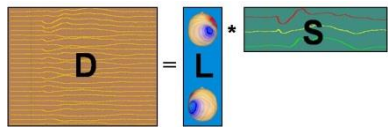
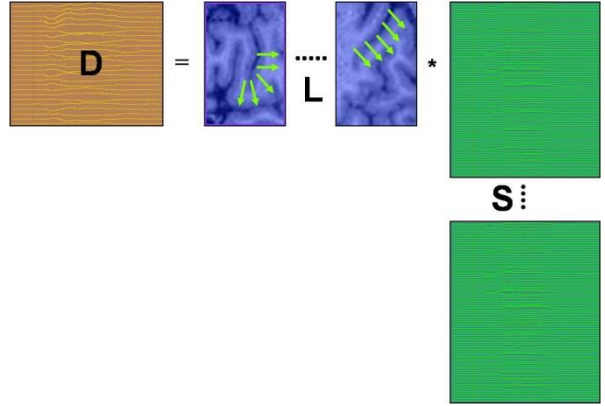
Each row of S contains the activity (in units of dipole moment, nAm) of one source as a function of time.

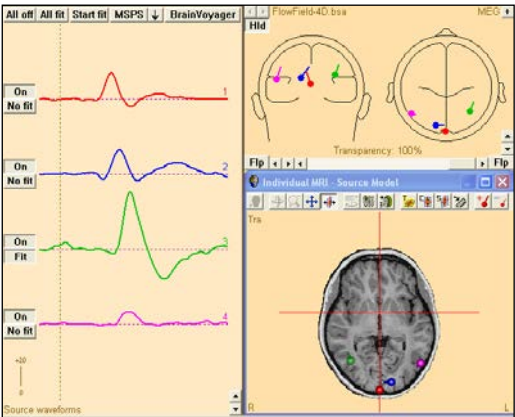
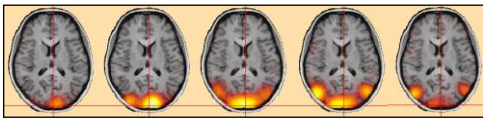
L: The leadfield matrix. The dimension of this matrix is [Number of sensors × Number of sources].

Each column of L contains the topography (the signal pattern) of one source, i.e. the signals that normalized activity of this source generates on the different EEG/MEG sensors. L contains all information about the source model (the multiple dipoles or regional sources) and the head model (the assumed electrical conductivity distribution inside the head).

L^T: The transposed leadfield matrix, i.e., rows and columns are swapped. Accordingly, the dimension of this matrix is [Number of sources × Number of sensors].

- λ : A regularization parameter. The formula in the table holds for Tikhonov regularization, which is just one way of regularizing a matrix.
- I: The identity matrix, containing ones in the diagonal elements and zeroes in the off-diagonal elements.
- V: A spatial weighting matrix on source level. The dimension is [Number of sources \times Number of sources].

Discrete source analysis	Distributed source analysis
Idea: Each equivalent current dipole represents an extended brain region	Idea: Each current dipole represents one small brain segment
	
Number of sources < Number of sensors Overdetermined problem	Number of sources >> Number of sensors Underdetermined problem
Source model is defined by fitting or seeding	Source model is predefined (e.g. along the brain surface or on a regular volume grid)
$D = L \cdot S$ 	$D = L \cdot S$ 
The leadfield L has more rows (number of sensors) than columns (number of sources)	The leadfield L has more columns (number of sources) than rows (number of sensors)
Reconstructed source waveforms: $S = L^{-1} \cdot D$ where $L^{-1} = (L^T \cdot L)^{-1} \cdot L^T$	Reconstructed source waveforms: $S = L^{-1} \cdot D$ where $L^{-1} = L^T \cdot (L \cdot L^T)^{-1}$
Regularization in source space, e.g., Tikhonov: $L^{-1} = (L^T \cdot L + \lambda \cdot I)^{-1} \cdot L^T$	Regularization in sensor space, e.g., Tikhonov: $L^{-1} = L^T \cdot (L \cdot L^T + \lambda \cdot I)^{-1}$
	Spatial weighting: $L^{-1} = V \cdot L^T \cdot (L \cdot V \cdot L^T + \lambda \cdot I)^{-1}$

Discrete source analysis	Distributed source analysis
<p>Result:</p> <p>Multiple source model and source waveforms</p> 	<p>Result:</p> <p>3D Volume image, one for each time point</p> 
<p>Properties:</p> <ul style="list-style-type: none"> • Crosstalk: (+) If the source model contains all active brain regions, the source waveforms represent their activity, i.e. they separate and mutually contrast their activities with minimum crosstalk. • Effort: (-) Source model needs to be defined by fitting or seeding. This requires user interaction (decision on the number of sources, fit intervals etc.). 	<p>Properties:</p> <ul style="list-style-type: none"> • Crosstalk: (-) Smeared, non-focal activity. Substantial crosstalk between sources. Reconstructed activity at any location is contaminated by activity from other brain regions. Activity of brain regions close to each other can hardly be separated. • Effort: (+) Pre-defined source model. Source images are generated easily and quickly. However, parameters must be specified (V, λ). They can have a large impact on the quality of the obtained source image.

In BESA Research, distributed source models consist of regional sources at each source location. In the 3D volume images demonstrated in this tutorial, the sources are located on a regular cubic grid spanning the whole brain volume. The grid spacing in Talairach units can be specified by the user.

Spatial weighting: Minimum norm, LORETA and LAURA

Because distributed source models contain more sources than recording sensors, there are many different source current distributions that perfectly model the recorded data. Therefore, side constraints need to be defined that allow the selection of the optimum solution. These side

constraints are represented in the spatial weighting matrix V (see above). Different methods have been published in literature. The following is an overview of the imaging methods implemented as standards in BESA; variations and combinations of them can be specified as a user-defined image (see the corresponding chapter below). More detailed descriptions are given in the BESA Help menu.

- **Minimum norm** (Hämäläinen & Ilmoniemi 1984): In its simplest form, V is set to the identity matrix. This results in the image with the smallest overall energy (the sum of squares of all sources magnitudes). Usually, depth weighting is used by applying a diagonal matrix V , whose entries are inversely proportional to some measure for the magnitude of the respective sources lead field vector (i.e., deep sources get a larger a-priori weight than superficial sources).
- **LORETA** ("Low Resolution Electromagnetic Tomography", R.D. Pascual-Marqui, International Journal of Psychophysiology. 1994, 18:49-65): Here, V is non-diagonal and contains both a depth weighting term and a representation of the 3D Laplacian matrix. This leads to the image with the smoothest distribution of activity across the source space.
- **LAURA** ("Local Auto Regressive Average", R. Grave de Peralta Menendez 2001, Brain Topography 14(2), 131-137): In LAURA, V is non-diagonal and contains both a depth weighting term and a representation of a local autoregressive function.

Standardization with the resolution matrix: sLORETA and swLORETA

All distributed source images suffer from smearing and crosstalk, leading to the following effects:

- Even in data generated by focal brain activity, the reconstructed 3D image is blurred and non-focal. Activity of the active brain region gets projected onto neighboring sources.
- Consequently, the reconstructed activity at one source location is representing not only brain activity at the modeled location but is also reflecting activity of other brain regions.

These effects are captured mathematically by the resolution matrix R , defined as:

$$R = L^{-1} \cdot L$$

The diagonal elements of R are a measure for the percentage of the reconstructed activity of the respective source that is due to brain activity at the modeled location. The idea behind sLORETA and swLORETA is to divide (standardize) the reconstructed minimum norm activity of each source with this measure. This serves as a compensation for the non-uniform depth sensitivity of the minimum norm approach.

- **sLORETA** (“standardized LORETA”, R.D. Pascual-Marqui, Methods & Findings in Experimental & Clinical Pharmacology 2002, 24D:5-12): Unlike the name suggests, this method is not a standardization of LORETA, but rather of the unweighted minimum norm image. The sLORETA activity at location r : is estimated from the minimum norm source estimate $S_{MN,r}$ as:

$$S_{sLORETA,r} = R_{rr}^{-1/2} \cdot S_{MN,r}$$

In simulated data sets with only one focal activity and no noise, the sLORETA image has its maximum exactly at the simulated location. However, this property does not hold anymore in the realistic case of noisy data and multiple simultaneously active brain regions.

- **swLORETA** (E. Palmero-Soler et al 2007 Phys. Med. Biol. 52 1783-1800) is a standardized version of the depth-weighted minimum norm.

Iterative approaches: CLARA and sSLOFO

One approach to make distributed source images more focal is to apply them iteratively. The spatial weighting matrix V in each iteration step contains contributions that reflect the image obtained in the previous iteration step. CLARA and sSLOFO are such approaches:

- **CLARA** (“Classical LORETA Analysis Recursively Applied”) is an iterative application of the LORETA algorithm with an implicit reduction of the source space in each iteration. First a regularized LORETA image is computed as initialization. Then in each iteration step the following actions are carried out:
 1. The obtained image is spatially smoothed (this step is left out in the first iteration).
 2. All grid points with amplitudes below a threshold of 1% of the maximum activity are set to zero, thus being effectively eliminated from the source space in the following step.

3. The resulting image defines a spatial weighting term (for each voxel the corresponding image amplitude). A LORETA image is computed with this additional spatial weighting term for each voxel. By the default settings in BESA Research, the regularization values used in the iteration steps are slightly higher than that of the initialization LORETA image.

After a specified number of iterations (default: 2), the computation stops, and the image computed in the last iteration is displayed.

- **sSLOFO** (“standardized shrinking LORETA-FOCUSS”, H. Liu et al. 2005, IEEE Transactions on Biomedical Engineering 52(10), 1681-1691.) is an iterative application of weighted distributed source images with a reduced source space in each iteration. As initialization step, an sLORETA image is computed. Then in each iteration step the following operations are performed:

1. The obtained image is spatially smoothed (this step is left out in the first iteration).
2. All grid points with amplitudes below a threshold of 1% of the maximum activity are set to zero, thus being effectively eliminated from the source space in the following step.
3. A depth-weighted, standardized minimum norm is being computed, where V has additional diagonal weights proportional to the image amplitudes in the previous iteration steps.

After a specified number of iterations (default: 3), the computation stops and the image computed in the last iteration is displayed.

An overview of these methods is provided in the next page.

Tutorial 7 – Distributed Sources I: Volume Methods

Method name	Type	Regularization	Spatial weighting	Operator	Optimization / specific features	Pros	Cons
Multiple dipoles / Regional sources	discrete	optional	no	$s = (L^T L + \lambda I)^{-1} L^T * D$	Adjust L minimize $ D_{\text{model}} - D_{\text{measured}} $	Provided that all brain regions are modeled, little cross talk and good separation of source	Takes skill to model and sequentially fit sources; user-dependent
Minimum norm (L_2)	distributed	mandatory	optional (diagonal only)	$s = L^T (L L^T + \lambda I)^{-1} * D$ $s = V L^T (L V L^T + \lambda I)^{-1} * D$	With spatial weighting V : diagonal matrix with depth weighting	No user interaction necessary after definition of λ and V	cross talk, smearing; activities of nearby brain regions cannot be separated
LORETA	distributed	mandatory	yes (with off-diagonal elements)	$s = V L^T (L V L^T + \lambda I)^{-1} * D$	V holds depth weighting (diagonal) and Laplace operators (off-diagonal)	No user interaction necessary after definition of λ and V	Very smeared signal
LAURA	distributed	mandatory	yes (with off-diagonal elements)	$s = V L^T (L V L^T + \lambda I)^{-1} * D$	V holds depth weighting (diagonal) and a local autoregressive function (off-diagonal)	No user interaction necessary after definition of λ and V	Very smeared signal
sLORETA	distributed	mandatory	yes (diagonal only)	$s_r = R_{rr}^{-1/2} L^T (L L^T + \lambda I)^{-1} * D$, where $R = L^T (L L^T + \lambda I)^{-1} L$	R is a measure of the percentage of the reconstructed activity at a source location that is due to the brain activity at	cf. Minimum norm	cf. Minimum norm
swLORETA	distributed	mandatory	yes (diagonal only)	like Minimum norm	With spatial weighting V : diagonal matrix with standardized depth weighting	cf. Minimum norm	cf. Minimum norm
CLARA	distributed	mandatory	yes (with off-diagonal elements)	like LORETA	Iterative approach, reduce source space and use image as spatial weighting term	No user interaction necessary after definition of parameters (no of iterations, ...)	some smearing
sSLOFO	distributed	mandatory	yes (diagonal only)	like sLORETA / Minimum norm	Iterative approach, reduce source space and use image as spatial weighting term. Initial solution uses LORETA,	No user interaction necessary after definition of parameters (no of iterations, ...)	some smearing

Regularization

Distributed source images require the inversion of a term of the form $L \cdot V \cdot L^T$. This term is generally regularized before its inversion. In BESA, selection can be made between two different regularization approaches.

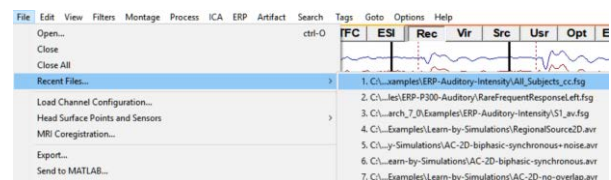
- **Tikhonov regularization:** In Tikhonov regularization, the term $L \cdot V \cdot L^T$ is inverted as $(L \cdot V \cdot L^T + \lambda \cdot I)^{-1}$. λ is the regularization constant, and I is the identity matrix.
- **Truncated singular value decomposition (TSVD):** Here, an SVD decomposition of $L \cdot V \cdot L^T$ is computed as $L \cdot V \cdot L^T = U \cdot X \cdot U^T$, where the diagonal matrix S contains the singular values. All singular values smaller than the specified percentage of the maximum singular values are set to zero. The inverse is computed as $U \cdot X^{-1} \cdot U^T$, where the diagonal elements of X^{-1} are the inverse of the corresponding non-zero diagonal elements of X .

As we will see, regularization has a critical effect on the obtained distributed source images. The results may vary substantially with the choice of the regularization parameter (see examples below). Therefore, it is important to evaluate the generated image critically with respect to the regularization constant, and to keep in mind the uncertainties resulting from this fact when interpreting the results.

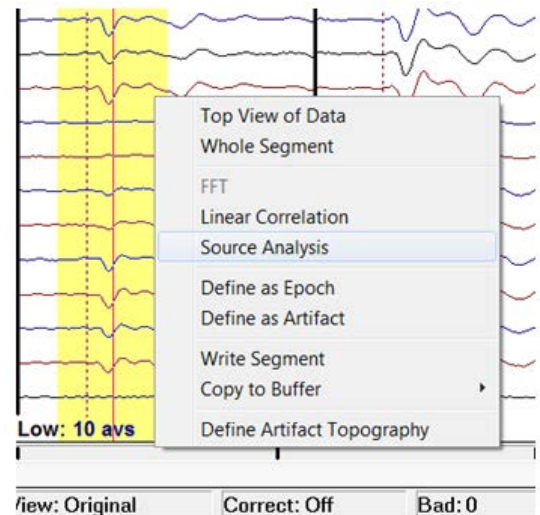
B. Comparison of different distributed source imaging methods

We will now return to the grand average data of the auditory intensity experiment to compare distributed source analysis methods with one another as well as with the regional source model we fitted earlier on.

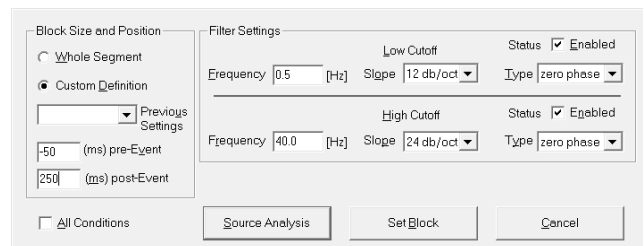
1. Select the file **All_Subjects_cc.fsg** from **File / Recent Files**.



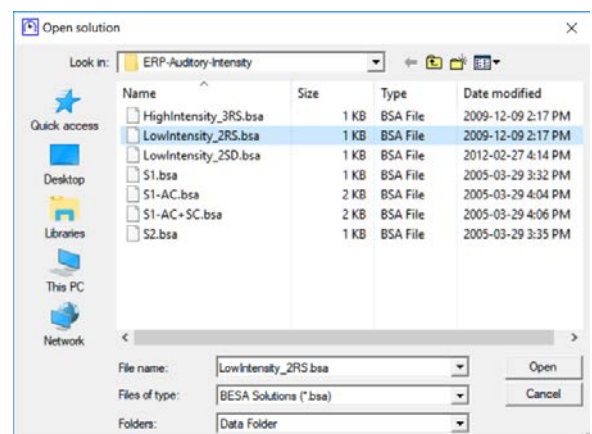
2. Select condition **Low**, **left-drag** a block and send it to source analysis by **right-clicking** and pressing **Source Analysis**.



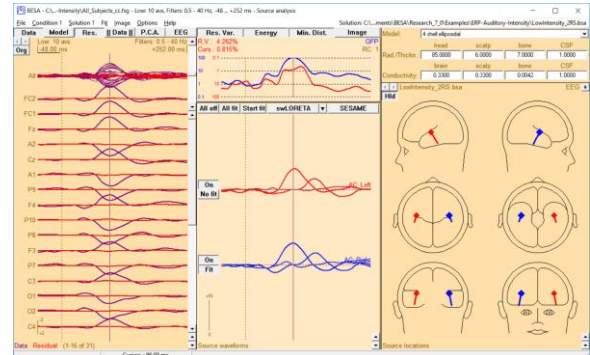
3. Select a time range from **-50 to 250 ms**, and specify a **Low Cutoff filter of 0.5 Hz, 12dB/oct, zero-phase** and a **High Cutoff filter of 40 Hz, 24 db/oct, zero-phase**. Press **Source Analysis** to open the specified data in the source analysis window.



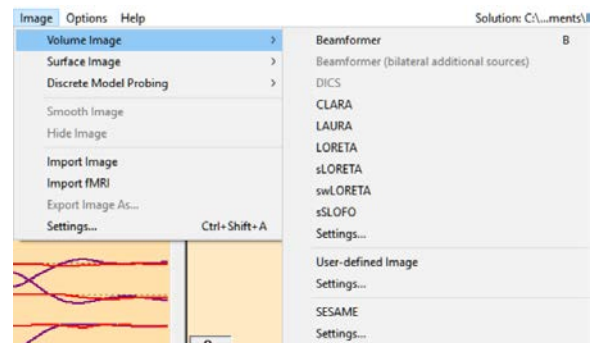
4. As a reference and for comparison, load the regional source model we created in Tutorial 4, steps D1-7. Press **File / Open Solution...** and load file **LowIntensity_2RS.bsa**.



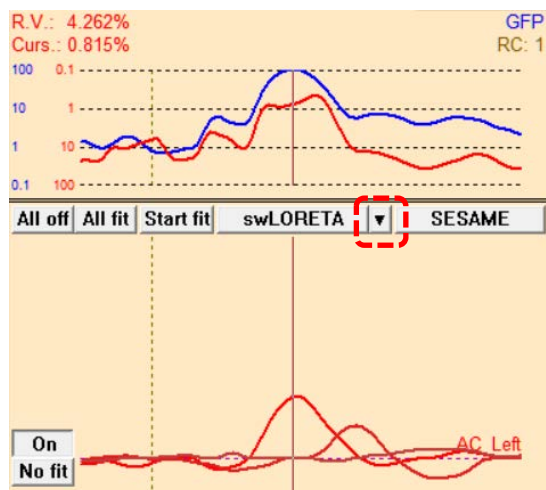
- Set the cursor at 96 ms, at the peak of the N100 component.



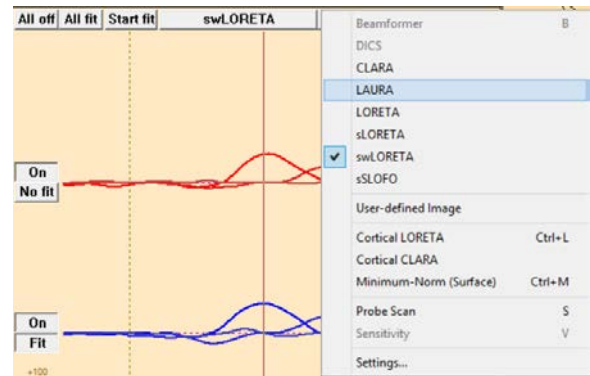
- Distributed 3D volume images are generated with a single click in BESA. They can be generated by selecting the corresponding method from menu entry **Image / Volume Image**, or from the dropdown menu of the image selector button (the arrow left of the SESAME button in the middle of the source analysis window).



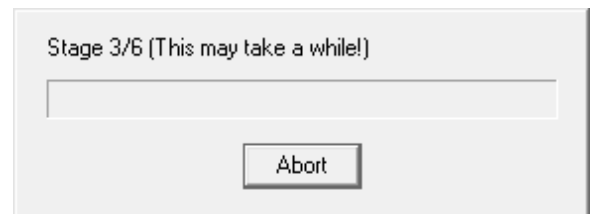
In this chapter, we will use the default parameters for all 3D images. The importance and potentially large influence of these parameters on the obtained result will be illustrated in the next chapter.




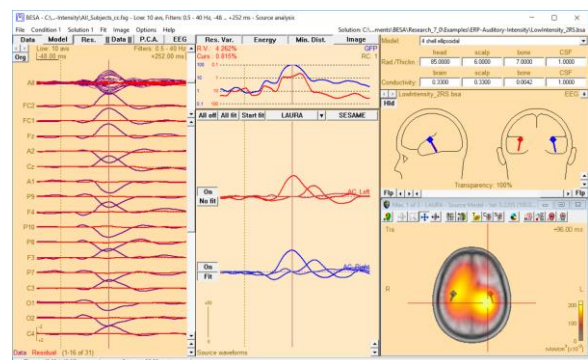
- First, compute a LAURA image at the cursor latency. Simply select **LAURA** from the Image selector button dropdown menu.




- The computation of a LAURA (and LORETA) image is divided into 6 steps. A dialog window informs you about the processing stage. When computing a LAURA image for the first time for a data set, steps 2 and 3 can take some time to complete (depending, among others, on the selected grid spacing, see below). The results of this intermediate steps are stored to disk, however, so that these steps will be omitted in all future LAURA images. This speeds up the image calculation.

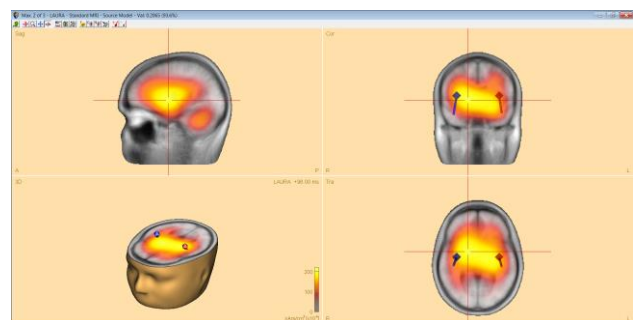
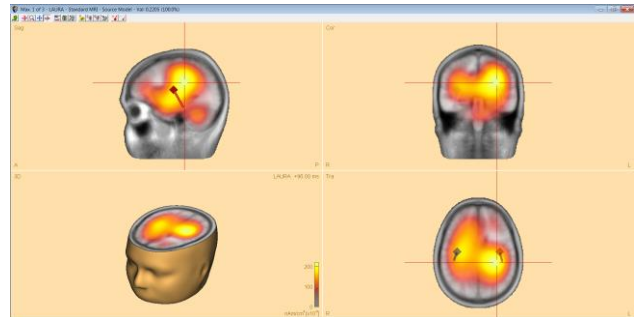


- The result is displayed superimposed to the anatomical MR image in the 3D window in the lower right corner of the source analysis window. Because for this subject, no individual MRI is available, BESA automatically uses a standard MRI. The regional source model is also shown and superimposed on the LAURA image. Press the  button in the 3D window to get a 4-head view. (You may also maximize the 3D window to get a larger view of the obtained LAURA image.)

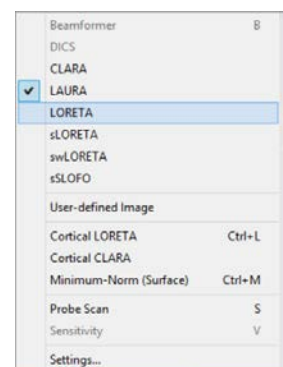


10. The units of the displayed LAURA images are nAm/cm³. The image correctly shows activity in both hemispheres. However, the focal activity is substantially blurred – a negative effect inherent in all distributed source images. It becomes evident from this example that this does not allow to draw any conclusion on the extent of the active brain regions.

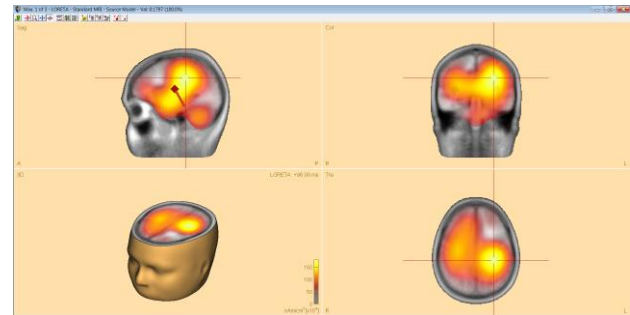
The LAURA image detected 3 maxima. The largest maximum is in the left hemisphere, roughly in the temporal lobe. Compared to the regional source it is located more medial, posterior, and superior. You can jump to the next maximum using the  **Button** (4th button from the right in the 3D window). The second maximum is roughly in the right-temporal lobe and located more medial inferior and anterior to the corresponding regional source. LAURA also detected a third maximum in the left cerebellum. The regional source model does not suggest activity there.



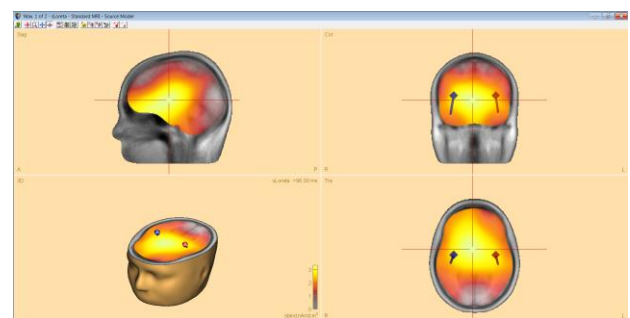
11. Compare the LAURA method with LORETA: Select **LORETA** from the image selector button dropdown menu. Like LAURA, LORETA includes a spatial cross-voxel weighting term, which increases the computational load, so that the first LORETA image computed for a data set



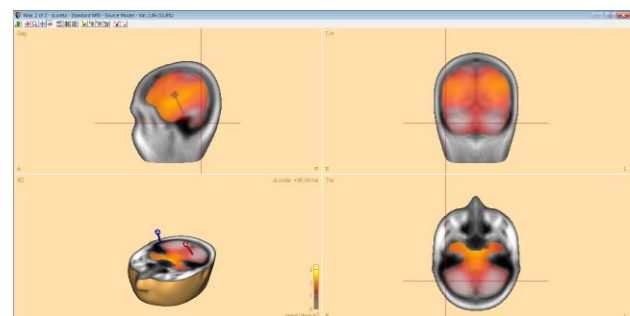
takes a longer time to complete than sLORETA or swLORETA. LORETA and LAURA often produce similar results: The first two maxima are located roughly in the temporal lobes; a third maximum is located in the cerebellum.



12. Compare the LORETA method with **sLORETA**: Select **sLORETA** from the image selector button dropdown menu. The result is an image (units: standardized nAm/cm3) with two maxima. The first maximum is located roughly in the middle of the head, the second maximum is located in the right cerebellum. There is no convergence between the discrete source solution and the sLORETA image.

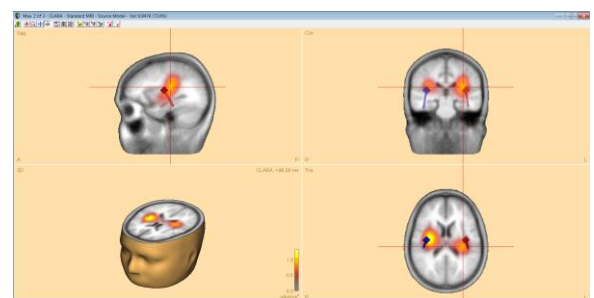
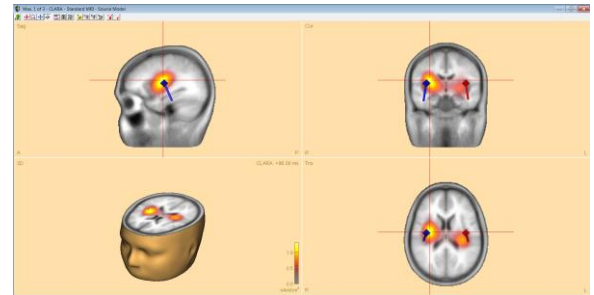


swLORETA additionally uses depth weighting but will come up with a very similar result; we will not pursue this method now.



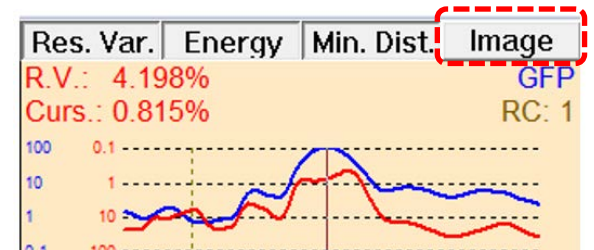
13. Iterative methods aim at combining advantages of discrete and distributed source images. Implemented as default methods in BESA Research are sSLOFO and the new CLARA method. Both methods iteratively apply distributed source images with a successive shrinking of the source space. They differ from each other in the type of distributed source images applied in this procedure.

14. Let us try out the **CLARA** method, an iterative application of weighted LORETA images. Select **CLARA** from the image selector button dropdown menu and observe that the result is much more focal than the previous methods, shrinking the activity substantially, and indicating bilateral activation of the supra-temporal lobes. The first two maxima are very close to the discrete source solution. CLARA detected a third maximum, again located in the cerebellum.

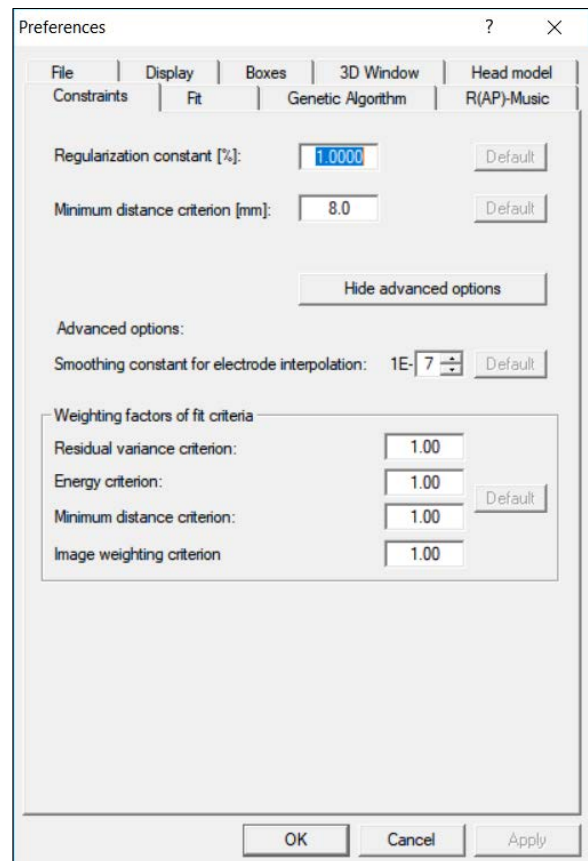


The other iterative method **sSLOFO** has a similar approach to CLARA but uses sLORETA during the iterative refinement of the initial result. The result is similar to CLARA; however the two main maxima do not coincide quite as closely with the regional sources. You can try it at your own discretion.

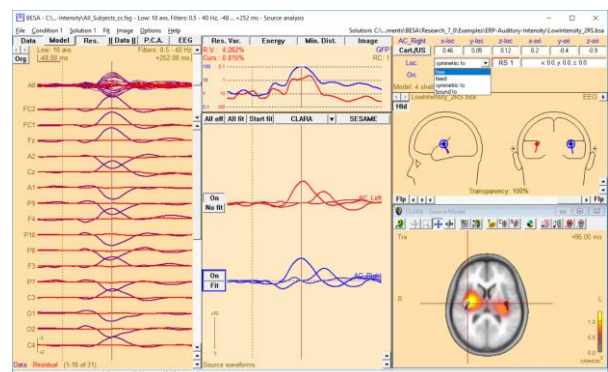
15. Next, we want to re-fit our discrete sources using Image weighting. Press the **Image** button in the top-right corner of the GFP and residual variance field. By default, only buttons for criteria Residual Variance,



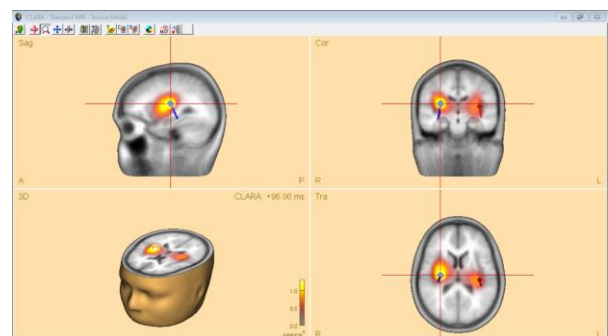
Energy and Minimum Distance are pressed. **Right-click** on the **Image** button and click on **Weighting Factors** to bring up the Preferences dialog. You can see that by default weighting factors Residual Variance, Energy, Minimum Distance and Image Weighting are treated equally (all are set to 1). This can be altered if desired. We will leave the default settings and press **OK**.



16. Click on the right-hemispheric source and change the symmetry constraint to **free** in the **Loc** drop-down menu.



17. Press **All Fit** and **Start Fit**. The regional sources are now fitted again with additional weighting by the current image. Maximize the MRI view to observe the new fitting-results. Close the source analysis window without saving anything.



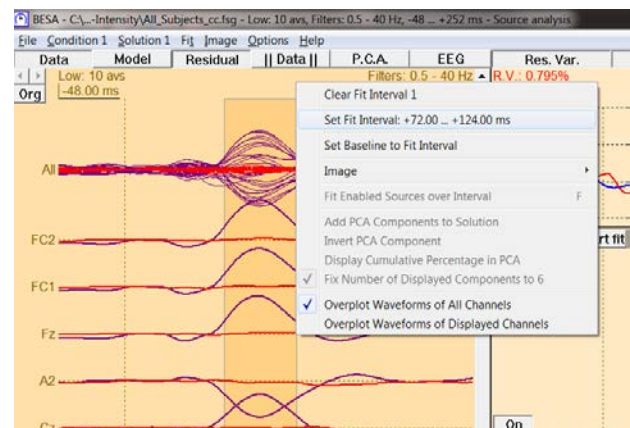
This first glance at the different imaging methods on our example dataset illustrates both the advantages and disadvantages of distributed source images: While they allow to get a very quick result at a certain latency, they all suffer from severe blurring (least in CLARA and sSLOFO), which can make it impossible to separate brain regions that are located close to each other. The different methods do not necessarily agree in their image maxima. It is not straightforward to determine which method is the most appropriate right away – the answer may be different in different data sets. Therefore, generally, a comparison of different methods is advisable.

To be able to interpret distributed source images, it is essential to understand their sensitivity towards the parameters that are applied during the computation. Especially regularization has a crucial effect on the result; this is demonstrated in the following.

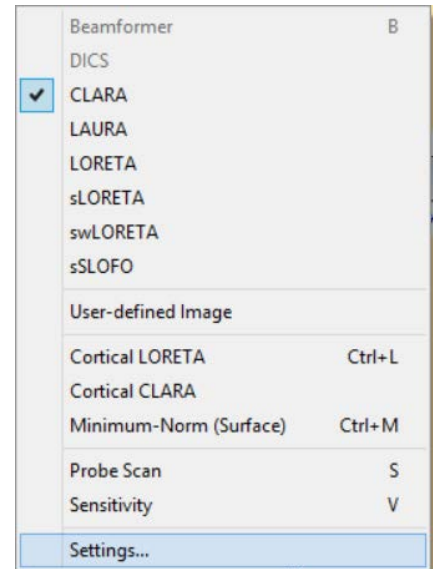
C. Settings for distributed source images: The effect of regularization

Distributed source images apparently have a big advantage over discrete multiple source models: They are quickly generated by a single mouse click, and the experimenter does not have to decide on the number of sources and the respective fit intervals. However, there is an important parameter also for distributed source images that has to be decided on: the regularization parameter, which can have a large impact on the quality of the obtained source images. This is illustrated in the following.

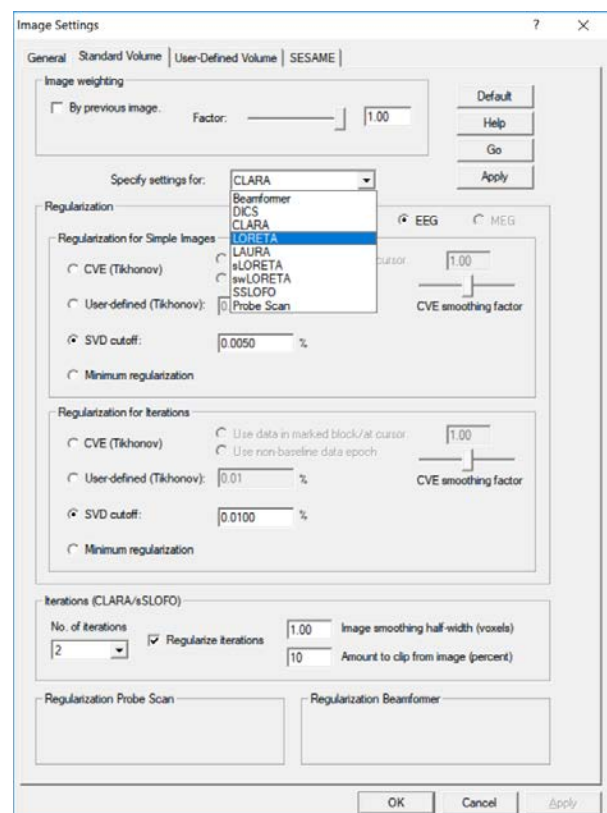
1. As an example, we will compare **LORETA** images with different regularization settings. We could use images computed for the cursor time only, as we did in the previous chapter. Alternatively, we can mark an extended latency interval. By default, BESA research will then compute a mean image over that interval. This is of advantage in noisy data because it reduces the noise influence. **Left-drag** to mark a fit interval from **72 to 124 ms** to include the time range around the N100 peak. Note that you can drag the edges of the interval, or right-click into it and select **Set Fit Interval** to adjust the time range.



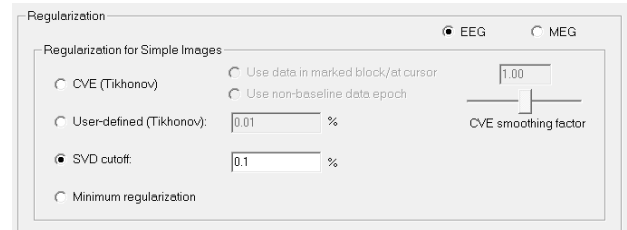
- Regularization and other imaging parameters can be specified in the **Image Settings** dialog window. Open it by pressing **Image / Settings** or from the bottom of the image selector button dropdown menu.



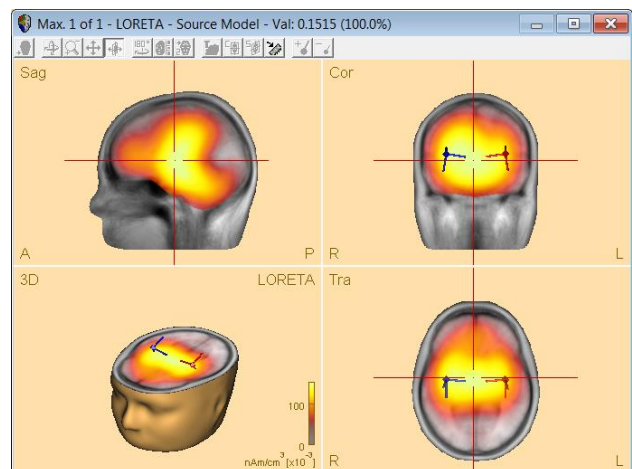
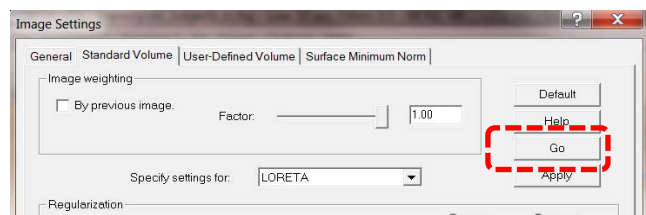
- The **Image Settings** dialog window for volume imaging consists of three tabs: The **Standard Volume** tab lists all adjustable parameters of the standard distributed volume images. We will focus here on the effect of the **regularization** parameter, which has a critical influence on all distributed source images. Parameters can be specified separately for each imaging method (and differently for EEG and MEG). The window displays the parameters of one method at a time only. From the upper dropdown menu, select **LORETA** to adjust the LORETA parameters only.



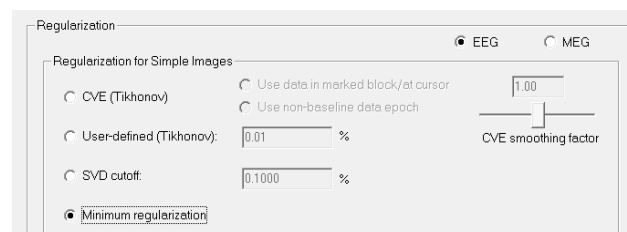
- We will now compute and compare images with different regularization constants. The default is an SVD cutoff of 0.005%. First observe the effect of too high regularization: Increase the SVD cutoff to **0.1%**.



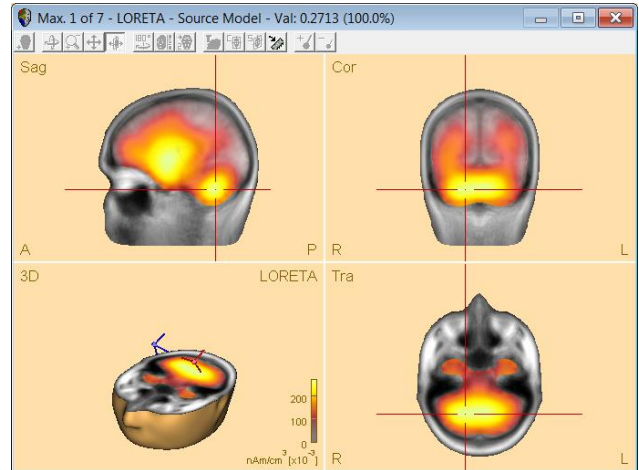
- Press **Go** in the Image Settings dialog window to apply the current settings and compute a LORETA image with too high regularization: In contrast to the result of the multiple dipole model, the LORETA image suggests a single midline generator of the recorded signals. This is a typical result of a too strong regularization: This tends to lead to deep, widely distributed image maxima. In our example, the bilateral activity of the left and right auditory cortex are combined and mis-localized in the middle of the head.



- Now compare too high with too low regularization: Select **Minimum regularization** to use only the minimum regularization required for numerical reasons.

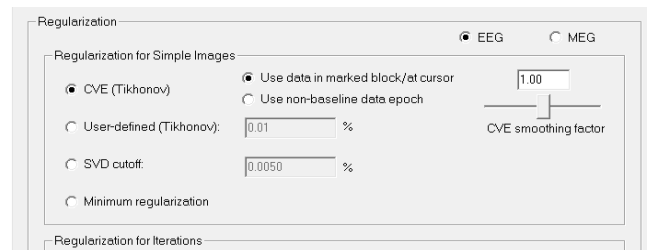


7. Press **Go** again to recompute the LORETA image. In contrast to a too high regularization constant, we now obtain a solution with many maxima. This is a typical effect of too low regularization.

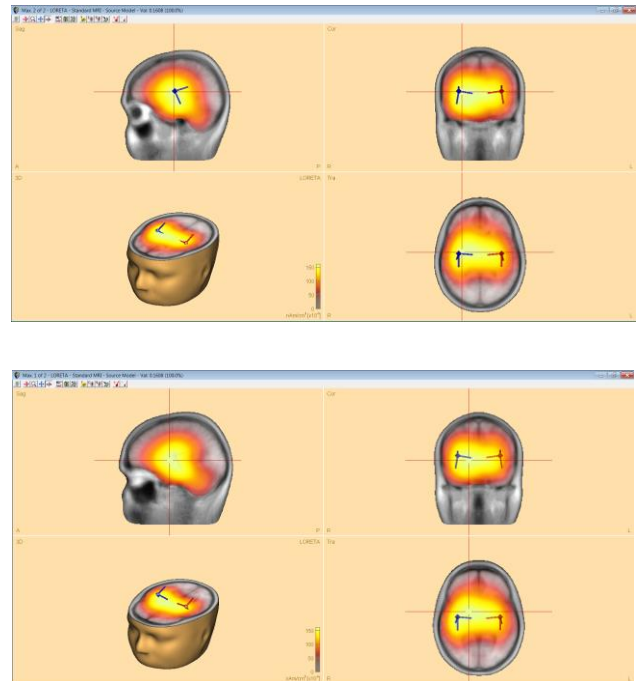


The above examples were computed with SVD regularization, but the same principle holds for Tikhonov regularization as well. You may test this by selecting the user-defined Tikhonov regularization in the Image Settings dialog window and compute LORETA images with different parameters.

8. How to determine the optimum regularization parameter for a given data set and imaging method is still an unsolved problem. Minimization of the generalized cross validation (CVE) is an attempt to achieve this. However, this method is not guaranteed to work properly in every data set and with every method. We will compute a LORETA image with the regularization determined automatically by CVE minimization. Select **CVE** and have the regularization optimized to the **Data in marked block**. Press **Go**.



9. The resulting automatically chosen regularization appears to be slightly higher than the default value of 0.005% (the image contains 2 rather than 4 maxima). The *second* maximum corresponds well with the regional source in the right hemisphere, but the *first* maximum mislocalizes to a right medial temporal area.

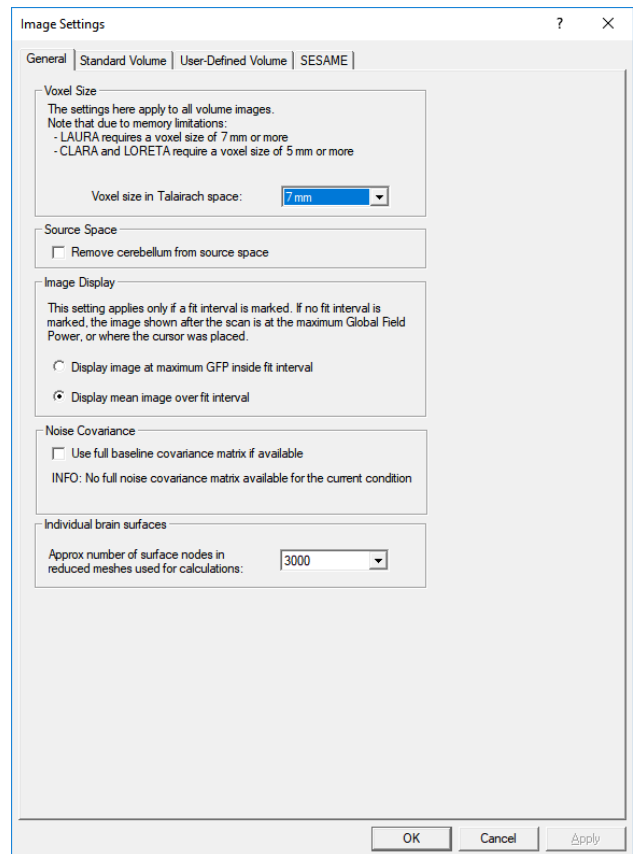


BESA uses predefined default regularization constants specific for each method and channel type. These default values are appropriate in many situations. However, the optimum regularization depends on the signal-to-noise ratio of the data, the number of channels and other properties of the specific data at hand. **There is no strict objective criterion for the choice of the optimum or correct regularization parameter.** However, it is generally recommended to adjust the regularization parameter such that the obtained image neither shows too many, superficial maxima (too low regularization) nor only one or two very broad midline maxima (too high regularization).

D. Other image settings

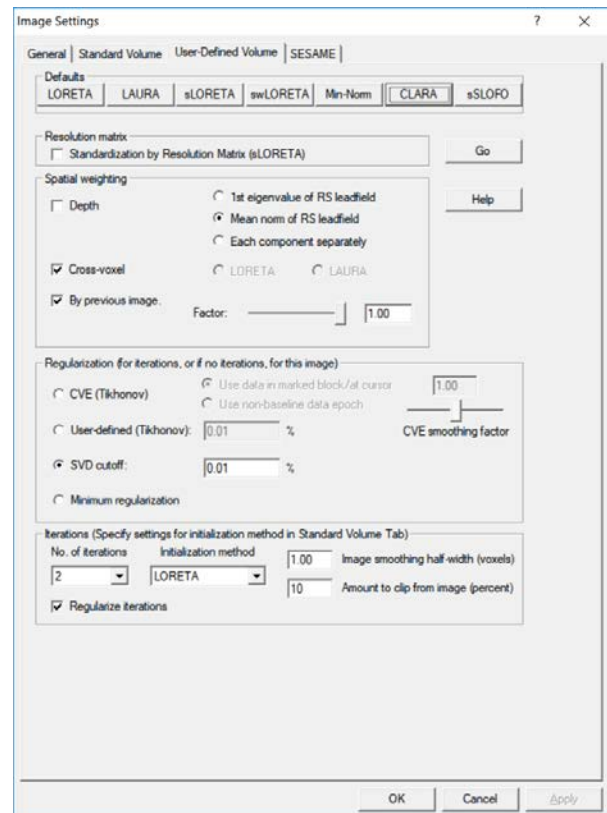
1. The Image Settings dialog window not only allows to modify parameters of the pre-defined imaging methods. Select the **General** tab. Here the **grid spacing** of the source grid used for the 3D volume imaging methods can be specified. The default setting is a spacing of 7 mm, which is appropriate for the rather distributed images in most situations.

Another setting allows to specify which kind of image to display when a fit interval is marked. BESA Research computes a separate image for each latency within the fit interval. With the default setting, the **mean image** across the different latencies in the fit interval is computed and displayed. Alternatively, you can have BESA Research to automatically set a cursor at the latency of **maximum global field power** and display the corresponding image.

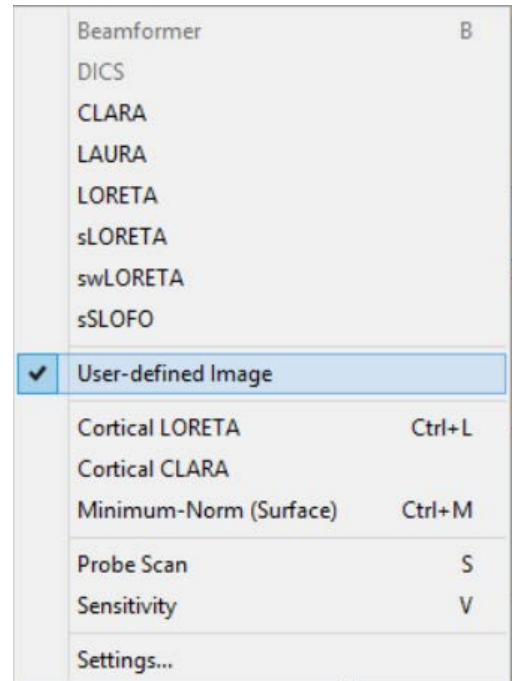


2. It is also possible to create a user-defined volume imaging method: Switch to the **User-Defined Volume** tab. Here, a wide range of parameters can be specified.

- In box **Resolution Matrix**, specify whether you would like to standardize your image with the resolution matrix entries as in sLORETA.
- In box **Spatial Weighting**, different types of depth weighting can be selected. Cross-voxel weighting as in LORETA (3D Laplacian) and LAURA (local autoregressive function) can be applied. In addition, an additional spatial weighting can be imposed by the previously generated or imported 3D image (e.g. an imported fMRI image). The strength of the image weighting can be adjusted by the Factor sliding bar.
- The **Regularization** parameters specified in this tab are in analogy to those in the Standard Volume tab.
- The **Iterations** box allows to define iterative methods in which the source space is shrunk in each step, leading to more focal images. An initialization image can be selected, defining the initial voxel weight (this image is regularized as specified in the Standard Volume tab). In each iteration step, the image is then smoothed, and the source space clipped with the parameters specified here.
- The **Default** buttons in the upper row set the parameters to those of the respective pre-defined imaging method so that you can understand the details of those methods and can easily modify them if you wish to.



3. After specifying the settings, you can compute a user-defined image by selecting the corresponding entry from the list of images.



E. Brain atlases

A brain atlas can be overlaid on discrete or distributed sources in the 3D window. Please remember that brain atlases are created using either averaged data or single-subject post mortem data, and might not fully correspond to your subject's individual MRI data. For details about how each atlas is created please refer to the author's publication. If you use a brain atlas in your publication, please cite the corresponding work as reference. In BESA Research, the following atlases are available:

- **Brainnetome** (Fan, Lingzhong, Hai Li, Junjie Zhuo, Yu Zhang, Jiaojian Wang, Liangfu Chen, Zhengyi Yang, et al. 2016. The Human Brainnetome Atlas: A New Brain Atlas Based on Connectional Architecture. *Cerebral Cortex* 26 (8): 3508–26)
- **AAL** (Tzourio-Mazoyer, N., B. Landeau, D. Papathanassiou, F. Crivello, O. Etard, N. Delcroix, B. Mazoyer, and M. Joliot. 2002. Automated Anatomical Labeling of Activations in SPM Using a Macroscopic Anatomical Parcellation of the MNI MRI Single-Subject Brain. *NeuroImage* 15 (1): 273–89)
- **Brodmann** (Damasio, Hanna, and Antonio R. Damasio. 1989. *Lesion Analysis in Neuropsychology*. Oxford University Press, USA)
- **AAL2015** (Rolls, Edmund T., Marc Joliot, and Nathalie Tzourio-Mazoyer. 2015. Implementation of a New Parcellation of the Orbitofrontal Cortex in the Automated Anatomical Labeling Atlas. *NeuroImage* 122 (November): 1–5)
- **Talairach** (Talairach, J, and P Tournoux. 1988. *Co-Planar Stereotaxic Atlas of the Human Brain. 3-Dimensional Proportional System: An Approach to Cerebral Imaging*. Thieme)
- **Yeo7 and Yeo17** (Thomas Yeo, B.T., Krienen, F.M., Sepulcre, J., Sabuncu, M.R., Lashkari, D., Hollinshead, M., Roffman, J.L., Smoller, J.W., Zollei, L., Polimeni, J.R., Fischl, B., Liu, H., Buckner, R.L., 2011. The organization of the human cerebral cortex estimated by intrinsic functional connectivity. *Journal of Neurophysiology* 106, 1125–1165)

F. Atlas based source montages

In addition to the atlases, we created atlas-based source montages. Montages are available for the following atlases:

- AAL (Automated Anatomical Labeling)
- AAL_2015 (Automated Anatomical Labeling revision 2015)
- Brainnetome
- Brodmann
- Desikan-Killiany*
- Talairach

*(Desikan, R.S., Ségonne, F., Fischl, B., Quinn, B.T., Dickerson, B.C., Blacker, D., Buckner, R.L., Dale, A.M., Maguire, R.P., Hyman, B.T., Albert, M.S., Killiany, R.J., 2006. An automated labeling system for subdividing the human cerebral cortex on MRI scans into gyral based regions of interest. *NeuroImage* 31, 968–980.

There are three types of source montages:

- Regional source (RS)
- dipole-source (SD)
- Beamformer source (BF)

The sources in dipole-source based montages have radial orientations, pointing towards the center of the brain. All sources are regularized with a regularization constant of 1%.

These montages (except Desikan-Killiany) were generated using [Brain Atlases](#) available in source analysis. Each source in the atlas-based montage was created in the center of gravity of the corresponding region in the atlas.

Desikan-Killiany atlas is a surface-based atlas therefore different method for defining the position of sources had to be used. We adopted the approach proposed in [brainGraph v.3.0.0](https://github.com/cwatson/brainGraph) (<https://github.com/cwatson/brainGraph>) that exploits graph theory analysis for brain MRI data.


The sources in the cerebellum and deep brain as well as sources lying in very small regions, were removed from the montages (except for Brodmann). The coloring of the sources as well as labels correspond to the Brain Atlases. For each montage the information about exclusion criteria together with removed sources and the corresponding solution file (*.bsa) that can be [loaded as a solution](#) in the Source Analysis module are located in the public user documents folder: **<Public>\Documents\BESA\Research_7_1\Montages\Atlas Montages**

The Regional source and single dipole atlas-based source montages are available in main BESA Research window and can be enabled either from toolbar (**SRC** button) or from top menu **Montage\Source\AtlasMontages**.

In addition to this, there is also an additional solution file for each atlas ending in the suffix **_BF** located in aforementioned directory. This solution file contains Beamformer virtual sensor sources and can be used to create a source montage from Beamformer in Time-domain analysis results. This will be described in detail in **Error! Reference source not found**.

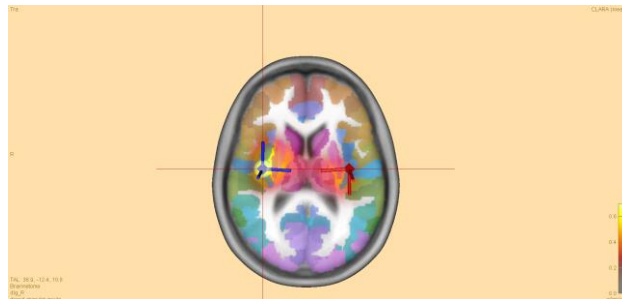
Below it is illustrated how to turn on the brain atlas and how to change settings.


1. Use the dataset and fitting interval in source analysis settings from chapter C of this tutorial (**72 to 124 ms**). Go to **Image / Volume Image /Settings...** and switch to settings for **CLARA**, then press the **Default button** and **Go button** afterwards. Close window by pressing **OK button**. The CLARA results are displayed alongside the discrete solution (two regional sources).

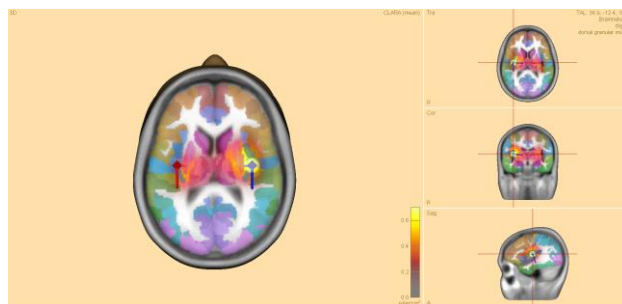
Press  on the toolbar (or **Shift-A**) to turn on brain atlas overlay. A Brainnetome atlas will be displayed using contour blending mode. Note that the crosshair position in Talairach coordinates along with the region name is provided.





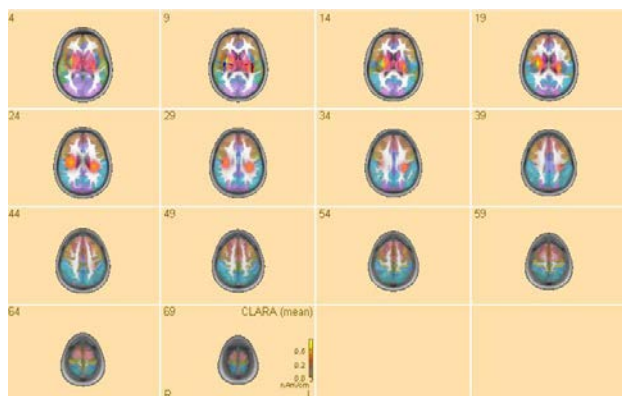
2. **Right click** on the empty area in the 3D window and from the popup menu select **Atlas Blending Mode / brainCOLOR**.



3. Press  on the toolbar (or **Shift-U**) to switch to **Multiple view**.

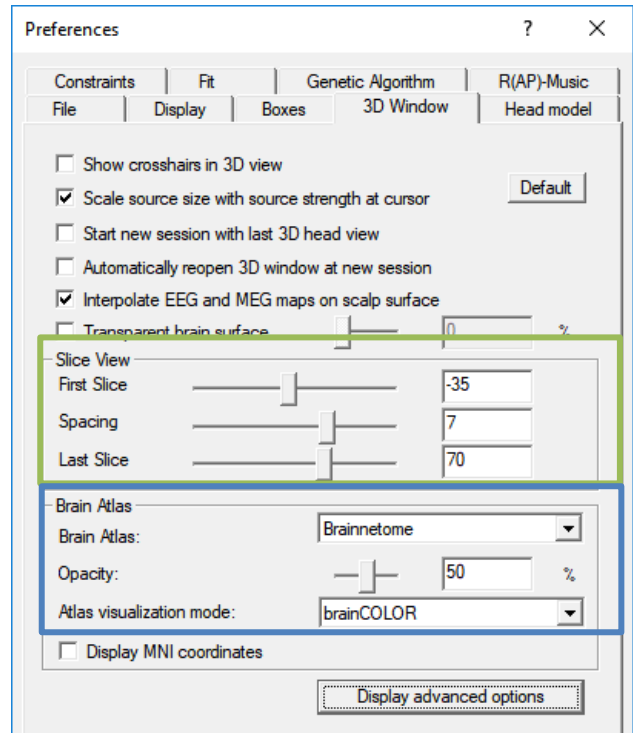


4. Now the icon has changed to . Press this icon on the toolbar (or **Shift-U**) to switch to **Slice view**. This view can help better visualize the results and provides a succinct overview over multiple slices. To return to the default single view press this icon  (or **Shift-I**).



Note: Multiple slice view is the preferred display mode in scientific publication as it gives a wide overview of the whole brain activity. For such purposes you can also easily switch all BESA Research windows to a color neutral theme by unchecking the **Color Background in Result Windows** under **Options\Display** in the main **BESA Research** window menu bar.

5. **Right click** on the empty area in the 3D window again and from the popup menu select **Options....** Here more settings for slice view (in green) can be adjusted. The First and the Last slice can be selected to focus on a particular area. Spacing of the slices can be adjusted to view the desired number of slices in a single view. Similarly, more settings for brain atlas (in blue) can be adjusted from here. From the **brain atlas** drop-down menu, different brain atlases can be selected. With the slider **opacity** the opaqueness of the brain atlas overlay over the MRI image can be adjusted. Finally, the **visualization mode** can be changed here by selection of the mode from the drop-down menu.

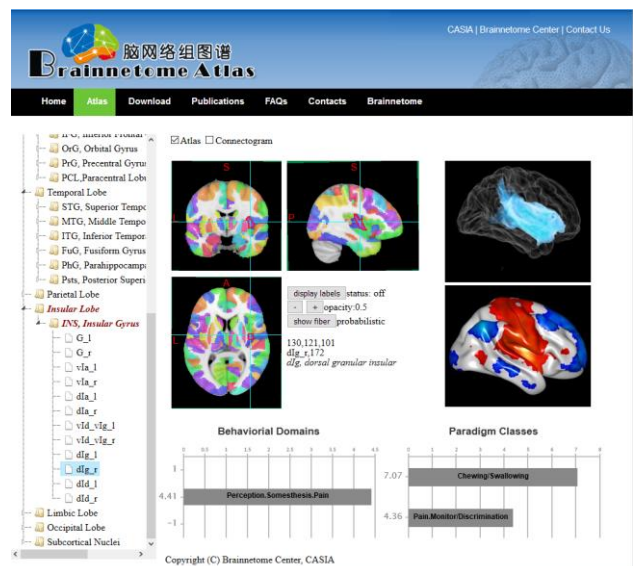


6. The Brainnetome atlas project provides additional details about parcellated regions. **Please visit:**

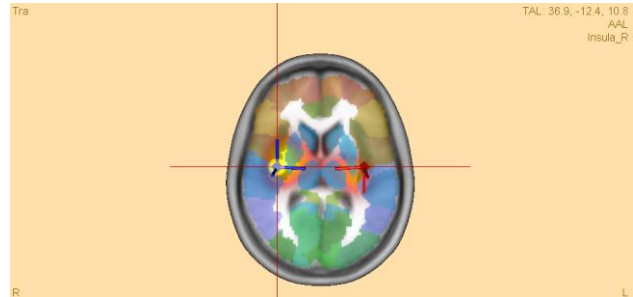
<http://atlas.brainnetome.org/bnatlas.html>

In the online version of the atlas the following information can be found about every brain region (indicated in BESA Research):

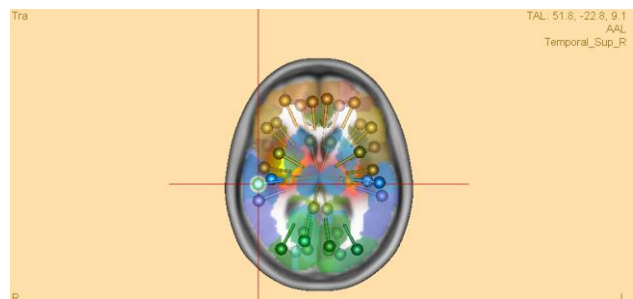
- Anatomical connections to the other brain regions (white matter)
- Behavioral domains
- Paradigm classes
- Connectogram



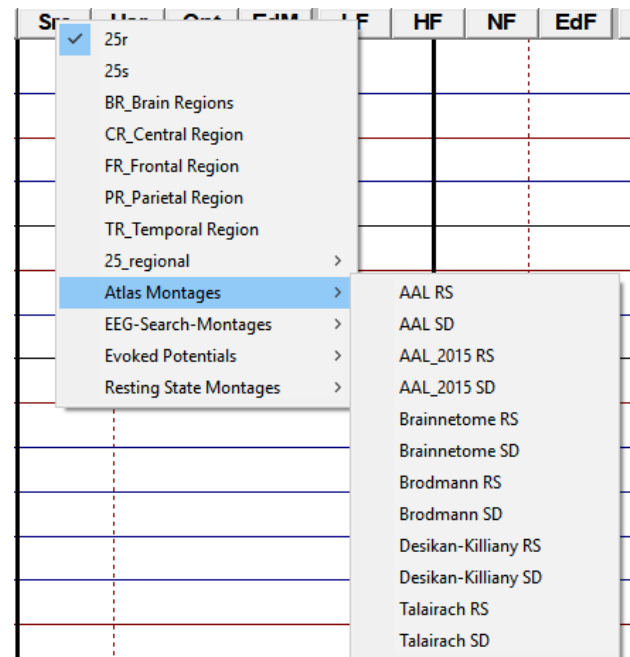
- Go back to BESA Research Source Analysis window. The preference dialog will still be open. Change the **Brain Atlas** option to **AAL** and click **OK**. The Brain Atlas is now switched to **AAL**.



- Press **File / Open Solution** (or **Ctrl-O**) and select **User Montages** under **Folders**. Go one level up and inside the **Atlas Montage** folder select the **AAL_SD.bsa**. Press **Open**. A solution based on **AAL** Atlas is opened with **85** sources. See how the atlas compares with the previous solution.



- Close the **Source Analysis** window. In the main BESA Research window press the **SRC** button and click **Atlas Montages** option. A list of montages based on various atlases is shown. Click the **AAL SD** option. The data is now displayed as a montage based on **AAL**. Review the data, note that sources in the temporal atlas region picks up more signal when compared to the other regions.



G. Export and import options

All images obtained in BESA Research can be exported for further analysis (e.g. for averaging and statistics in BrainVoyager or MATLAB). Images can also be imported into BESA Research.

These will then be displayed superimposed to the available MR image (the BESA standard MRI or the individual MRI of the corresponding subject). In addition, images can be used to define an initial spatial weighting for the different brain regions – both for distributed 3D images (see above) and for a discrete multiple source fit, as will be demonstrated in the following.

- Image ASCII Files (*.dat), BrainVoyager VMP Files (*.vmp) and ANALYZE files (*.hdr): Selection of one of these three formats leads to the export of exactly the currently displayed 3D volume image. The resulting image file contains one image intensity for each grid location (as specified in the Volume Grid Spacing tab of the Image Settings dialog window. The ASCII format contains the image in its original resolution (as specified in the Volume Grid Spacing tab of the Image Settings window). ANALYZE files will be interpolated to a 1x1x1mm³ resolution. The BrainVoyager format allows for both options.
- Same as above but type all latencies: These options not only export the currently displayed image at the cursor latency, but rather multiple images (one for each latency in the available data set). In the present example, selecting one of these file types would export LORETA images for each latency into one file. This file then contains the image intensities for each location at each latency. This option is not available for iteratively generated source images.
- Image Ascii Voxel Time Series (*.vts): Exports the image intensity of the voxel at the current crosshair position at all latencies.
- Voxel values for each dipole orientation (*.dat): This generates an ASCII file that not only contains the image intensities (i.e. the magnitude of the regional source activity at each grid location), but rather exports the activity of all 3 components of each regional source separately. This results in 3 activity values for each grid location.

Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

What does BESA Research provide?

- ✓ SESAME
- ✓ Cortical LORETA
- ✓ Cortical CLARA
- ✓ Minimum Norm
- ✓ Age-appropriate template head models

Distributed Sources: Bayesian Source Imaging, Surface Methods and Age-Appropriate Template Head Models

This tutorial will explore the different methods available for surface imaging, and also introduce the age-appropriate template models as an alternative to a realistic head model.

A. Background

Volume imaging using Bayesian methods

Bayesian source imaging uses the idea of sampling the posterior probability distribution using assumptions about prior distributions. BESA Research implements the method **Sequential Semi-Analytic Monte-Carlo Estimation** (SESAME) of sources (Sommariva and Sorrentino 2014, Sorrentino et al. 2014). It allows to automatically estimate simultaneously the number of dipoles, their locations and time courses requiring virtually no user input.

The algorithm is divided in two blocks:

The first block consists of a Monte Carlo sampling algorithm that produces, with an adaptive number of iterations, a set of samples representing the posterior distribution for the number of dipoles and the dipole locations.

The second block estimates the source time courses, given the number of dipoles and the dipole locations.

The Monte Carlo algorithm in the first block works by letting a set of weighted samples evolve with each iteration. At each iteration, the sample (a multi-dipole state) approximates the n -th element of a sequence of distributions p_1, \dots, p_N , that reaches the desired posterior distribution ($p_N = p(x|y)$). The sequence is built as $p_n = p(x) \cdot p(y|x) \alpha(n)$, such that $\alpha(1)=0$, $\alpha(N) = 1$. The actual sequence of values of alpha is determined online. Dipole moments are estimated after the number of dipoles and the dipole locations have been estimated with the Monte Carlo procedure. This continues until a steady state is reached.

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Prior distribution assumptions are:

- Poisson distribution for the number of sources
- Uniform distribution for the source locations
- Gaussian distribution for the dipole moments

Dipole locations are constrained to pre-defined grid points. Perturbation of the dipole locations exploits a neighbours matrix. The output is a posterior probability for number of dipoles, and a 3D probability map for dipole locations.

References:

Sommariva S and Sorrentino A: Sequential Monte Carlo Samplers for Semi-Linear Inverse Problems and Application to Magnetoencephalography. Inverse Problems 30(11):114020, 2014

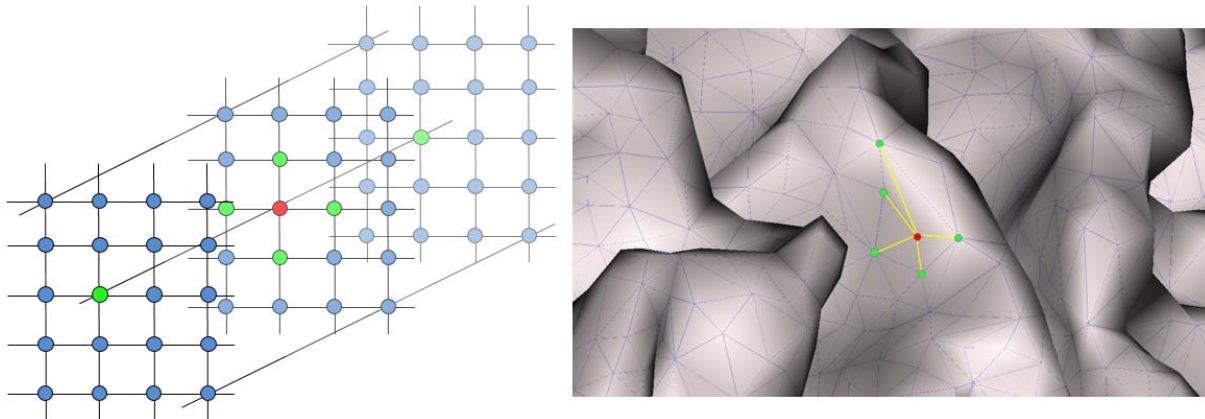
Sorrentino A, Luria G, Aramini R: Bayesian Multi-Dipole Modeling of Single MEG Topographies by Adaptive Sequential Monte-Carlo Samplers. Inverse Problems 30(4):045010, 2014

Surface imaging methods

Volume imaging methods typically work on a regular grid that spans the brain, which serves as source space for potentially active sources. There are no particular constraints as to where in this source space a source is allowed to be, or how it should be oriented.

Surface imaging methods use a mesh which reconstructs the brain surface. The source space is then usually constrained to this cortex region. In some cases, orientations are also constrained to be perpendicular to the surface, or allowed to vary in a cone around the perpendicular orientation.

Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models



Left: In a volume image, neighborhood is defined on a grid. **Right:** On the surface, the neighborhood relationship depends on the mesh.

If spatial weighting terms are used, then the neighborhood comes into play. Considering the formulation of the inverse problem introduced in Tutorial 7 – Distributed Sources I: Volume Methods, the spatial weighting matrix V has diagonal terms, and off-diagonal terms. The diagonal terms can be used for e.g. depth weighting. Off-diagonal terms describe the influence of neighboring nodes in the grid or mesh.

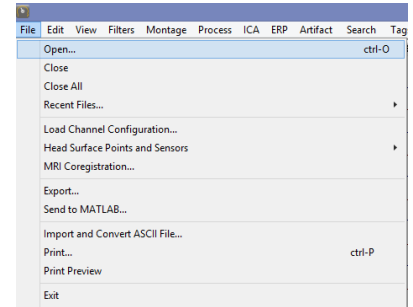
The cortical methods discussed here in more detail, Cortical LORETA and Cortical CLARA, use a surface Laplacian operator. The Minimum Norm method uses no neighborhood information – only diagonal weights are applied in the V matrix.

Cortical CLARA is a method which iteratively applies a Cortical LORETA to the data set. After each iteration, the source space is reduced by eliminating the sources with the smallest signal. Also, the result of the current iteration will be used as an additional spatial weighting term for the computation of the next iteration. After several iterations, the solution approaches a focal solution, which, if a large number of iterations are applied, may result in a focus of activity on few individual mesh nodes, which makes it comparable to a solution using discrete sources.

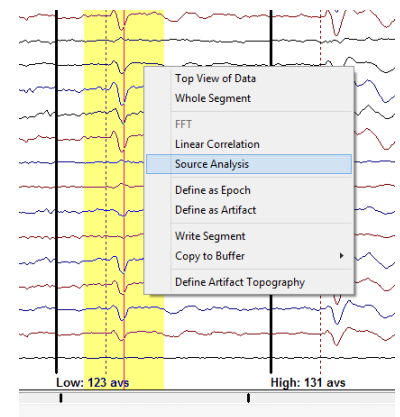
B. Source imaging with SESAME

Let us apply the Bayesian approach to the auditory data example.

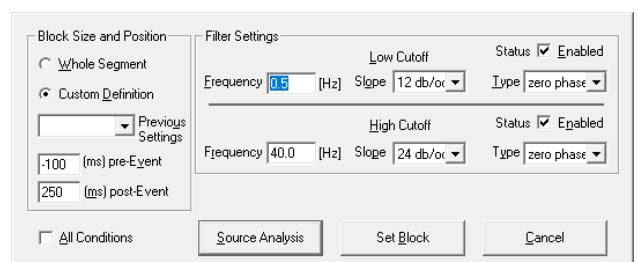
1. Select the file **All_Subjects_cc.fsg** from the folder **ERP-Auditory-Intensity**.



2. Select condition **Low**, **left-drag** a block and send it to source analysis by **right-clicking** and pressing **Source Analysis**.




3. Select a time range from **-100 to 250 ms**, and specify a **Low Cutoff filter of 0.5 Hz, 12dB/oct, zero-phase** and a **High Cutoff filter of 40 Hz, 24 dB/oct, zero-phase**. Press **Source Analysis** to open the specified data in the source analysis window.

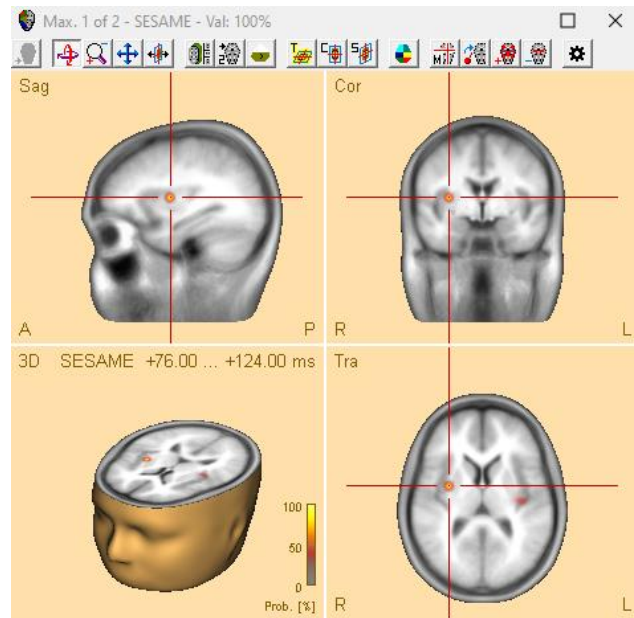



4. Drag a fit interval from **76 ms to 124 ms** over the data. Then press the **SESAME** button in the center of the screen.

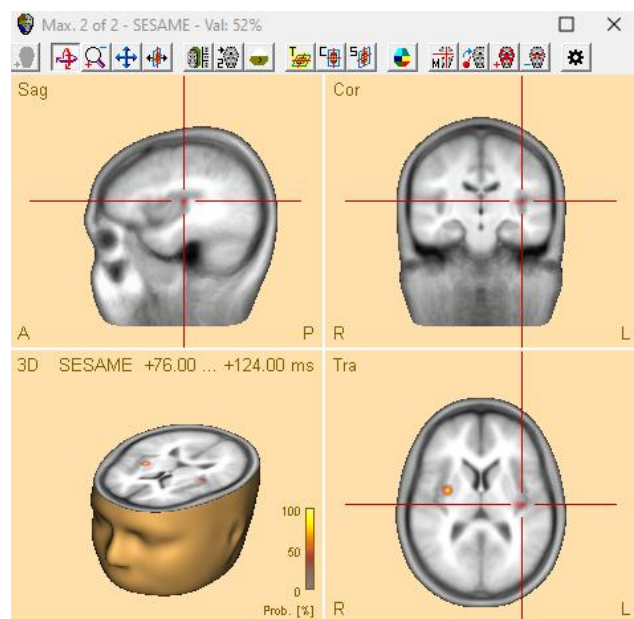
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5. During computation, press the  button in the toolbar of the 3D window to follow the live update (you may have to press it twice to enforce the action). Note how the number of maxima indicated in the title bar of the 3D window changes over time.

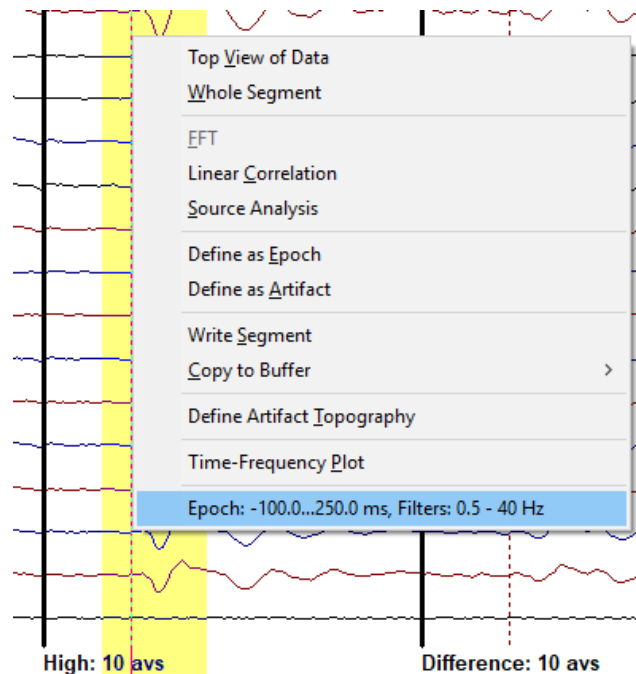


6. Toggle through the maxima using the **Maxima** button  in the toolbar. Note that after the end of computation, there are only two maxima; they appear in lateralized areas, one slightly anterior and medial, the other one very close to where the auditory cortex is expected.

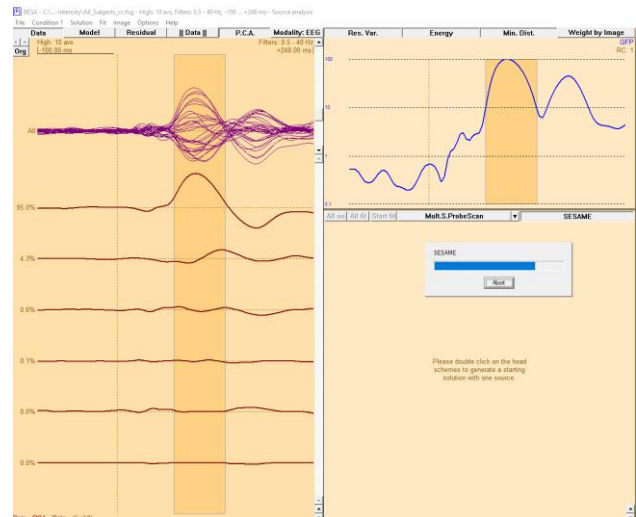


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- Minimize the Source Analysis window. Now **drag** over the condition **High**, **right-click** and select the **last entry in the popup menu**. This will send the **High** condition to the Source Analysis window.

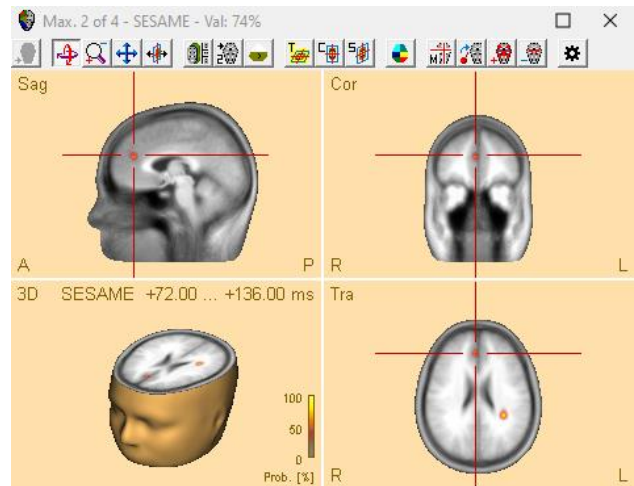


- In the Source Analysis window, **drag** a block in the **global field power display** to mark an interval from **72 ms** to **136 ms**, which covers the interval where global field power exceeds 10%, and the main activity in the butterfly plot. Then press the **SESAME** button again.



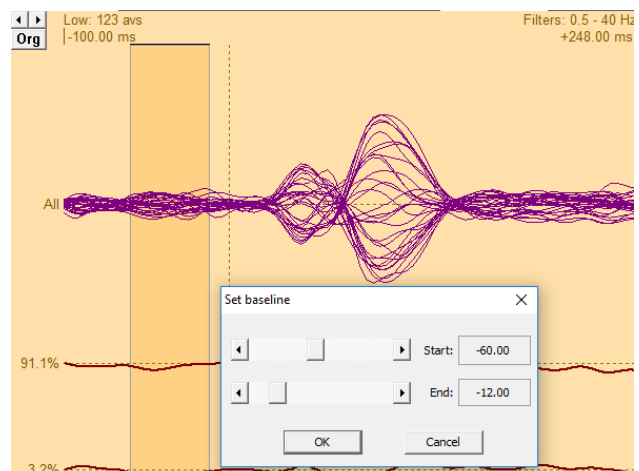
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9. One peak shows the cingulate activity that we modelled in the discrete source analysis earlier. Toggle through the other maxima: Two of them represent the auditory activity; the last one is insignificant. Note that this result was obtained without the need for sequential dipole fitting, in a completely automated fashion.



10. Open the Image Settings (available from the [dropdown arrow](#) in the centre of the screen). When you browse to the **SESAME** tab, you can see that the noise variance computed over the baseline interval is shown at the bottom. There are two parameters that can be adjusted: **Noise Scale Factor**, and **Source Scale Factor**. Close the dialog box.

11. We have seen a very good solution obtained with a fully automated approach. For the sake of argument, let us assume that the baseline interval was not well defined, or not defined at all (possible e.g. if you used pattern search for finding peaks of activity in the data, and averaged these). In this case, you can change the baseline interval definition:



12. Above the butterfly plot, [click](#) on the **left arrow** at the top left of the window to switch

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back to the previous condition. Then [click](#) on the **baseline indicator** at the top left above the butterfly plot (or use the menu entry [Condition / Baseline interval](#)) to open the dialog for setting the baseline. Adjust the baseline to **-48 ms ... -12 ms** using the sliders. Press OK. Note that the horizontal line showing the baseline has changed.

13. Open the **Image settings** again and browse to the **SESAME** tab. Note that the noise variance has changed from 0.12 to 0.08. This reduced noise variance estimate would now potentially result in an image with less regularization, which could lead to more maxima. Similarly, increasing the values for **Noise Scale Factor**, and **Source Scale Factor** would have the effect of more regularization. Leave with [OK](#) and [close](#) Source Analysis.

Notes for using SESAME:

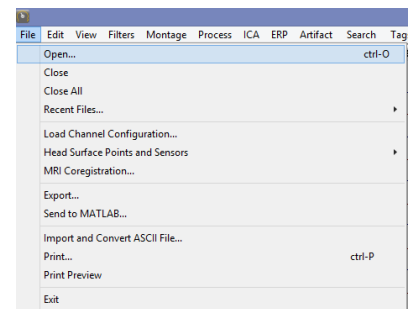
The noise variance is a very important parameter for the SESAME method. It should be ensured that the data set contains a large enough baseline interval. You can manually adjust the baseline interval by clicking on the baseline indicator at the top left. This is especially important when pattern search was used to create an average.

Computation time rises non-linearly with the number of channels used. One measure to reduce the computation time is to increase the spacing between grid points, e.g. to 10 mm.

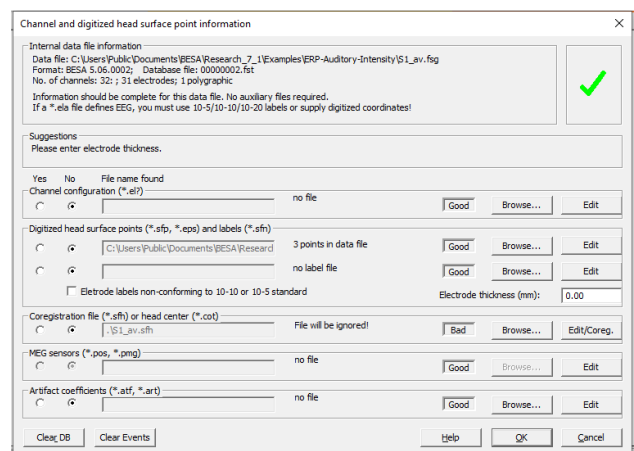
C. Comparison of different surface imaging methods

We will now compare the different surface imaging methods using the auditory intensity experiment data. When investigating surface data, we often want to use the individual anatomy, or a representation that is as close as possible. We will first look at one subject from our auditory intensity pool.

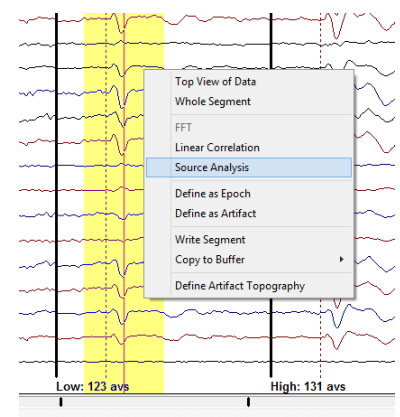
1. Open the file **S1-av.fsg** in the folder **ERP-Auditory-Intensity**.



2. Press **CTRL-L** on the keyboard and ensure that the additional files we loaded in a previous tutorial will not be used to begin with – we will use these again later. So, please make sure that the rows for Digitized Head Surface Points and Coregistration file are set to “No”. Leave with **OK**.



3. Select condition **Low**, **left-drag** a block and send it to source analysis by **right-clicking** and pressing **Source Analysis**.




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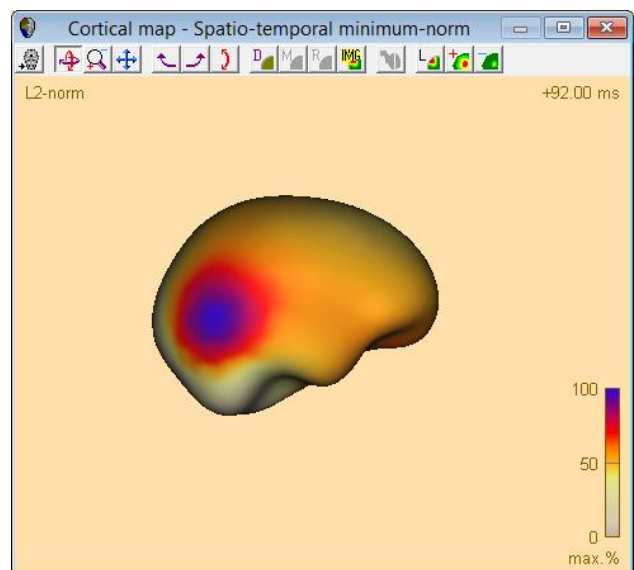
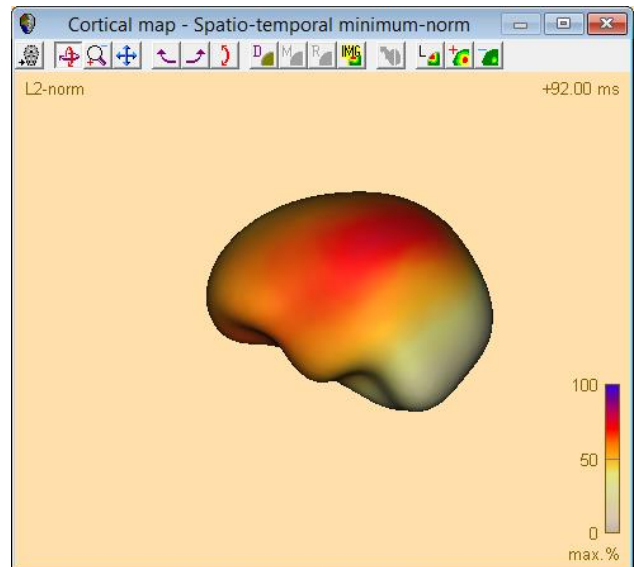
- Select a time range from **-50 to 250 ms**, and specify a **Low Cutoff filter of 0.5 Hz, 12dB/oct, zero-phase** and a **High Cutoff filter of 40 Hz, 24 db/oct, zero-phase**. Press **Source Analysis** to open the specified data in the source analysis window.

- Ensure that the head model is set to “**4-shell ellipsoidal**”. Then use the arrow button in the centre of the Source Analysis window to select **Minimum Norm** from the popup menu.

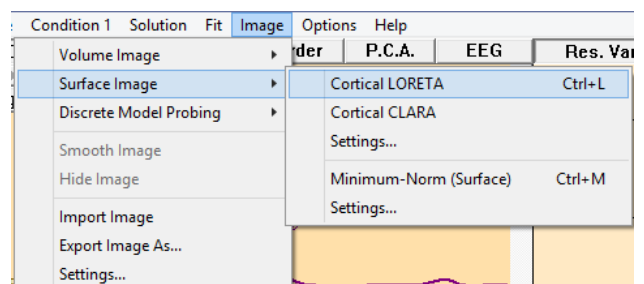
Beamformer	B
DICS	
CLARA	
LAURA	
LORETA	
sLORETA	
swLORETA	
sSLOFO	
User-defined Image	
Cortical LORETA	Ctrl+L
Cortical CLARA	
✓ Minimum-Norm (Surface)	Ctrl+M
Probe Scan	S
Sensitivity	V
Settings...	

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6. A cursor is automatically set at the peak of the global field power at 92 ms. A minimum norm estimate is computed with the default settings and is displayed on the standardized smoothed surface reconstructed from an average of 50 brains. The result is a broadly smeared distribution in the left hemisphere. Use the toolbar buttons  to rotate the brain. A more focal maximum is visible in the right hemisphere, posterior to the Sylvian fissure where we would have expected the bulk of activity.

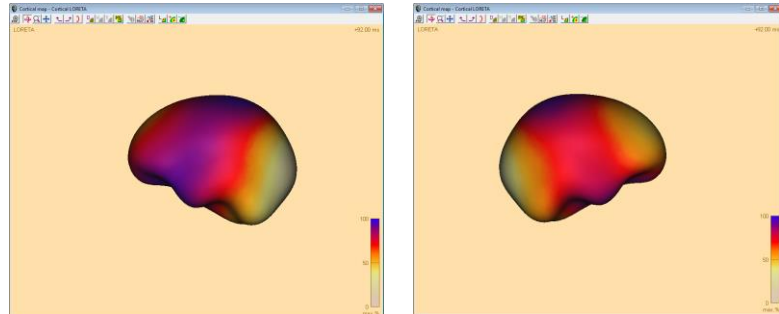



7. Use the **arrow** in the centre of the screen again to select **Cortical LORETA**, or select the entry from the menu **Image** and the sub-menu **Surface Image**.

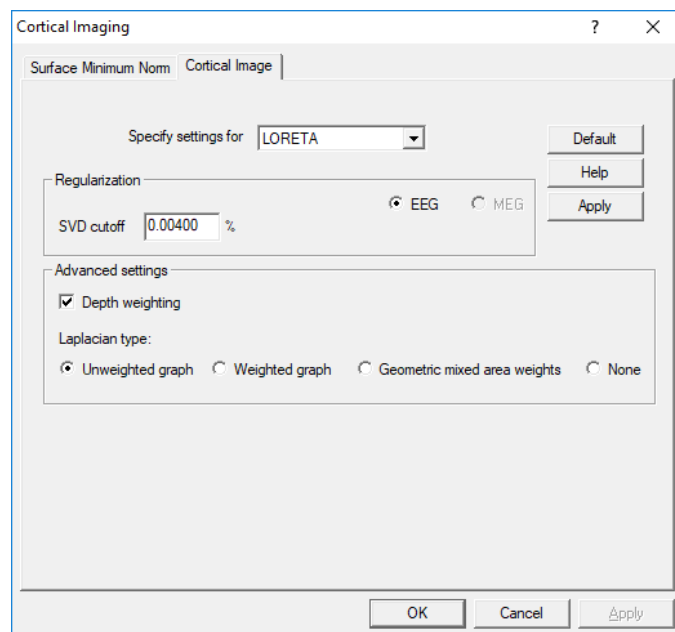


Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

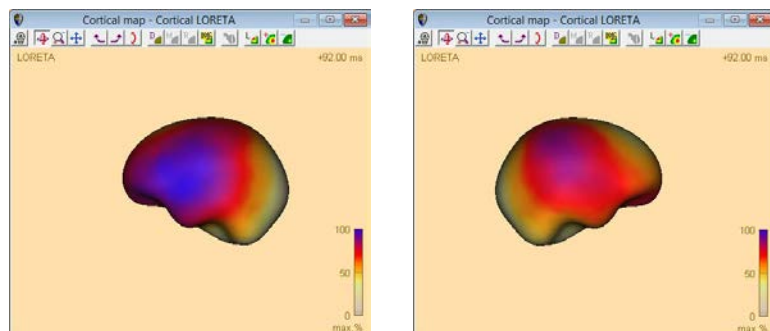
8. The display changes and now shows more activity in lower brain regions, but still a maximum in a central location.



9. We will slightly adapt regularization to get a better separation: [Click](#) the down-arrow  in the centre of the screen to open the popup menu, and select the bottom menu entry [Settings](#). In the dialog, change the regularization to 0.004%. Then press [OK](#).

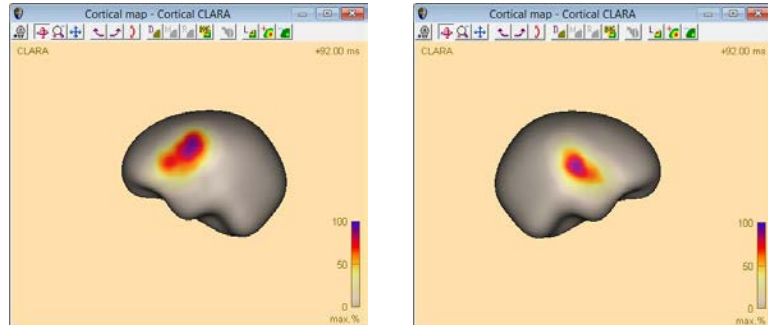


10. The display changes to show two maxima which are now more frontal, closer to the Sylvian fissure.



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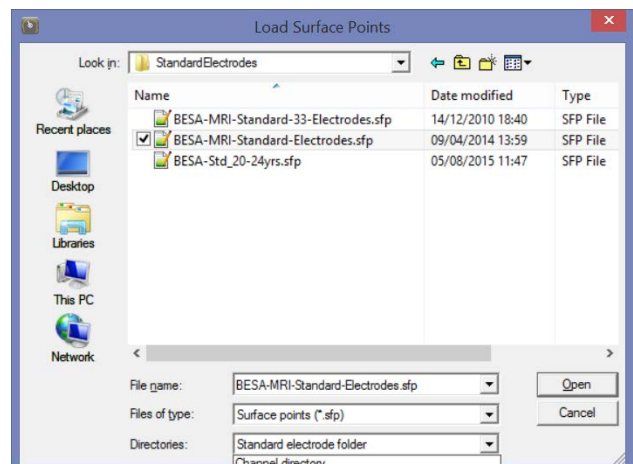
11. Select Cortical CLARA from the popup menu or from the menu **Image / Surface Image**.



The display now shows two clear maxima, one for each hemisphere, which are much more focal than with the previous methods. In the right hemisphere, the location looks approximately correct; however, in the left hemisphere the maximum is too anterior.

We now want to use the individual anatomy of this subject for the estimation of activity on the cortex. We follow the same steps as earlier in the Tutorial on **Coregistration and FEM Modeling, part B**.

12. Close the Source Analysis module. Press **CTRL-L** and in the dialog box that appears, in the row for **Digitized Head Surface Points**, press **Browse**. Then select the **Standard Electrode** folder in the File Open box, choose **BESA-MRI-Standard-Electrodes.sfp**, and open it.



13. Close the Channel and digitized head surface point information dialog with **OK** and select **File / MRI Coregistration**.
14. If you had previously coregistered the file, you will be taken again to the dialog you just

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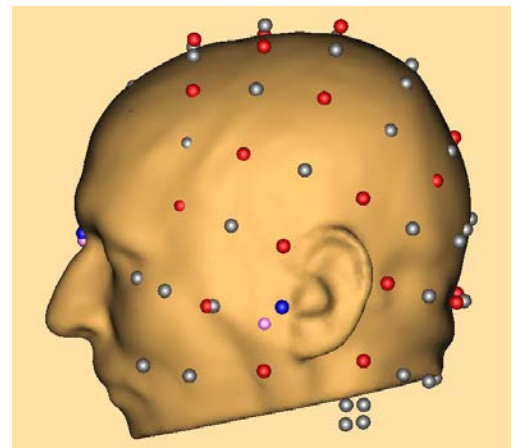
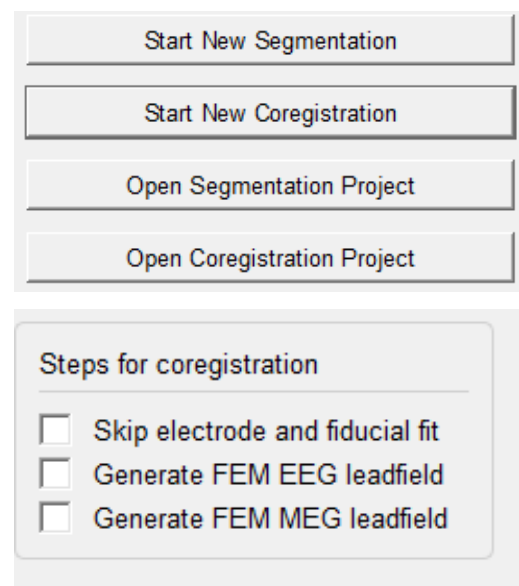
closed. Now you simply have to check the box for using the already existing coregistration file. Leave with **OK**. In case you are asked to write a surface point file, press **Cancel**. Select **File / MRI Coregistration** again. All information should be there. Leave with **OK**.

If there is no previous coregistration, then you will be prompted to save an *.sfh file. BESA MRI will start. In **BESA MRI**, click the button **Start New Coregistration**.

In **Steps for coregistration**, do not check anything.

Press **Next**. Select the input project that we used in the tutorial on **Coregistration and FEM Modeling**. Press **Next**.

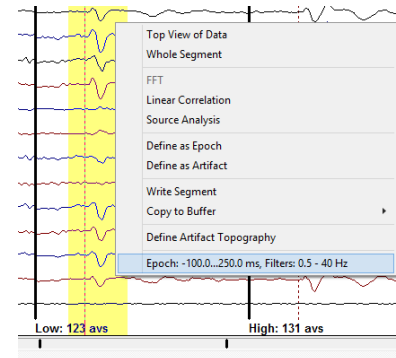
Press **Select Coregistration File** and open the file that you just saved from BESA Research. Then simply press **Next** and **Finish** to complete the Coregistration. Save the project and return to BESA Research. If you click into one of the fields in the dialog box, a green tick mark should appear to indicate that coregistration was successful. Leave the MRI Coregistration dialog with **OK**.



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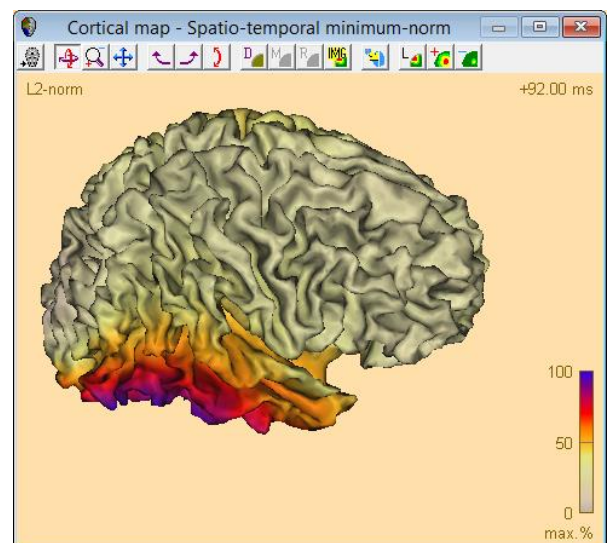
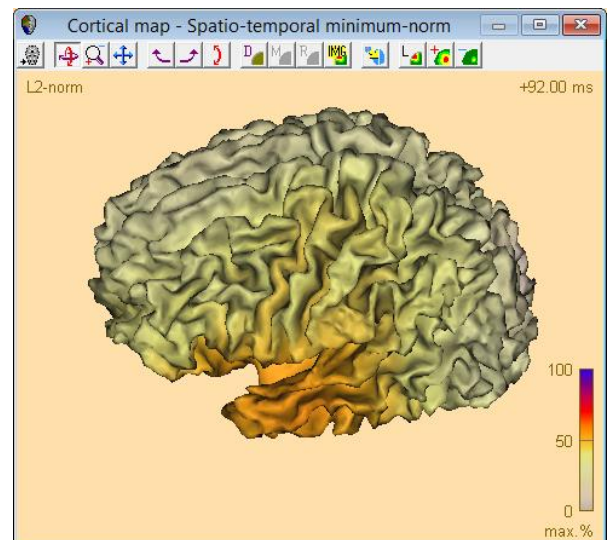
Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

15. Left-drag across condition **Low** again to mark a block, **right-click** and select the previous entry from the popup menu to start **Source Analysis** with the previous parameters.



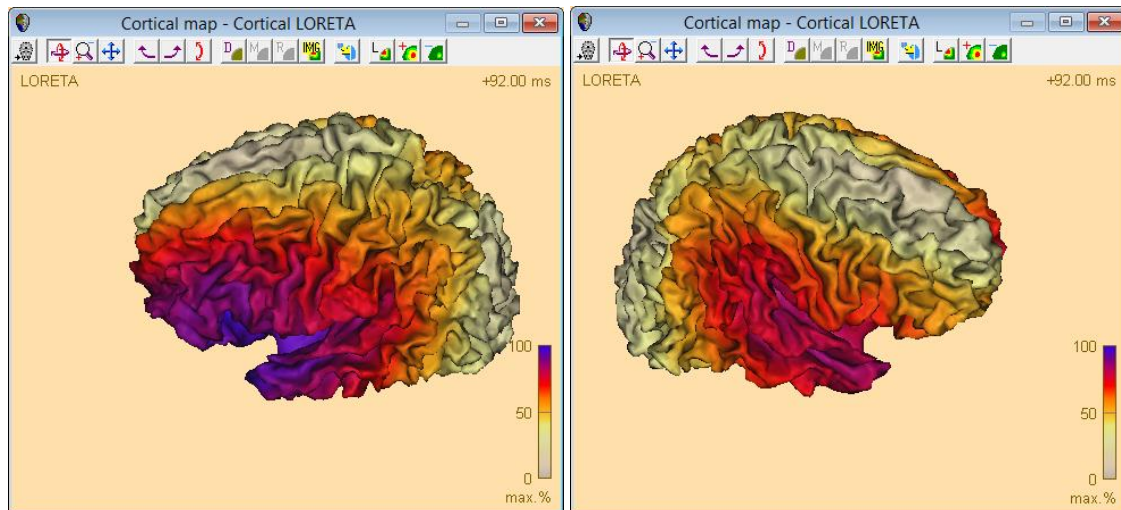
16. Now press the **arrow button** in the centre of the window again and start **Minimum Norm**.

It now shows the individual anatomy, and the activity is estimated lower than before. The Minimum Norm solution places the main activity in the temporal lobe.

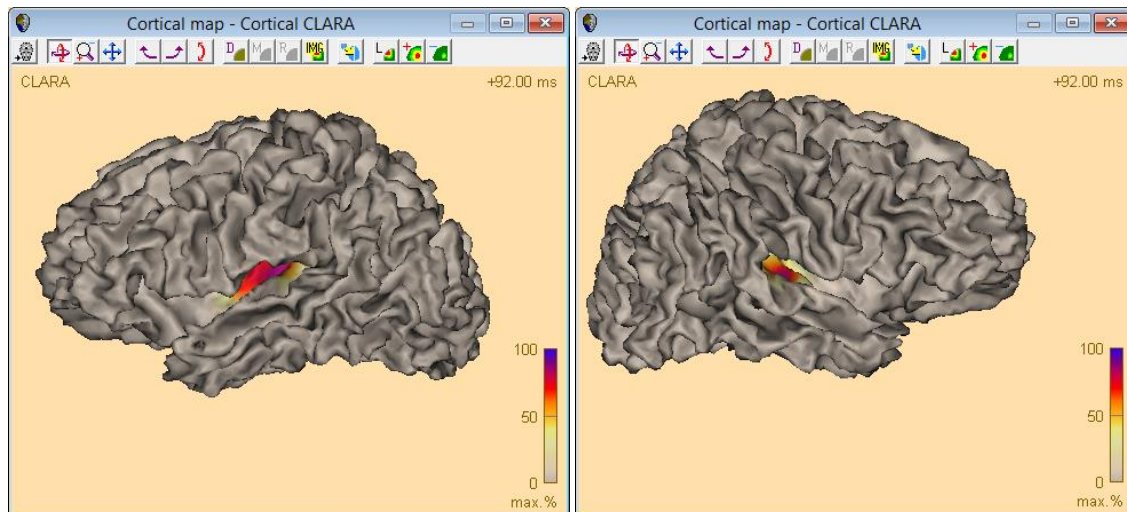


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17. Use the **arrow button** again and select **Cortical LORETA**. The activity now moves closer to the Auditory Cortex.

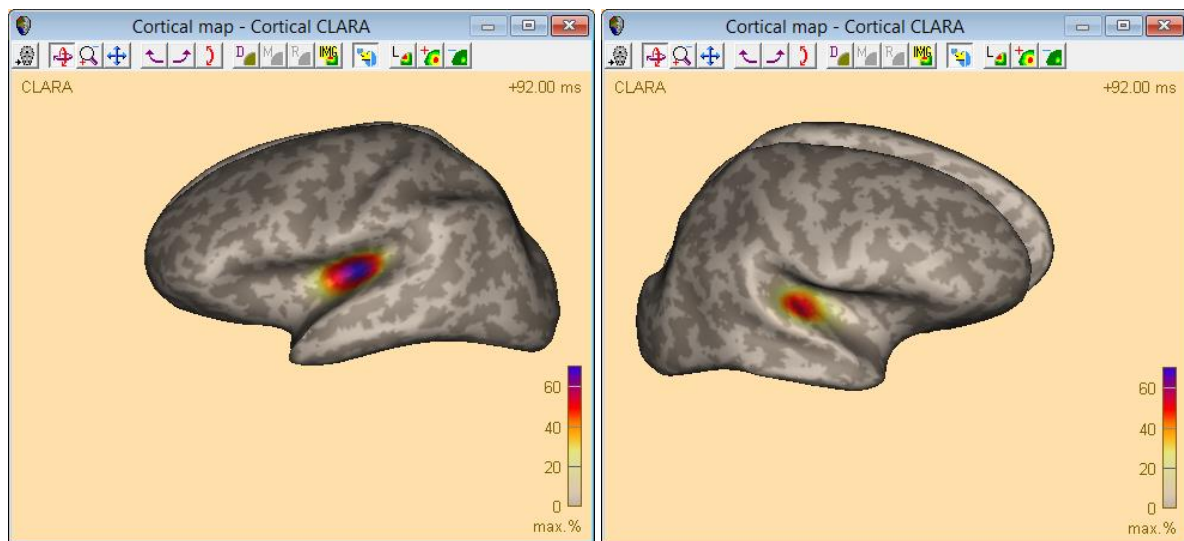


18. Use the **arrow button** again and select **Cortical CLARA**. The activity now shows in the area of the Heschl's gyrus. It is actually not easy to detect – you may need to rotate and zoom the display.



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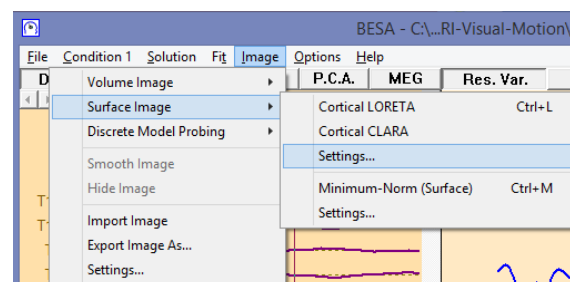
19. Press the inflation icon  on the toolbar. On the inflated brain, it is clearly visible that the reconstructed activity is almost exactly on Heschl's gyrus. You may want to scale up once to see the focal spot more clearly.



D. Settings for surface imaging methods

So far, we have worked with the default settings for the Cortical Imaging methods. We will now explore some of the settings that can be changed, and see the effect on the source images.

1. Select the menu entry **Image / Surface Image** and then the first **Settings...** entry.



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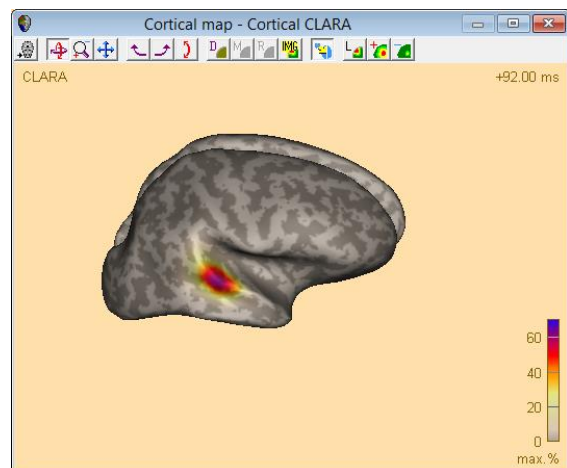
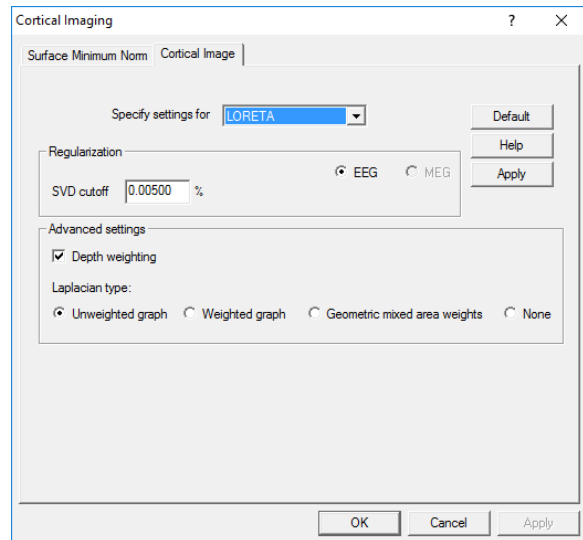
- Note that the dialog that appears contains two tabs – one for Minimum Norm, and the other one for Cortical Images. In the **Cortical Image** part, LORETA is selected by default. You can adjust the following parameters:

- SVD cutoff
- Depth weighting on or off
- Type of Laplacian

Note that SVD cutoff can be adjusted separately for EEG and MEG.

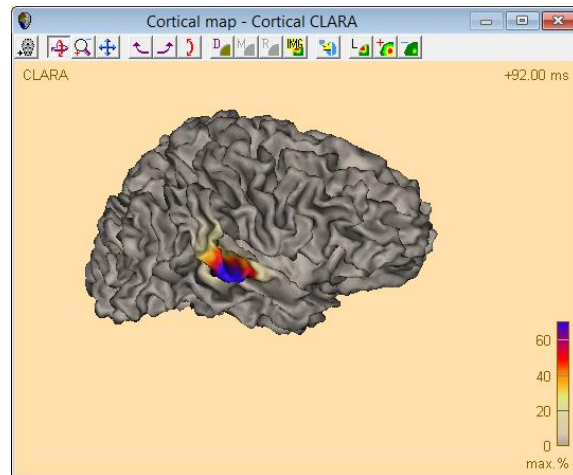
Since Cortical CLARA is an iterative application of the Cortical LORETA solution, these parameters for Cortical LORETA also affect the Cortical CLARA settings.

- Un-tick the **Depth Weighting**. Press the **OK** button. The dialog box closes and Cortical CLARA is re-computed. Note that the activity patch has moved.



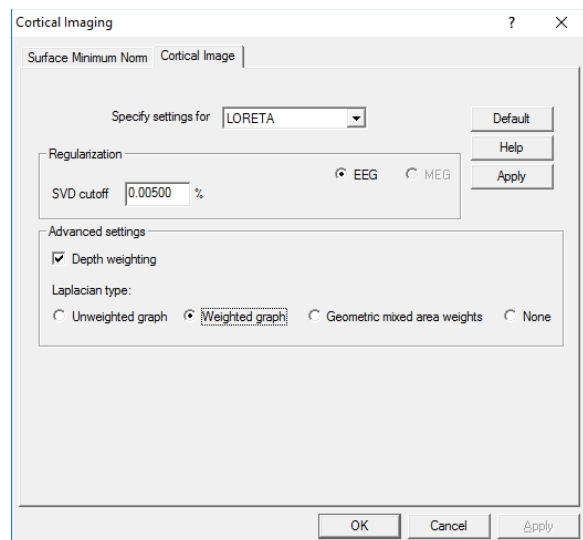
Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

4. Press the inflation toolbar button to show the cortex again. It is evident that the activity has moved towards more superficial locations on the cortex.

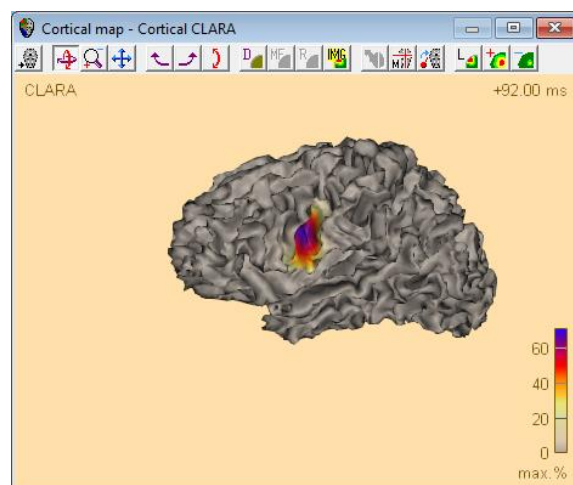


5. Use the **arrow button** in the center of the window to select the last entry **Settings**. It will automatically open the settings for **Cortical Imaging** again since the last selected image was a cortical map.

Now change the **Laplacian** from **Unweighted graph** to **Weighted graph**. Press **OK**.

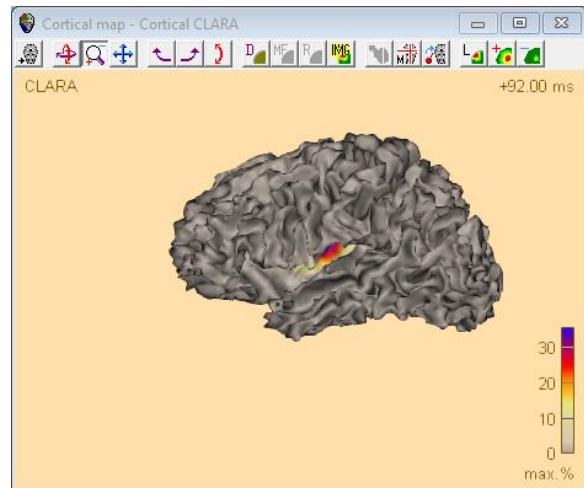


6. This Laplacian applies weights to the Laplacian operator terms depending on the distance to the respective neighbor. The result here is that the activity moves to another gyrus in the left hemisphere.



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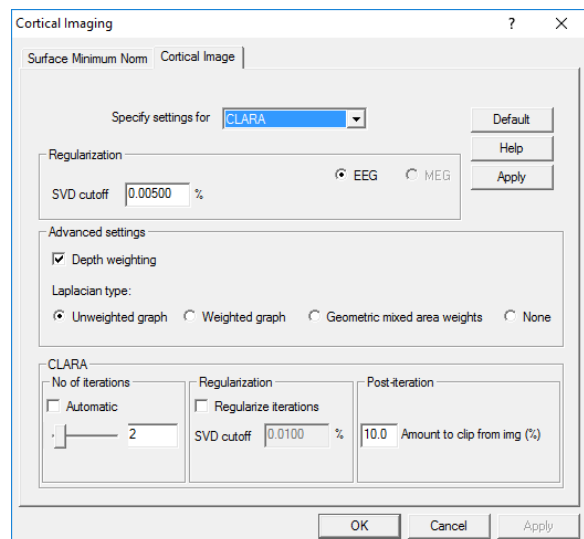
7. Change the settings again to re-activate **depth weighting**. Activity moves back to the Heschl's gyrus.



8. Now select the third option for the **Laplacian**: **Geometric mixed area weights**. This changes the result again slightly.

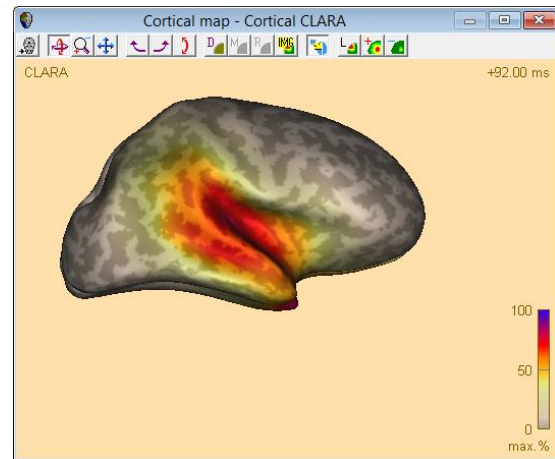
Open the **Settings** once more, and now select **CLARA** from the dropdown list. Three new sets of settings appear.

Change the **Laplacian type** back to **Unweighted graph**, and change the **number of iterations** to **2**. Leave the other settings unchanged. Press **OK**.



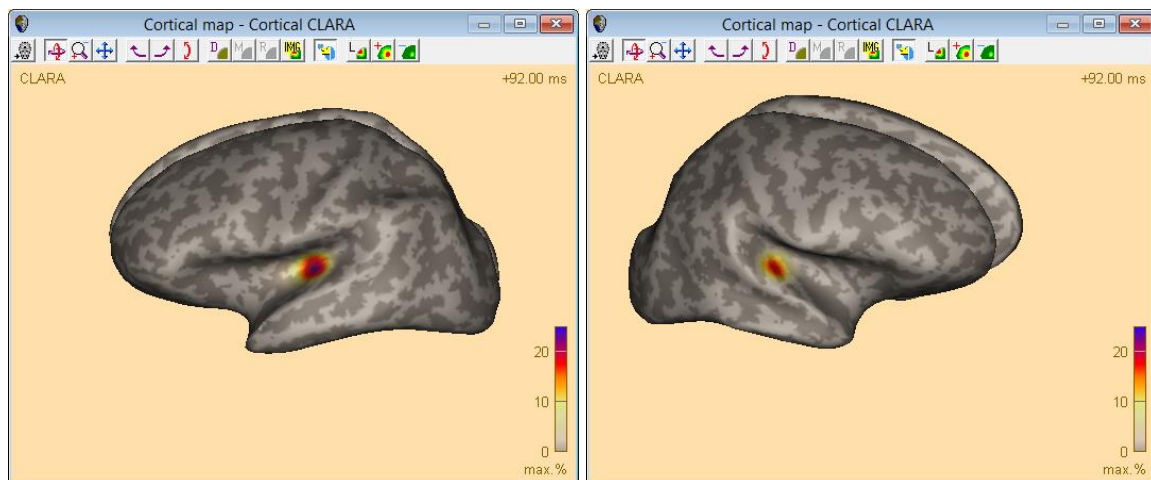
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9. Change scaling back to **100** and press the **inflation** button on the toolbar again. It is evident that the solution now resembles the Cortical Loreta solution more closely.



10. Now try a larger number of Cortical CLARA iterations: Open the **Settings** again and now push the lever for **No of iterations** to the maximum value of **25**. Press **OK**.

The maximum is now smaller in amplitude, and you will need to scale the image up a few times to see it clearly. A very focal maximum is visible on each of the two hemispheres, in a location which closely approximates that of Heschl's gyrus.



11. Close the Source Analysis module.

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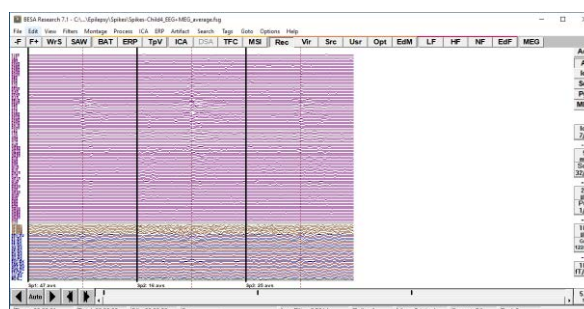
E. Head models

BESA Research offers several age-appropriate template head models, which were kindly provided by Dr. John E. Richards, University of South Carolina, USA¹¹. We will look into the effect of applying an appropriate head model for fitting dipole sources to an averaged epileptic spike.

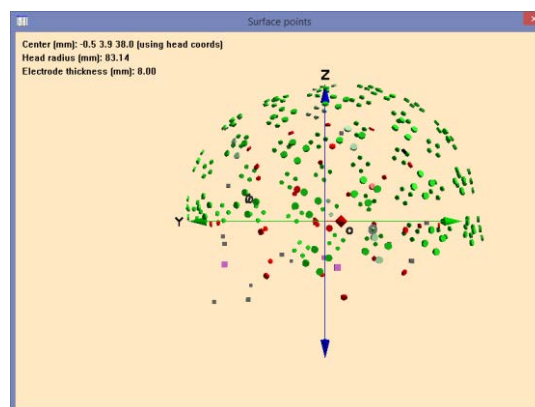
1. Select **File / Open** and browse to the folder **Examples/Epilepsy/Spikes**.

Open the file **Spikes-Child4_EEG+MEG_average.fsg**.

The file is a combined EEG-MEG recording, where occurrences of three different types of spikes in a 12-year old child were averaged.



2. Press **Shift-V** on the keyboard to view the sensor configuration. The red circles denote the electrodes. Coordinates were digitized. Grey donuts denote coils which were placed on the head to coregister the electrode cloud with the MEG sensor positions.

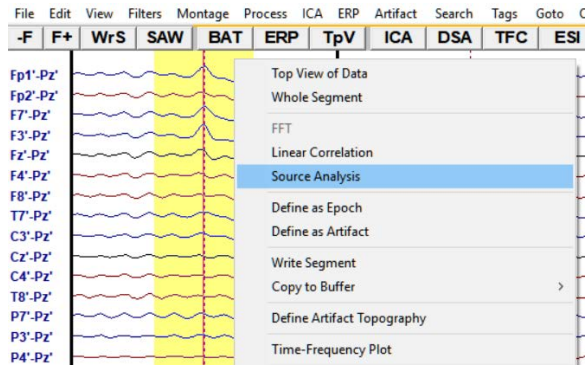


¹¹ If you would like to publish results obtained with the use of the age-specific models, please reference the publications below:

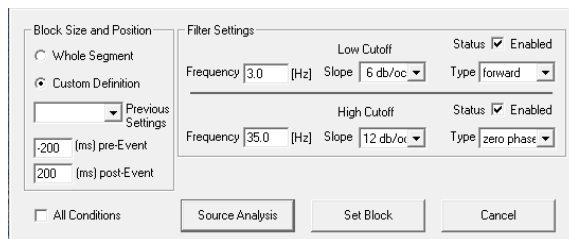
- Richards, J.E., & Xie, W. (2015). Brains for all the ages: Structural neurodevelopment in infants and children from a life-span perspective. In J. Bensen (Ed.), *Advances in Child Development and Behavior* (Vol 48, Chapter 1, pps 1-52)
- Richards, J.E., Sanchez, C., Phillips-Meek, M., & Xie, W. (2015). A database of age-appropriate average MRI templates. *Neuroimage*, doi:10.1016/j.neuroimage.2015.04.055.

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- Press the **Scp** button on the right to show only EEG channels. You can see activity on most channels. **Drag** over the first segment which has the most averages of spike events. **Right-click** and select **Source Analysis**.

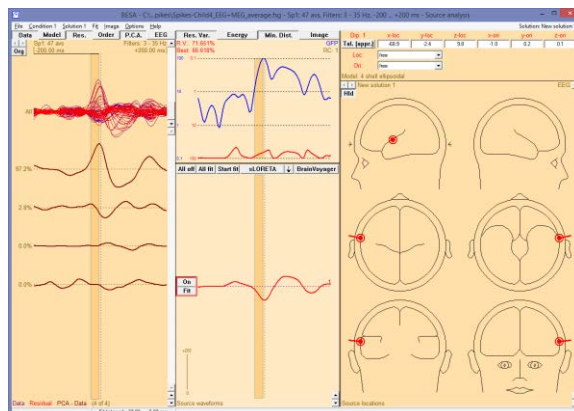


- Define the interval and filters as follows: **-200 ms .. 200 ms, 3.0 Hz forward with 6dB slope, and 35 Hz zero phase with 12 dB**. The reason for using a forward filter for the high pass is that in epilepsy, the initial (crucial) activity is often smaller than the later activity, and can be compromised by signal from later components bleeding back into the early components if a zero phase shift filter is used.



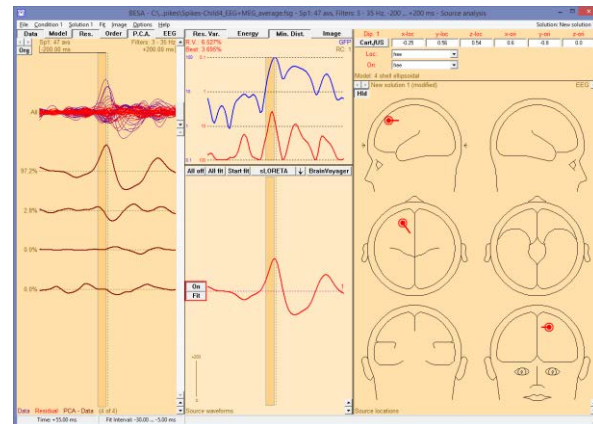
Press the **Source Analysis** button.

- Check that the selected model is the **4-shell ellipsoidal model**. **Double-click** into the head schemes to create a dipole. Click the **P.C.A. button** and **mark a fit interval** over the onset period from **-30 ms to -5 ms**, such that the first PCA component explains more than 97% of the overall variance in that interval.

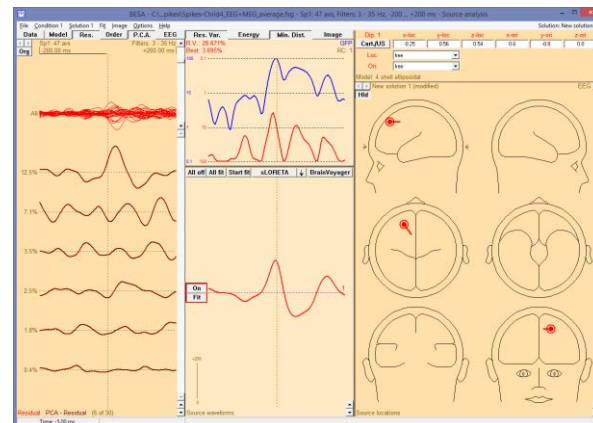


Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

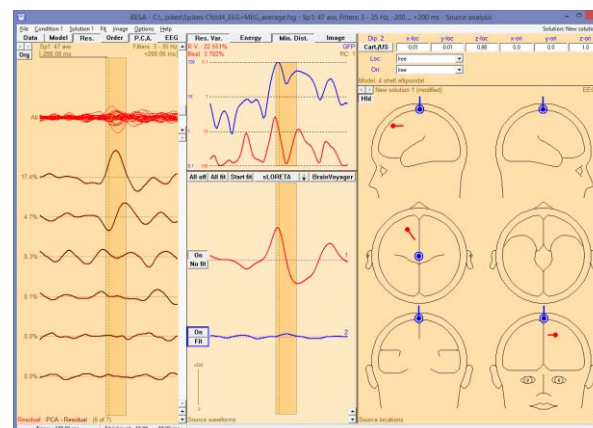
6. **Start the fit.** The dipole fits to a left frontal location.



7. Untick the **Data** button and click outside the fit interval to remove the fit interval. The residual variance PCA plot is shown on the left. The largest component holds 12.5%.

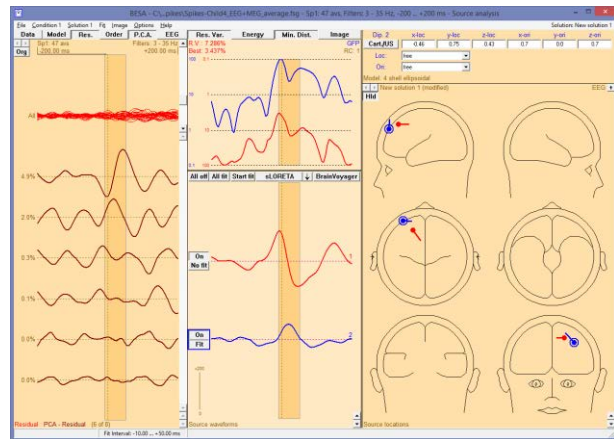


8. Double-click into the head schemes again to set a second dipole, and mark a fit interval over the PCA component from -10 ms to +50 ms.

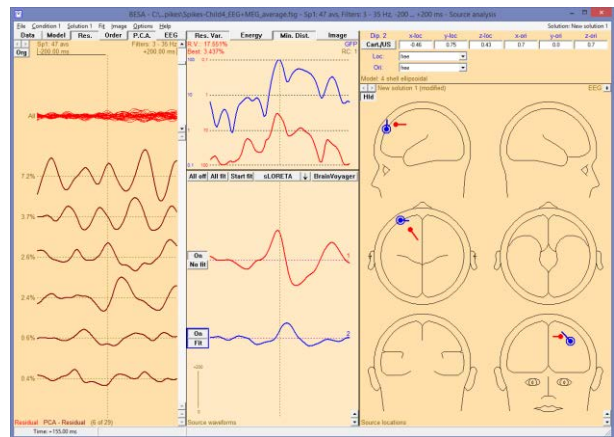


Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

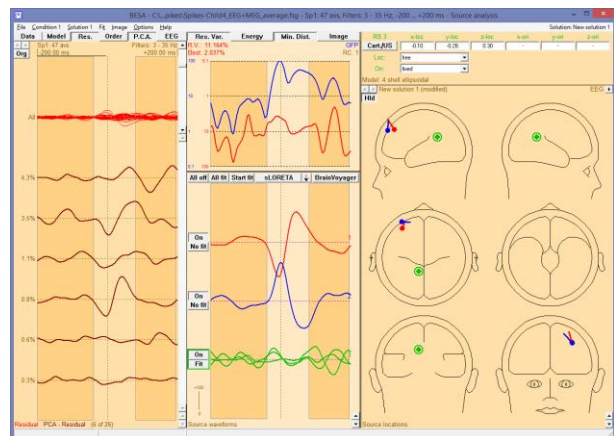
9. Press the **Start fit** button. The dipole localizes to a peripheral location.



10. Unmark the fit interval again. The largest unexplained component now is a rhythmic one. We will try and explain this component by a regional source.

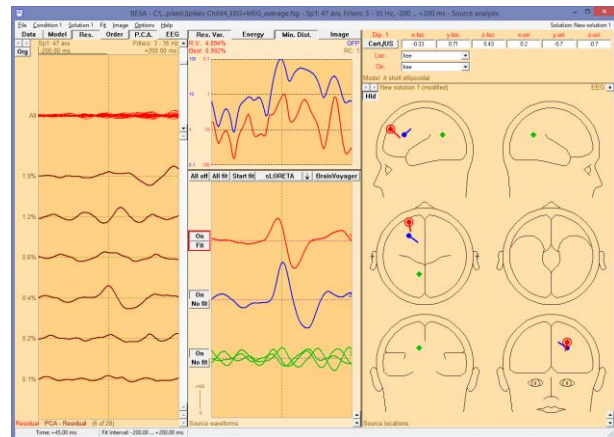


11. Double-click in the head schemes and press **C** on the keyboard to convert the source to a regional source. Mark a fit interval from **-200 ms to -40 ms**, where the two sources are not yet active. Press the **CTRL** key and drag from **+80 ms until the end**. The fit interval is now split into two. **Fit** the regional source. It moves to a posterior location.



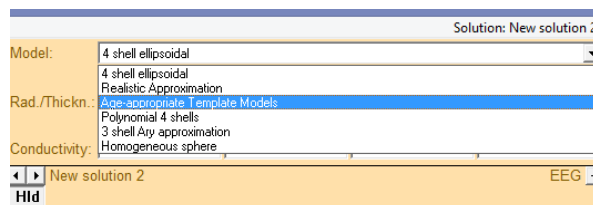
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12. Note that we fitted the first two sources not accounting for the rhythmic activity that is present also during the time when the two dipoles are active. Mark the complete interval and press the buttons **All fit** and **Start fit**. Then invert the first source by selecting its waveform and pressing the **I** key on the keyboard. We now have a solution with clearly separated waveforms and a small residual variance.



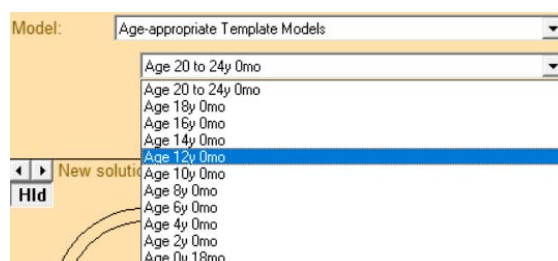
This solution was achieved using the standard 4-shell head model. However, a 12-year old child has vastly different conductivities from an adult. We will now take this into account for an alternative model.

13. Save the current model as **Spikes-Child4_EEG+MEG_average-4shell.bsa**.



Click into the box at the top right to display the model, and use the **dropdown list** to select **Age-appropriate Template Models**. When the warning concerning the source location appears, click **OK**.

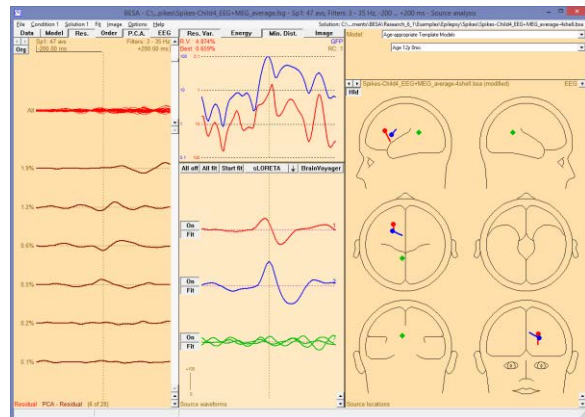
14. A new dropdown list appears below the first one. Select **Age 12y** from this list.




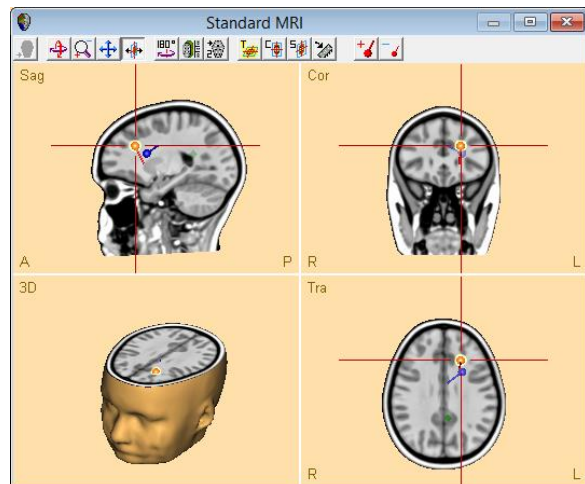
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Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

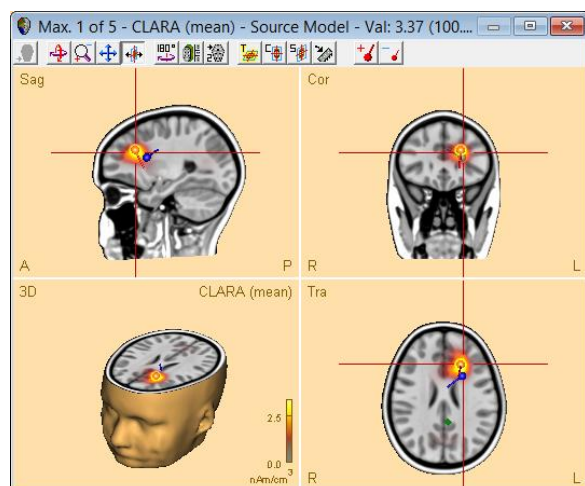
15. Now press the buttons **All fit** and **Start fit** again. The two sources move deeper into the brain volume. Press **CTRL-Z** and **CTRL-Y** to compare the situation before and after the fit. The source locations differ between 2 and 3 cm.



16. Press the **A** key on the keyboard to show the sources in the anatomy. Use the  button on the toolbar to show the different views. Select the first source to slice at that position.

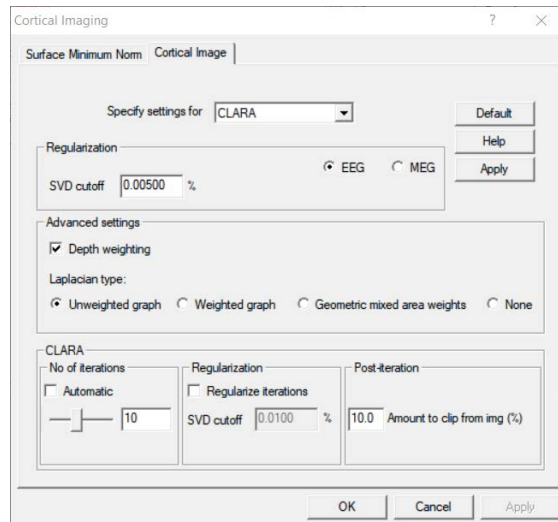


17. Now mark the interval where the first source becomes active, from **-40 ms to -10 ms**. Start **CLARA** to compute the average CLARA image during that interval. CLARA coincides very well with the location of the first dipole source.

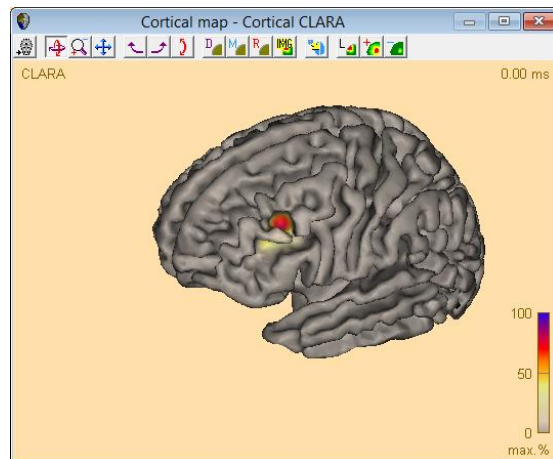


Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

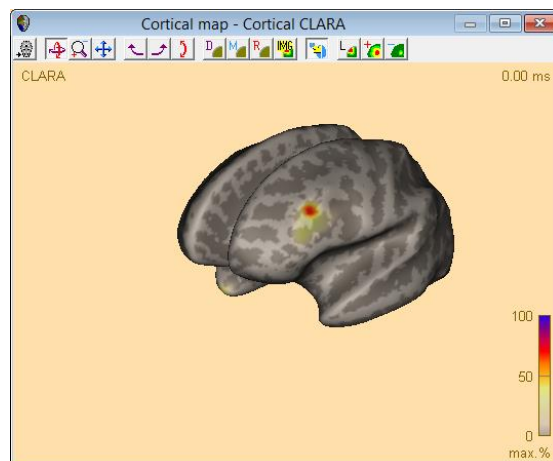
18. We will now try Cortical CLARA for this example as well. Select the menu entry **Image / Surface Image / Settings**. In the dialog box for Cortical Imaging, select **CLARA** and re-set all settings to **Default** using the button. Close the dialog box with **OK**.



19. Then, using the **arrow button** in the centre of the window, select **Cortical CLARA**. The cursor is automatically set at 0 ms where the maximum activity is, and the averaged brain for the 12-year old template model is shown. Activity centers around a sulcus in the frontal left lobe, consistent with the dipole and CLARA solutions.

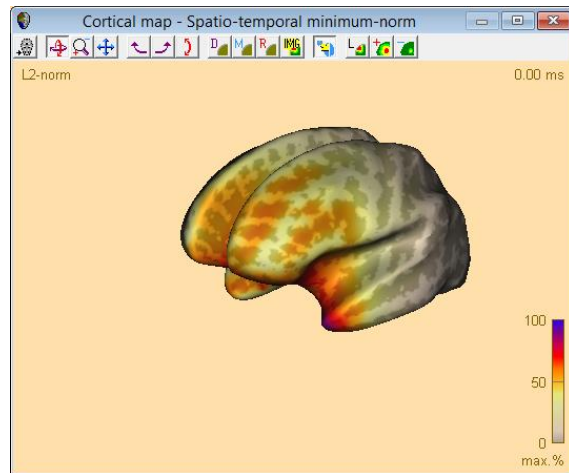


20. Press the **inflation** button on the toolbar to check for other maxima. There is a small activity visible at the tip of the right temporal lobe, but it is much smaller in amplitude.

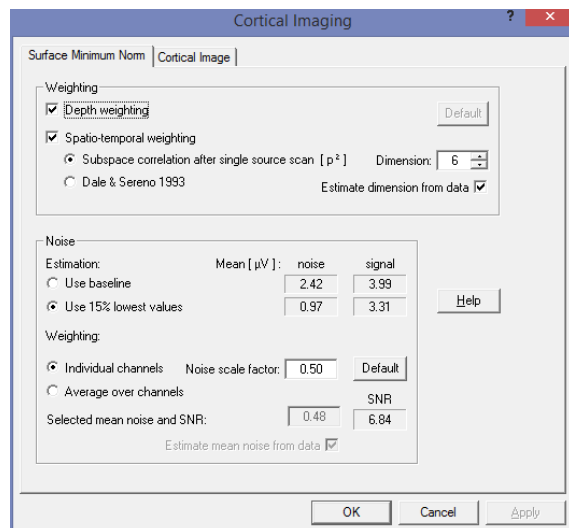


21. For comparison, select **Minimum-Norm (Surface)** button from the **arrow** drop list. It shows a wide-spread activity, with a maximum on the of the left temporal lobe.

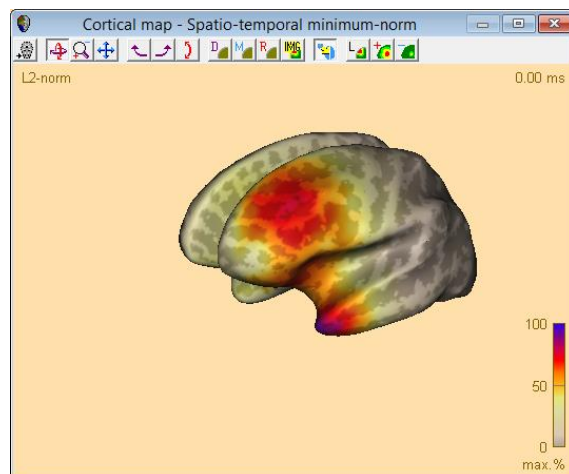
Note that this type of maximum can be an indicator of noise modelling. We will try and change the noise estimator for the minimum norm.



22. Select **Settings** from the **arrow** drop list. The dialog box for **Minimum Norm** settings comes up. The current noise estimator is set to **Use baseline**. However, this is not useful when dealing with epileptic spike averages, as there is no proper pre-stimulus baseline. Select **Use 15% lowest values** instead and change the **noise scale factor** to **0.5** to reduce regularization. Press **OK**.

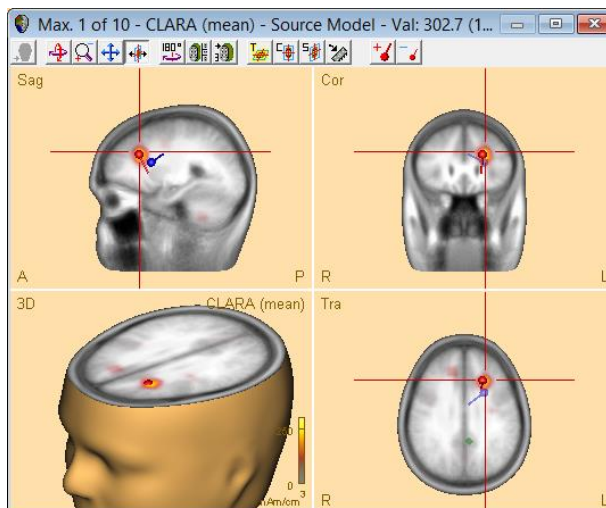


23. Minimum Norm is recomputed, and the result shows an improvement. However, there is still a larger spread of activity compared to the Cortical CLARA method.



24. Finally, we want to have a look at the MEG modality. Press the button **EEG** to toggle the measurement data and switch to MEG. Then mark an interval from **-30 ms to -5 ms** again as before and switch on the **Data** button to review the P.C.A. We can see that the variance explained by the first component is reduced to 88.6%.

Run **CLARA** over this interval. The result is almost the same as for EEG using the age-appropriate template model.



We have seen the influence of the head model onto the solution. In a different research project, the dataset used here was investigated with the patient's MRI and using a realistic head model, and it was shown that indeed the age-appropriate head model template resulted in the closest match to the location found with a realistic FEM, and to the anatomical lesion seen in the MRI (Lanfer et al., 2015)¹².

F. Combined MEG-EEG modeling with realistic head models

Especially in the analysis of epileptic spikes, accuracy and interpretation of source analysis results is of highest importance. We will now investigate how the accuracy of MEG can be combined with the robustness of EEG.

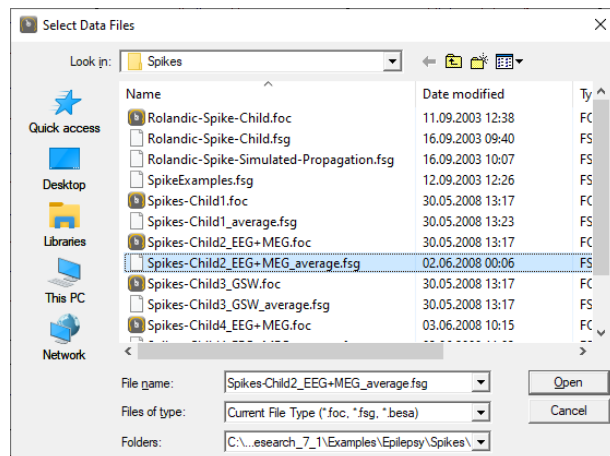
¹² Lanfer B, Spangler R, Richards JE, and Paul-Jordanov IP (2015) Age-specific Template Head Models for EEG Source Analysis. OHBM 2015. https://www.besa.de/wp-content/uploads/2015/07/Lanfer_OHBM2015_Poster.pdf

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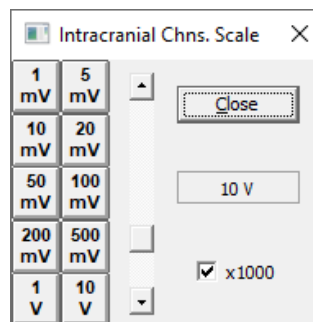
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The data set is another epileptic spike average, also in a child. We will again work with an age-appropriate head model for EEG.

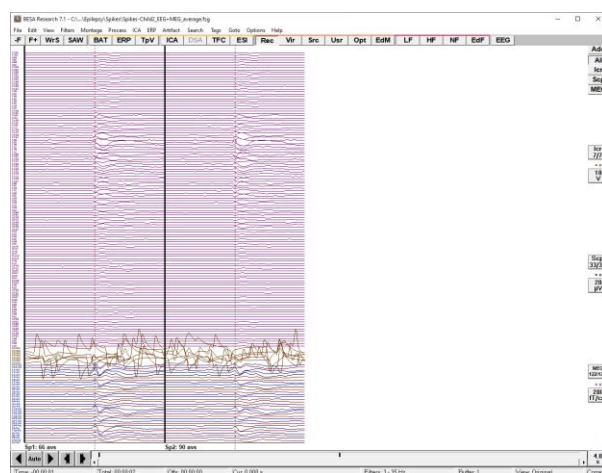
1. In BESA Research, select **File** → **Open** and browse to the Examples sub-folder Epilepsy, and to the folder Spikes. Open the data set **Spikes-Child2-EEG+MEG-average.fsg**.





2. The data set contains 122 MEG channels, and 33 scalp electrodes. Some disturbing signal in stimulus channels can be removed by clicking the **ICR** button and selecting the highest scale value of 10V, and checking the **x1000** box.

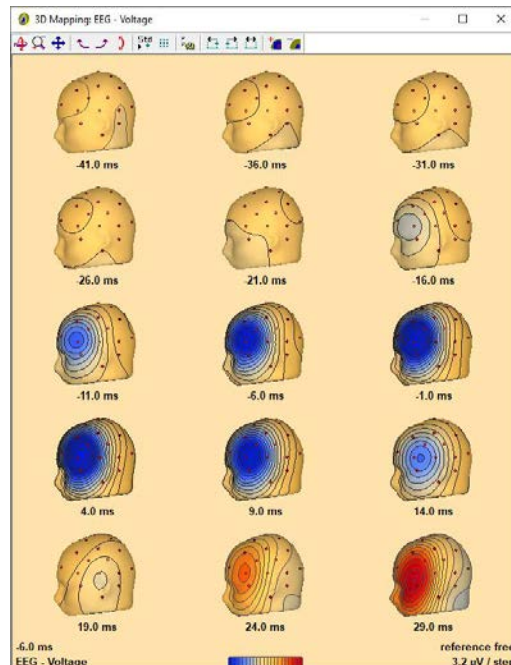


3. The first average contains 66 events.

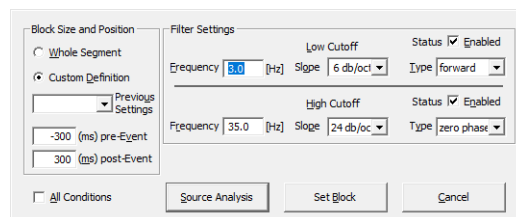


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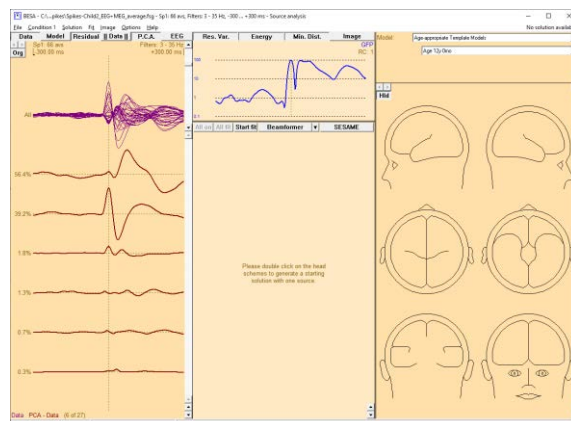
- Double-click on the dashed line denoting the first spike peak to start a map. In the mapping window, use the  icon in the toolbar to select a time series with 5x3 maps. Then rotate using the  icons. The map sequence shows that the initial peak moves somewhat from anterior of F7 (-11 ms) to between F7 and central left (14 ms).



- Drag over the first segment. Right-click and select **Source Analysis**. Adjust the time to -300 ms ... 300 ms and the filters to 3 Hz forward, 6 dB/Oct, and 35 Hz zero phase, 24dB/Oct. Press the **Source Analysis** button.

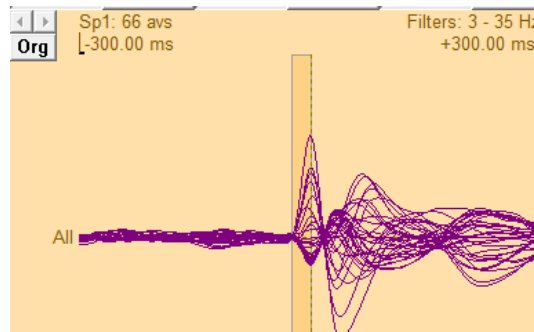


- In Source Analysis, there are two main PCA components. Adjust the head model to Age-appropriate template, age 12 years.

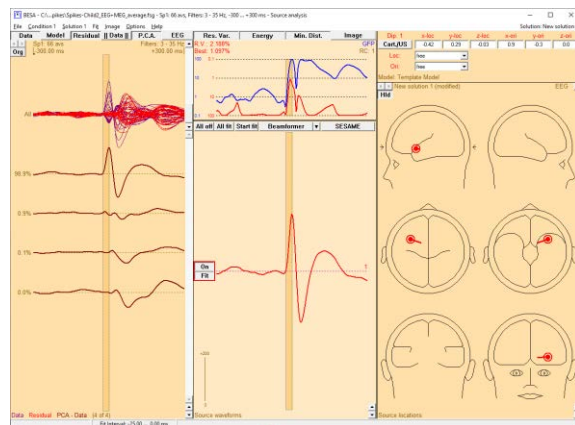


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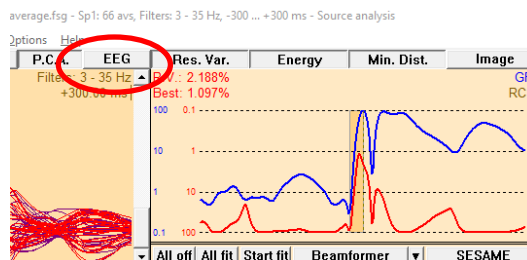
- Let us fit the EEG first. Mark a block from the onset of the butterfly plot to the peak (-25 ... 0 ms). The first PCA component should now explain almost 99% of the data in this interval.



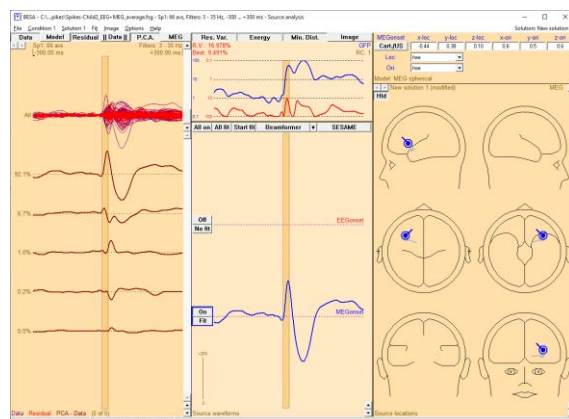
- Press the **Start Fit** button. This automatically inserts a dipole and fits it. If the initial peak of the waveform points down, invert it using the **I** key.



- Label the source "EEGonset" by clicking on the label "1" and editing it. Then move to MEG by clicking the **EEG** button at the top.

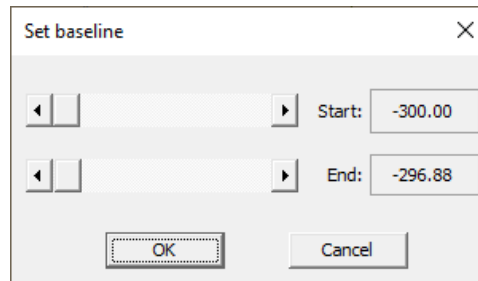


- Switch off the source by clicking the **On** button. Now we can see that the first PCA component explains about 92% of the MEG activity in this interval. Double-click into the head schemes to add a source. Then press **Start Fit**. The location is similar, but the orientation is not. Label the source "MEGonset".

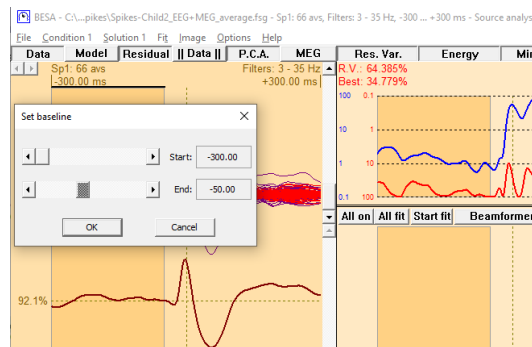


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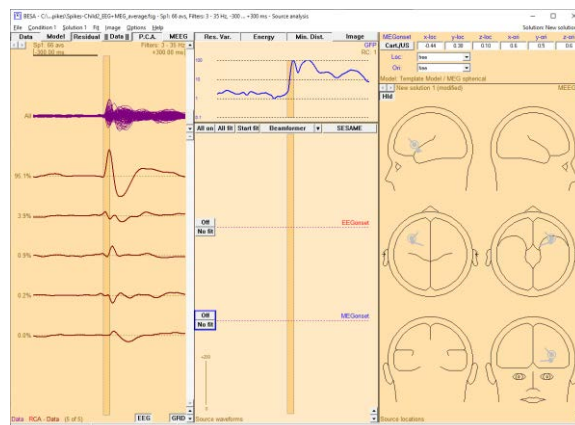
11. Now we want to combine EEG and MEG. To do this, we need to have the baseline interval properly assigned. The reason for this is that EEG and MEG signals need to be normalized to dimensionless parameters in order to be jointly used. This is done by dividing their signals by the baseline signal. A good baseline is important. Use menu **Condition 1** → **Set Baseline...** to open the baseline selection dialog.



12. Adjust the end of the baseline to -50 ms. It should end before the onset of the spike-related activity. Then press **OK**.



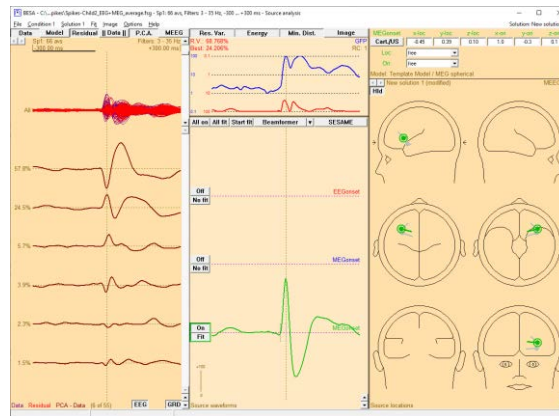
13. The baseline indicator is now clearly visible at the top left. Switch off the MEG source. Then click the button **MEG** in the top row. The button changes to **MEEG**. Note that two channel types are now listed at the bottom. The model information at the top right shows both models (EEG and MEG model). Head models cannot be changed in MEEG – to change, you will need to toggle back



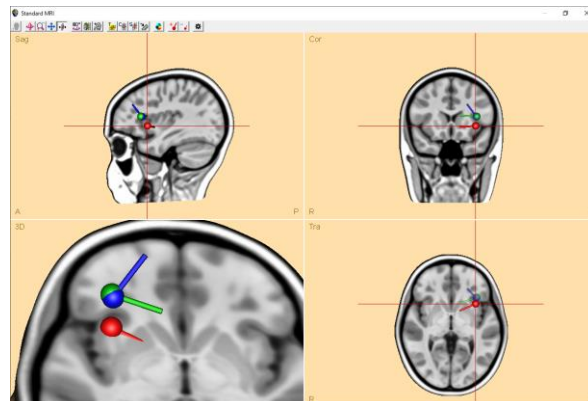
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to EEG or MEG, and then come back to MEEG.

14. Double-click into the head schemes to add another source and press the **Start Fit** button. The fit comes out with a similar location than before, but with different orientation. Label the source with MEEGonset.

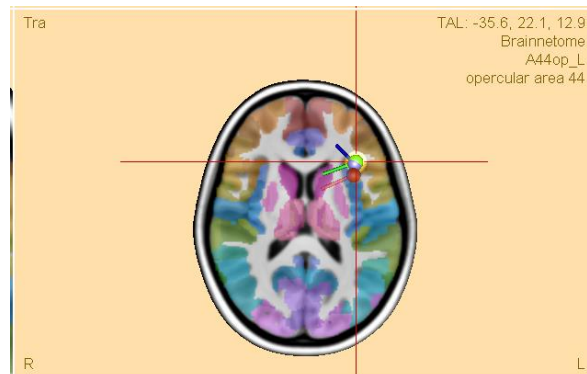


15. Now let us have a look at how the solutions compare in the anatomy. Click the **MEEG** button to toggle back to EEG. Then switch all sources to **On** and press the **A** key on the keyboard to show the anatomy (please note that in this example, we are using an averaged brain). Maximize the view and then zoom into the 3D brain display using **CTRL+SHIFT+Drag**. It can be seen that the localization of MEEG (green source) follows the MEG, but the orientation is much closer to the EEG orientation (red source; note that MEG is almost blind to radially oriented components).

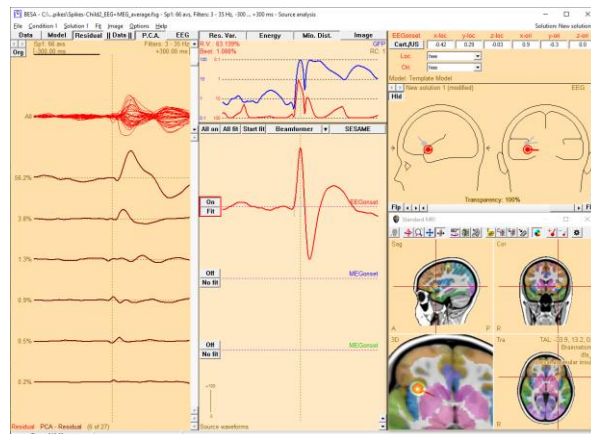


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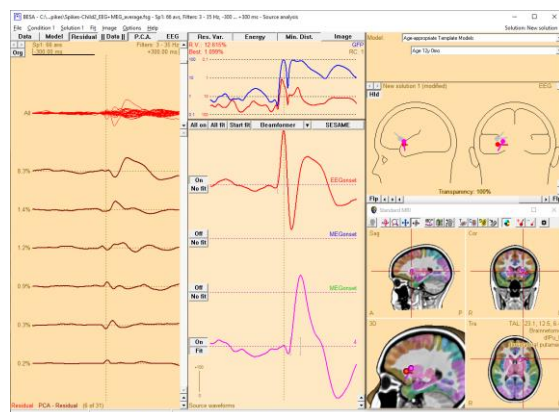
16. If we switch on the atlas, we can click on the different sources and compare their Talairach values to estimate the localization differences. The difference between EEG and MEEG is approximately 15 mm in this case.



17. To complete the source model, we need to investigate the propagation. Switch off the MEG and MEEG sources. Change the channel display at the left to **Residual**, and switch off any fit interval by clicking once into an empty space in the channel display. One major component still needs to be modeled.



18. Mark an interval from 50 ... 68 ms (onset to peak of the residual PCA component). This leaves very little variance for other components. Double-click into the head schemes to add a source, and fit it. The source fits slightly medial to the previous source. Label the source EEGprop.



19. We could now also model the propagation for MEG and MEEG. We will leave this for an extended example later. For now, please save the solution as **MEEG_onset.bsa**.

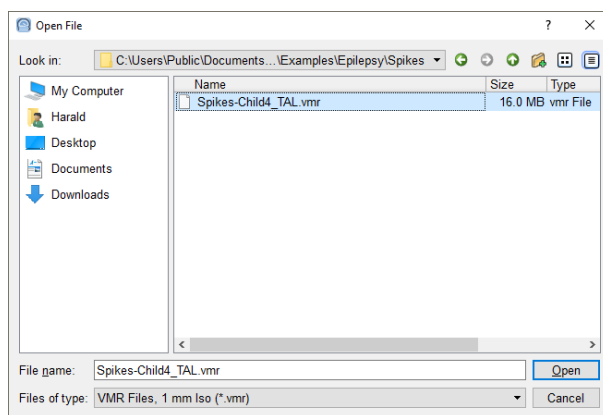
G. Optional - Confidence limits

To understand the limitations, especially in accuracy, of the modeling, it is useful to investigate the confidence limits. Confidence limits are only available for co-registered MRI data. They can be displayed in the Source Analysis module (in the Talairach space), or also in BESA MRI (in AC-PC space, without distortion of the anatomy).

Confidence limits are computed over the fit interval. Thus, the fit interval should be chosen to be small enough as to only incorporate time samples where the signal is much stronger than the noise. The confidence limits show a 95% confidence interval – however, this is computed solely due to noise. The real error will be higher, since other things need to be taken into account, e.g. head model errors, inaccurate electrode placement, and co-registration errors.

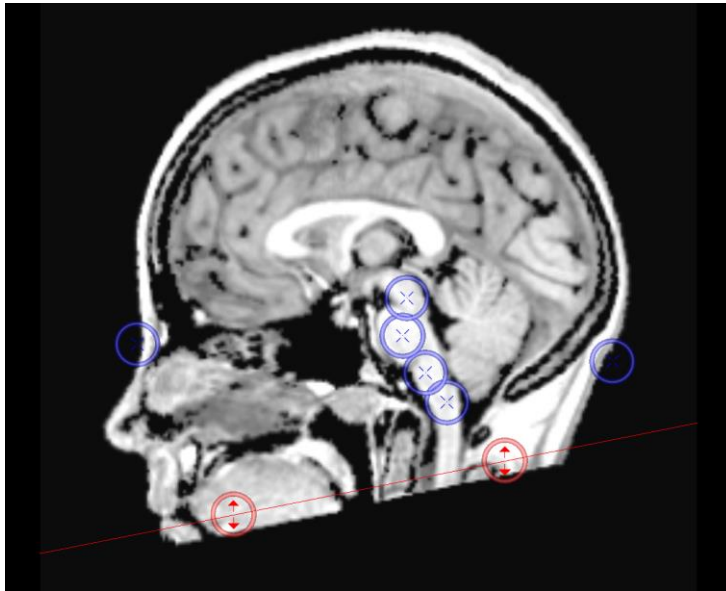
Here is an example on how to compute and display confidence limits in our first epilepsy example data set:

1. In BESA MRI: Start a segmentation project. In Project Targets, leave the defaults. In work step Read T1-weighted MRI Data, select file type VMR Files, and browse to **C:\Users\Public\Documents\BESA\Research_7_1\Examples\Epilepsy\Spikes**. Select data file **Spikes-Child4_TAL.vmr**.



2. In step Set Orientation of T1 data, leave all defaults. In step Set ACPC transformation, leave defaults for AC and rotation, and adjust the PC position slightly. In workstep Set Talairach Transformation, adjust to the brain boundaries. In Set Markers, set the nasion, inion, and 4 brain stem markers. Move the red line up so that it is inside the MRI as shown below.

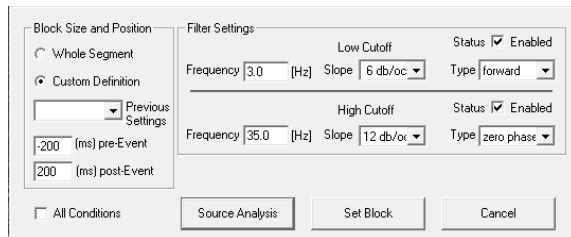
Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models



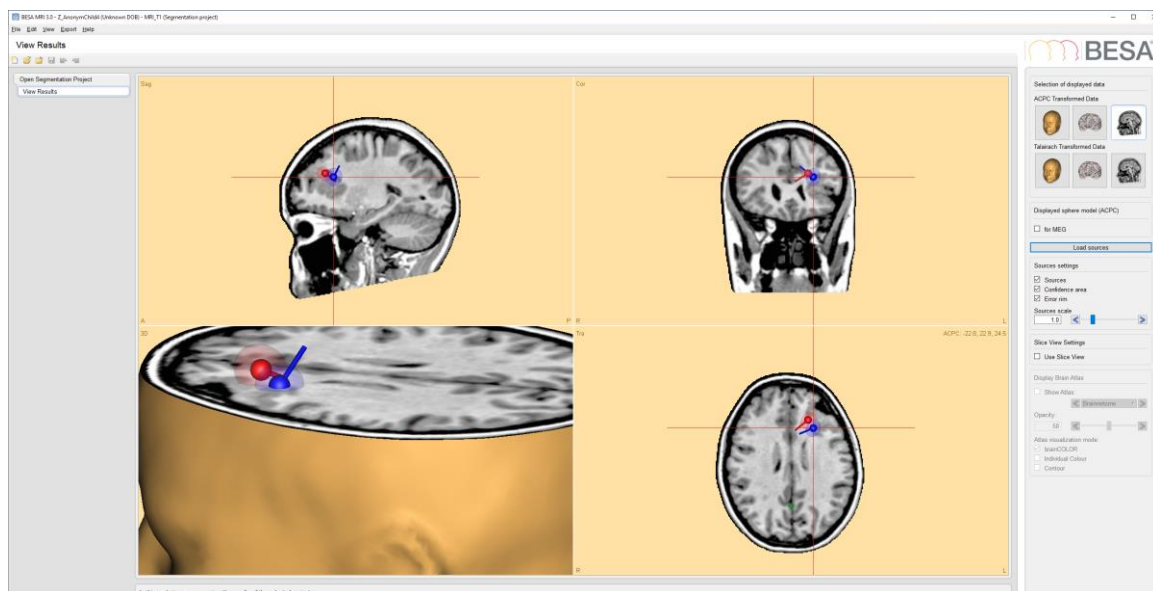
3. Then let the program automatically finalize the segmentation, and save the project upon finishing the workflow.
4. In BESA Research: Select **File / Open** and browse to the folder **Examples/Epilepsy/Spikes**. Open the file **Spikes-Child4_EEG+MEG_average.fsg**.
5. Co-register the data set: Use **File → MRI Coregistration**. Save the sfh file as required. Then BESA MRI will open and start the co-registration workflow. In the workstep Set Project Targets, check the boxes for EEG FEM and EEG BEM. In the next worksteps, simply press Next and OK to use defaults. In the workstep for head model calculation, select the age-appropriate entry for 12 years of age. Then press **Next** to calculate the FEM and BEM models. Finish and save the project.
6. In BESA Research, the dialog for co-registration shows the filled values and a green tick mark is shown (you may need to click into an edit box for it to update itself). Press **OK**.
7. Mark the first segment, right-click, and select Source Analysis. In the dialog, adjust the time to -200 ms ... 200 ms and the filters to 3 Hz forward, 6 dB/Oct, and 35 Hz zero phase, 12dB/Oct. Press the **Source Analysis** button.

BESA® Research 7.1

Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models



8. In Source Analysis, load the previously saved solution **Spikes-Child4_EEG+MEG_average-4shell.bsa**.
9. Change head model to EEG – individual FEM. Switch off the second dipole. Mark the onset activity from -30 ms ... -10 ms. Fit the first dipole again. Then switch on the second dipole. Mark the activity from -10 ms ... +5 ms. Fit the second dipole again.
10. Press **A** to open the anatomy. See the confidence ellipsoid display.
11. Select **File → Save solution** for BESA MRI.
12. In BESA MRI, open the segmentation project for Child4. Then click the button **Load Sources** and load the file that is visible in the dialog box. The confidence limits are shown in the ACPC view. They overlap with an area of cortical dysplasia.



Tutorial 8 – Distributed Sources II: Bayesian Source Imaging, Surface Methods and Template Models

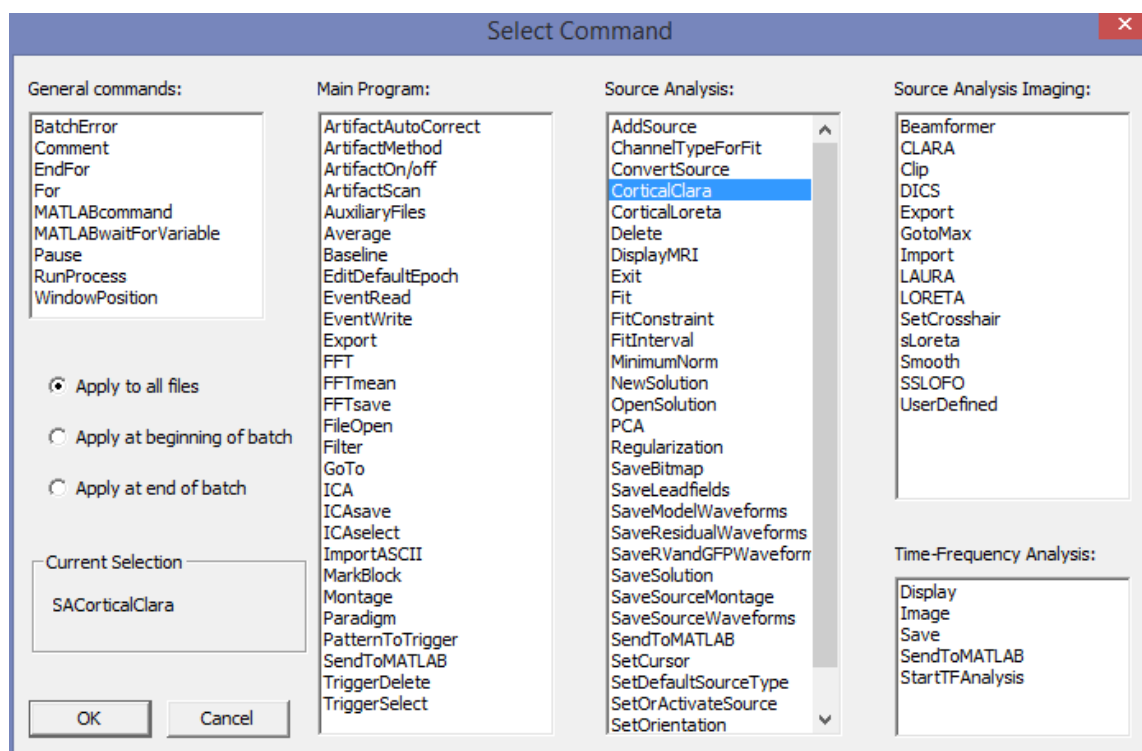
H. Batch processing and export of cortical results

Batch processing

The methods for Cortical Imaging can also be used in batch processing. For these methods, the following commands are available in the list of batch commands:

- CorticalClara
- CorticalLoreta
- MinimumNorm

The parameters can be entered after selecting one of the commands.



Export of results

Cortical images can be exported as ASCII files. There is a choice between current latency, or all latencies.

Each mesh node location is provided with x, y, and z coordinates, followed by the value for either the current latency, or for all latencies. In the case of all latencies, BESA Research calculates the values for each latency of the current condition during the export process.

Tutorial 9 – Beamforming and virtual sensor montages

What does BESA Research provide?

- ✓ Time-domain beamforming tools
- ✓ Several beamformer types
- ✓ Graphical user interfaces for using the tools
- ✓ Virtual sensor montages

A. Principles of beamforming

Beamforming (Van Veen et al., 1997) is a technique for the reconstruction of source activity that differs from other discrete or distributed modelling approaches:

- A spatial filter is used like in the other approaches, but for each brain voxel, a different spatial filter is computed.
- The measured data are directly considered for computing the beamformer result.
- Activity is contrasted against either a reference interval, or a reference condition.

Several methods for computing beamformers exist. We will explain them and their (sometimes subtle) differences, and work with them in the tutorial.

Beamformer ingredients are:

- Data covariance matrix
- Leadfield matrix derived from the head model and sensor configuration
- Spatial filters computed from the leadfield matrix and data covariance matrix

Let us start by looking at the “standard” beamformer (single-source beamformer):

If C_r^{-1} is the inverse of the regularized data covariance matrix C in the time range of interest; $L(r)$ is the leadfield matrix of the model containing a regional source at target location r and, optionally, additional sources, whose interference with the target source is to be minimized; $\text{tr}[\cdot]$ is the trace of the $[3 \times 3]$ (MEG: $[2 \times 2]$) submatrix of the bracketed expression that corresponds to the source at location r ; then $P(r) = \text{tr}[L^T(r)C_r^{-1}L(r)]^{-1}$ is the power at location r .

Beamformers can suppress noise sources that are correlated across sensors. However, uncorrelated noise will be amplified in a spatially non-uniform manner, with increasing distortion with increasing distance from the sensors (Van Veen et al., 1997). For this reason, estimated source power should be normalized by a noise power. In BESA Research, the output power $P(r)$ is normalized by the output power in a reference interval $P_{\text{ref}}(r)$, defining a value $q(r)$:

$$q(\mathbf{r}) = \begin{cases} \sqrt{\frac{P(\mathbf{r})}{P_{\text{ref}}(\mathbf{r})}} - 1 = \sqrt{\frac{\text{tr}[\mathbf{L}^T(\mathbf{r}) \cdot \mathbf{C}_r^{-1} \cdot \mathbf{L}(\mathbf{r})]^{-1}}{\text{tr}[\mathbf{L}^T(\mathbf{r}) \cdot \mathbf{C}_{\text{ref},r}^{-1} \cdot \mathbf{L}(\mathbf{r})]^{-1}}} - 1 & \text{for } P(\mathbf{r}) \geq P_{\text{ref}}(\mathbf{r}) \\ 1 - \sqrt{\frac{P_{\text{ref}}(\mathbf{r})}{P(\mathbf{r})}} = 1 - \sqrt{\frac{\text{tr}[\mathbf{L}^T(\mathbf{r}) \cdot \mathbf{C}_{\text{ref},r}^{-1} \cdot \mathbf{L}(\mathbf{r})]^{-1}}{\text{tr}[\mathbf{L}^T(\mathbf{r}) \cdot \mathbf{C}_r^{-1} \cdot \mathbf{L}(\mathbf{r})]^{-1}}} & \text{for } P(\mathbf{r}) < P_{\text{ref}}(\mathbf{r}) \end{cases}$$

$P_{\text{ref}}(\mathbf{r})$ can be computed either from the baseline of the same condition or from the corresponding range in a control condition.

Multiple source beamformer vs single source beamformer

Traditional single-source beamformers are known to mislocalize activity if several brain regions have highly correlated activity (Van Veen et al., 1997). The BESA multiple source beamformer tries to overcome this problem by extending the traditional single-source beamformer. The multiple-source beamformer can implicitly account for activity from possibly correlated brain regions (This is also called suppression beamformer (Dalal et al., 2006) or nulling beamformer (Hui et al., 2010)). This is achieved by using a multiple-source beamformer calculation that contains not only the leadfields of the source at the location of interest \mathbf{r} , but also those of possibly interfering sources.

BESA Research uses a bilateral beamformer, where specifically contributions from the homologue source in the opposite hemisphere are considered (the leadfield matrix $\mathbf{L}(\mathbf{r})$ thus being of dimension $N \times 6$ for EEG and $N \times 4$ for MEG, respectively, where N is the number of sensors). This allows for imaging of highly correlated bilateral activity in the two hemispheres that commonly occurs during processing of external stimuli.

Vector beamformer vs scalar beamformer

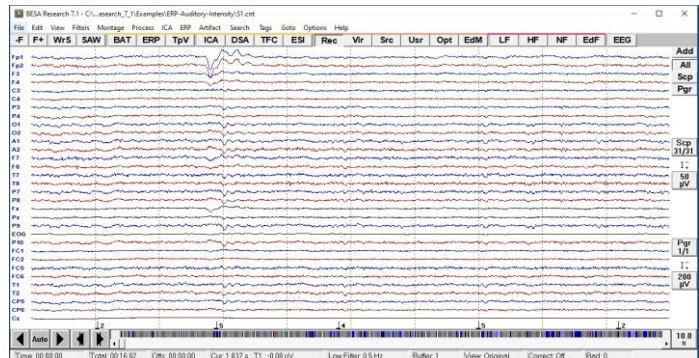
A beamformer source at position \mathbf{r} can have 3 orientations for EEG or 2 orientations for MEG. The beamformer can either optimize the orientation, “scalar beamformer” (Robinson and Vrba, 1998; Sekihara et al., 2004), or compute the mean amplitude over all orientations, “vector beamformer” (Van Veen et al., 1997).

References

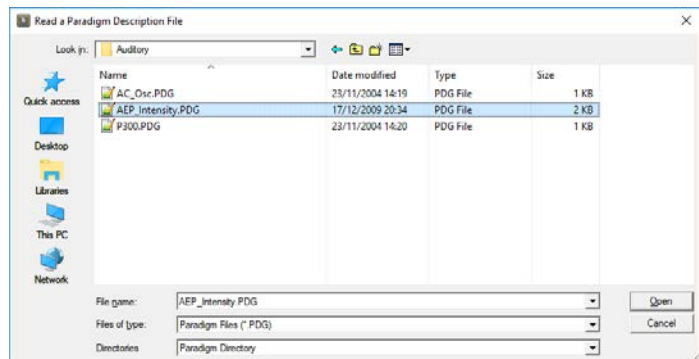
- Dalal, S. S., Sekihara, K., & Nagarajan, S. S. (2006). Modified Beamformers for Coherent Source Region Suppression. *IEEE Transactions on Biomedical Engineering*, 53(7), 1357–1363.
- Hui, H. B., Pantazis, D., Bressler, S. L., & Leahy, R. M. (2010). Identifying true cortical interactions in MEG using the nulling beamformer. *NeuroImage*, 49(4), 3161–3174.
- Robinson, S. E., & Vrba, J. (1998). Functional neuroimaging by synthetic aperture magnetometry (SAM). In: Yoshimoto T, Kotani M, Kuriki S, Karibe H, Nakasato N, editors. *Recent Advances in Biomagnetism*. Sendai: Tohoku University Press, 302–305.
- Sekihara, K., Nagarajan, S. S., Poeppel, D., & Marantz, A. (2004). Asymptotic SNR of scalar and vector minimum-variance beamformers for neuromagnetic source reconstruction. *IEEE Transactions on Biomedical Engineering*, 51(10), 1726–1734.
- Van Veen, B. D., Van Drongelen, W., Yuchtman, M., & Suzuki, A. (1997). Localization of brain electrical activity via linearly constrained minimum variance spatial filtering. *IEEE Transactions on Biomedical Engineering*, 44(9), 867–880.

B. Time-domain beamforming in EEG data

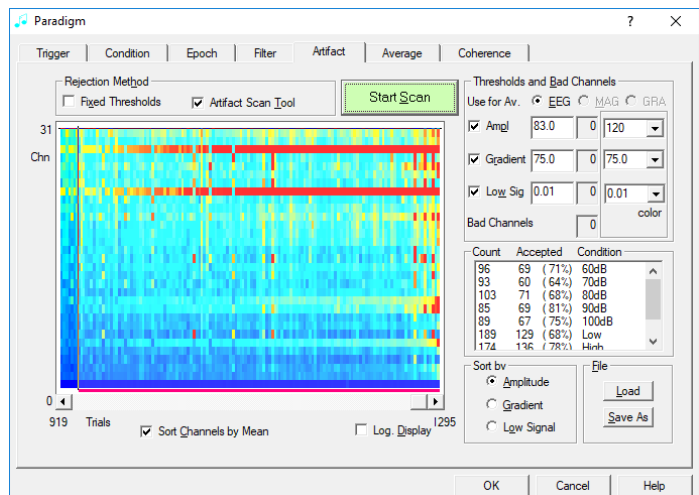
1. Open data set **s1.cnt** from the folder **/Examples/ERP-Auditory-Intensity/**. It contains 32 EEG channels and one polygraphic channel.



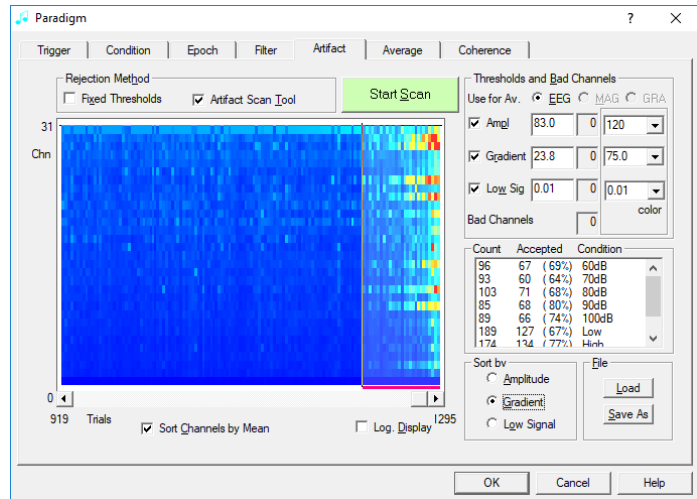
2. Click the **ERP** pushbutton. If the paradigm file for the data file was not loaded before, a dialog box opens, and you can browse to the sub-folder **Auditory** and open file **AEP-Intensity.pdg**. 8 conditions are visible. Switch to the **Artifact** tab and **start** the artifact scan.



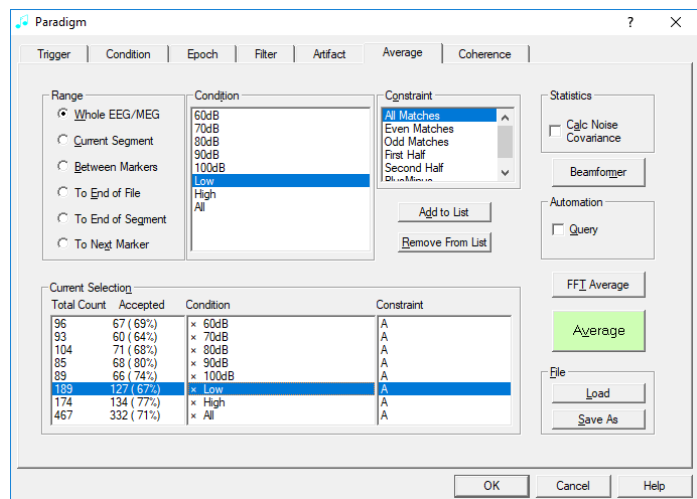
3. Move the vertical slider to the left until all eye blinks are excluded.



- Click the **Gradient** radio button and exclude some muscular activity by moving the slider to the left.



- Move to the **Average** tab. In the list of conditions, click once on the **Low** condition to select it.



- Click the **Beamformer** button. An additional dialog box appears for choosing the beamformer intervals for condition **Low**.

Set beamformer intervals

Target condition: Low ☐ Use Control Condition

60dB

Beamformer interval

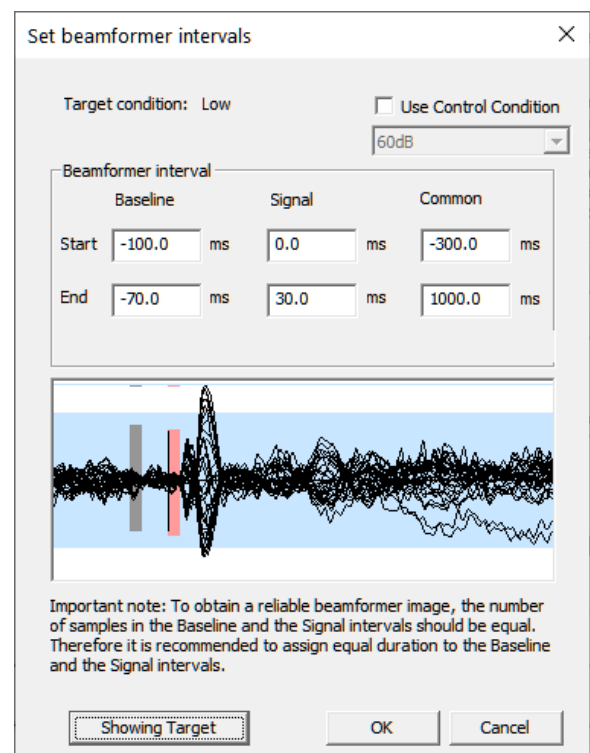
	Baseline	Signal	Common
Start	-100.0 ms	0.0 ms	-300.0 ms
End	-70.0 ms	30.0 ms	1000.0 ms

Important note: To obtain a reliable beamformer image, the number of samples in the Baseline and the Signal intervals should be equal. Therefore it is recommended to assign equal duration to the Baseline and the Signal intervals.

Toggle Butterfly Plot OK Cancel

- Click the **Toggle Butterfly Plot** button. The butterfly plot shows the average signal for all channels, and the currently defined intervals. Three intervals can be defined:

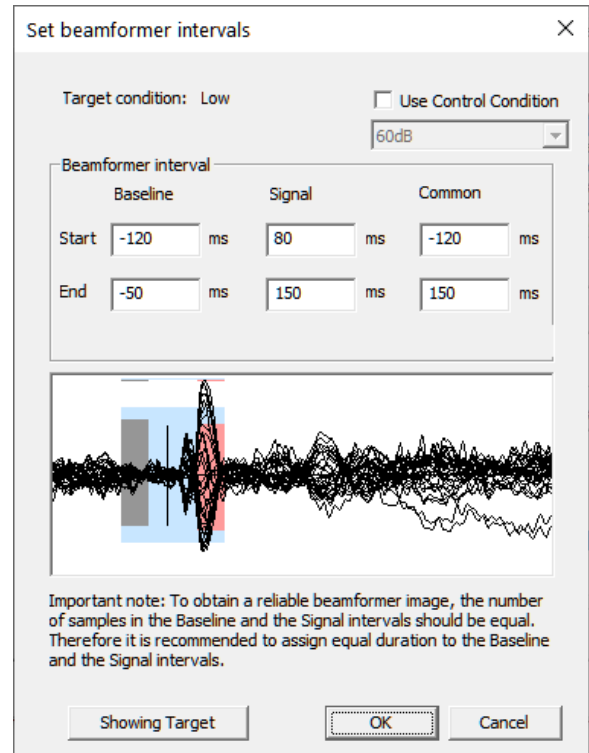
- Baseline
- Signal
- Common



8. Using the Edit boxes, set **signal** to **[80...150]** to cover the main activity of the N100. Set **baseline** to **[-120...-50]** (matching duration). **Common** can be set to **[-120...150]** to cover the complete duration.

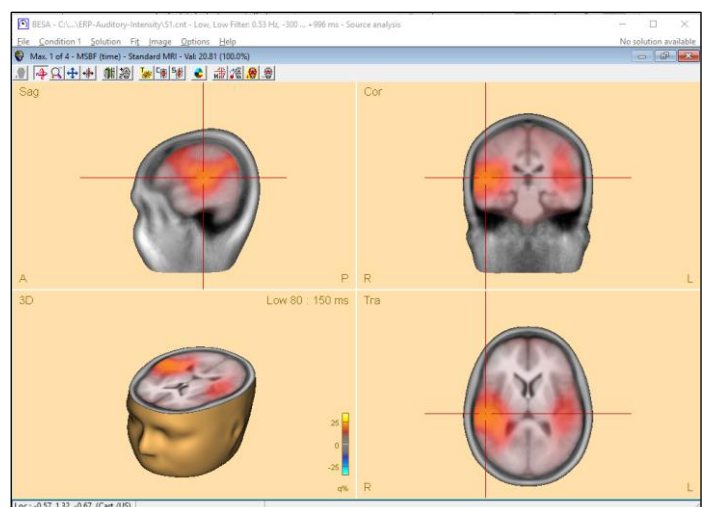
Tip: Contrasting the same interval of interest between two conditions


It is also possible to compare two conditions, instead of using one condition. Check the checkbox '**Use Control Conditions**' and select a condition in the drop-down list for this purpose. When the checkbox is checked, only the 'Signal' interval can be set because the signal interval of the selected control condition will be used as a reference instead of using the 'Baseline' interval. The 'Common' interval is also not used for this case since common beamformer spatial weights are computed using the signal intervals of the both target and control conditions.

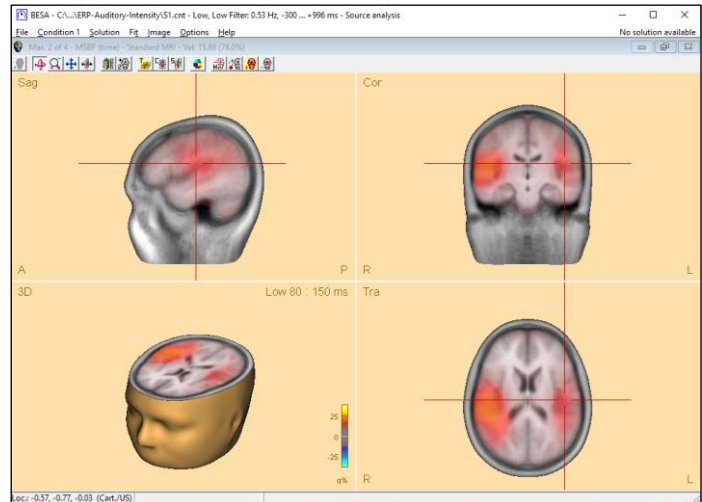


9. Click **OK** to start the beamformer computation. The Source Analysis module opens. Scale the beamformer result up several times to visualize the activation pattern using the **scaling**

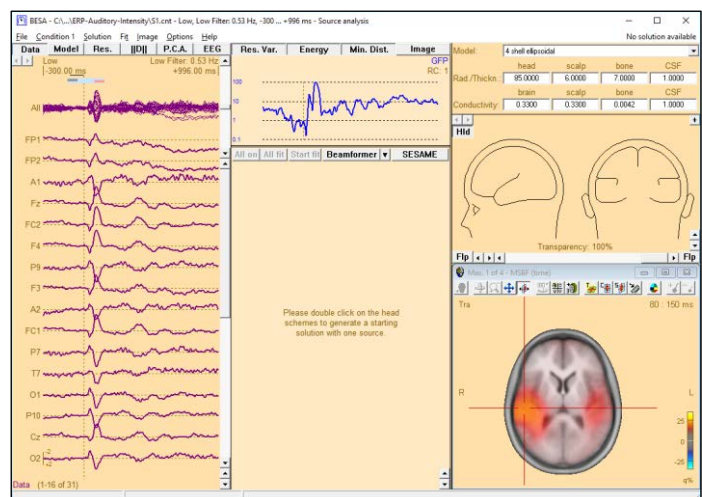
toolbar buttons




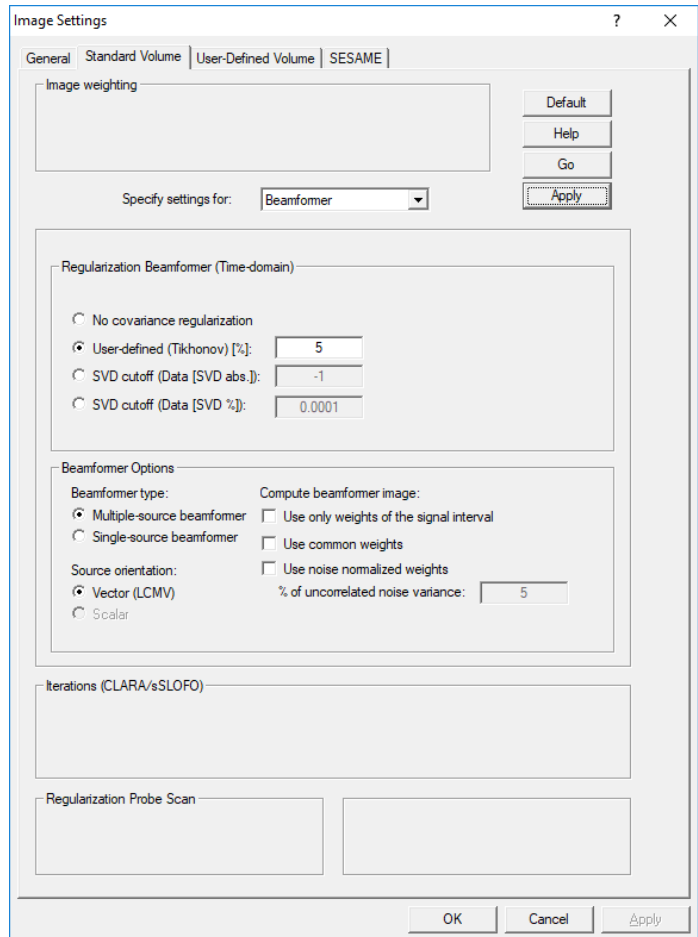
10. Click the **Maxima** toolbar button  to move the crosshair to the next image maximum. Two image maxima are close to auditory areas.




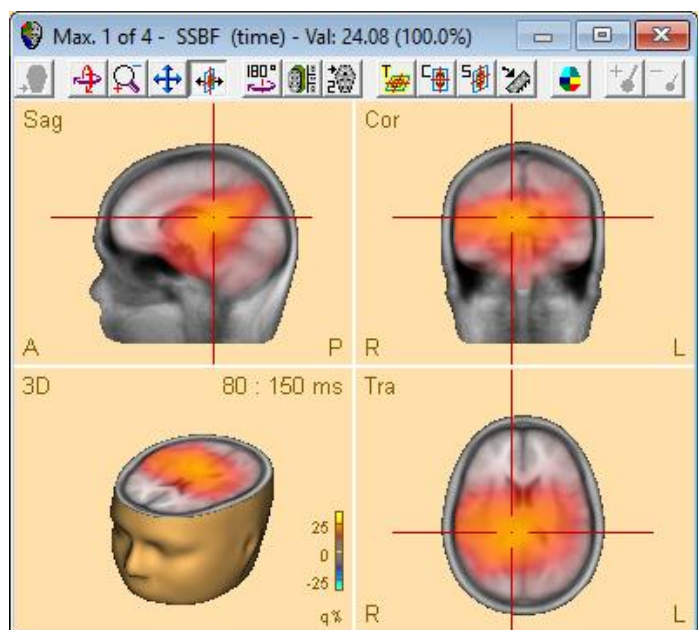
11. Click again the **Maxima** button to return to the first maximum. Then minimize the 3D window using the **Restore down** button at the top right, to visualize the data and global field power. You can see the beamformer intervals plotted above the butterfly plot on the left.



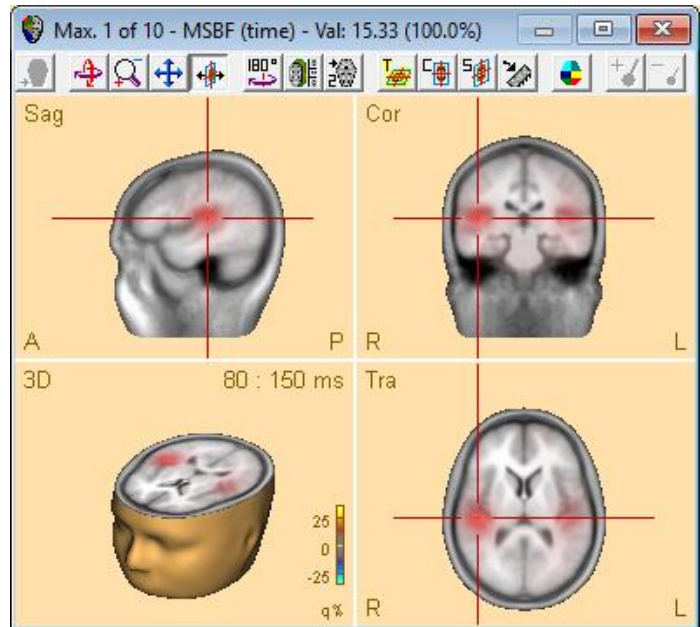
12. Click the **arrow** in the center of the display  to open a popup menu. Then select **Settings**. The dialog box for defining beamformer settings opens. Alternatively, you can use the menu and select **Image / Settings**.
13. The dialog contains settings for regularization, and the beamformer options. We can see that by default, the **Multipole-source beamformer** is selected, and a **Vector** type is used.



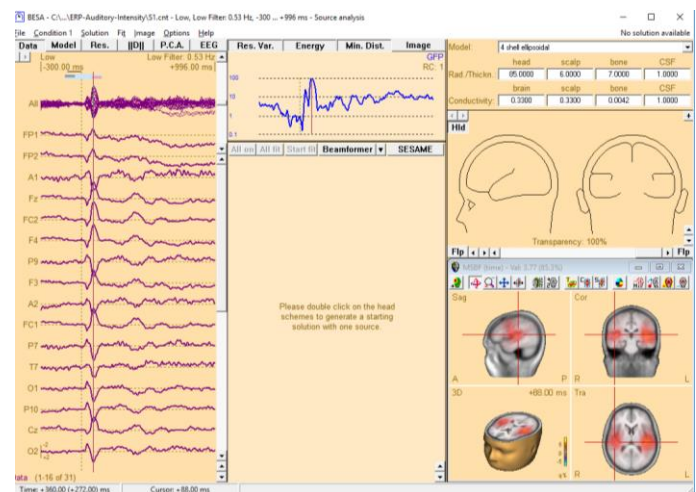
14. We will first try the single-source beamformer. Select **Single-source beamformer** and click the **Go** button at the top right of the dialog. The result changes. To check on what the new result means, leave the dialog box with **OK**, and in the toolbar of the 3D window, activate the **2x2-view** with the button . Then click the **Maxima** button to jump to the first maximum. The first one is now much more central and explains both auditory activations.



15. Next, in the **Settings**, select **Multiple-source beamformer** and **Use noise normalized weights**. A Gaussian noise distribution is assumed, and the contribution of uncorrelated noise variance can be adjusted manually. Use the default value of **5**, then press **OK** and the **Beamformer** button. The result resembles the one where the signal interval was used. The first two beamformer maxima with the highest power percentage cover the auditory areas.



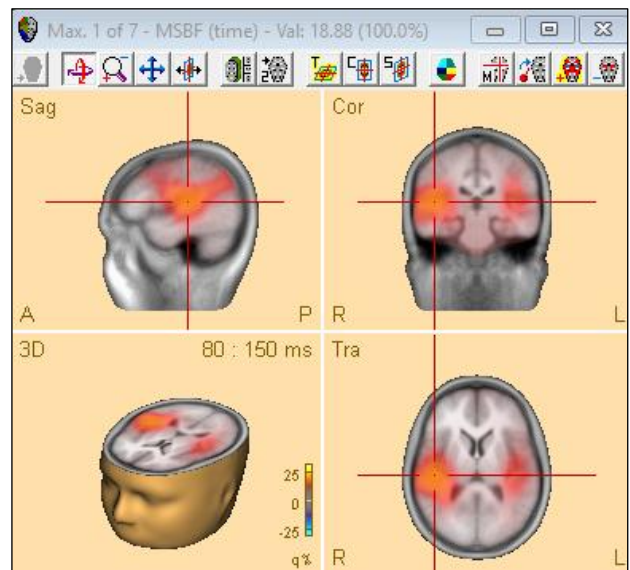
16. In the **Global field power** display at the top center of the screen, **double-click** into the plot to set a cursor. Scale the 3D window intensity up by pressing the **scaling toolbar button** several times, and then move the cursor around using the cursor keys on the keyboard. You can see that the intensity display is now updated with the cursor latency.




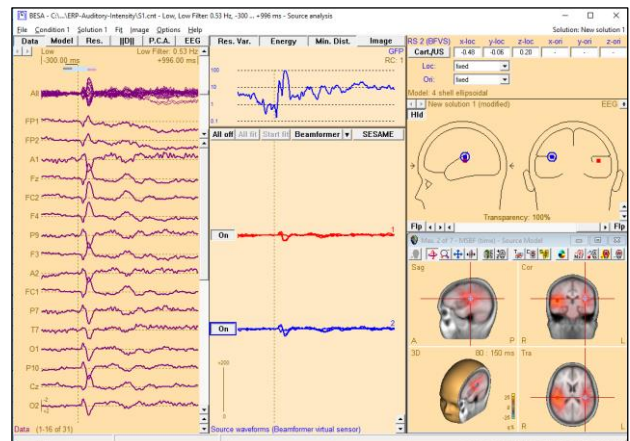
C. Virtual sensor montages

We will now look at further uses of beamformer imaging. One powerful application is the ability to create virtual sensors in a brain voxel of interest. The spatial filter that was computed for estimating its power can be applied not just to the covariance matrix, but also to the raw data.

1. Let us reconsider the good result we achieved with the bilateral vector beamformer. Once more, open the **Settings** dialog on the **Standard Volume** tab and select the **Multiple-source beamformer** with the check box **Use common weights**. Press **Go** and **OK**, and then the **Maxima** button to slice at the first maximum of the newly computed beamformer.

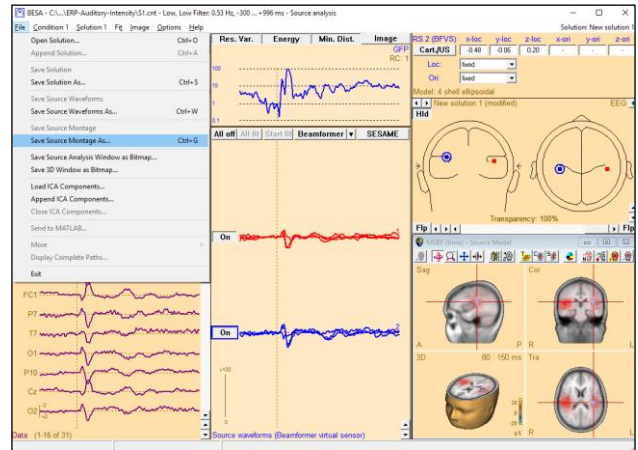


2. In the toolbar, press the **Insert** button  to insert a source at this particular location in the brain. Press the **Maxima** button to move to the second maximum. Then press the **Insert** button again. You have now created a solution of two virtual sensors for this data set.



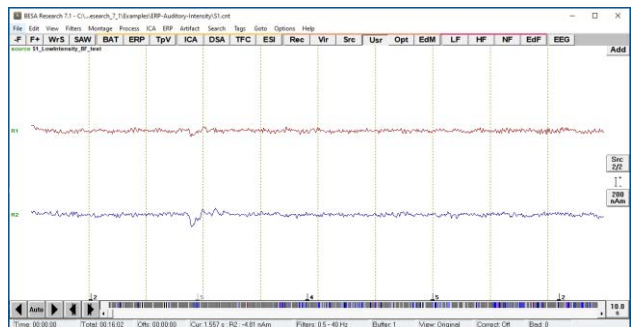
- This solution can be applied to the raw data.

From the **File** menu, select **Save Source Montage As...** In the dialog, save it with the name **S1_LowIntensity_BF_test.mtg**.



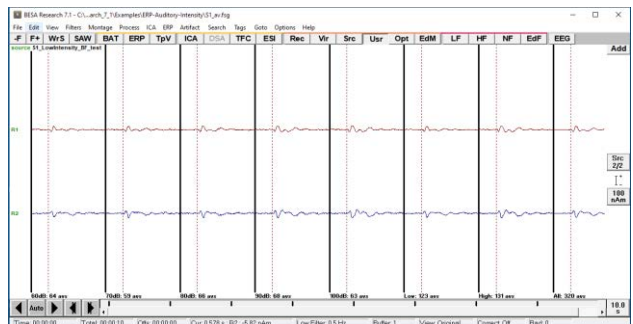
- Minimize** the Source Analysis Window.

The source montage is applied to the raw data. Two channels are visible. These show the orientation-optimized source waveforms of the two beamformer sources, which consist of 3 different orthogonal orientations.

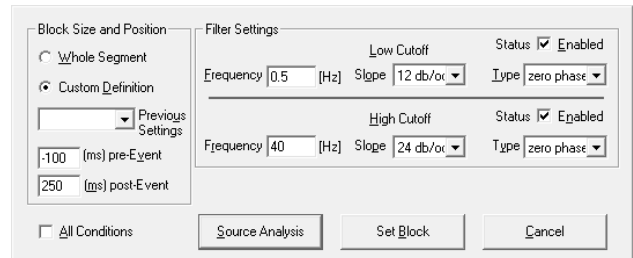


Tip: All waveforms of a source can be displayed using the **Montage / Options / Regional Sources All Traces** menu entry.

- Open the File **s1-av.fsg**. Then press the **Usr** push button and select the montage from the dropdown menu that appears. You can now see how the source channels reconstruct the auditory activity in the averaged conditions.



6. How does this compare with a standard source montage? Let us assume that we had defined a source montage with just two regional sources, fitted to the auditory cortex, for comparison:

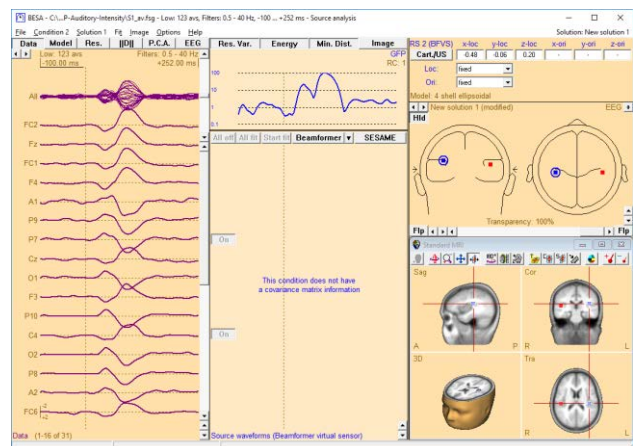


7. **Left-drag** over the condition **Low**, then **right-click** and select **Source Analysis** from the popup menu. In the dialog that appears, select:

- **custom definition** of **-100 to 250 ms**,
- **Low Cutoff Filter** of **0.5 Hz**, **12 dB/Oct.**, **zero-phase** and
- **a High cutoff Filter** of **40 Hz**, **24 dB/Oct.**, **zero-phase**.

Press the **Source Analysis** button.

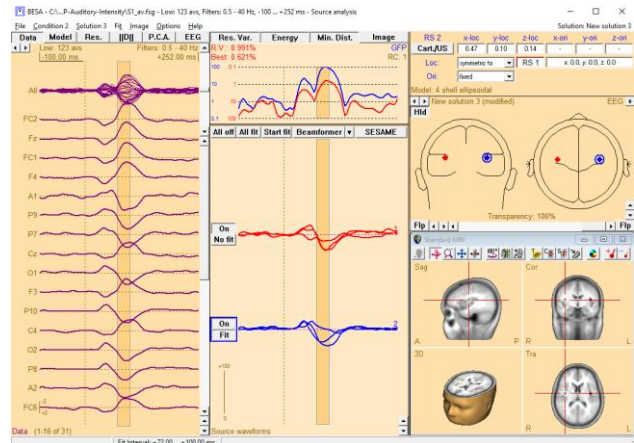
8. The beamformer virtual source condition cannot be applied to these data since no covariance matrix is present.



9. Create a new solution by pressing the **N** key on the keyboard and insert two regional sources.

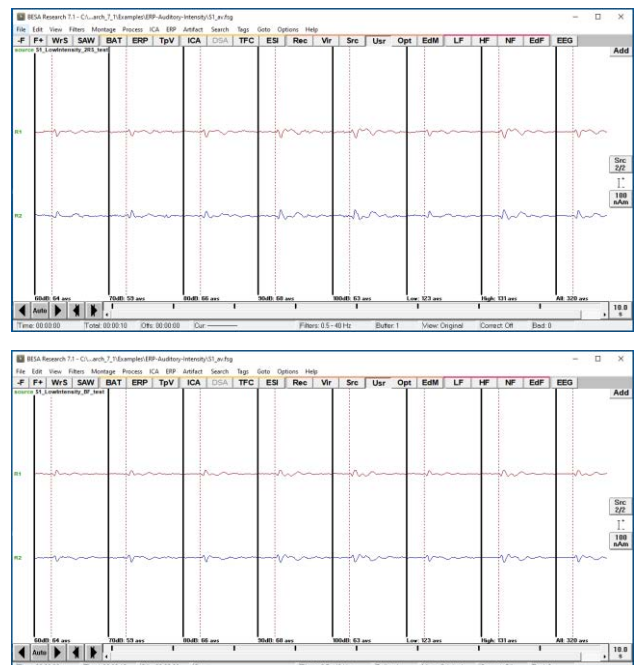
If dipoles are inserted instead, then convert the sources to regional sources by selecting each of them, then using the key **C** on the keyboard to convert.

Apply a symmetry constraint to one of the sources by selecting it, then using the **drop-down menu** beside **Loc** at the top right. Then, mark an interval from **72 –100 ms** and press the **All fit** and **Start fit** buttons. The sources fit into an area close to the auditory cortex.



10. Use the menu **File / Save Source Montage As...** to save this as a source montage with the file name **S1_LowIntensity_2RS_test.mtg**. Then **close** the Source Analysis window.

You can see that the auditory activation is also picked up by these sources as shown in the upper screen shot on the right; however, if you switch back to the beamformer virtual sensors using the **Usr** button, you will see the difference: The beamformer virtual sensors pick up much less background activity (lower screen shot). This is due to the fact that in classical source montages, any brain activity needs to be modelled; otherwise, background activity that is spatially correlated with the



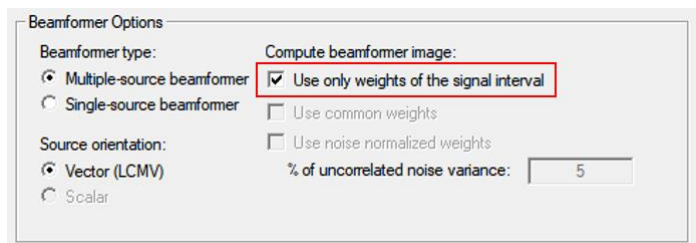
activity of interest will be projected onto the source of interest. In the beamformer case, the spatial filter is already optimized for each source, independent of the presence of other sources in the model.

D. (Optional section) More settings in the time-domain beamforming

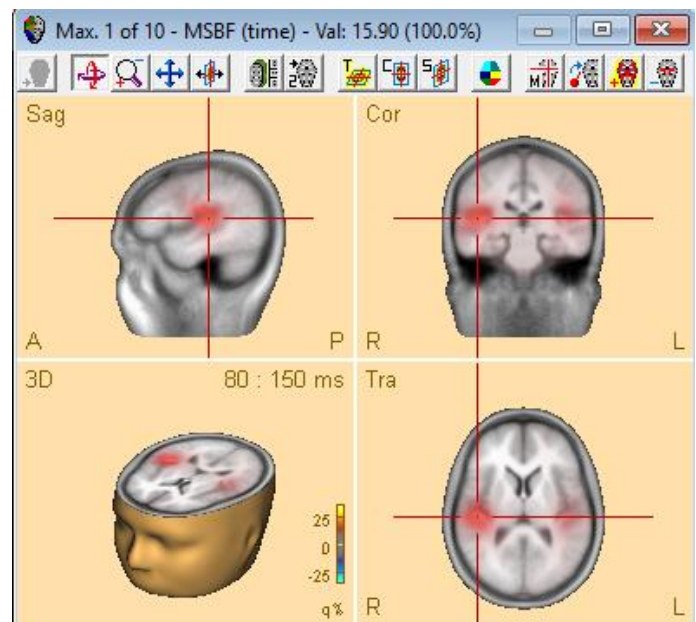
The options to reduce the influence of different spatial leakage profiles of the beamformer spatial weights for baseline and signal intervals.

- **Use only weights of the signal interval:** Beamformer spatial weights for *signal interval* is only used when a beamformer image is computed.
- **Use common weights:** Beamformer spatial weights for the *common interval* is only used when a beamformer image is computed.

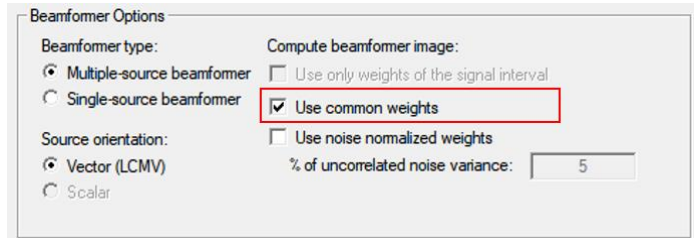
1. Open the **Image Settings** dialog again (hotkey: Ctrl + Shift + A). Select the **Multiple-source beamformer**, and check the box for **Use only weights of the signal interval**.



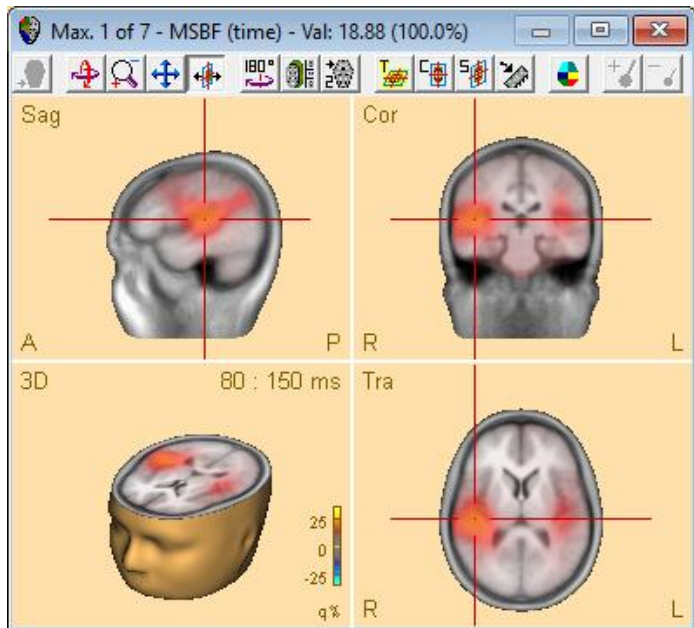
2. Press **Go** and then **OK**. Click on the **Maxima** button. The first two cover again the auditory activation. They are more focal than the initial ones.



3. In the **Image Settings** dialog, **uncheck** the previous box and check the **Common weights box** instead.



4. Press **OK**, then press the **Beamformer** button in the center of the screen. The beamformer is re-computed and automatically slices the MRI at the first maximum.

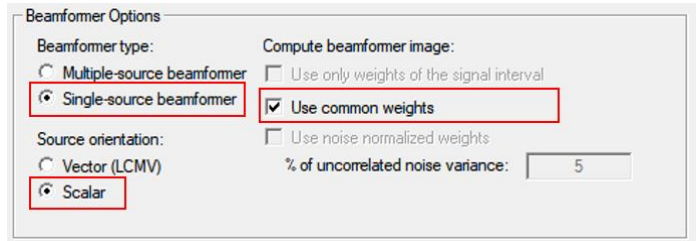


Scalar beamformer

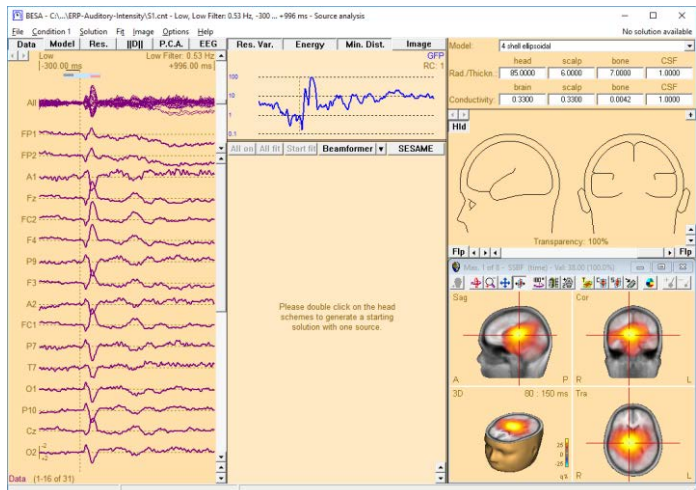
When vector beamformer is used, a beamformer source at position \mathbf{r} can have 3 orientations for EEG or 2 orientations for MEG. A single optimal orientation that gives the maximum power output at each location is considered in scalar beamformer (Robinson and Vrba, 1999; Sekihara et al., 2004). Therefore, single source waveform is computed for a virtual sensor of the scalar beamformer, while three waveforms (MEG: two waveforms) are estimated for a virtual sensor of the vector beamformer.

Note that this option cannot be used with “Multiple-source beamformer” or “Use noise normalized weights” option.

1. We will have a look at the Scalar beamformer. We go back to the Settings dialog, and now select **Single-source beamformer**, with the option **Use common weights**. With these options, the **Scalar beamformer** becomes available. Select this option and press **OK**, then click the **Beamformer** button.



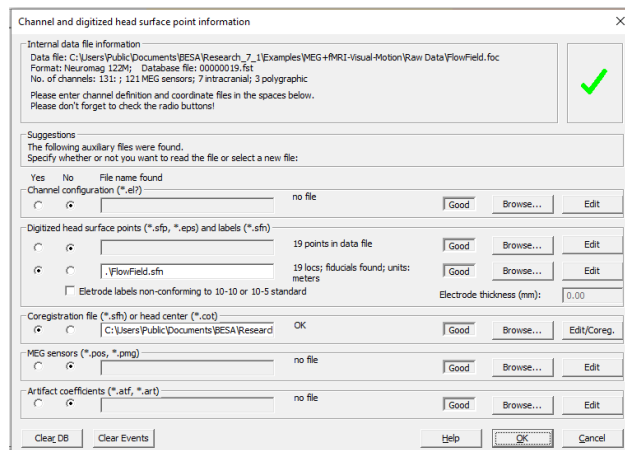
2. Slice the display at the first maximum using the **Maxima** button on the toolbar. Like in the vector beamformer case with single source, the maximum moves to a more medial location. The other maxima localize outside of auditory areas.
3. You can try to go back to the **Settings** and check **Common weights** and **noise-normalized weights** at the same time. This will not substantially change the result, however.



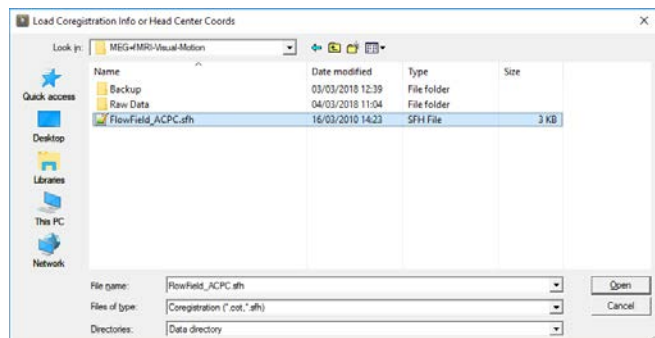
E. Time-domain beamforming in MEG data

We will now use the beamformer to analyze MEG data, and try to find out whether propagation of activity over time can be modelled via the beamformer.

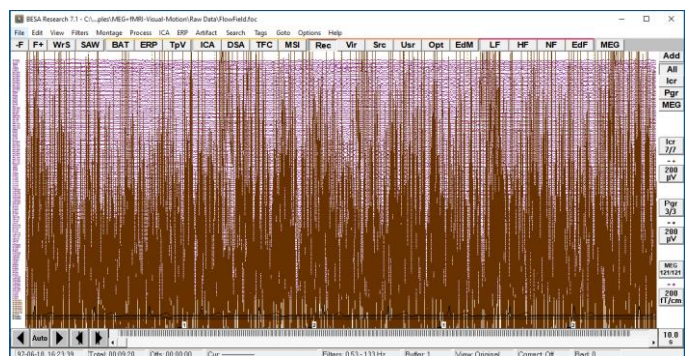
1. Select **File / Open** and browse to the folder **./Examples/MEG+fMRI-Visual-Motion/Raw Data**. Open the data set **FlowField.foc** (you may have to change the extension filter at the bottom of the dialog box to see the file in the list). The **Channel and digitized head surface information** dialog appears.



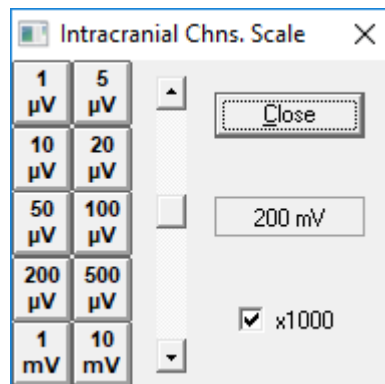
2. In the section **Coregistration**, click the **Browse** button. In the dialog that appears, go up one folder, and select file **FlowField_ACPC.sfh**.



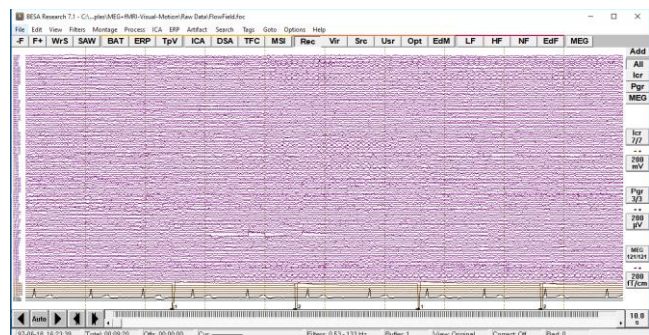
3. Press **OK** to close the **Channel and digitized head surface information** dialog. The file opens. Display of MEG waveforms is obscured by the large signal of the stimulus channels, which have been assigned to channel type **ICR**.



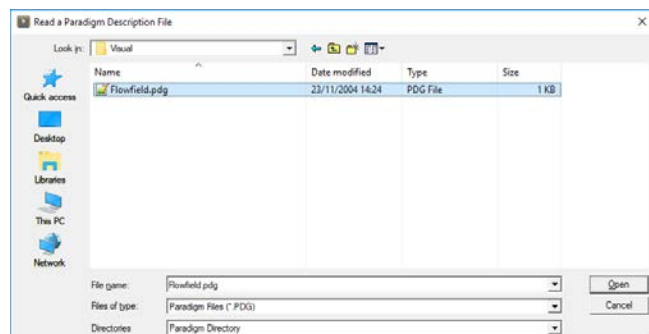
- Click the **scaling button** of the **lcr** channel type at the right side of the screen and check the **x1000 check box** to change scaling to **200 mV**.



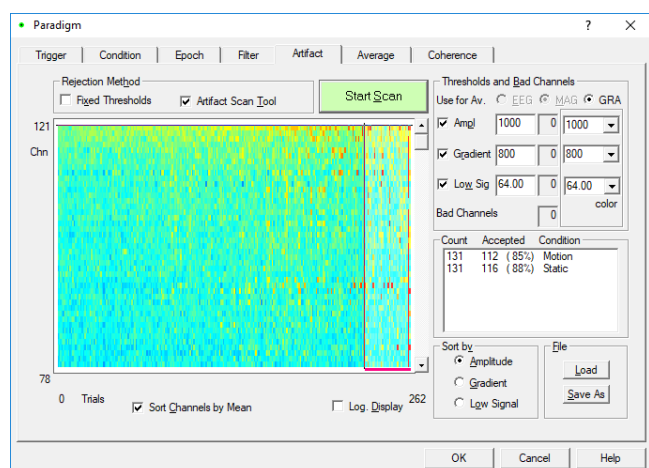
- Now the MEG is visible. Trigger codes 1 and 2 were applied.



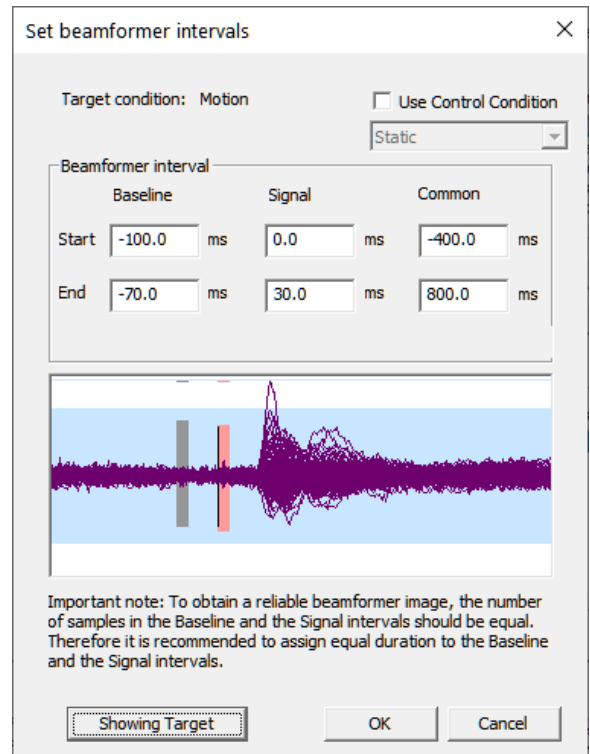
- Press the **ERP** push button. Then, in sub-folder **Visual**, open the paradigm file **Flowfield.pdg**.



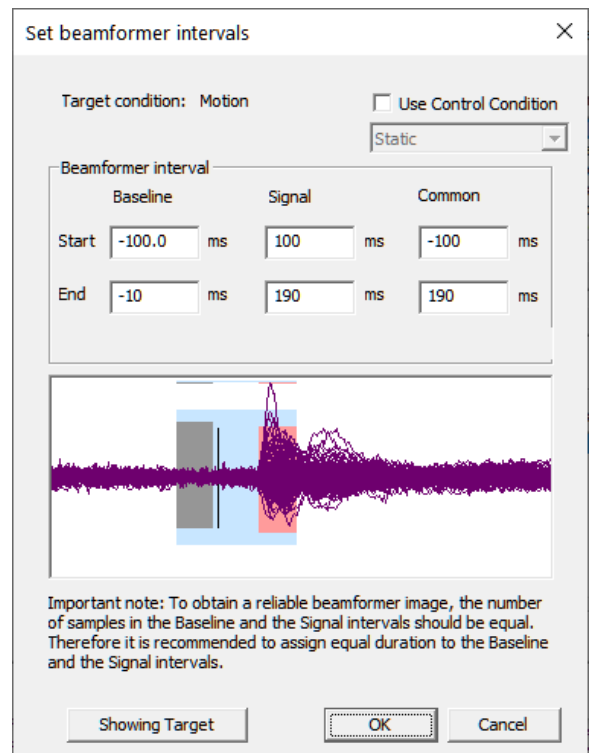
- Move to the **Artifact** tab and press **Start Scan**. The current thresholds are appropriate. You can check for gradient and Low Signal criterion, too.



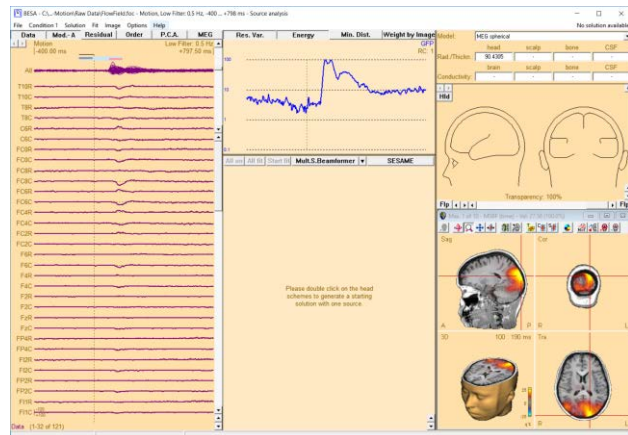
8. Move to the **Average** Tab. Select the first condition **Motion** and press the **Beamformer** button. In the **beamformer intervals** dialog, press the **Toggle Butterfly Plot** button. MEG channels are shown in a dark purple colour.




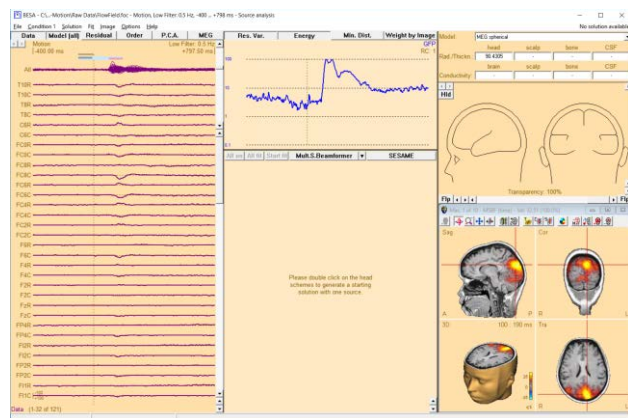
9. From the tutorial 7, we know that the activity related to Motion happens later than the initial visual evoked activity that follows the stimulus. Let us mark a signal interval from **100 to 190 ms**. Accordingly, set the baseline interval from **-100 to -10 ms** and the Common interval from **-100 to 190 ms**.



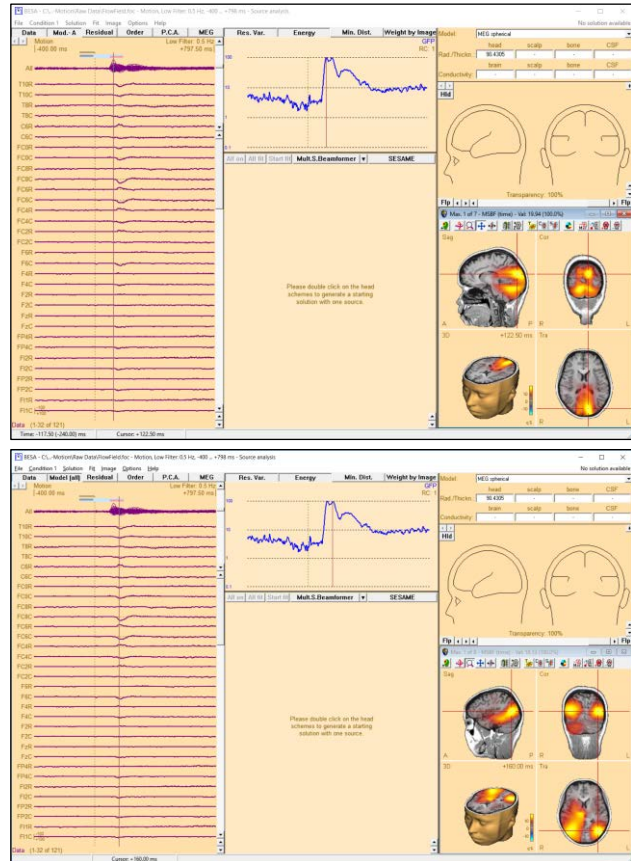
10. Press the **OK** button to start the beamformer computation. The Source Analysis module opens.




11. Click the **arrow** in the center of the display  to open a popup menu. Then select **Settings**. The dialog box for defining beamformer settings opens. Select **Multiple-source beamformer** and **Vector (LCMV)** options, and check the boxes for **Use common weights** and **Use noise normalized weights**. Then, click the **Go** button. The results change.

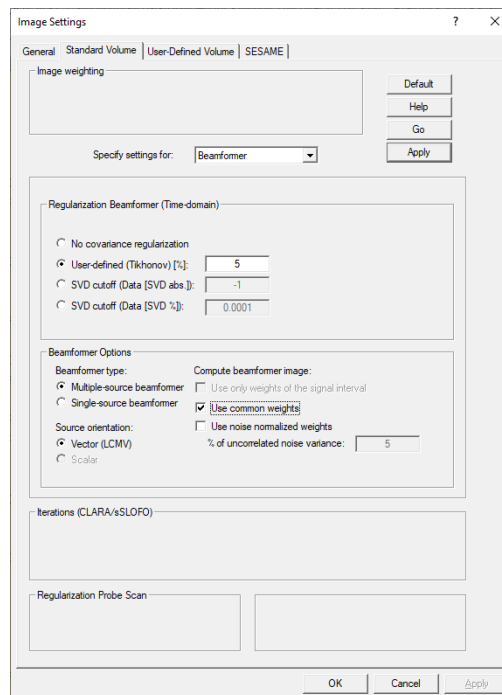


12. In the **Global field power** display at the top center of the screen, **double-click** into the plot to set a cursor. Then move the cursor around using the cursor keys on the keyboard. You can see that the beamformer image is now updated with the cursor latency. Check the beamformer image at 122.50 ms and 160 ms.

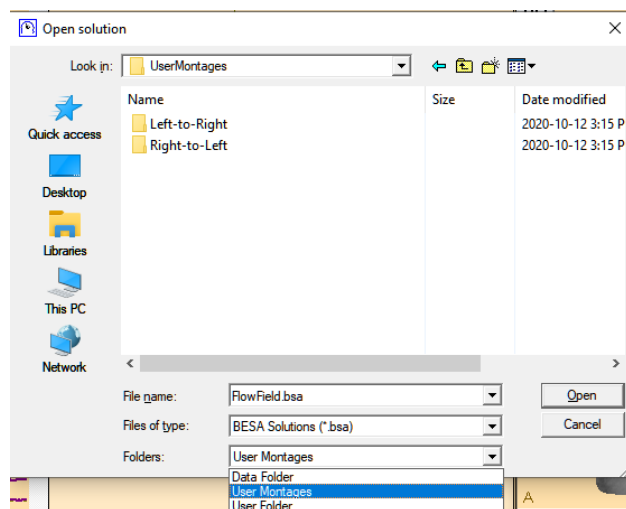


In the next steps, we will create an atlas-based beamformer source montage using the predefined source locations based on a brain atlas.

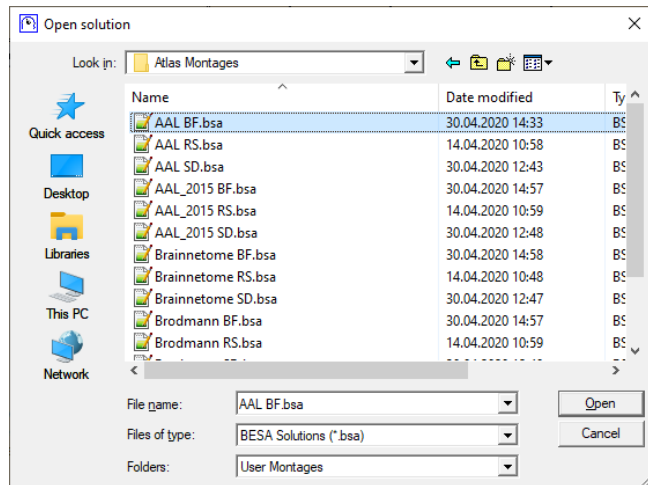
13. Click the **arrow** in the center of the display  to open a popup menu. Then select **Settings**. The dialog box for defining beamformer settings opens. Select **Multiple-source beamformer** and **Vector (LCMV)** options, and check the box for **Use common weights** (uncheck the **Use noise normalized weights** option if the option is already checked). Then, click the **Go** button. The results change. Leave the box with **OK**.



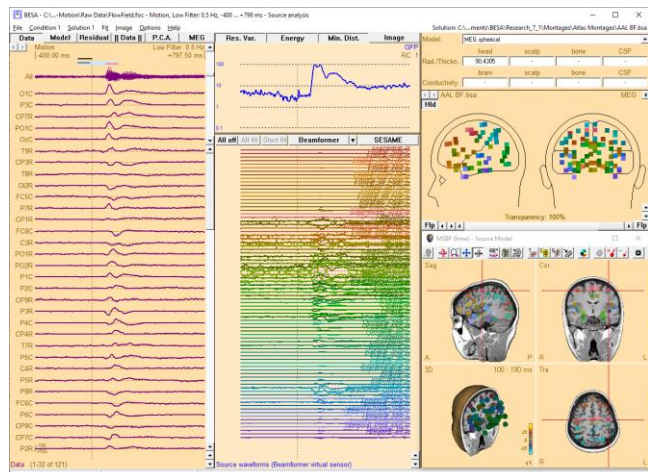
14. Now we have a robust inverse operator that covers the activation. We want to apply it to an atlas source montage that will place virtual sensors in all atlas regions. To do this, select **File → Open solution** and select the folder **User Montages** at the bottom of the dialog box.



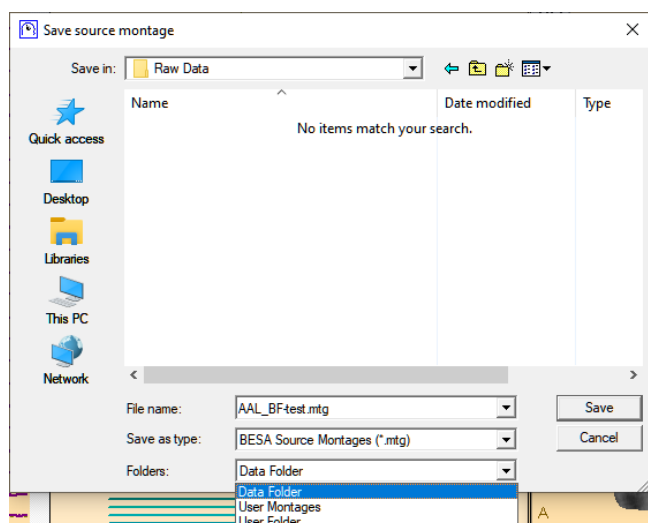
15. Move up one folder level and into the folder **Atlas Montages**. Open the file **AAL_BF.bsa**.



16. The beamformer solution is loaded and shows activation mainly in the green and blue sources. You may set a cursor to see the symbol sizes change over time.



17. Now we will create a beamformer virtual sensor montage to operate on the raw data. To do this, use **File → Save Source montage as....** Change the **Folders** to **Data folder**. Assign the name **AAL_BF-test.mtg**.
The saved beamformer virtual sensors will be use in **Tutorial 12** for time-frequency and connectivity analyses.



Tutorial 10 – Advanced Artifact Correction

What does BESA Research provide?

- ✓ Artifact correction based on surrogate models,
- ✓ Artifact correction based on adaptive artifact correction,
- ✓ ICA based artifact spatial filtration and artifact free data generation

A. Artifact Correction

In the following we will learn about the background of artifact correction. Artifact correction always aims at extracting unwanted signals like EOG, EKG or external noise from the data, while leaving all brain activity of interest as undisturbed as possible. To achieve this, artifact and brain topographies must be separated. Depending on whether one is dealing with spontaneous or evoked activity, different approaches for artifact correction are appropriate. These will be discussed and demonstrated in this tutorial.

Principles of artifact correction

For artifact correction, artifact and brain activities must be identified and separated. In general, artifact and brain topographies will be spatially correlated. Hence, a simple regression or the projection of the data onto the subspace orthogonal to the artifact topographies will severely distort the data (see Subspace Projection approach below).

For a correction without distortion, it is not sufficient to define the artifact topographies (to be removed), but it is equally necessary to create a model or a spatial description of the brain topographies (to be retained). The first two of the following three methods also create a model for the brain activity:

- 1) Adaptive artifact correction:** (Ille N, Berg P, Scherg M. Artifact correction of the ongoing EEG using spatial filters based on artifact and brain signal topographies. J. of Clin. Neurophysiol. 19:113-24, 2002.)

This method estimates the brain activity from the data currently displayed on the screen. The data is scanned in specified time intervals. Those segments are considered to represent brain activity where 1) the correlation between data and artifact topography does not exceed a certain threshold and 2) the signal amplitudes are below a specified threshold. Of the remaining segments a principal component analysis (PCA) is performed. All PCA components explaining more than the minimum variance specified in the box Adaptive Model: PCA Topography are maintained. They span the brain signal subspace.

In a next step, the recorded data is decomposed using all topographies into a linear combination of brain and artifact activities. Thus, the estimated artifact signals are much

less overlapped with brain activity and can be subtracted from the original signals without much distortion.

This approach is recommended, in particular, for the review of continuous EEG or MEG data.

- 2) Surrogate Model approach:** (Berg P, Scherg M. A multiple source approach to the correction of eye artifacts. *Electroencephal. Clin. Neurophysiol.* 90:229-41, 1994.)

Here, brain activity is modeled by a model consisting of multiple equivalent current dipoles. The artifact topographies are added to this model and the combined model is then applied to the recorded data. Again, the estimated inverse signals separate the brain activity associated with the surrogate sources from the artifacts to a high degree. Thus, the artifact signals can be subtracted without considerable distortion of the activities originating in the modeled regions. This approach considers the activity in the modeled brain regions while the on-going EEG is not modeled accurately.

Therefore, the surrogate method is especially recommended for the correction of data to be averaged if the average signal is smaller than the EEG or MEG background. In this case a model cannot be estimated from the on-going data. Therefore, a-priori knowledge of the involved brain regions should be employed to create an appropriate surrogate model.

- 3) Subspace projection (SSP, regression):** This approach has been commonly applied in the literature. SSP does not contrast artifacts and brain activity. Rather, the complete subspace spanned by the artifact topographies is projected away from the recorded data. This leads to undistorted data only in the highly unlikely case when artifact and brain activity have exactly orthogonal topographies. This is generally not the case in real data. In the likely event that evoked brain activity has a topography correlated with the artifact, this method removes the correlated fraction of the brain activity. As one of the negative consequences, maps of the corrected brain activity will be severely distorted after SSP correction, as we will see below.

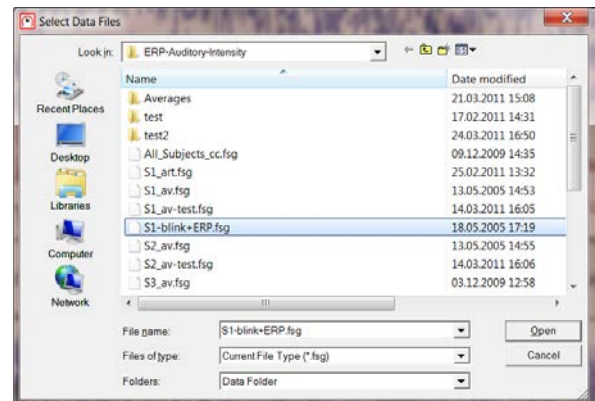
Therefore, this method is not recommended.

The following chapters demonstrate the practical application of these different approaches.

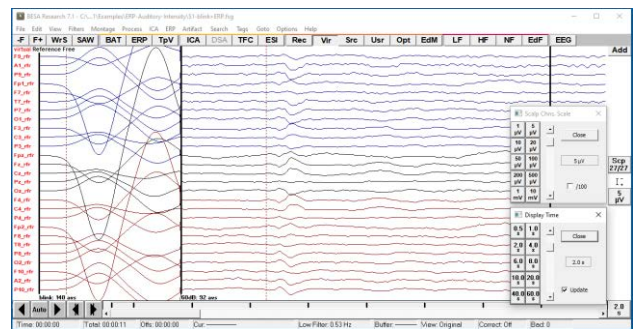
B. The Effect of Artifact Correction on Averaged ERP data

For a traditional ERP analysis (e.g. analysis of peak channel amplitudes and latencies), artifact correction can be applied to the averaged ERP data. This chapter demonstrates how the different correction methods affect the obtained result.

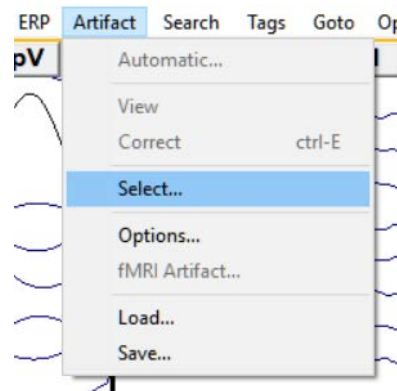
1. Please **open** the file **S1-blink+ERP.fsg** located in the **ERP-Auditory Intensity folder**. This file contains the average of conditions 60 to 100 dB, Low, High and All along with an **averaged eyeblink**. Change to the virtual reference-free montage by pressing the **Vir** button and selecting the entry **Reference Free**.



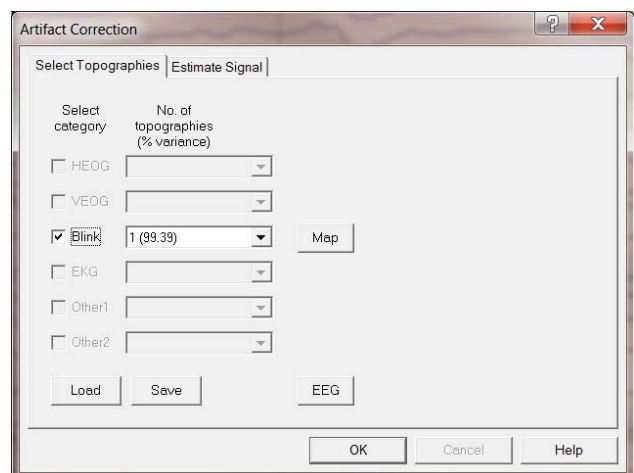
2. We will demonstrate the effect of artifact correction with focus on the 60dB condition. Use the **time scaling button** at the bottom right of the window to set the time scaling to **2.0 s**. Press the **amplitude scaling button** under the **Scp** button to increase the displayed scalp channel amplitude to **5 μ V**.



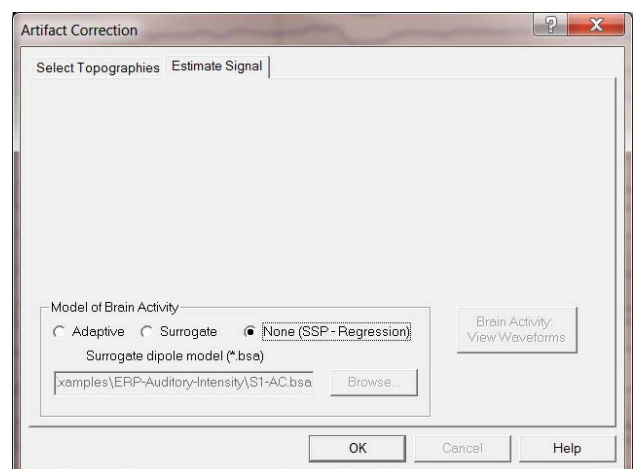
- From the **Artifact** menu, choose **Select....**



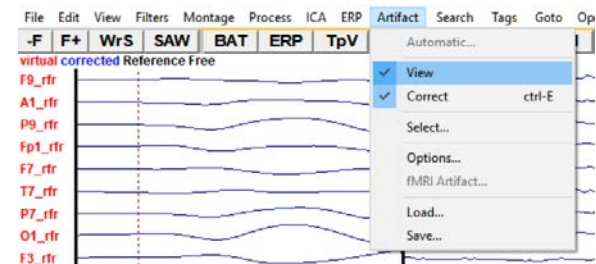
- Note that the blink artifact topography that we defined in the raw data has been assigned automatically to the averaged file as well, but is not selected by default. **Set the checkmark** next to the **Blink** category.



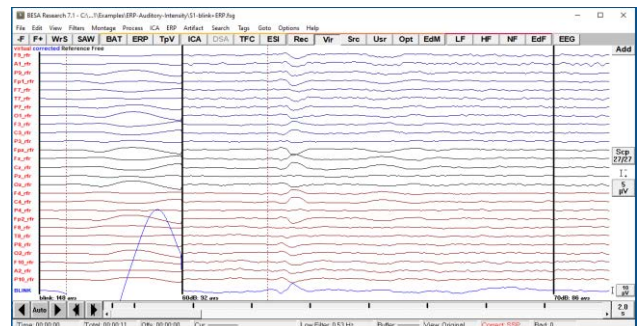
- Switch to the **Estimate Signal** tab. We will compare the three different approaches for artifact correction offered by BESA Research. First, select **None (SSP-Regression)** in the **Model of Brain Activity** box to correct the data by subspace projection. Press **OK**.



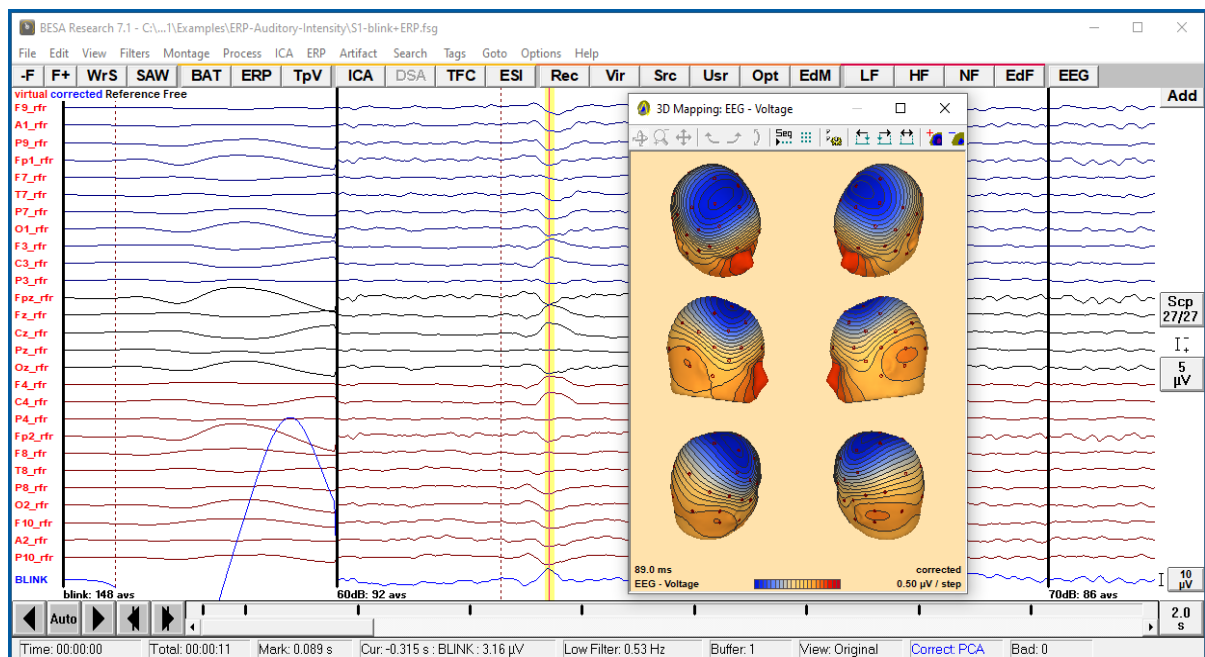
- Make sure that artifact correction and view is selected in the **Artifact** menu.



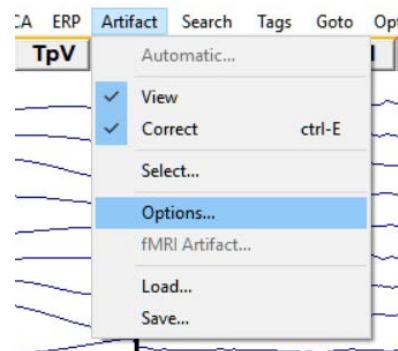
- Press the **scaling button** for the Blink channel to scale it up to **10 μ V**. The blink activity has been largely corrected. Remaining activity in the first segment is due to the 0.6% of variance that is not explained by the first PCA component. Including a second or third PCA component in the Select Topographies tab would improve the correction. However, the more artifact topographies are being defined, the more likely the brain activities become distorted.



8. **Double-click** in the second segment at the latency of the N100 component (ca. **90 ms**) to obtain a 3D whole head map of the corrected data at this latency. The map is severely distorted by the SSP correction: Instead of the N100 topography, a strong frontal positivity is observed that is typical for the blink topography. The reason is that SSP is not able to contrast the artifact topographies with the brain signals. Since the N100 topography is correlated with the blink topography, the correlated fraction of the N100 contribution is removed from the data by the subspace projection. The correlation can be seen in the bottom trace which depicts the blink signal estimated using its topography throughout the data set. At the time of the N100, it shows an upward deflection. Hence, SSP subtracts this part weighted with the blink map. Thus, a more inferior frontal positivity is introduced. The net resulting map, however, has been made orthogonal to the blink topography over all electrodes.

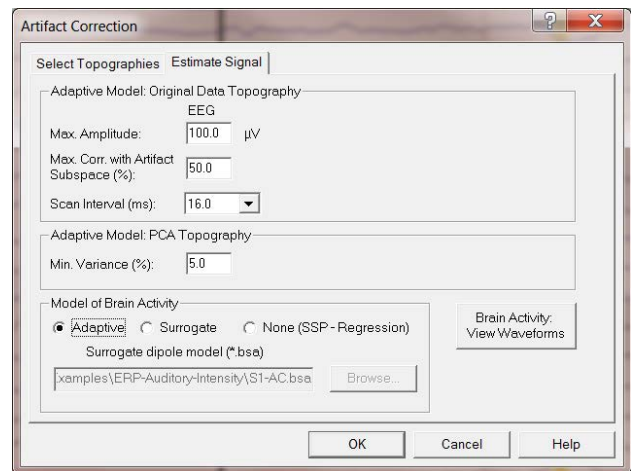


9. To see how the adaptive method improves the result, **select Artifact / Options**.

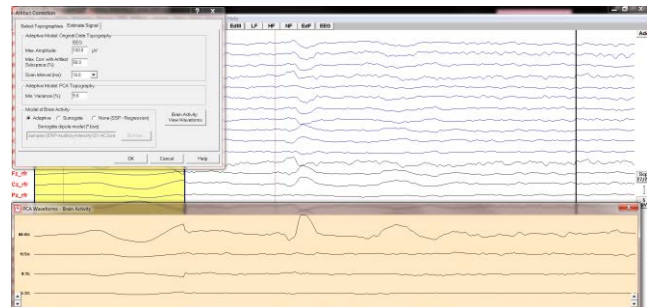


10. As Model of Brain Activity select **Adaptive**.

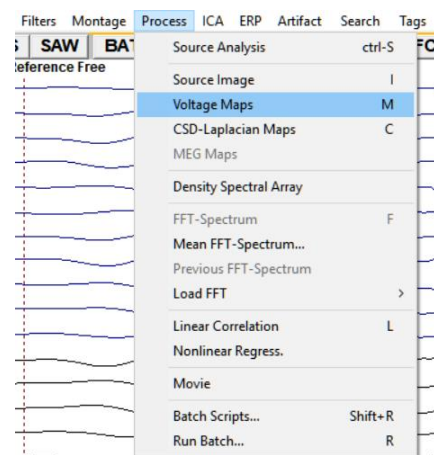
The **Minimum Variance** threshold determines the number of topographies that are considered brain activity which is contrasted against the artifact topography. Set the threshold to **5%**. To view the time course of the brain topographies, press **Brain Activity: View Waveforms**.



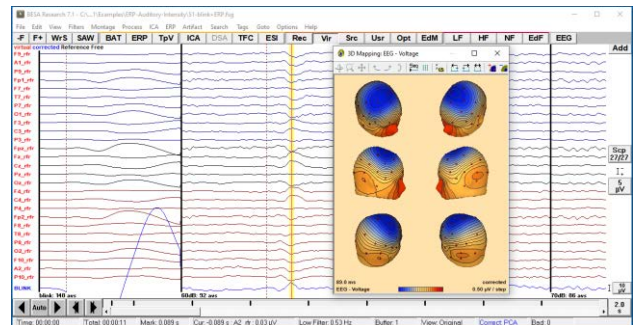
11. Three PCA topographies serve as model for the brain activity. In their time courses, the auditory N100 component is mainly represented by the first component. Note that the 4 displayed components have topographies that are orthogonal to each other, but they are not orthogonal to the artifact topography. Accordingly, this approach will retain brain activity even when it is spatially correlated to the artifact topography.



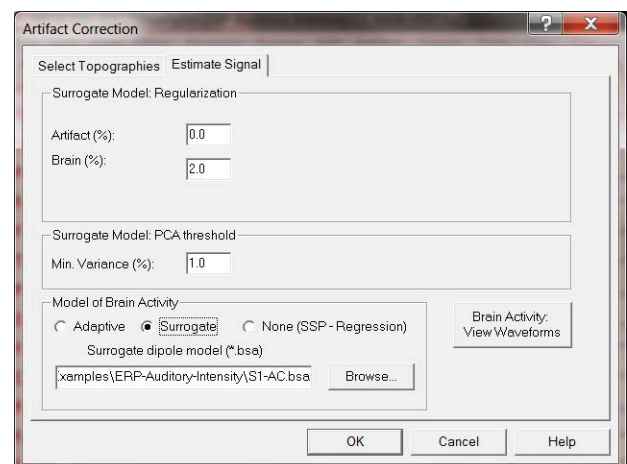
12. To see this, close the PCA Waveforms and Estimate Signals windows. If the cursor at ca. **90 ms** is still set in the second condition, select **Process / Voltage Maps** or type the hot key **M** on the keyboard to obtain the 3D map of the adaptively corrected data.



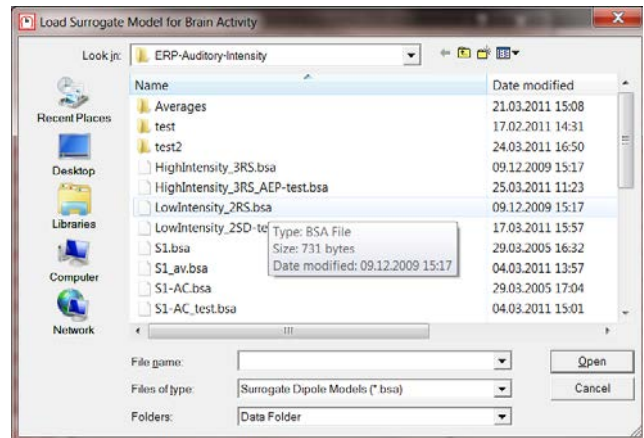
13. The maps are nearly undistorted by the artifact correction and show the typical N100 topography. As a correlate, note that the blink waveform does not show any interaction with the auditory evoked components. This indicates that blink and brain activities have been very well separated by the adaptive method.



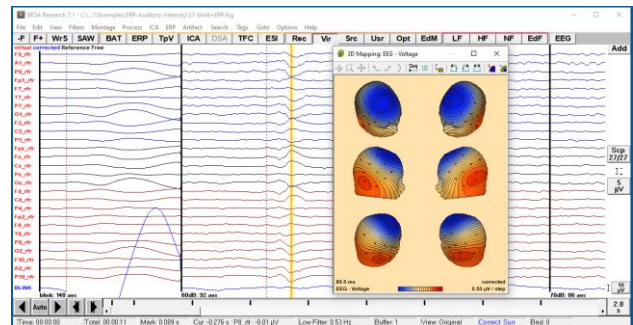
14. Press **Artifact / Options** and check **Surrogate** in the Model of Brain Activity box. The surrogate model approach is useful if evoked activity is to be contrasted against eye movement artifacts and if the evoked activity is small as compared to the background EEG / MEG. In this case, the adaptive model does not well model the evoked activity and artifact correction is likely to create distortion. Therefore, a surrogate source model should be established *a) on the basis of a priori functional-anatomical knowledge*, or *b) by using a multiple source model* or spatial components defined by a PCA from an average with all artifact epochs rejected and fewer trials.



15. Press the **Browse** button to load the solution **LowIntensity_2RS.bsa** that was created earlier on, consisting of a symmetrical pair of regional sources in the auditory cortex. The stored two regional sources model the bilateral brain activity in the supratemporal region and are combined with the defined artifact topography to separate artifact and brain signals¹³.



16. Press **OK** and press **M** to view the 3D map of the surrogate-corrected data at the cursor latency. Similar to the adaptive method applied to the averaged data, the brain topographies are nearly undistorted. The blink waveform does not show any interaction with the auditory evoked components.

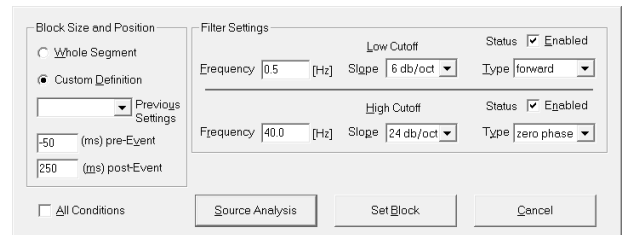


C. Source analysis of artifact-corrected data (not recommended)

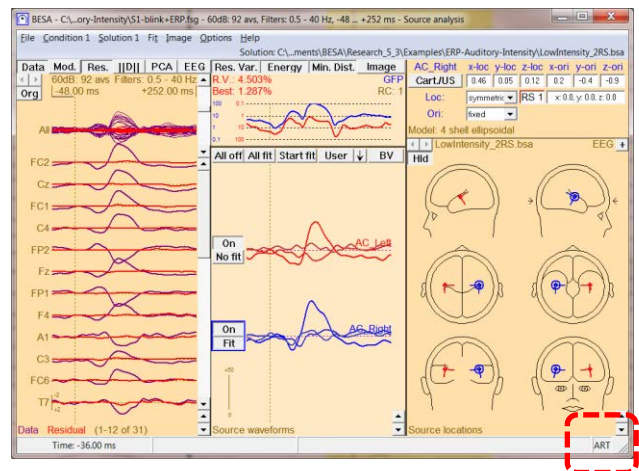
Accurate source analysis of artifact-corrected data requires knowledge of the artifact topographies that were removed from the data. Otherwise, source activities will also be distorted. If an (averaged) data segment has been created (and/or stored as binary segment) by the program, BESA Research knows the artifact coefficients as indicated by corrected at the upper left. Otherwise, an ASCII file (*.art) with the artifact topographies must be provided.

¹³ It is not necessary to create a surrogate source model. Predefined surrogate models are provided by BESA Research.

1. **Left-drag** over the second segment to mark a block. **Right-click** and send it to **source analysis** with settings **-50 to 250 ms**, **Low Cutoff filter of 0.5 Hz**, **6 db/oct**, **forward** and **High Cutoff Filter of 40 Hz**, **24 db/oct**, **zero-phase**.



2. Load the source model **LowIntensity_2RS.bsa** by pressing **File / Open Solution**. The letters **ART** in the status bar at the bottom right corner of the window indicate that this data is artifact-corrected and that BESA Research knows the topographies of the corrected artifacts.



Depending on the correction method, a fraction (adaptive, surrogate) or the complete (SSP) dimension of the artifact subspace is missing. Despite this fact, the source analysis window ensures correct localization and correct source waveforms (S) of fitted sources. This is achieved by a SSP method that projects both the data (D) and the source topographies (L) onto the subspace orthogonal to the subspace that is spanned by the artifact topographies. Accordingly, the display shows the SSP-corrected data, independent of the correction method used in the main window. The fact that the source waveforms are recovered correctly by this approach can be seen from the following equations:

Uncorrected data:

$$D = L * S$$

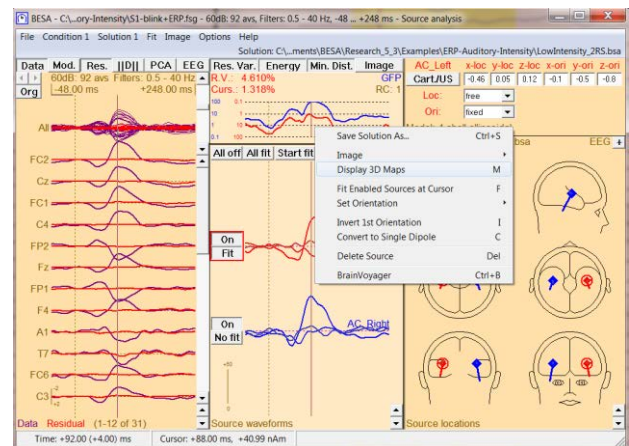


Corrected data:

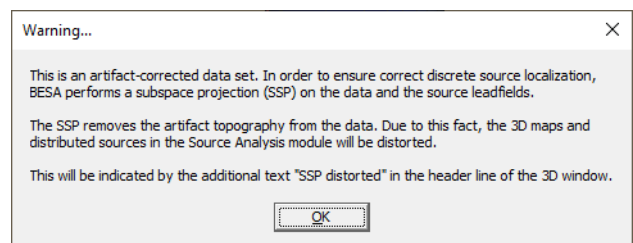
$$(P*D) = (P*L) * S$$

Here, P is the operator that projects into the subspace orthogonal to the subspace spanned by the artifact topographies.

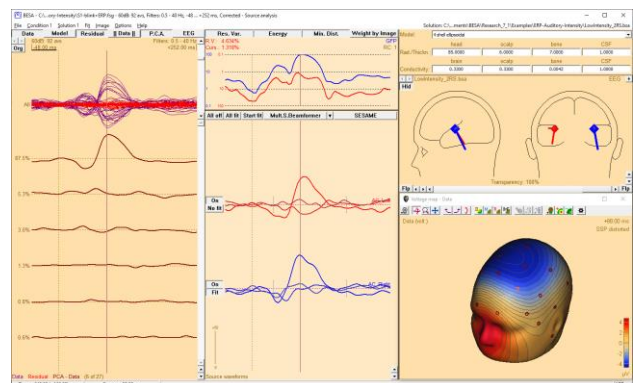
3. **Double-click** in the waveform box to set a cursor at the N100 latency. **Right-click** and select **Display 3D Maps** or type the hot key **M** on the keyboard.



4. BESA Research displays a warning message. It explains why the following map will be distorted. Press **OK** to confirm.



5. The topography is severely distorted by the subspace projection that was applied to the data. Although the source waveforms obtained by modeling the corrected data are undistorted, the data displayed in the channel box and in the global field power (GFP, blue line in the upper middle box) are distorted. As a consequence, *loading corrected data into the source analysis window is less recommended*. Close the source analysis window.



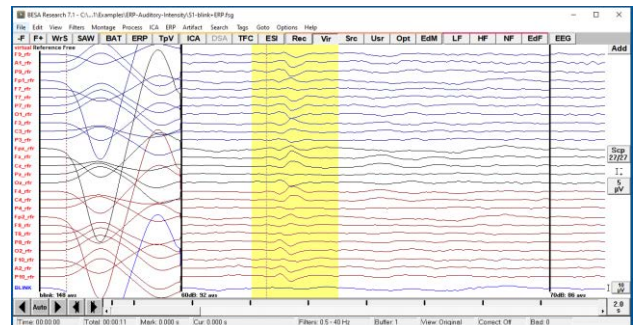
D. Contrasting artifact and brain topographies – the Optimizing method (recommended)

In order to obtain correct source localization, the presence of blink artifacts in the averaged segments must be taken into account. This is done by including the artifact topography in the multiple source model during source analysis.

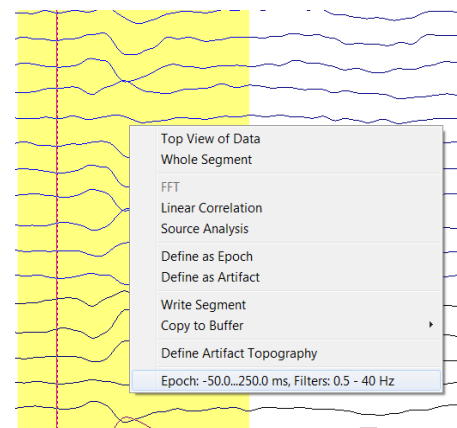
BESA® Research 7.1

Tutorial 10 – Advanced Artifact Correction

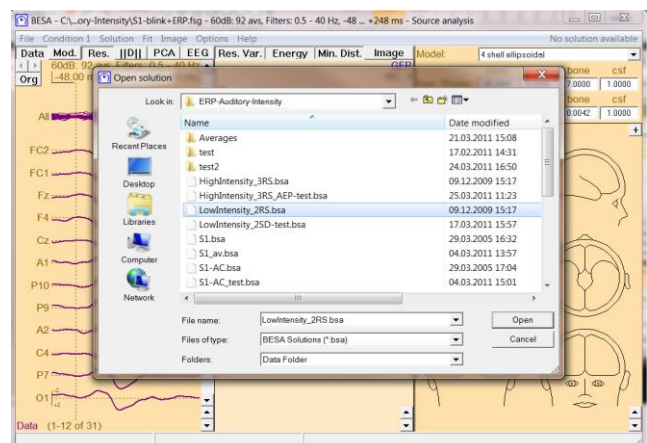
1. **Switch off artifact correction** by pressing **ctrl-E**. You can confirm it is switched off as corrected is no longer displayed in the top left corner of the main window.



2. **Left-drag** over the second segment to mark a block. **Right-click** and send it to **source analysis** with settings **-50 to 250 ms**, **Low Cutoff filter of 0.5 Hz**, **6 db/oct**, **forward** and **High Cutoff Filter of 40 Hz**, **24 db/oct**, **zero-phase**.

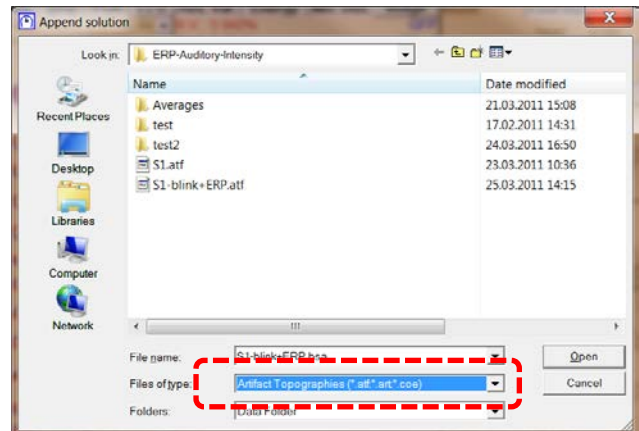


3. Load the source model **LowIntensity_2RS.bsa** by pressing **File / Open Solution**.

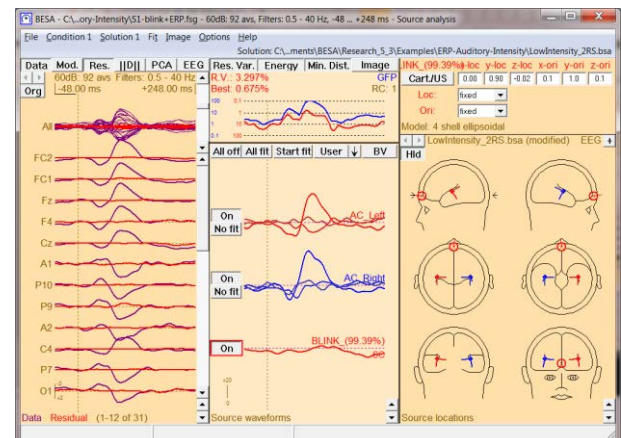


4. Next, we will load the artifact topography into the source analysis window. This will create a spatial component explaining the blink topography.

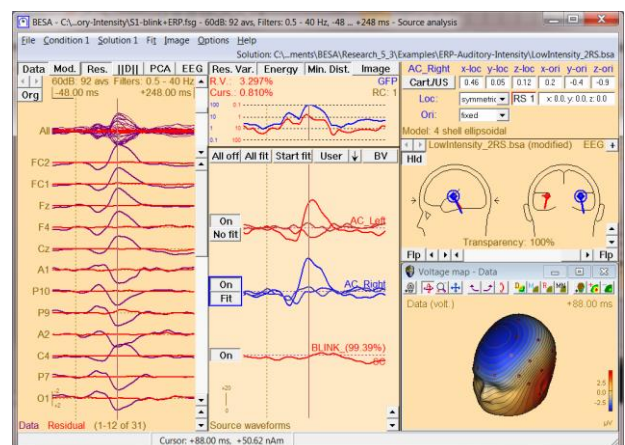
- Press **File / Append Solution....** In the drop-down menu **Files of type:** select **Artifact Topographies (*.atf;*.art;*.coe)**. Select **S1-blink+ERP.atf** and press **Open**.



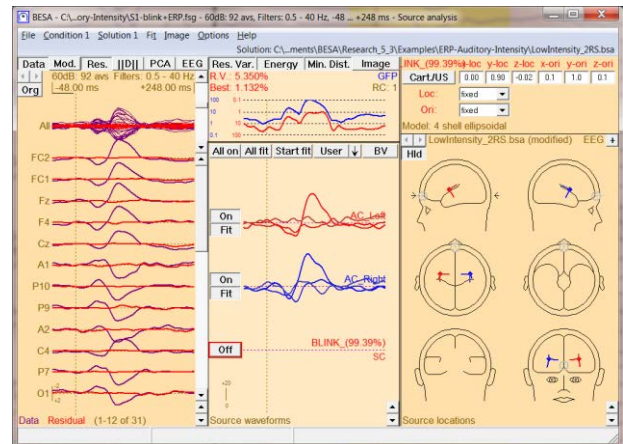
- The topography of the main PCA component of the blink artifact is now appended to the current solution. The corresponding waveform and the equivalent location are shown in the source analysis window. This is the component explaining 99.4% of the artifact variance that was selected during the artifact definition.



- Again, **double-click** in the waveform box to set a cursor at the N100 latency. **Right-click** and select **Display 3D Maps** or type the hot key **M** on the keyboard. Note that the map is not distorted but shows the typical N100 topography.



8. Switch off the spatial blink component by pressing its **On** button and close the 3D mapping window. Press **All Fit** and **Start Fit** to see how the fit changes if we don't take eyeblink activity into account. Note that the auditory sources locate more anterior and medial than before. Switch the spatial blink component back on and repeat the fit for comparison. Close the source analysis window without saving anything.



E. Artifact Correction of raw data using ICA – spatial filtration

Independent Component Analysis (ICA) allows decomposing EEG/MEG data into independent components. Independent components (IC) can be used for artifact correction, as spatial components in source analysis or for creating ICA-reconstructed data only containing signal from specified IC. ICA is performed on the current screen and can be started from the ICA entry in the menu bar or by pressing the ICA button located in the button menu. The amount of data available in the current screen can be manipulated by using the time scaling button in the bottom right corner of the main window (max. 1200 s).

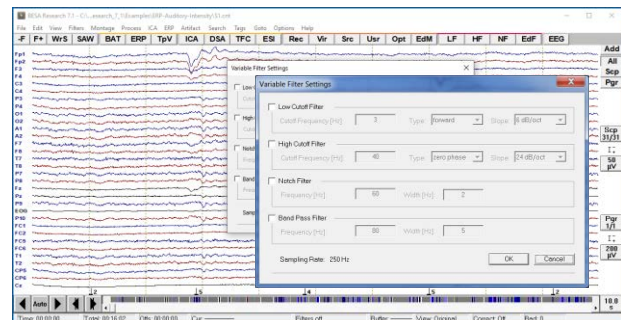
The method behind ICA can be chosen between the extended Infomax algorithm (Lee TW et al., Independent component analysis using an extended infomax algorithm for mixed sub-Gaussian and super-Gaussian sources. Neural Computation 11(2), 1999, 409-433) or Second-order blind identification – SOBI (Belouchrani A et al. A blind source separation technique using second-order statistics. IEEE Transactions on Signal Processing, 45(2), 1997, 434-444). Before the ICA is calculated, the dimensionality of data is optionally reduced by PCA. By default, all PCA components are ignored that explain less than 1% variance. The use of PCA can be switched off or the variance cutoff can be altered by pressing **ICA / Options**.

While ICA is being computed, the current analysis step is displayed in a dialog box along with the changing weights. The first ICA step may take longer for many samples than the subsequent steps. ICA analysis stops when the change of weights from 1 step to the next is

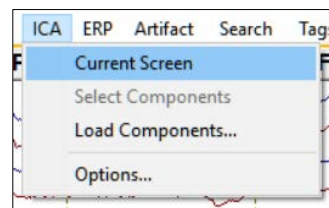
smaller than $1.0e-6$ or after max. 500 steps. ICA analysis can be stopped by pressing the **Abort** button in the dialog box.

In case EEG and MEG data are both available, ICA analysis will only run on the data type that is selected by the EEG/MEG button. Running ICA on combined gradiometer/magnetometer data is not possible as it can only run on one channel type at a time.

1. Open file **S1.cnt** from the **ERP-Auditory-Intensity Examples** folder. Make sure, the **Rec** button is pressed, that you are displaying the **first screen** and that **artifact correction** and all **filters** are **switched off**.

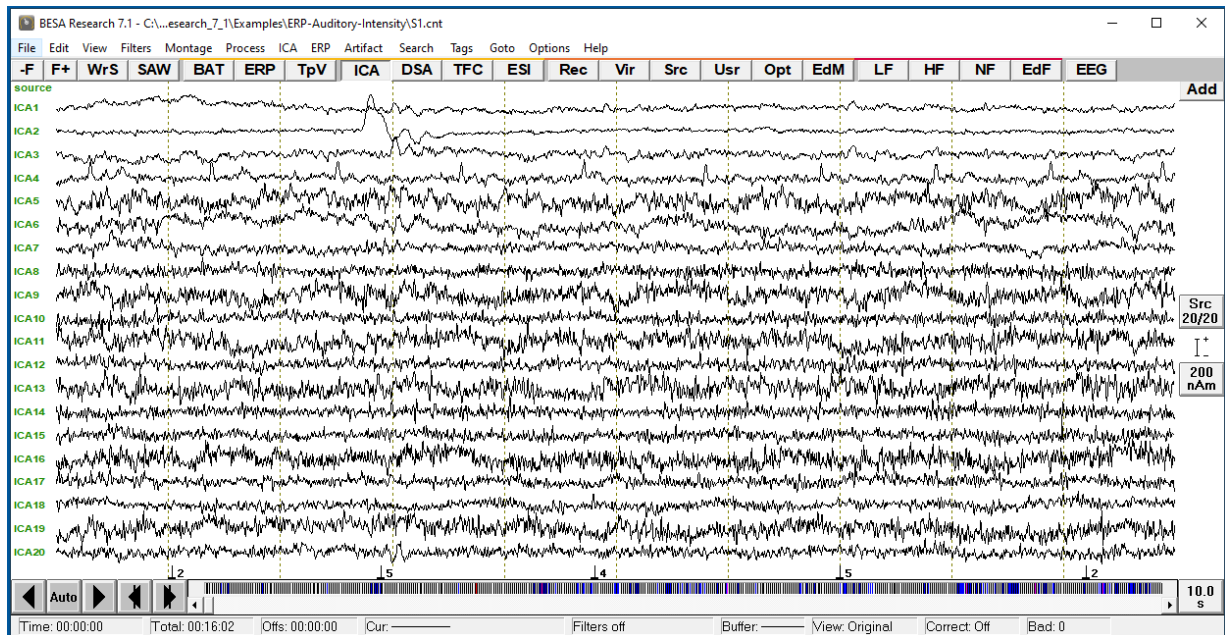


2. Please select **ICA / Current Screen** to start ICA analysis.

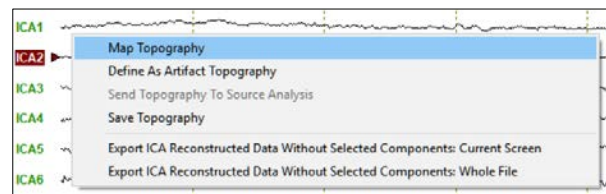


3. The results of the ICA analysis are displayed like a montage. The units of the waveforms are nAm since ICA waveforms can be described as source activity of a spatial component localized at the center of gravity of the corresponding map. ICA waveforms have the labels ICA1 – ICAn. The menu item ICA / Current screen is ticked and the ICA button is pressed. ICA components are sorted in descending order of their explained variance. The displayed ICA montage is automatically recomputed whenever ICA options change or the data change, e.g. when filtering, changing the time-range to display, etc.

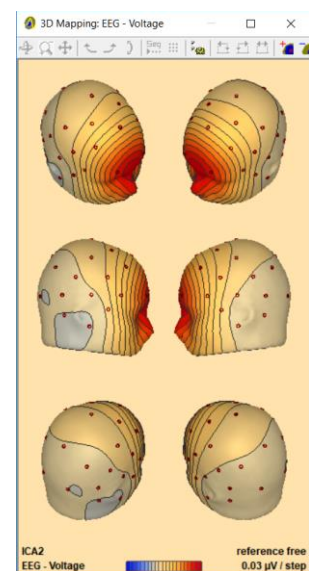
Here, ICA decomposition delivers 21 independent components. It appears that the second ICA component represents an eyeblink and the fourth ICA component represents a cardiac artifact.



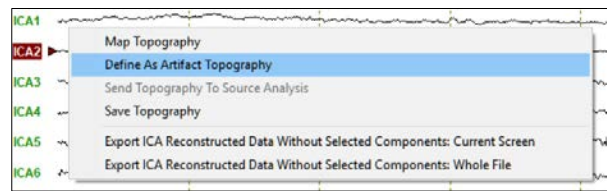
4. Right-click on the **second ICA** component and select **Map Topography**.



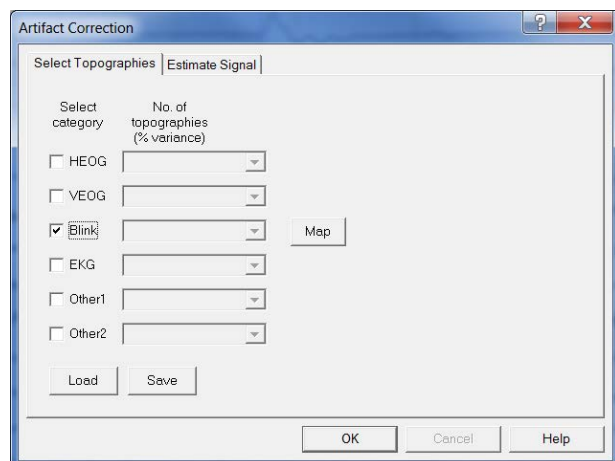
5. The map indicates that the second ICA component indeed reflects an eyeblink.



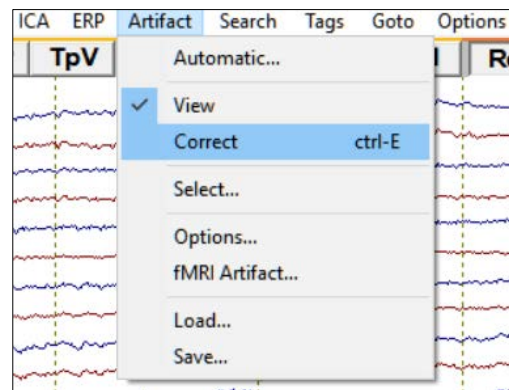
6. We can now use this topography for artifact correction. Close the mapping window, **right-click** on the **second** ICA component label and choose **Define As Artifact Topography**.



7. The Artifact Correction window opens. Please **check the box** next to **Blink**. Close the mapping window and press **OK**.

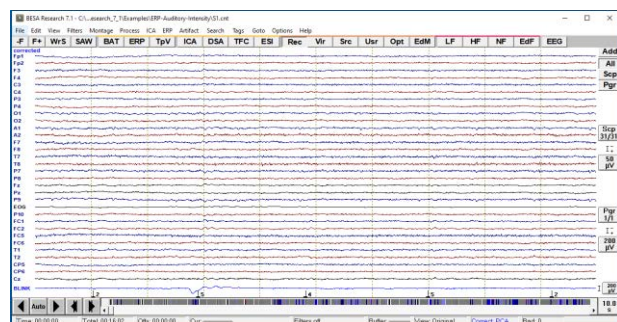


8. Return to the original recording by pressing the **Rec** button. Now press **Artifact / Correct** to switch on artifact correction.

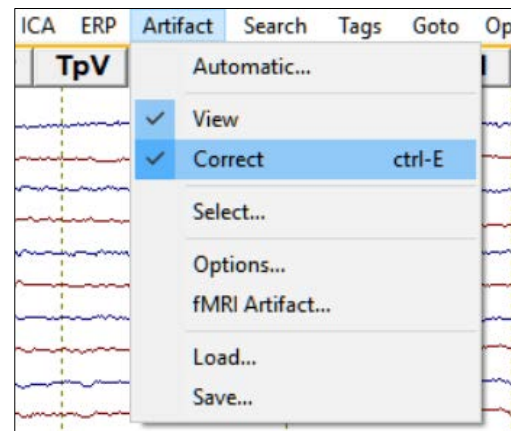


9. Note that the eyeblink has now disappeared. The topography of the second ICA component is now subtracted from the data.

We will learn more about the background and other methods of artifact correction throughout the tutorial.



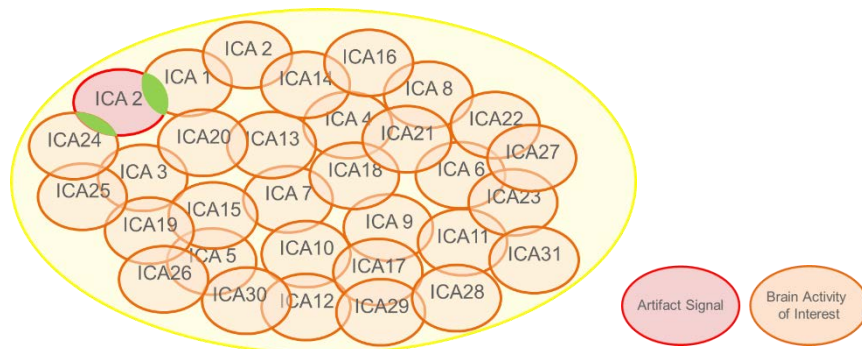
10. Please switch off artifact correction again by pressing **Artifact / Correct**.



F. Artifact Correction of raw data using ICA – data reconstruction

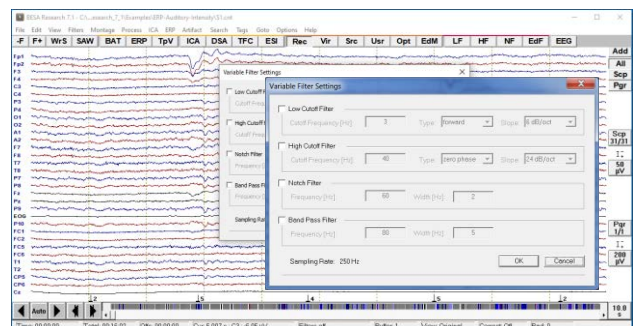
We already saw that it is possible to use ICA components for artifact correction. However, we only used ICA to determine the artifact topography and proceeded with artifact correction also using the adaptive or surrogate method. Thus, we used ICA decomposition as a different technique to estimate the artifact topography (in contrast to averaging the artifact and decomposing it using PCA). There is an alternative way to use ICA decomposition for artifact correction by creating ICA-reconstructed data, i.e. creating a “new” dataset only consisting of non-artifact-related ICA components.

EEG/MEG data can be considered as a summation of topographies that are differentially active at each sampling point. Subtracting an artifact *topography* reduces the data by one dimension. This can potentially lead to severe distortion of brain activity of interest (as previously demonstrated by the SSP correction method) if the brain activity of interest is not modeled. Creating ICA-reconstructed data leaving out artifact topographies poses the same problem. However, ICA decomposition has the advantage that ICA components must be as independent as possible, but they may overlap to some degree. This means that if the artifact topography is correlated with a topography representing brain activity of interest, some other ICA components will also most likely be correlated with brain activity of interest.

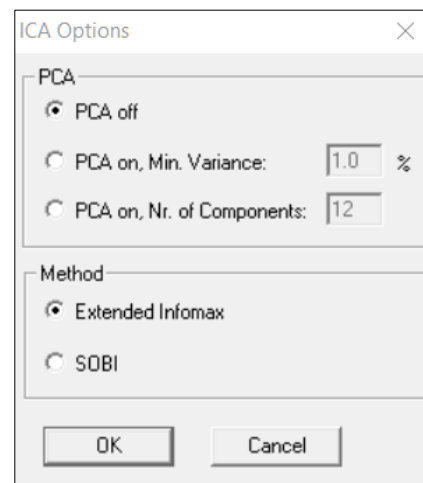


Thus, subtracting an ICA component will not cause distortion as pronounced as SSP correction does, as the correlated part of the signal will still be represented by the remaining ICA components at least to some degree. Nevertheless, there will be some distortion as it cannot be fully prevented. The distortion effect gets the more reduced, the more electrodes are available, as the number of electrodes determines the number of ICA components. The more ICA components are available that represent brain activity of interest, the less likely data will be distorted after subtracting an artifact topography.

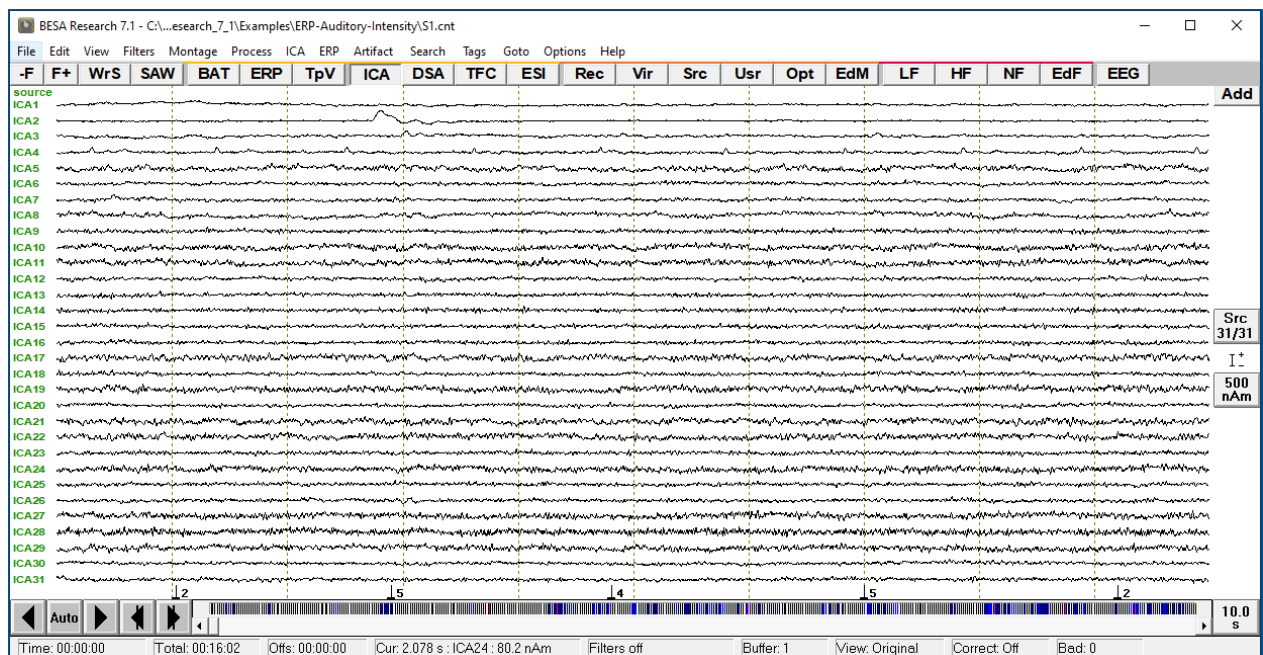
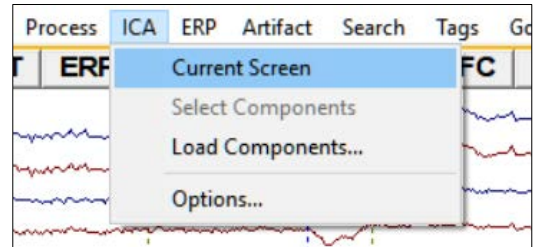
1. Make sure that **S1.cnt** file is opened and, the **Rec** button is pressed. Press **CTRL-E** to switch off artifact correction. Check if you are displaying the **first screen** and that **artifact correction** and all **filters** are **switched off**.



2. Press **ICA / Options** and select **PCA off**. Switching PCA off will lead to ICA decomposition running on all data. PCA on, Minimum Variance of 1% (default) will reduce the data by all PCA components explaining less than 1% variance before running ICA. PCA on, Nr. of Components 12 (default) will reduce the data by the smallest 12 components before running ICA.



- Press **ICA / Current Screen** to start ICA decomposition.



- ICA will output 31 ICA components, the same number as EEG channels are present on the current screen. Some of the channels will represent brain activity, and some will represent artifact signal. Each ICA component is associated with a topography, and a source waveform. Source waveforms can be estimated by assuming a spatial component at the center of gravity of each ICA topography. Multiplying the data with the pseudo-inverse of the matrix containing the ICA topographies will yield the ICA source waveforms.

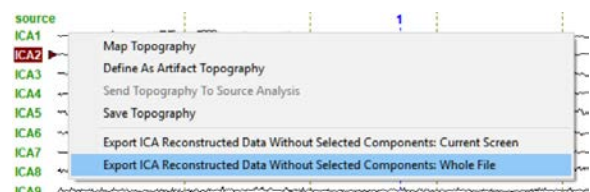
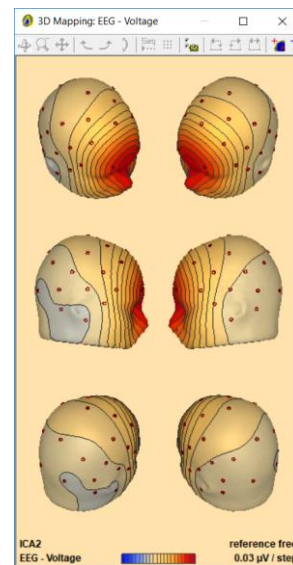
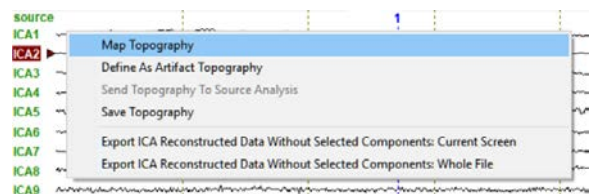
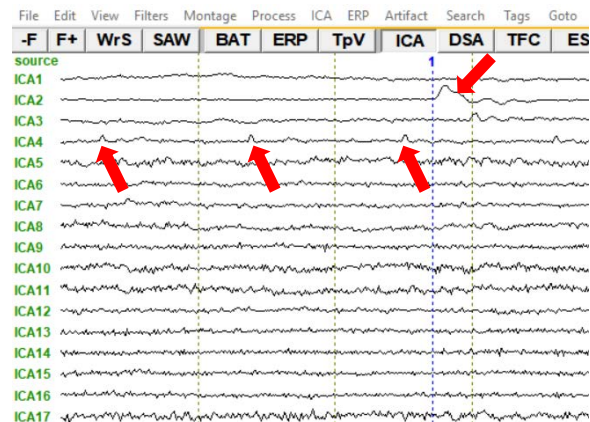
- ICA2 seems to represent an eyeblink and ICA4 seems to represent cardiac activity, which we had not noticed previously.

Note: it is possible that in your case the ICA components representing the blink/EKG are not ICA2 and ICA4. If this is the case, locate the respective ICA components and use their according label in the following!

- Right-click** on the label **ICA2** and select **Map Topography**.

- The map confirms that ICA2 does indeed represent blink activity. In the following, we want to neglect ICA2 and create a new dataset containing all ICA components but ICA2. **Close** the mapping window.

- Make sure to **left-click** on ICA2 only in order to select it. **Right-click** and choose **Export ICA Reconstructed Data Without Selected Components: Whole File**. BESA Research will now create a new file containing ICA-reconstructed data.

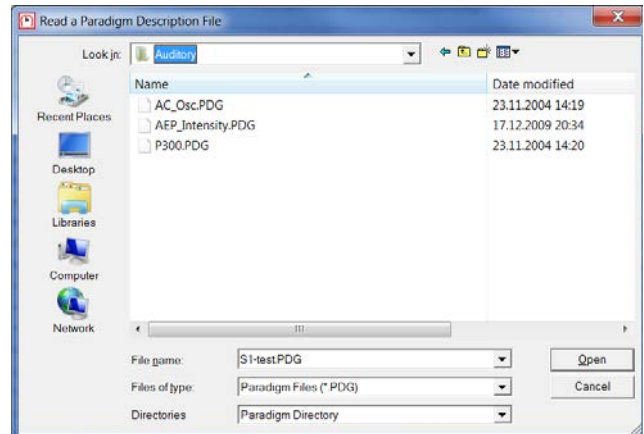


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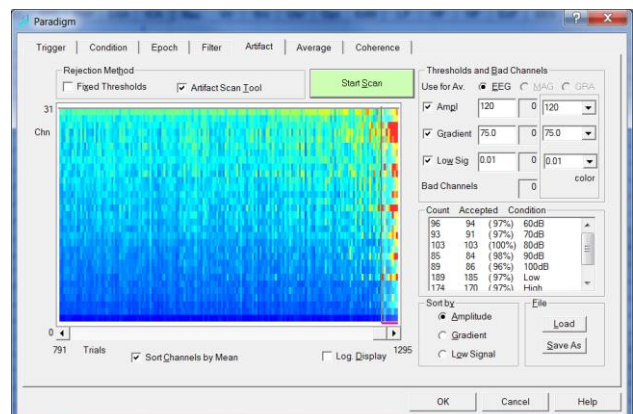
Tutorial 10 – Advanced Artifact Correction

To investigate, we will average the data again to look at evoked potentials.

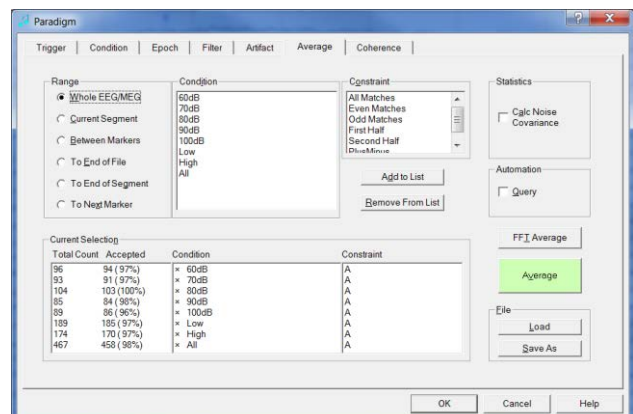
13. Press **ERP / Open Paradigm**. Browse to the **Auditory** folder and select **AEP_Intensity.PDG**. Press **Open**.



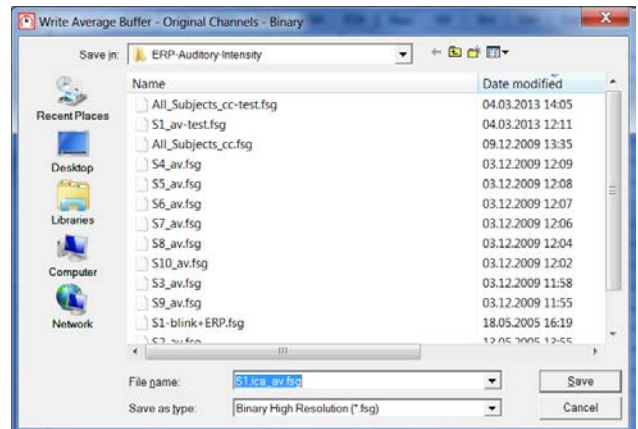
14. Move to the **Artifact** tab and press **Start Scan** to exclude artifacts from averaging.



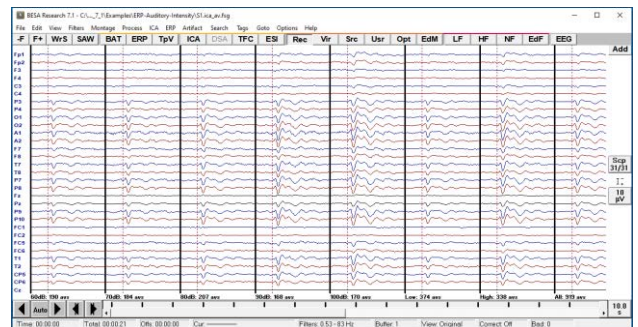
15. Move to the **Average** tab and press **Average**.



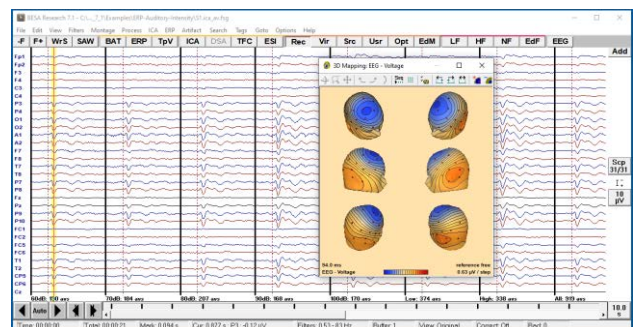
16. **Save** the average file under the suggested name **S1.ica_av.fsg**. When prompted to specify a segment comment, press **Stop Asking** to use the suggested names from the paradigm.



17. The new average file will be automatically opened along with the TopView window. **Close** the TopViewer.



18. **Double-click** at the N100 peak in condition **60dB** to bring up the 3D window. Make sure to move to **94 ms** using the left and right arrow keys. Scale up the topographic view to **0.63 µV / step**. The N100 map appears nearly undistorted.

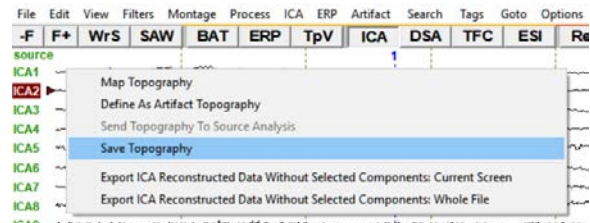


G. Applying the Optimizing method when using ICA-reconstructed data for source analysis

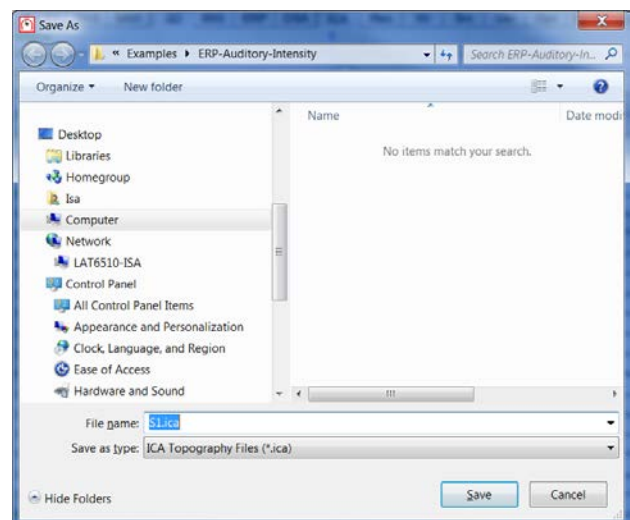
Despite the apparent lack of distortion of the N100 component in the example of ICA-reconstructed data in section F, it is recommended to account for the artifact topographies that were subtracted during source analysis. Whenever artifact correction is performed, a spatial dimension of the data (the topography) is changed. This can distort the data. To prevent this distortion from affecting source analysis, the same distortion should be applied to the leadfields. Alternatively, the spatial dimension can be projected out of the leadfields. As BESA Research does not save any

information about the topographies that were subtracted when creating ICA-reconstructed data, the artifact topographies need to be saved manually and later loaded in source analysis.

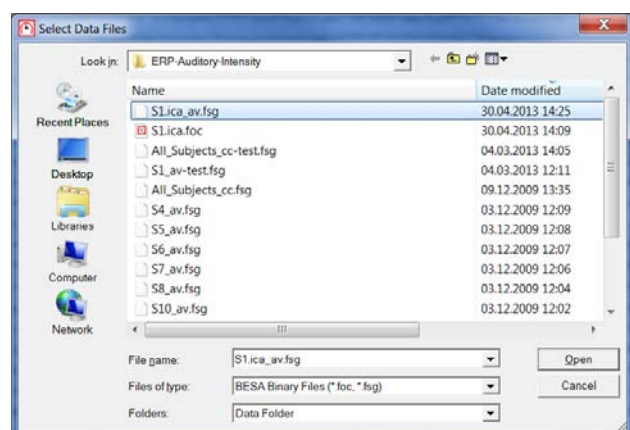
1. Follow **steps 1 to 4 of section F** in the present tutorial to run ICA decomposition on the first screen of **S1.cnt**. Locate the ICA component reflecting the blink (usually ICA2). **Right-click** on the label and select **Save Topography**.



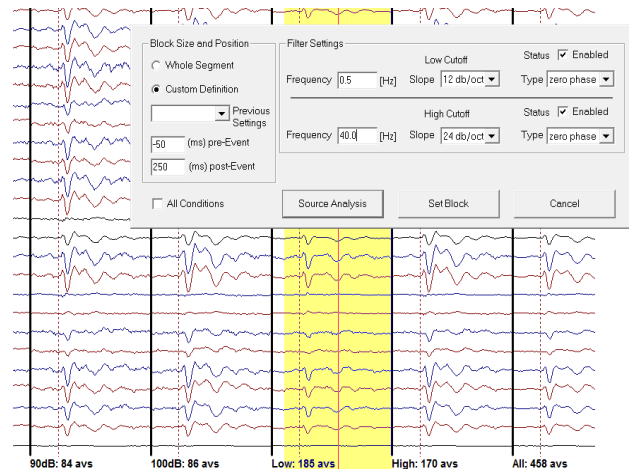
2. **Save** the topography under the suggested name **S1.ica**.



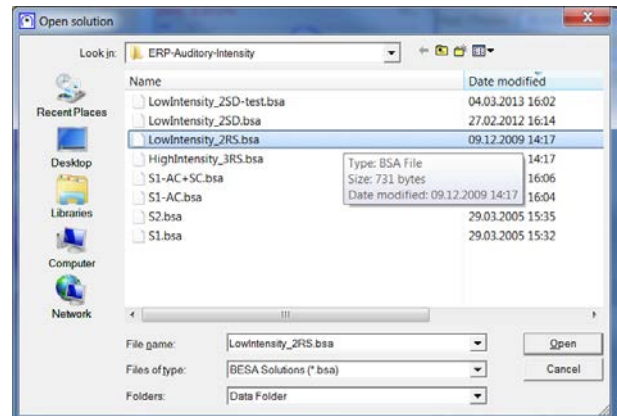
3. **Open** dataset **S1.ica_av.fsg** we created in section G of the present tutorial. It should be located in the **Auditory Intensity examples folder**.



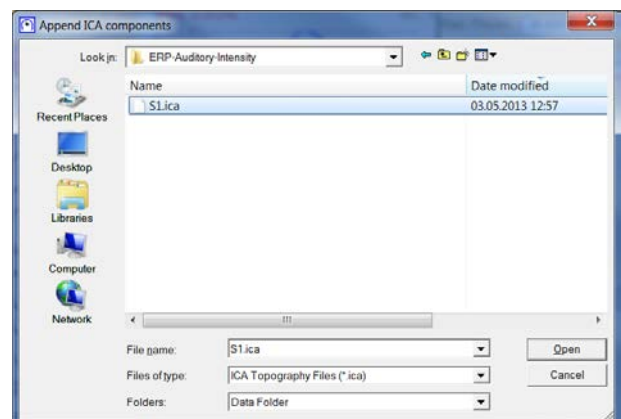
- Send **condition Low** to source analysis by **left-dragging a block, right-clicking** and selecting **Source Analysis**. Use a custom definition of **-50 to 250 ms**, a **Low Cutoff Filter of 0.5 Hz, 12 dB/Oct, zero-phase** and a **High Cutoff Filter of 40 Hz, 24 dB/Oct, zero-phase**. Press **Source Analysis**.



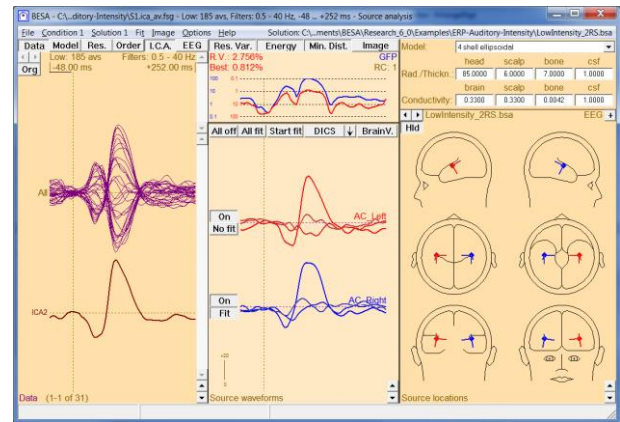
- In the Source Analysis Window press **File / Open Solution** and select our source model **LowIntensity_2RS.bsa**. Press **Open**.



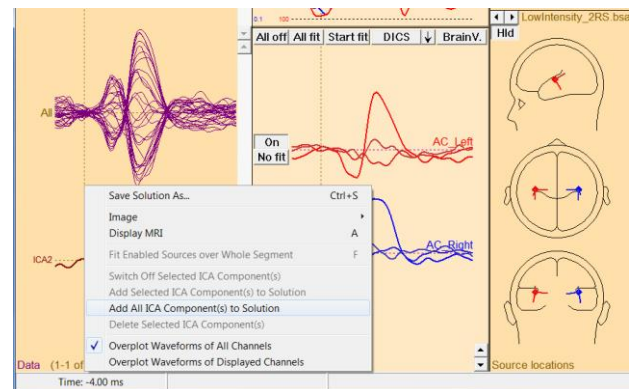
- Now we will append the ICA blink component to the current solution. Press **File / Append ICA Components**. Change Folders to **Data Folder** and select **S1.ica** that we created in step 2. Press **Open**.



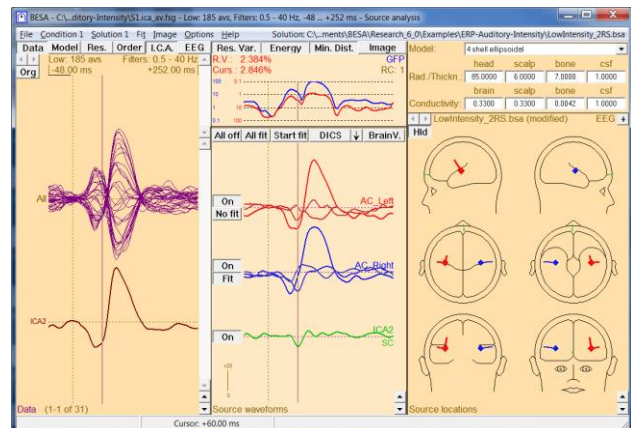
- You will see the waveform associated with the blink topography plotted beneath the EEG butterfly plot. We want to utilize it in our source model.



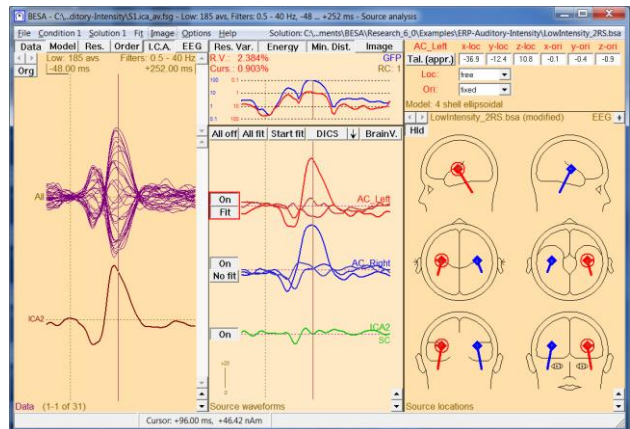
- Right-click** on the ICA waveform and press **Add All ICA Components to Solution**.



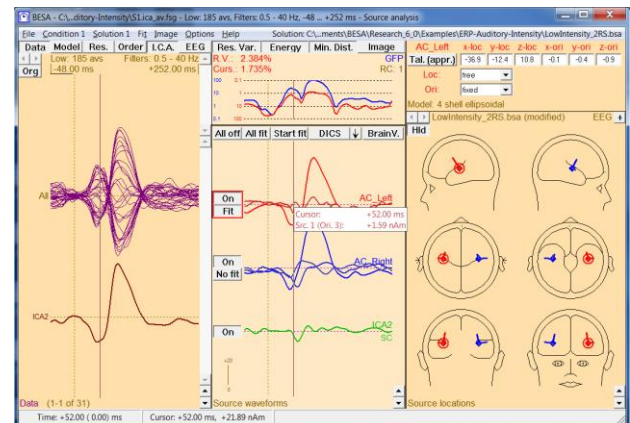
- We will now see that the blink was added to our source model as a spatial component. Its activity pattern for the current data can be seen in the middle panel.



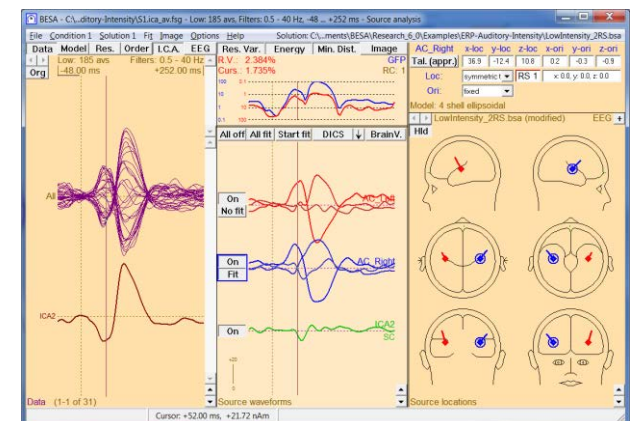
10. **Double-click** at the N100 peak at around **96 ms**. The green source waveform is nearly 0 at this point, suggesting that there was indeed no blink activity at the N100 peak.



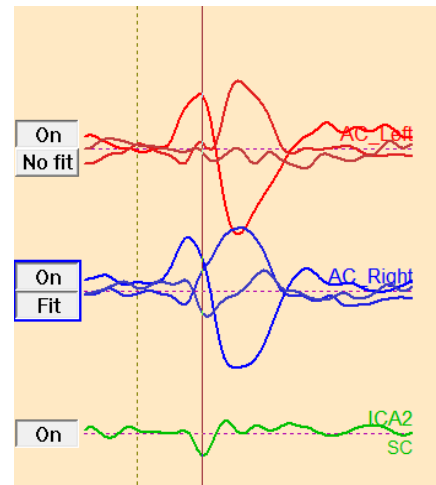
11. **Double-click** in the red source waveform (AC_Left) and move the cursor to **52 ms** using the arrow keys on your keyboard. **Press O** on the keyboard to orient the first regional source approximately at the P50 peak.



12. **Repeat** for the blue source (AC_Right). Now both regional sources are oriented so that the first orientation optimally reflects the P50 peak.

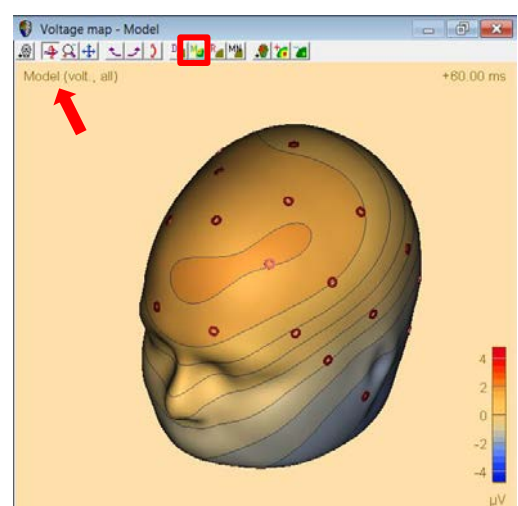


13. Use the arrow keys on your keyboard to **move the cursor** to the peak of AC_Left at **60 ms**. This coincides with the peak of the blink component!

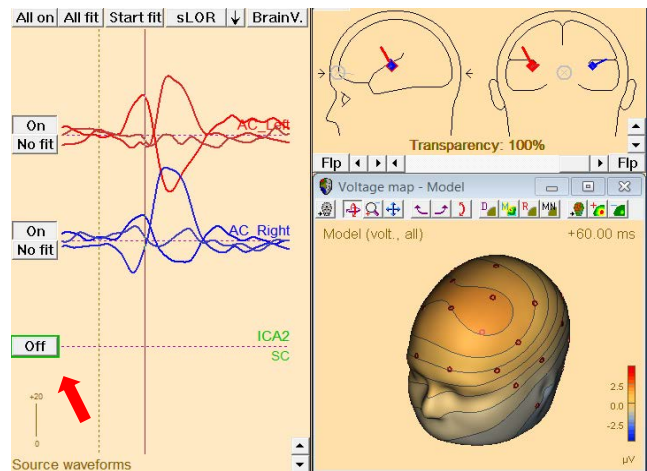


When we created ICA-reconstructed data without the blink topography, we subtracted an ICA component that was not correlated with the N100 topography. Thus, if we now tried to localize the N100 activity in the present example, we would not make an error. However, the ICA component we subtracted did correlate with the P50 topography! Thus, we subtracted part of the P50 topography when creating ICA-reconstructed data. If we now tried to localize the P50 activity, we would end up with a localization error caused by artifact correction with ICA. Therefore, it is vital to use the subtracted ICA component in the source analysis window in order to prevent this error. Adding the blink as a spatial component corrects the distortion of the P50 topography and allows correct reconstruction of the underlying sources.

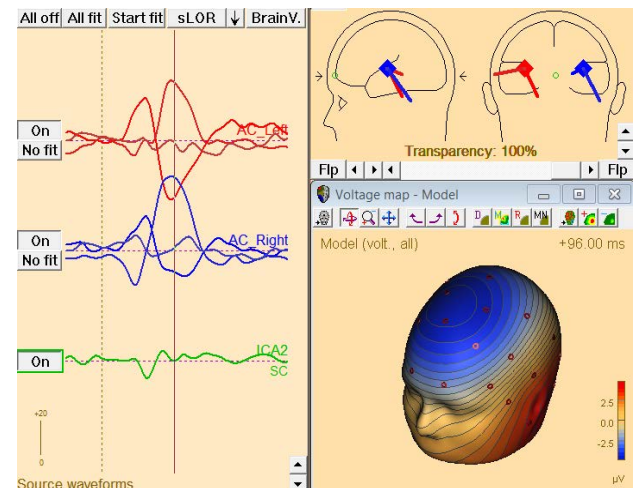
14. Press **M** on the keyboard to bring up 3D mapping. Press the 6th **button** from the right labeled **M** until the 3D window is labeled **Model (volt, all)**.



15. **Switch off** the ICA component in the middle panel by clicking on the **On** button. Note how the map changes if the blink component is left out of the model. This difference corresponds to the distortion imposed on the P50 map by subtracting the blink topography.



16. Move the cursor to the N100 peak at **96 ms** by using the arrow keys on your keyboard. **Toggle** between on and off for the ICA component. Note that the N100 map is barely influenced by the blink topography.



The above steps illustrate that creating ICA-reconstructed data will lead to some distortion of the data. Therefore, the recommended strategy for performing source analysis on ICA-reconstructed data is to use the subtracted topographies as spatial components in the source model.

Tutorial 11 – Simultaneous EEG-fMRI

What does BESA Research provide?

- ✓ fMRI artifact gradient removal
- ✓ Ballistocardiograph (BCG) artifact reduction
- ✓ fMRI-informed source analysis

Note: Currently data collected during simultaneous EEG-fMRI is not intended to be used in any diagnostic procedures. Following this guideline, fMRI artifact removal implemented in BESA Research may also not be used for any diagnostic procedures. This tool was developed for research purposes only.

For acquisition of simultaneous EEG-fMRI, please use only EEG hardware that is certified for MRI! Remember that bringing any metal or other (para-)magnetic parts into the magnetic field area is dangerous.

When EEG data is recorded during an fMRI session there are plenty problems waiting to be solved before being able to analyze the real brain signal. Here we going to investigate the following:

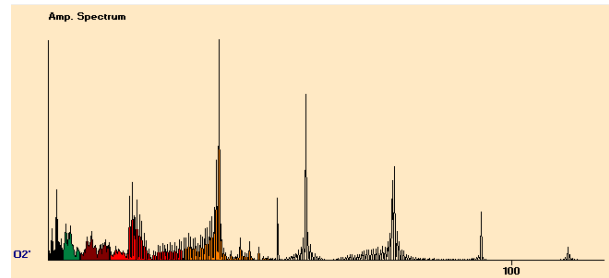
- removal of fMRI gradient artifact
- reduction of heart beat-induced ballistocardiogram (BCG) and blinking artifacts
- performing source analysis of EEG-fMRI data

A. Removal of fMRI gradient artifact

The fMRI gradient artifact results from fast switching of MRI gradient coils which is a part of volume acquisition in the Echo-Planar sequence used for fMRI imaging. This switching introduces variable magnetic fields that in turn induce variable electrical fields in the EEG recording system (electrodes and wires namely), as described by Maxwell's second law. The induced artifact is typically very large in amplitude (i.e. approximately 16 mV in a 3T MR scanner). Also, the frequency range of the artifact overlaps with the frequency band of physiological EEG signal.

The artifact frequency and its harmonics can be easily assessed using the following equation (Rusiniak et al., 2013b):

$$f_x = \frac{S(x + 1)}{TR}$$



where f_x is the harmonic frequency, x is the harmonic number, NS represents the number of slices, and TR stands for Repetition Time of fMRI volume acquisition. As will be explained further, each fMRI gradient removal algorithm has its limitations, so using this equation allows to set up fMRI acquisition in a way that minimalizes frequency coupling with the band of interest. For example, consider that we want to investigate the alpha frequency range (7-13 Hz). Using 37 slices and TR equal to 2 s ensures proper spectral separation since the first frequency peak of fMRI gradient artifact will be at 18.5 Hz.

One of the known methods to deal with the fMRI gradient induced artifact is based on moving average subtraction, first introduced by Allen and colleagues (2000). This type of method works only satisfactorily when the following assumptions are true:

- ***Each artifact occurrence is identical***

Each fMRI volume acquisition is identical (gradient switching does not alter between volumes). This assumption is true when we take into consideration only fMRI acquisition. However, if the subject moves during the acquisition the artifact changes since electrode positions in relation to the local magnetic field have altered.

- ***EEG signal is stationary***

In principle this assumption is true for the EEG signal. The signal stationarity can be affected by the paradigm, therefore jitter between trigger events is strongly advised.

- ***Each start point of artifacts has to be precisely indicated***

This can be achieved either by hardware clock synchronization between EEG system and MRI machine, or by a very high sampling rate (> 10 kHz). All modern EEG hardware units designed for simultaneous EEG-fMRI registration are capable of clock synchronization.

Filtration Methods

Allen et al., 2000

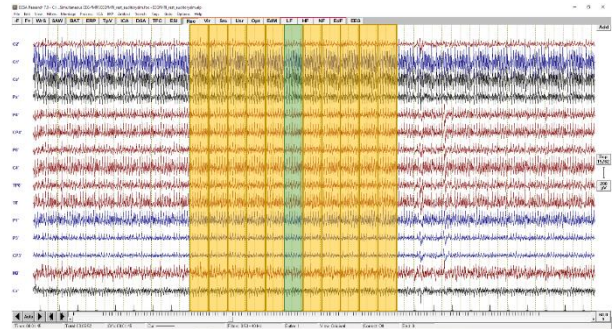
This method is a starting point for two other methods as well. In all methods available in BESA Research, a moving average artifact subtraction algorithm is used and the difference between methods can be noted in the template creation matrix.

To obtain artifact clean data **C**, at epoch **n**, the artifact template **B** has to be subtracted from artifact contaminated data **A**. The mathematical principle for creating the artifact template at the **n**-th epoch (**B_n**) is:

$$B_n = \frac{1}{k} \sum_{i=n-\frac{k-1}{2}}^{n+\frac{k-1}{2}} A_i$$

$$B_n = \frac{1}{k} \sum_{i=1}^k A_i \text{ for } n \leq (k-1)/2$$

$$B_n = \frac{1}{k} \sum_{i=m-k+1}^m A_i \text{ for } n \geq m - \frac{k-1}{2} + 1$$



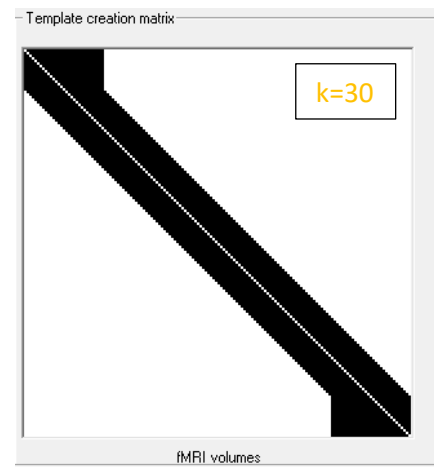
,where **m** is the number of fMRI volumes recorded, **k** is the number of artefact volumes used for template creation (averaging). Once an artifact template was created for every epoch, the final subtraction can be performed:

$$C_n = A_n - B_n$$

For example, to clean the epoch indicated by the green shaded box in the image above, the surrounding epochs – indicated by yellow color – have to be averaged first (here the averaging constant is **k** = 10). After the template is created, it is subtracted from the recorded data (at each channel independently) to obtain artefact free data. Next this procedure is repeated for all epochs related to fMRI acquisition as indicated in the template creation matrix on the left:

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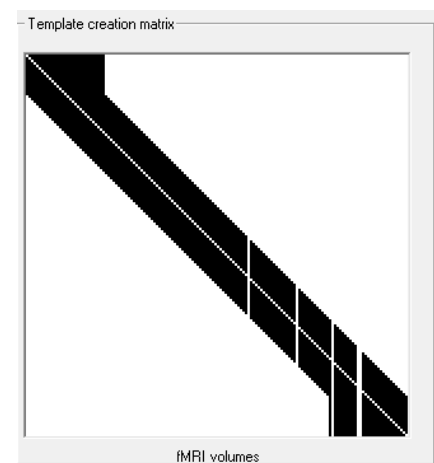
Tutorial 11 – Simultaneous EEG-fMRI



Note how the template creation matrix on the right changes when the number of artifact occurrence used for averaging is increased to $k = 30$.

Allen et al., 2000 Modified

This method is available only if a matching realignment file is provided. Also, the changes in filtration will be visible only if there is significant movement in the data. In the modified Allen method, the epochs where subject's movement exceeds the threshold (a recommended value for the movement threshold is 0.3 mm) are not taken into account during artefact template creation, as shown in the template creation matrix at the right. Note the vertical white lines, which indicate the moments where movement exceeded the threshold. As a result, the data will be filtered but less artifact occurrences will be used for template creation in the (temporal) vicinity of a movement area.



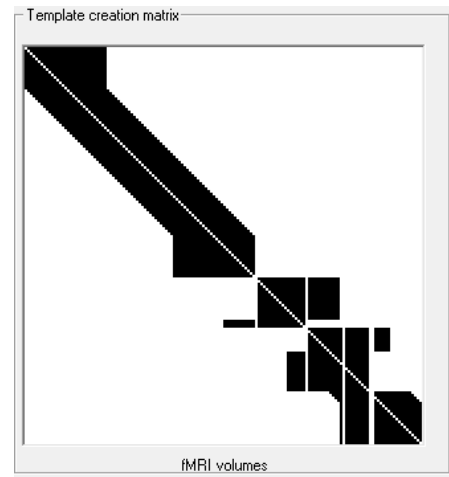
Moosmann et al., 2009

This method (Moosmann et al., 2009) is also available only if a matching realignment file is provided. The adjustment of the template creation matrix is much more advanced than in the modified Allen method and can be explained by following equation:

$$B_n = \frac{1}{k} \sum_{i=n-\frac{k-1}{2}}^{n+\frac{k-1}{2}} A_i \text{ for } n < z - \frac{k-1}{2} \text{ or } n > z + \frac{k-1}{2}$$

$$B_n = \frac{1}{k} \sum_{i=z-k}^{z-1} A_i \text{ for } n \geq z - \frac{k-1}{2} \text{ or } n > z$$

$$B_n = \frac{1}{k} \sum_{i=z+1}^{z+k} A_i \text{ for } n \leq z + \frac{k-1}{2} \text{ or } n < z$$



, where all parameters are defined as above and **z** means an epoch number when movement exceeds the threshold. The result of this operation is shown in the template creation matrix above.

Note that this operation results in a different shape of the template create matrix. Importantly there are now also horizontal white lines. This indicates that there was more than one epoch affected by movement. In such a situation the matrix is transformed to fit to the largest movements and smaller movements are treated as in the Allen et al., 2000 Modified method.

B. Reduction of heart beat-induced ballistocardiogram (BCG)

This artifact is one of the most challenging artefacts in the EEG when acquired simultaneously with fMRI. The artifact is related to following phenomena:

- **Head movement due to blood ejection by the heart**

Each heartbeat results in a very slight movement of the whole body due to its inertia.

In most of the cases we are not able to notice this. This tiny movement results in

movement of the electrodes, which in turn results in local magnetic field changes. Considering the fact that in an MR scanner the static magnetic field is usually 3T this normally negligible effect induces an artifact of amplitude larger than 100 μ V.

- **Arterial pulsation**

The blood flow induced by the heart beat can introduce an additional factor of the artifact. If some blood vessels are close to the skin surface the changes in blood volume result in skin pulsation. This pulsation also moves electrodes up and down in the rhythm of the heart beat.

- **Hall effect**

Blood by itself is an electrically conductive fluid, therefore the changes in blood flow velocity related to the heartbeat add another factor altering the artefact.

All aforementioned factors contribute to the ballistocardiographic artefact and make it particularly difficult to determine and reduce. It is worth mentioning that this artifact, as related to the heartbeat, cannot be controlled and varies during the time of experiment. A different approach to fMRI gradient removal has to be used to reduce its influence on data. In the literature many different approaches (both software and hardware) can be identified, please refer to Abreu and colleagues work (2018) for more details. Here we focus on spatial filtration where individual artifact topographies are estimated using the PCA method. Also, we recommend to use a surrogate model to separate brain signal from artifact subspace. More details about this method can be found in the BESA Research Tutorial 9.

C. Example data

The example data set provided with BESA Research installation is a mixture of real and simulated data. We used a 64-channel EEG data recorded during a simultaneous EEG-fMRI session. It was a 5-minute resting state session with eyes open. We added simulated ERP data to this recording. It consists of two bilateral dipolar sources simulating auditory cortex activity. The dipoles positions in brain were set as described by Gutschalk and colleagues (2002). Waveforms were replicated from the *Low* condition ERP in the Auditory Intensity experiment also available in the example directory. The ERPs were added to the resting state

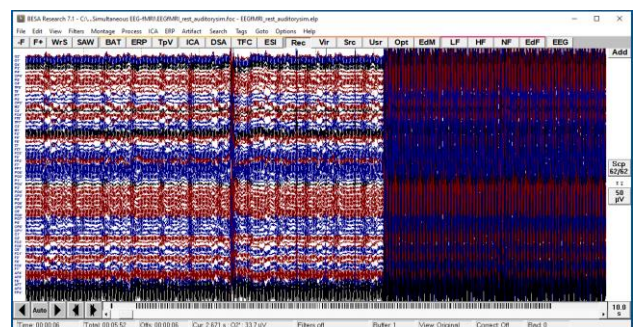
BESA® Research 7.1

Tutorial 11 – Simultaneous EEG-fMRI

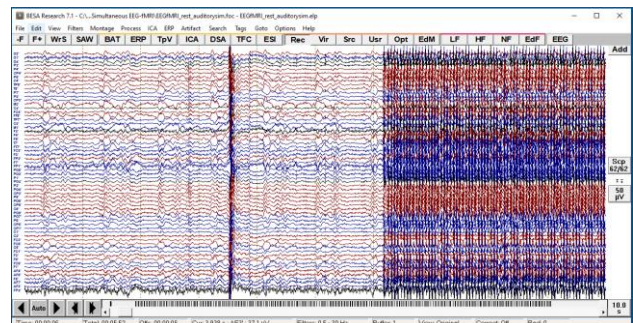
EEG, thus simulating an ERP experiment in fMRI. The first ERP is present after the start of the fMRI session, the inter-stimulus interval was 1.5 s with a jitter of ± 200 ms.

Consider the fact that in a real ERP experiment, the ERP signal would be a pure brain signal independent of MRI scanning. Therefore, using the provided data example, we can see what the influence of the MRI scanner environment on the data is and assess filtration results by comparing the filtration outcome with the pure stimulation signal.

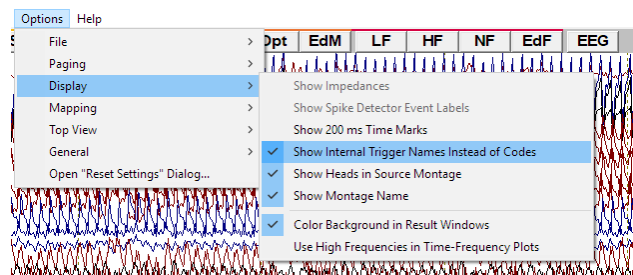
1. From the folder **/Examples/Simultaneous EEG-fMRI/** open data set **EEGfMRI_rest_auditorysim.foc**. It contains 64 EEG channels. Data is very noisy from the beginning, but from around 12 seconds the data is not readable – this is the time when the fMRI sequence starts.



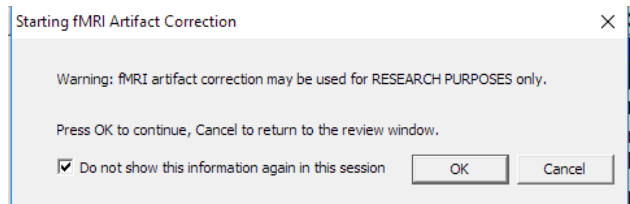
2. Press the **EDF button** and specify **Low Cutoff filter** of **0.5 Hz, 6 dB/Octave, forward** and **High Cutoff filter** of **30 Hz, 12 dB/Octave, zero-phase shift**. Note that the data is still not interpretable because of the fMRI gradient artifact.



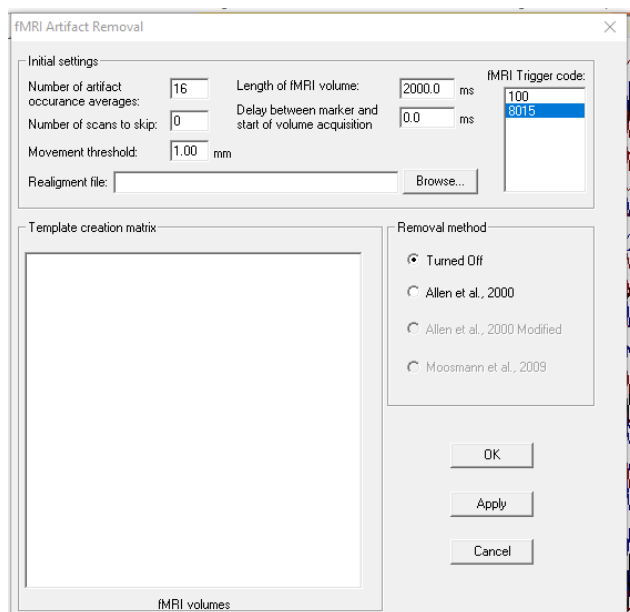
3. **Goto Time 00:00:12**. For this data set internal trigger names are not available, so select **Options / Display / Show Internal Trigger Names Instead of Codes** to uncheck this option if checked. Now you will see two trigger codes **8015** and **100**. The first indicates the start of fMRI volume acquisition, the other one the simulated ERPs.



4. Select **Artifact / fMRI Artifact...** to open the dialog where all the settings for fMRI artifact filtration can be set. If you work with the international version of BESA Research, you will need to acknowledge that this can be used for Research purposes only before you are able to use this feature. Please **check the checkbox** and press **OK** on the displayed notification window.

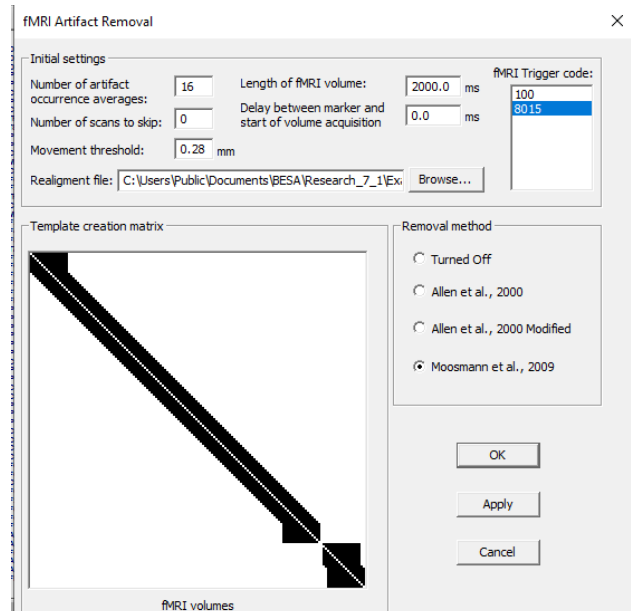


5. You will see the **fMRI Artifact Removal** dialog. Note that **fMRI Trigger code** and **length of fMRI volume** was automatically detected from the data. The automatic detection of length works only for continuous data. If you use so-called *sparse* fMRI acquisition you must adjust this value manually. The **Number of artifact occurrence averages** is set to a default value.

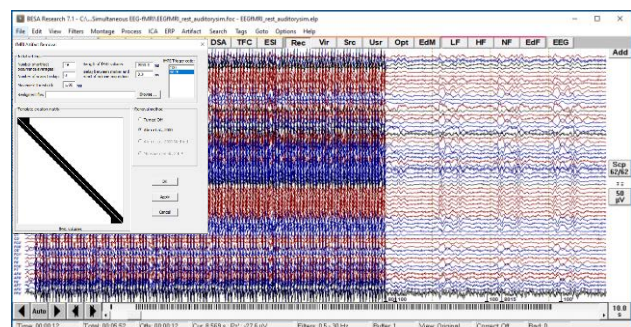


- Change the value of **Movement Threshold** to **0.28 mm**. Press **Browse...** button to select Realignment file. In the dialog box that comes up, choose **EEGfMRI_rest_auditorysim.txt** and press **Open**. Now two additional methods are available: **Allen et al., 2000 Modified** and **Moosmann et al., 2009**.

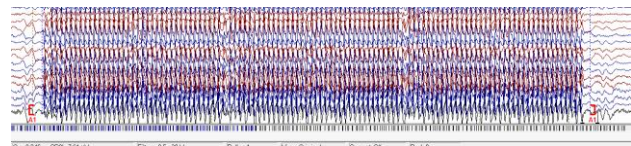
Change the method to **Moosmann et al. 2009**. The **template creation matrix** is filled instantaneously.



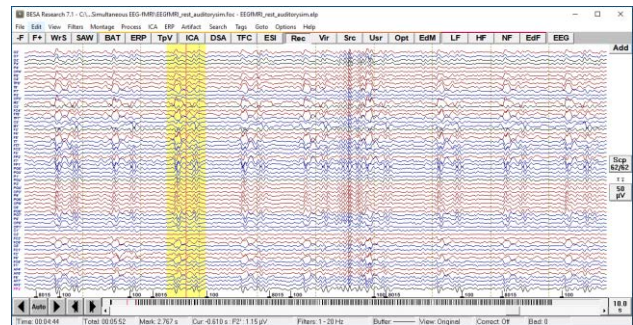
- Press **Apply** to perform artifact removal. Please note that the first six seconds of the artifact are not removed. This fMRI sequence starts with dummy scans that do not have associated triggers. The fMRI images are not collected for these, so no stimulation should be performed either. Press **OK** to close dialog box.



- While keeping the **left mouse button** pressed, **drag** the mouse over this noisy part of signal at beginning of recording, to highlight it. Then **right click** within the yellow marked area and select the **Define as artifact** option from the popup menu.

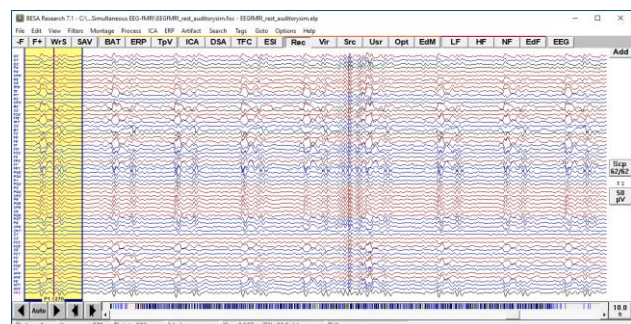


9. Now we will reduce the influence of the ballistocardiogram (BCG). First press the **EdF button** to adjust filters to the BCG frequency band. Specify a **Low Cutoff filter** of **1 Hz, 12 dB/Octave, zero-phase shift** and **High Cutoff filter** of **20 Hz, 24 dB/Octave, zero-phase shift**. For the provided dataset the Fpz channel (last in the list) is also highly contaminated with noise, **right click** on the channel label and select **Interpolate this channel** from the popup menu. The BCG is now clearly visible.



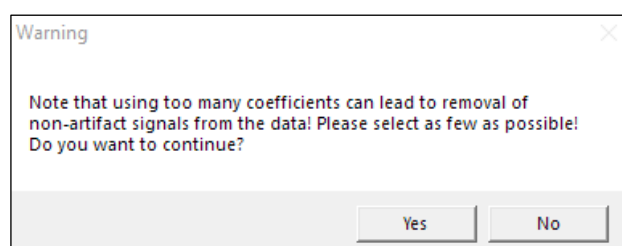
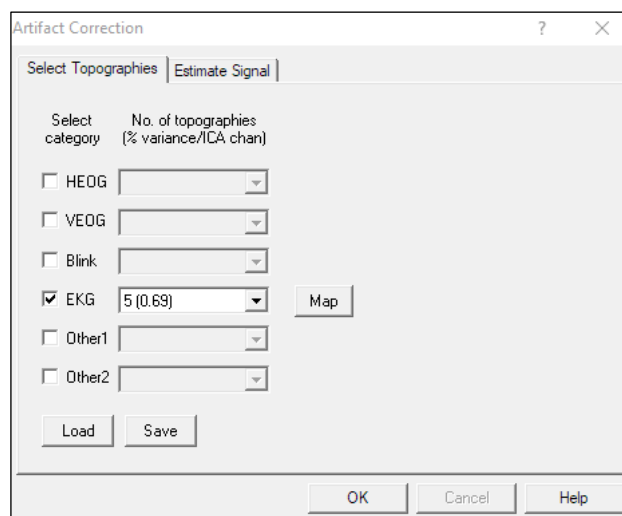
10. Select **Search / Search, Average, View** to turn off automatic saving of averaged buffer. Note that the 4th button in the control ribbon changed from **SAW** to **SAV**. Highlight one of the BCG occurrences and press the **SAV button**. Select a radio button to use **All** channels, **Current** filter, **Current** Buffer Width. Leave **Threshold** on the default value of **60%** and Search Range on **Whole File**. In **Options** you may uncheck **Selected View after Search** and **Selected view 300.0% width**. Press the **OK button** to start searching.

11. After the search is finished an averaged buffer with averaged BCG is shown on the left side of the screen. **Right click** on it and select **whole segment**. The whole buffer will be highlighted. **Right click** again on the highlighted area and select **Define Artifact Topography**.



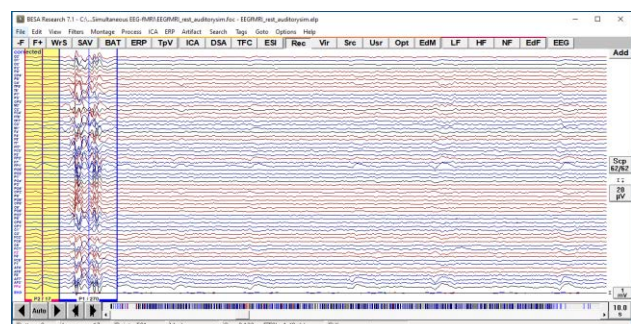
12. The Artifact Correction window will be displayed. **Check** the **EKG** check box. When a warning is displayed, check **Do not show this message again** and press **OK**. Change the **No of topographies** from the drop-down menu adjacent to EKG. The number of topographies has to be selected with caution, however here select a number with value close to **1%** (i.e. 5 components). Note that there will be a warning that **using too many coefficients can lead to remove non-artifact signal**. The BCG is a very strong and complex artifact and it is ok to use a slightly stronger filtration; thus press the **Yes button** to continue. After this operation the data should look much better. Press **OK** to close the dialog. Increase scaling using the **up arrow** on the keyboard. Verify if data is BCG free; if not the number of used coefficients used during artifact correction can be adjusted.

Please note that BCG artifact correction can be automatized using a pre-defined batch. (To do so just mark the R peak in the BCG artifact with **Pattern 1** – place a cursor and press 1 on your keyboard. Then press the **BAT** button on the toolbar and select **BCG_removal.bbat**, press **OK**.)



13. Now you can see that the F2 channel does not carry a correct signal (the cable was broken). **Right click** on the channel label and select **Interpolate this channel** from the popup menu. Press the **EdF** button to adjust filters to the blink frequency band: **Low Cutoff filter** of 1 Hz, 6 dB/Octave, **forward** and **High Cutoff filter** of 10 Hz, 12 dB/Octave, **zero-phase shift**. **Go to 00:01:30**. You will see some clear blinks. **Left Click** on the Fp1 label to select this channel and **highlight** data contaminated with one of the blinks. Press the **SAV** button again. All the settings should be used as previously, except for **Channel** selection, where **Selected** should now be checked. Note that the **second buffer** will be used and that for single channel based searching the default threshold is **85.00%**. Press **OK** to start searching.

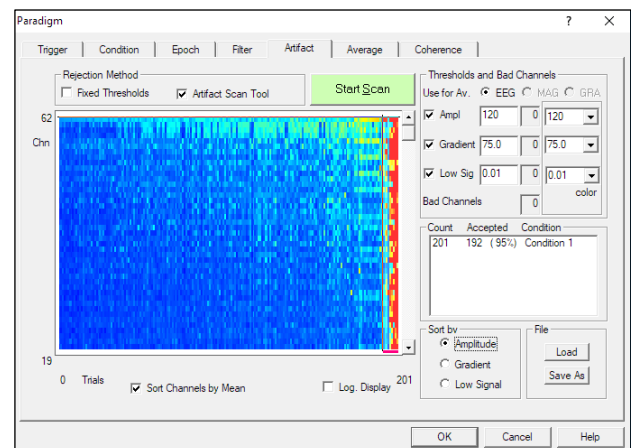
14. After the search is finished average buffers with averaged BCG and blink are shown on the left side of the screen. **Right click** on the first displayed buffer indicated with red color and select **whole segment**. The whole buffer will be highlighted. **Right click** again on the highlighted area and select **Define Artifact Topography**.



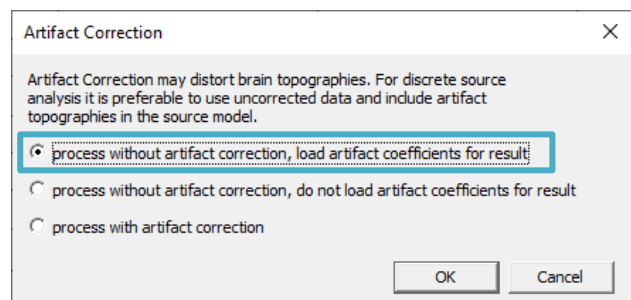
BESA® Research 7.1

Tutorial 11 – Simultaneous EEG-fMRI

15. In the displayed Artifact Correction dialog box **check** the **Blink** checkbox, leave **No of topographies** at 1, and press **OK**. Data can be now considered artifact free.
16. Press the **ERP** button, select **EEGfMRI_rest_auditorysim.PDG** file and press **OK**. Switch to the **Artifact** tab and press **Start Scan**. The threshold values may be left at default values.

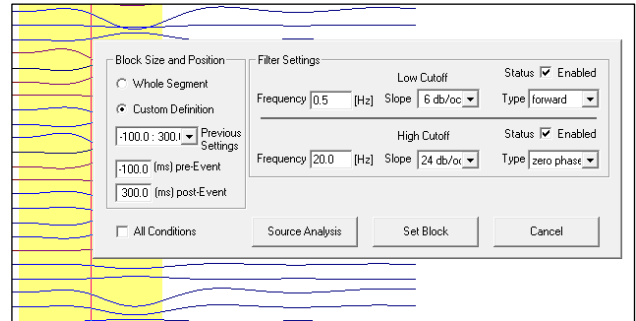


17. Switch to the **Average** tab and press **Average**. To perform averaging without artifact correction and load artifact topographies afterwards **select first option** and press the **Yes** button on the display dialog to turn off the artifact correction during averaging process. We will perform artifact correction in the next step.
18. Save the result of averaging using the file name **EEGfMRI_rest_auditorysim_av2.fsg**. Press **OK** on the displayed dialog.

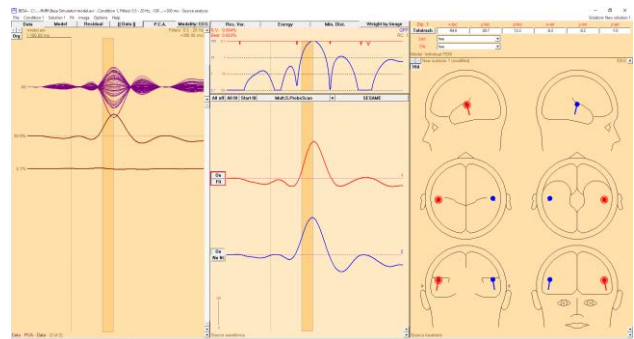


19. Open the **Besa Simulator \ model.avr** file.

This is a modeled ERP data which was used during simulation. Press **CTRL-L** on the keyboard. In the displayed dialog, press **Browse...** in the section **Coregistration file** (***.sfh**). Select file **EEGfMRI_rest_auditorysim.sfh** file from the experiment's main folder. Highlight a block of data and **right-click** on it. Select **Source Analysis** from popup menu. Select an interval from **-100 to 300 ms** and set filters as specified: **low cutoff filter** of **0.5 Hz**, **6 dB/Octave**, **forward** and **high Cutoff filter** of **20 Hz**, **24 dB/Octave**, **zero-phase shift**.

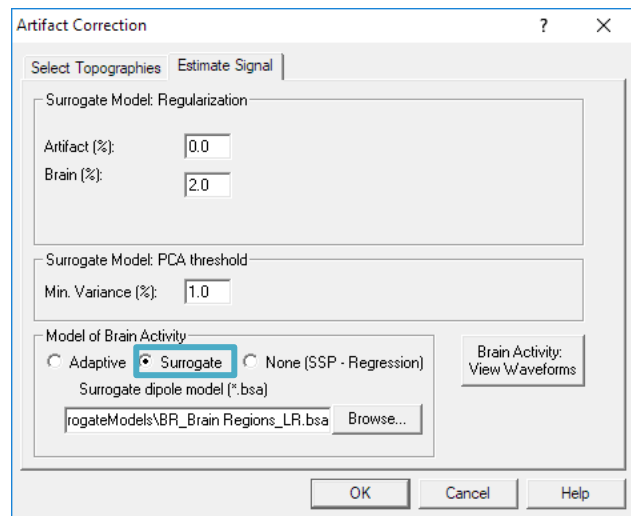


20. In the Source Analysis window, insert two dipolar sources by **double clicking twice** into the head schemes in the right area of the window. Select a fitting interval of **70 ms to 95 ms**. Select **Individual FEM** as head model. Press the **All fit** button and then the **Start fit** button. Dipoles are located perfectly in the auditory cortex and the residual variance is almost equal to zero.

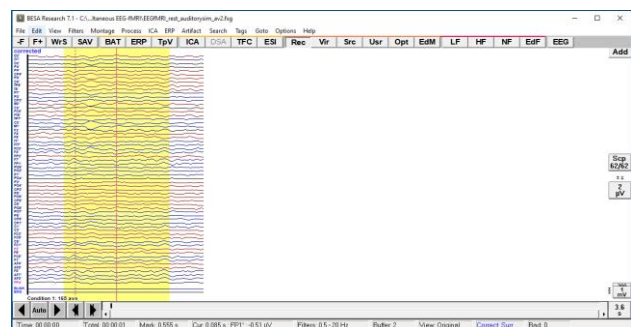


21. Minimize the Source Analysis window and go back to the main BESA Research Window. Press the **-F** button to go back to the averaged file: **EEGfMRI_rest_auditorysim_av2.fsg**.

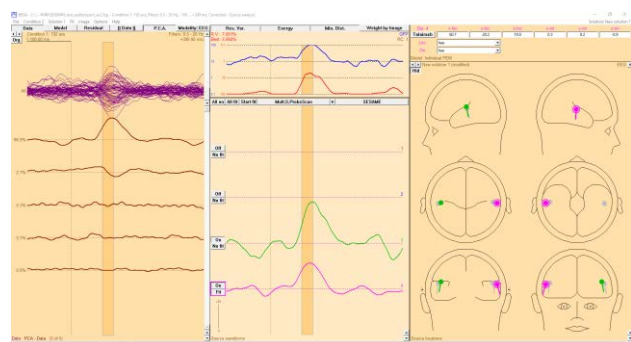
22. Press **Artifact / Options...** and switch **Model of Brain Activity** to **Surrogate** (use the default model: **BR_Brain Regions_LR.bsa**). Press **OK** to close the dialog.




23. Increase the High cutoff filter to **20Hz**, **24dB/Octave**, **zero-phase shift**. Highlight a block of data by left mouse-drag and **right-click** on it. Select **Source Analysis** from the popup menu. Select an interval from **-100 to 300 ms**. Make sure that the following filters are specified: **low cutoff filter of 0.5Hz**, **6dB/Octave**, **forward** and **high Cutoff filter of 20Hz**, **24dB/Octave**, **zero-phase shift**.

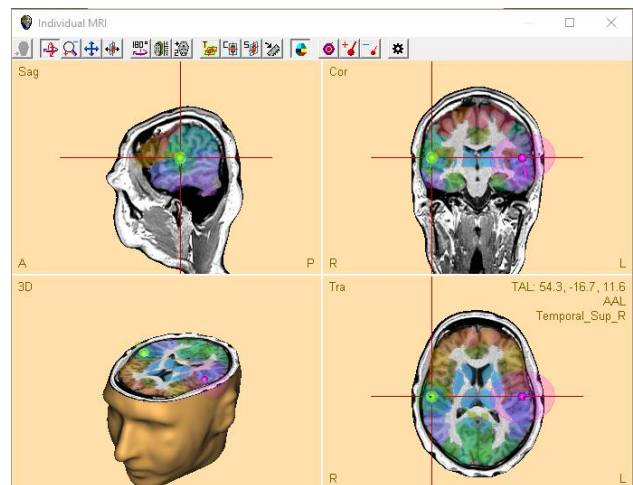


24. Note that the previous model does not explain all of the signal. **Disable** both dipoles from the previous model by clicking on the **On** button beside each dipole waveform to switch to **Off**. Insert two new dipolar sources by **double clicking twice** in the head schemes in the right window area. Select a fitting interval from **70 ms to 95 ms** by **left mouse-drag** over the waveforms. Make sure that **Individual FEM** is selected as head model at the top right.



Press the **All fit button** and the **Start fit button**. Dipoles are located in the auditory cortex, but in slightly different positions. Residual variance is smaller than before but still not close to zero due to noise in the data.

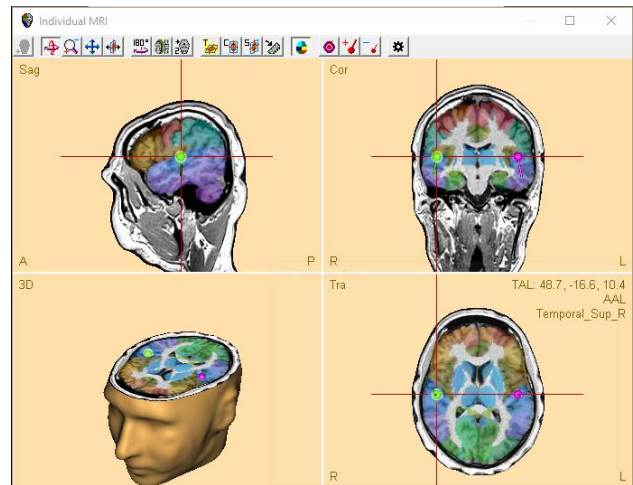
25. Press **A** on the keyboard to show the anatomy. Press  on the toolbar to switch to multiple view. Press **Shift-A** to display the brain atlas. **Right-click** on the 3D area and select **Options...** from the popup menu. Change Brain atlas to **AAL**, visualization mode to **brainCOLOR** and press **OK**. Now you can see that one of the sources is in the Rolandic operculum, and the second one in the Superior Temporal Gyrus.



Please note that around sources are visible confidence ellipsoids that are described in detail in Tutorial 8G. Due to high residual noise in data the confidence ellipsoids are noticeable, especially in the left source (as its location is forced to be symmetric).

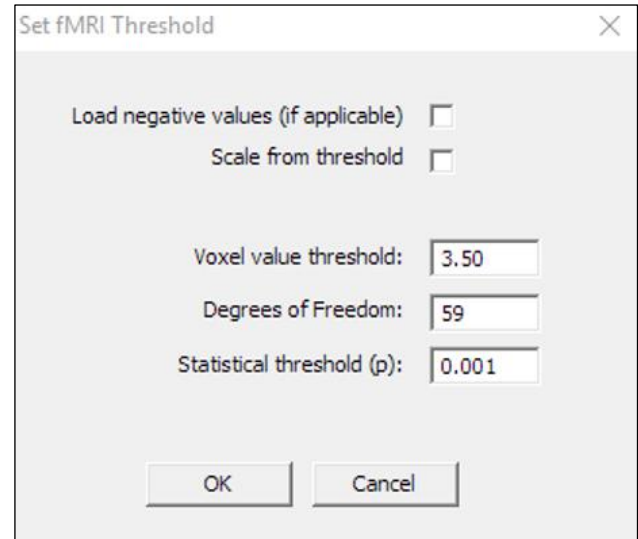
26. Go to menu **Condition** and select condition **model.avr** (or just press small **left arrow** in left top corner to switch condition).

Now the confidence ellipsoids are barely visible due to no noise in the data.



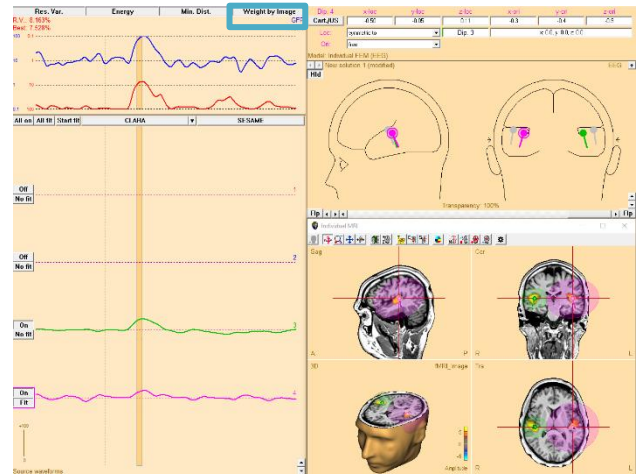
27. Go to menu **Condition** and select condition **EEGfMRI_rest_auditorysim_av2.fsg** (or just press small **right arrow** in left top corner to switch condition again).

28. Press **Image / Import fMRI**. Change filter to **ANALYZE/NIfTI files** and select **sound vs silence.nii** file. On the next dialog box **uncheck** **Load negative values**, set **Degrees of Freedom** to **59** and **statistical threshold** to **0.001**. The voxel value threshold will adjust automatically. Press **OK**.



29. Press **Shift-A** to turn off the atlas. Note that dipoles are not matched perfectly with fMRI results, however they indicate the same region. In the button row above the Global Field Power section (top center part of the window) press the **Weight by Image**

button. Again, press the **All Fit** button and the **Start Fit** button. Turn the brain atlas off again (**Shift-A**) and note that both sources are now located in the superior temporal lobe.



D. Good practice

Please keep in mind that simultaneous EEG-fMRI recording is a difficult yet powerful technique. The following rules could help one to perform a successful experiment:

- For an ERP experiment remember to introduce temporal **jitter between trials** (e.g. a random value in the range of ± 200 ms). Also, applying a pure EEG or a pure fMRI paradigm will probably have the effect that one of the modalities will not show satisfying results. Proper paradigm preparation is essential for success. Some further guidelines can be found here: (Rusiniak et al., 2013a).
- Inform your subject how important it is **not to move**.
- Keep electrode to skin **impedance as low as possible**.
- The EEG-fMRI recording session should be long enough to allow for proper artifact creation. Usually the experiment should **last at least 6 minutes**.
- At the same time try to **limit the time of experiment to a minimum** and preferably perform EEG-fMRI registration before other sequences to limit movement due to an inconvenient supine position.
- From the standard position, move the **subject about 4 cm towards caudal direction** to reduce artifacts: The MRI laser crosshair should be not in the Nasion position but in the middle of forehead (Mullinger et al., 2011).
- Especially for the first few registrations **repeat the experiment outside of the MR bore** to compare results.

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Moosmann, M., Schönfelder, V.H., Specht, K., Scheeringa, R., Nordby, H., Hugdahl, K., 2009. Realignment parameter-informed artefact correction for simultaneous EEG–fMRI recordings. *NeuroImage* 45, 1144–1150. <https://doi.org/10.1016/j.neuroimage.2009.01.024>

Mullinger, K.J., Yan, W.X., Bowtell, R., 2011. Reducing the gradient artefact in simultaneous EEG–fMRI by adjusting the subject’s axial position. *NeuroImage* 54, 1942–1950.

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Rusiniak, M., Wolak, T., Lewandowska, M., Cieśła, K., Skarzynski, H., 2013b. The relation between EPI sequence parameters and electroencephalographic data during simultaneous EEG–fMRI registration: an initial report., in: *ESMRMB 2013 Congress, Book of Abstracts*, Saturday. Presented at the ESMRMB, Springer, Toulouse, p. 661. <https://doi.org/10.1007/s10334-013-0384-5>

Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

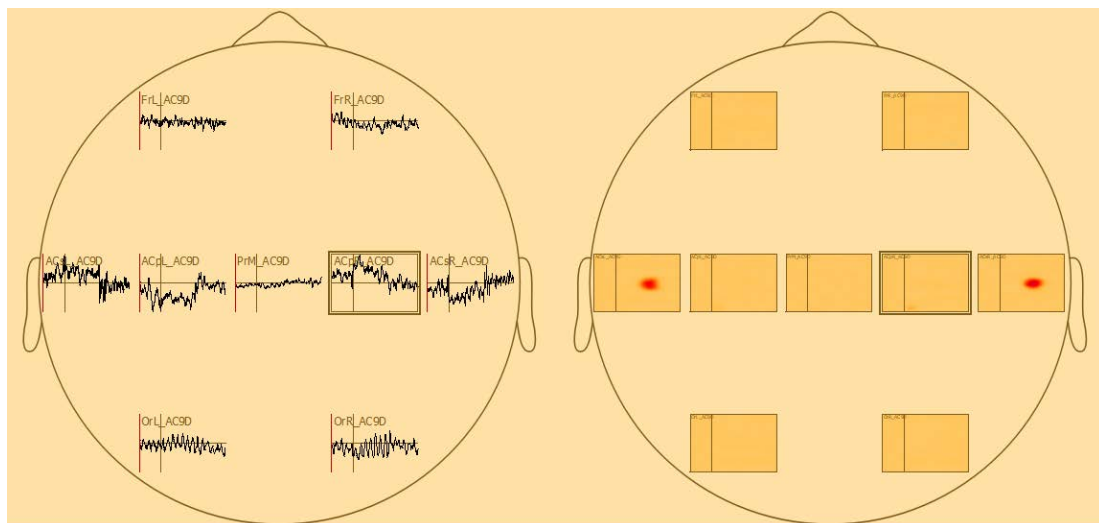
What does BESA Research provide?

- ✓ Time-Frequency Analysis
 - Complex Demodulation
 - Wavelets (Morlet / Mexican Hat)
- ✓ Connectivity Analysis
 - Coherence
 - Imaginary Part of Coherency
 - Phase Locking Value
 - Non-parametric Granger Causality
 - Non-parametric Partial Directed Coherence
 - Non-parametric Directed Transfer Function
- ✓ Multiple Source Beamforming
- ✓ Dynamic Imaging of Coherent Sources (DICS)

A. Introduction to Time-Frequency Analysis

Recently, an increasing number of papers on oscillatory coupling between brain regions and on time-frequency analysis of human EEG and MEG data has been published. BESA Connectivity provides several tools for fast and user-friendly time-frequency analysis.

Due to the fact that oscillatory components in EEG or MEG signals are not necessarily time-locked to an event, these components will be cancelled out when averaging across trials and therefore, will not be represented in an ERP / ERF analysis. Time-frequency analysis is able to reveal signal that are related to a stimulus, but not perfectly time-locked. It reveals which frequencies have the most power at specific latencies and how their phase synchronizes across time. The decomposition of a time-series into complex numbers for specified latencies and frequencies provide the magnitude and phase angles of the oscillations. To extract this information, a sliding time-window is used that compares the EEG / MEG signal to a reference template at multiple frequencies. This multiplication of a time-series with a windowed transformation function is a mathematical operation called convolution. Common templates are Morlet and Mexican Hat wavelets, as well as sine and cosine waves.



BESA Connectivity uses TSE (temporal-spectral evolution) plots to visualize changes in power or amplitude over time normalized to the mean power or amplitude of the baseline epoch for the respective frequency (see figure above).

B. Introduction to Connectivity Analysis

Brain connectivity is based on two central principles that form the functional organization of the brain. These principles are characterized by segregation and integration of information being processed. Modes of brain connectivity of large-scale brain networks are divided up into three separate, but related aspects: structural connectivity, functional connectivity and effective connectivity.

- Structural connectivity, also called anatomical connectivity refers to the anatomical structure of the brain.
- Functional connectivity is defined as the temporal correlation of spatially separated brain areas.
- Effective connectivity combines anatomical and functional connectivity, as it provides a measure for the directional influence of one neural system over another.

BESA Connectivity provides the following methods to estimate functional or effective connectivity collected from EEG and MEG recordings:

- Coherence (Rosenberg et al., 1989)
- Imaginary Part of Coherency (Nolte et al., 2004)
- Phase Locking Value (Lachaux et al., 1999)
- Non-parametric Granger Causality (in the frequency domain; Granger, 1969; Geweke, 1982)
- Non-parametric Directed Transfer Function (Kaminski and Blinowska, 1991)
- Non-parametric Partial Directed Coherence (Baccala and Sameshima, 2001)

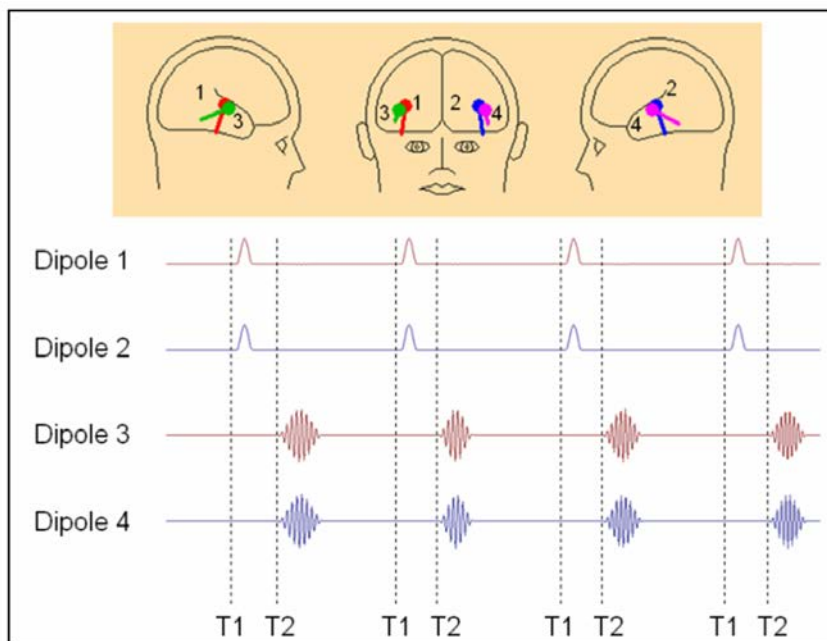
Non-parametric Granger causality, Directed Transfer Function and Partial Directed Coherence are based on a non-parametric estimation of the transfer matrix (Wilson, 1972; Dhamala et al., 2008).

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- Lachaux, J.-P., Rodriguez, E., Martinerie, J., Varela, F.J., 1999. Measuring phase synchrony in brain signals. *Human Brain Mapping* 8, 194–208.
- Nolte, G., Bai, O., Wheaton, L., Mari, Z., Vorbach, S., Hallett, M., 2004. Identifying true brain interaction from EEG data using the imaginary part of coherency. *Clinical Neurophysiology* 115, 2292–2307.
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C. Simulation of evoked activity and oscillations in the auditory cortex

The simulated data sets can be found in subfolder **Learn-by-Simulations\AC-Coherence** of the BESA Research Examples folder. The data have been generated by superimposing a real



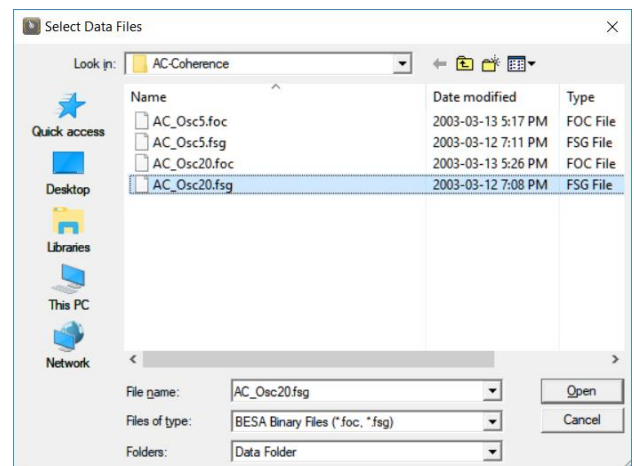
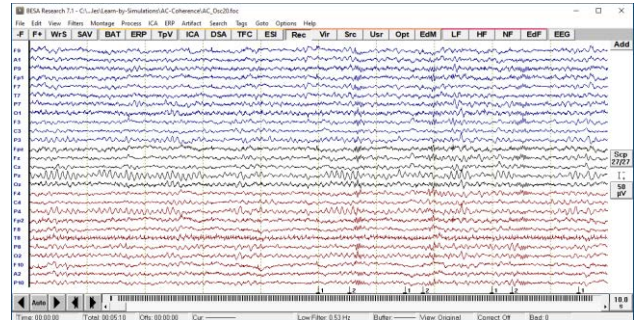
continuous 27-channel EEG-recording with the simulated activity of two pairs of bilateral sources in the auditory cortex (AC). The purpose of this combination was to understand the sensitivity of time-frequency analysis to reveal oscillatory activity and coupling in a realistic ongoing EEG. The figure below displays the underlying source configuration. Sources 1 & 2 were simulated as simultaneous evoked monophasic activity with a time-locked onset of 50 ms after a hypothetical auditory stimulus (trigger T1). The duration of this monophasic activity was 150 ms, and the amplitude was chosen to generate a signal of 10 μ V at Cz. Dipoles 3 & 4 simulate a more antero-lateral secondary area of AC with an orientation differing by about 30° from dipoles 1 & 2. They reflect oscillatory activity (trigger T2) that jitters in latency (300-550 after T1), duration (300-450 ms) and frequency (20-28 Hz). The envelope of this oscillatory activity had the same amplitude in all 200 simulated trials. The amplitude generated at electrode Fz was 5 μ V (file AC_Osc5.foc) and 20 μ V (file AC_Osc20.foc), respectively. The oscillation of dipole 4 follows that of dipole 3 with a constant delay of 5 ms.

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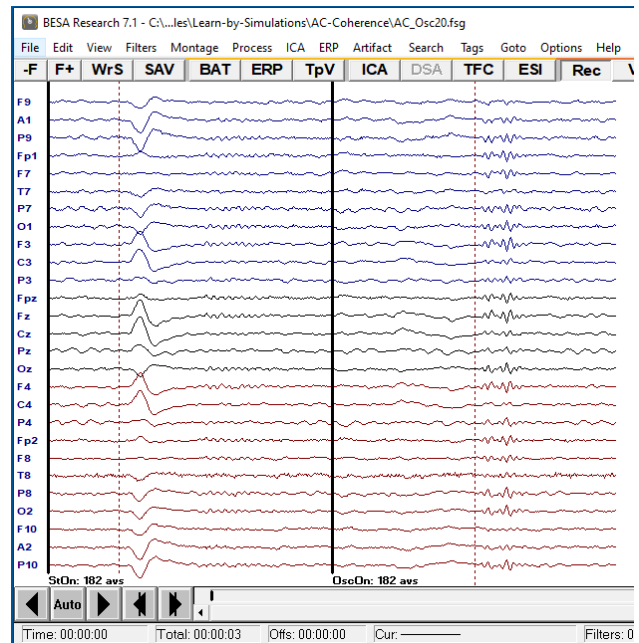
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

D. Prepare Data for Time-Frequency Analysis

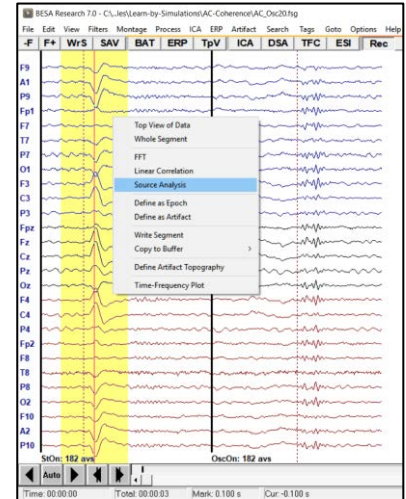
1. **Open** file **Learn-by-Simulations\AC-Coherence\AC_Osc20.foc** in the **BESA Research Examples** folder. Note that e.g. at electrode C3 the evoked monophasic response locked to trigger 1 is just visible on top of the background noise. The oscillatory activity following trigger 2 can be observed as well.
2. In order to better understand the properties of the simulated activity, we load the averaged evoked response file. Open file **AC-Coherence\AC_Osc20.fsg**.



- The first segment contains the average triggered by the stimulus onset, the second averaged segment is time-locked to the onset of the jittering oscillations. Relative to stimulus onset, the induced oscillations cancel out in the average. The jitter in the frequency range of the oscillation (20–28 Hz) also reduced the signal average relative to the onset of the oscillation. Note that the wave shape of the monophasic activity is altered by low cutoff filtering applied to the average to reduce slow drifts in the data.

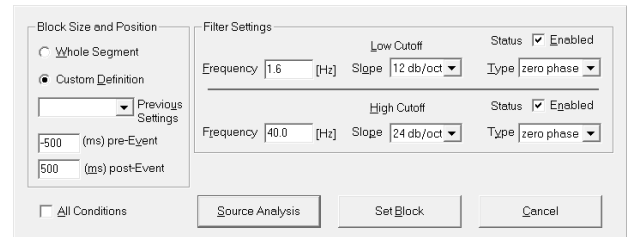


- To see how the averaged surface activity is transformed into brain space, we use the source analysis module. **Left-drag** over the first segment. **Right-click** and select **Source Analysis**. For this segment, we use an interval from **-50 to 1000 ms** and choose a **Low Cutoff** filter of **1.6 Hz**, **12 dB/Oct zero-phase** and set the **High Cutoff** filter to **40 Hz**, **24 dB/Oct, zero-phase**.

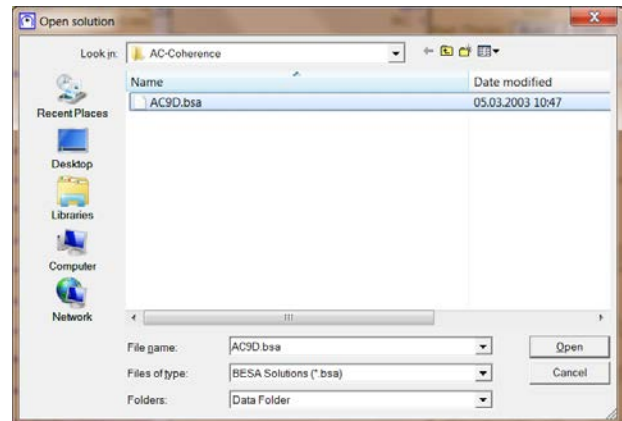


Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

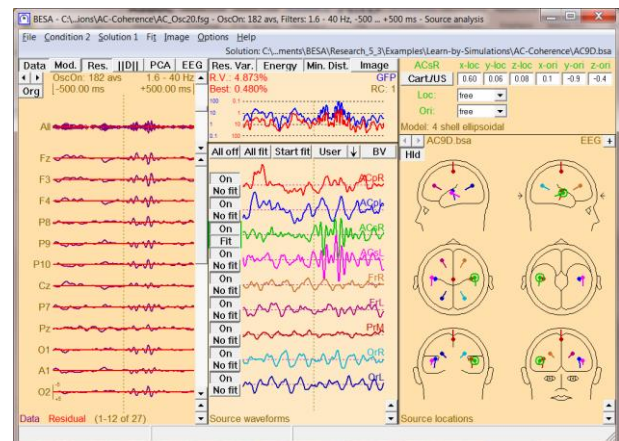
- The source analysis window opens. Minimize this window to load the **second segment** as well, but now select an epoch from **-500 to +500 ms** relative to the onset of the oscillation.



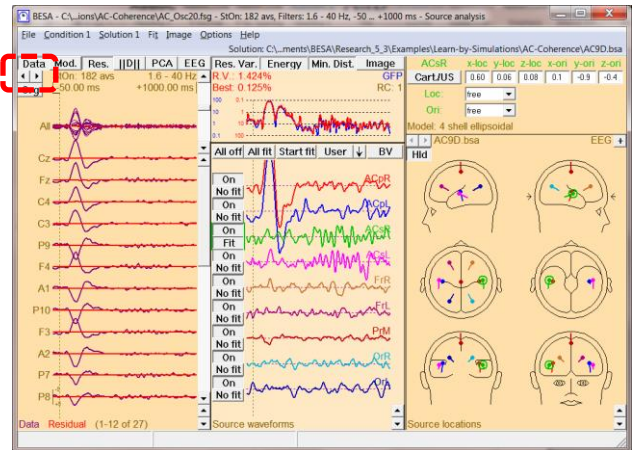
- Select **File / Open Solution** to load the predefined solution **AC9D.bsa**.



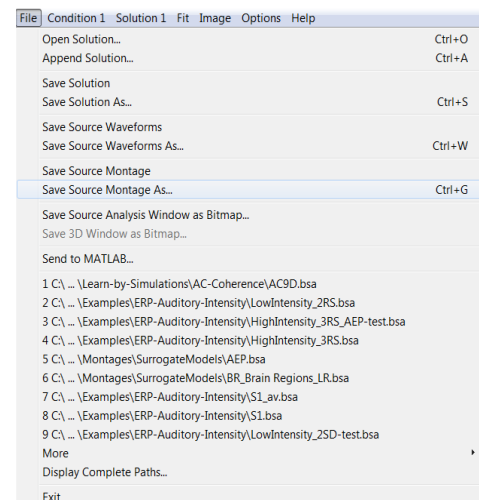
- The model contains the two pairs of dipoles that were used for the simulation. In addition, five probe sources are included that pick up background EEG activation. In condition OscOn (containing the oscillation-locked averages), dipoles 3 and 4 show small oscillatory activities. The evoked activation in sources 1 and 2 is barely visible, because of its large onset jitter with respect to trigger 2.



8. Use the **arrow buttons** in the upper left corner to switch to condition 1. The time-locked evoked activity appears only in the related sources 1 and 2. The induced oscillations in source waveforms 3 and 4 cancel out almost completely. The five probe sources show only small background noise activity. Note the almost complete separation of the activities in the different brain regions as compared to their wide distribution in the scalp waveforms.

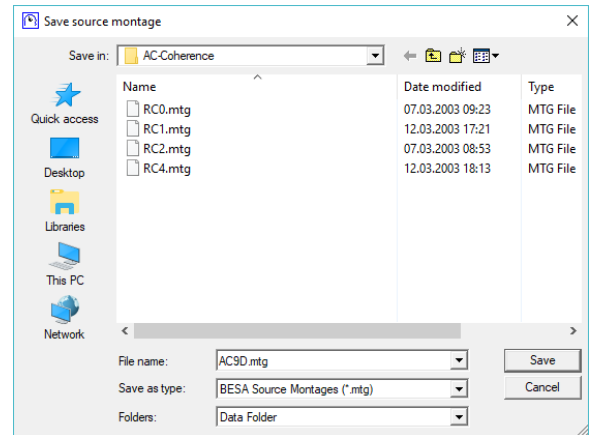


9. We want to use our nine-dipole model as a source montage for the continuous data. Create a source montage from the displayed multiple source model by selecting **File / Save Source Montage As...** Note that the source montage not only contains the source coordinates, but also stores the selected regularization constant (set to 1 by default).

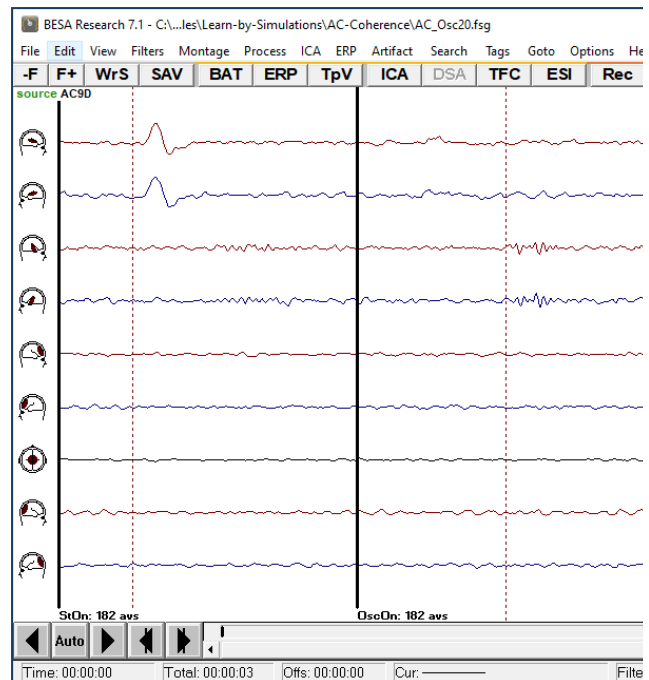


Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

10. When prompted for a name for the montage to be saved, enter **AC9D**. Press **Save**. This will create the new source montage and automatically apply it to the current file in the main window.



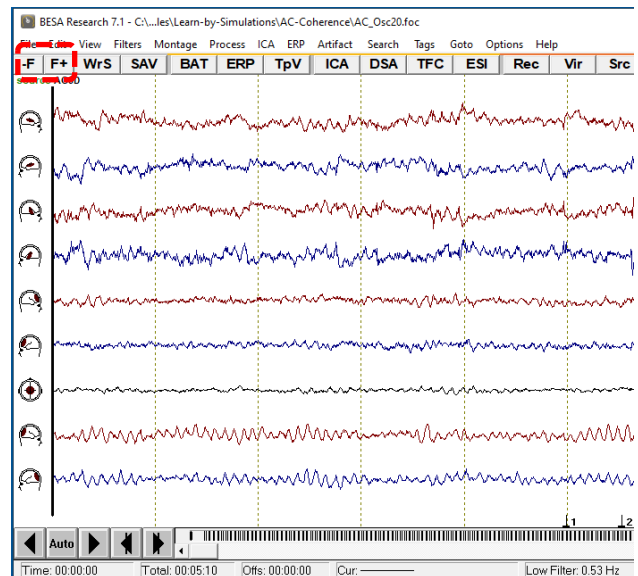
11. **Close** the source analysis window. The display now shows the averaged data segments transformed into brain space by the generated source montage. Note the advantage of the source montage: instead of the distributed overlap of the different activities at the surface channels, we now obtain largely separated activities of the modeled brain regions with the evoked time-locked activity in source 1 & 2 and the induced oscillatory activity in sources 3 & 4.



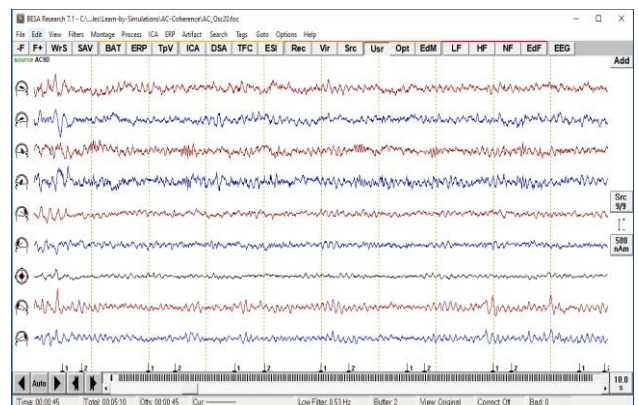
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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

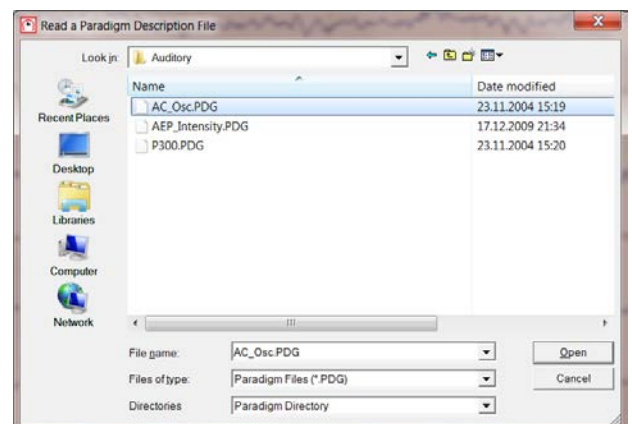
12. Next, we want to apply this source montage to transform the continuous data. Press the **-F** button to switch back to file **AC_Osc20.foc**. Press the **USR** button in the push button bar to show all user-montages that are available for this file. Select the predefined montage **AC9D**.



13. The continuous 27-channel EEG data has been transformed to nine source waveforms. We want to use the advantage of having contrasted the activities of the different waveforms to apply time-frequency analysis to the nine source waveforms and analyze the connectivity between them.

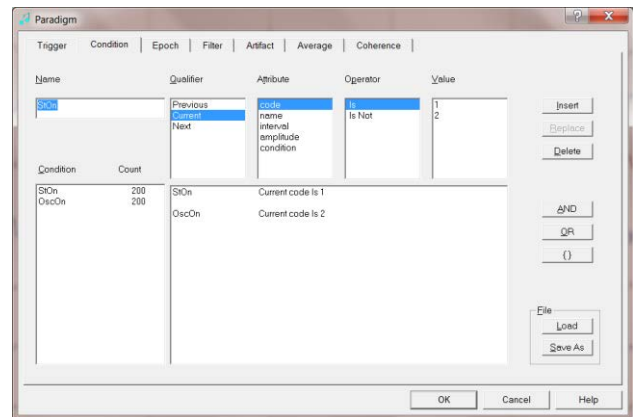


14. Select **ERP / Open Paradigm** to load the predefined settings in file **Auditory\AC_Osc.pdg** in the Paradigm directory.

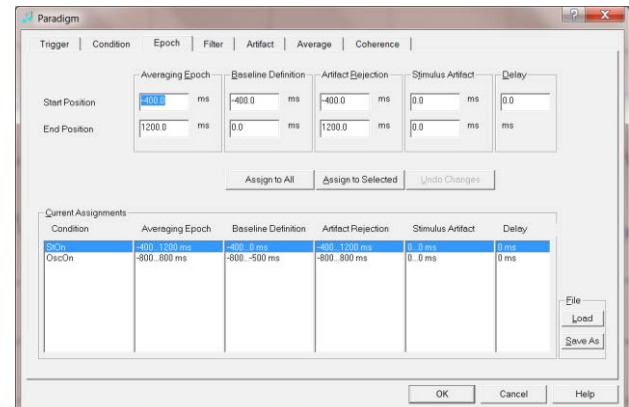


Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

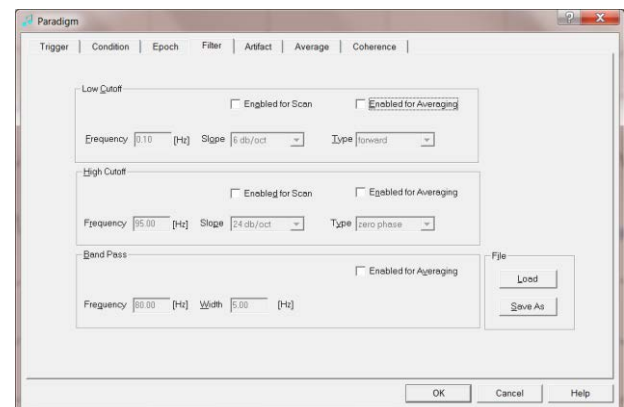
15. Conditions StOn and OscOn were predefined to represent triggers 1 and 2. 200 events are detected for stimulus onset and oscillation onset.



16. View the Epoch tab. The epoch settings have been predefined to span a sufficiently long epoch including a baseline of 400 ms for TSE. Note the different settings for both conditions. The later oscillatory onset requires an earlier baseline prior to stimulus onset.



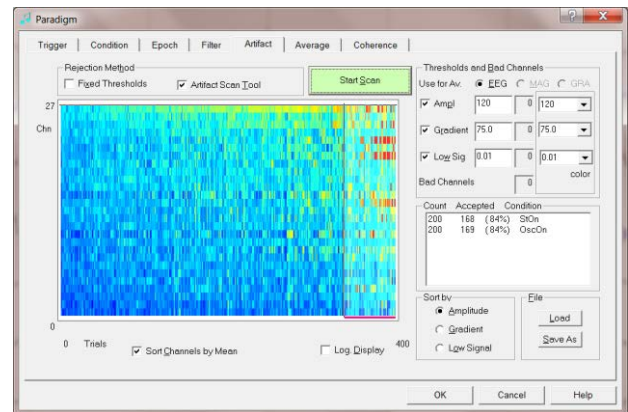
17. In the Filter tab no filters are selected, in order to obtain undistorted results of the time-frequency analysis. In the presence of strong low frequency activity, it can be useful to set a low cutoff of 0.2, 0.5, 1, or 1.6 Hz.



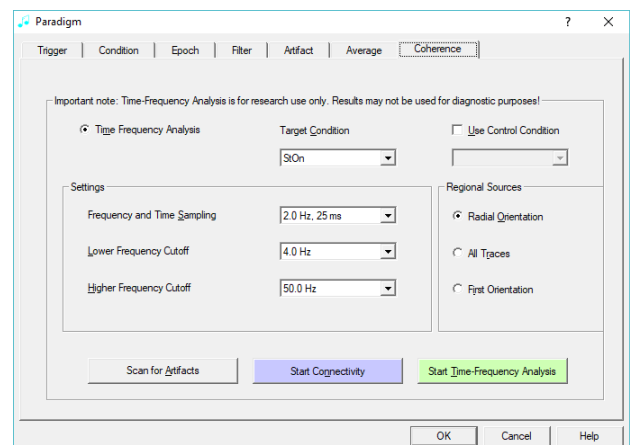
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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

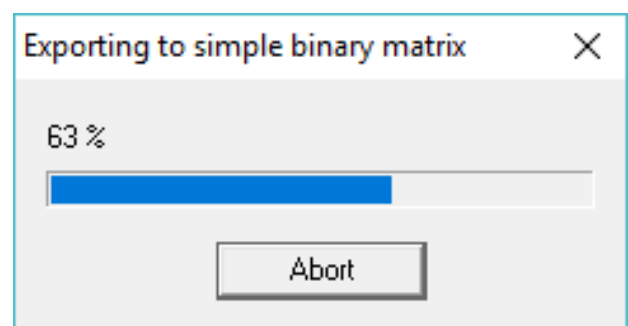
18. Select the **Artifact** tab and press **Start Scan**. Artifact epochs are automatically identified and excluded according to the default thresholds displayed in the upper right corner. Sort by amplitude, gradient and low signal by checking the corresponding item in the **Sort by** box. The suggested threshold settings do not have to be modified for the current file.



19. Select the **Coherence** tab. The Condition drop down menu allows choosing one condition for event-related time-frequency analysis. The time-frequency sampling settings in the **Settings** box are only relevant if you want to use the built-in Source Coherence module. We can ignore them for the moment.



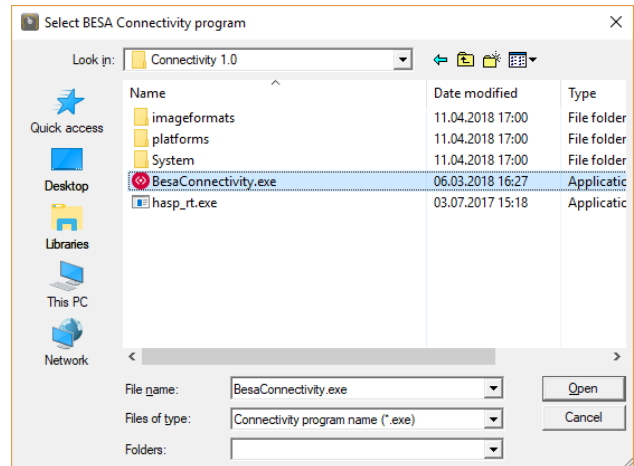
20. Press the button **Start Connectivity**. Data is exported for BESA Connectivity.



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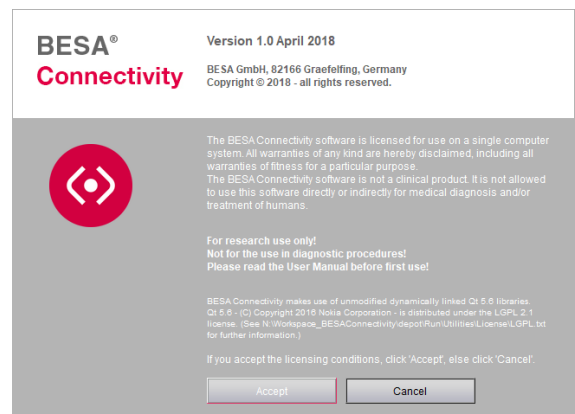
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

- Subsequently, a file dialog is opened to select the BESA Connectivity program. Please select the file **BESAConnectivity.exe** in the installation directory of BESA Connectivity (default: **C:\Program Files\BESA\Connectivity 1.0**) and press **Open**. Note that this step only needs to be performed once, when starting BESA Connectivity for the first time. (To change this assignment at a later stage, hold down the **Shift** key when clicking the **Start Connectivity** button).

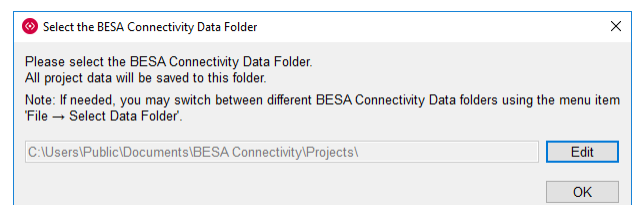


E. Time-Frequency Analysis with Simulated Data

- BESA Connectivity will open. Press **Accept** in the welcome screen.



- When BESA Connectivity is opened for the first time, the project folder needs to be defined. This is the folder where BESA Connectivity stores and reads all project and result data. A dialog box appears. Press **OK** to confirm the pre-selected folder.



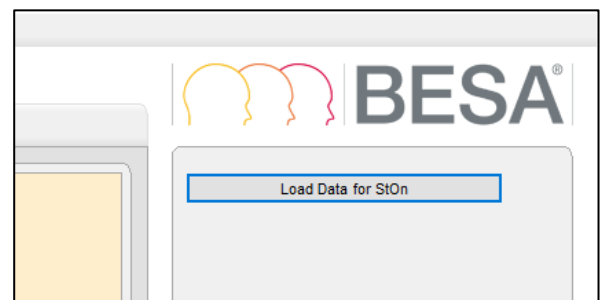
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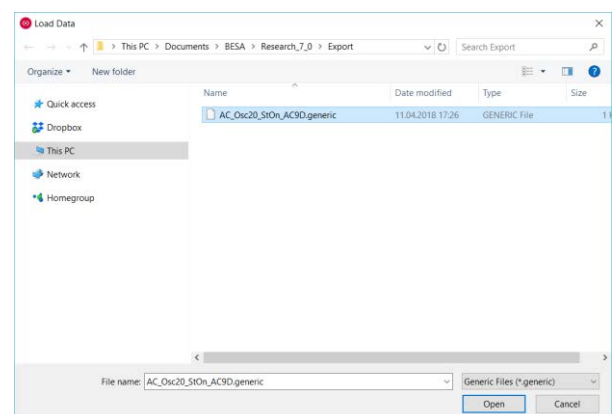
3. A new time-frequency project is started automatically. To compare results from different time-frequency decompositions, also enable **Wavelet Transform** using Morlet wavelets. Press **Next** on the bottom right (or hit the space bar).



4. Press **Load Data for StOn** in the interaction window.



5. Please browse to the folder **C:\<UserName>\Documents\BESA\Research_7_1\Export** (or **Documents\BESA\Research_7_1\Export**) and select the **AC_Osc20_StOn_AC9D.generic** file we previously exported for condition “StOn”. Press **Open**.



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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

6. A summary of the loaded file will be displayed in the main window and a green tick-mark will appear next to the **Load** button. Press **Next** on the bottom right (or hit the space bar) to go to the next work step.

StOn	
Condition name (from file):	StOn
Filename:	C:/Users/Robert/Documents/BESA/ Research_7_0/Export/ AC_Osc20_StOn_AC9D_generic
Number of trials:	168
Number of channels:	9
Sampling rate:	320 samples/s
Epoch start:	-400 ms
Epoch end:	1200 ms
Epoch length:	1600 ms
Pre-stimulus interval:	400 ms
Baseline start:	-400 ms
Baseline end:	0 ms
Padding:	2000 ms

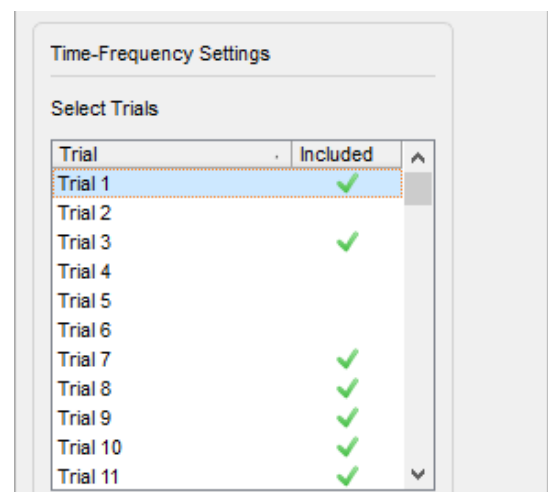


Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

- Waveforms of the currently loaded dataset are visualized in this work step. The signals of all sources for the currently selected trial are displayed in the main window. An average over all trials for the selected source channel is displayed in the left detail window. The right detail window shows the waveform of the current trial for the selected source.

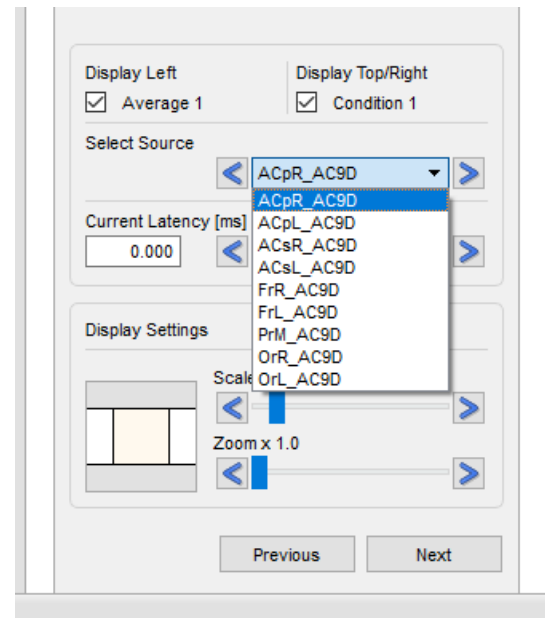
- Trials containing artifacts and/or noisy signals can be excluded from further analysis by removing the green checkmark icon to the right of the corresponding trial with a **left-click**. However, this is not necessary for this dataset since artifact rejection was already performed in BESA Research.

After removing unwanted trials, the average is recomputed and displayed in the left detail window for the currently selected source channel.

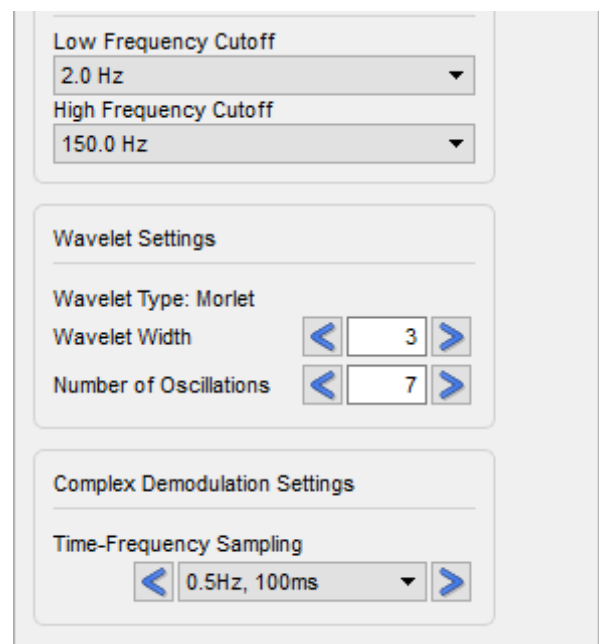


Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

9. Different source channels can be selected in the **drop-down menu** of the **interaction window**.



10. The **Time-Frequency Settings** section provides drop-down boxes to define the frequency interval. We will use the default frequency range of **2.0 Hz** to **150.0 Hz**.



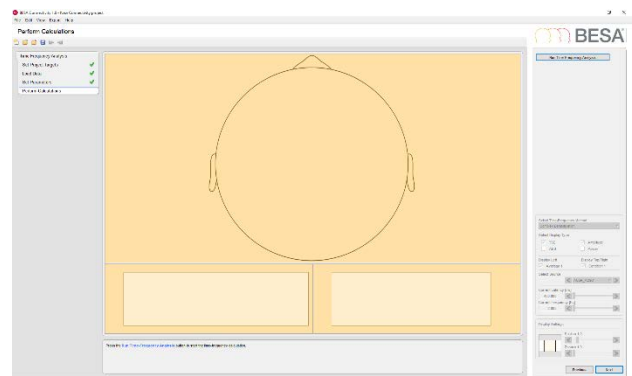
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

11. If **Wavelet Transform** was selected in the first work step, the **Wavelet Settings** section is displayed. The parameter **Wavelet Width** determines the length of the used wavelets in standard deviations of the implicit Gaussian kernel. The parameter **Number of Oscillations** defines the width of the wavelets in number of cycles. 'Shorter' wavelets will provide a finer temporal resolution at the expense of a coarser frequency resolution and vice versa.

The **Complex Demodulation Settings** section is displayed if the method was selected in the Set Project Targets work step. For the time-frequency sampling, a compromise has to be made between high frequency and low temporal resolution or low frequency and high temporal resolution. Default time-frequency sampling is intermediate with a frequency sampling of **1.0 Hz** and a time sampling of **50 ms**.

Press **Next** or hit the space bar to continue.

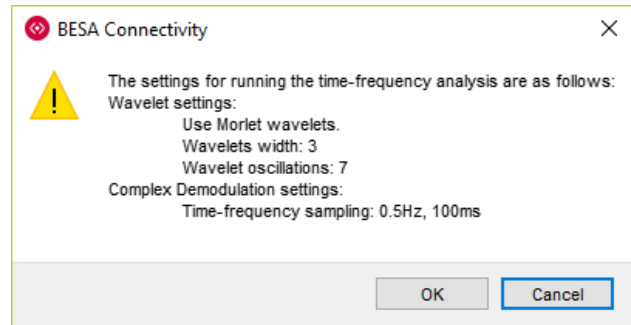
12. Press **Run Time-Frequency Analysis** to start the time-frequency decomposition using the selected methods and defined settings.



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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

13. An information window appears summarizing the settings for the time-frequency methods. Press **OK** to continue. Please note that the following calculations can be time-consuming depending on the selected methods, settings, type of data and the data length.



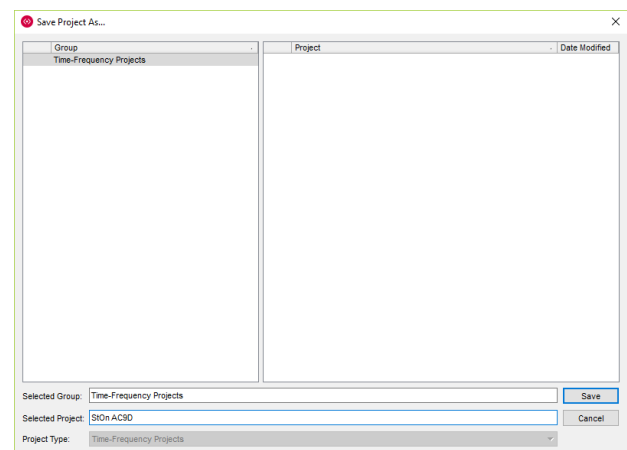
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

14. After all calculations are completed, the Temporal-Spectral Evolution (TSE) visualization for the selected time-frequency method is displayed in the main window. TSE shows the power/amplitude for each time-frequency bin, normalized to the mean power/amplitude of the baseline epoch for that frequency. Whether amplitude or power is used for visualization can be chosen in the **Select Display Type** section of the interaction window. Absolute power or amplitude values can be displayed when selecting the **ABS** option.

The left detail window shows the averaged waveform of the currently selected source, whereas the TSE/ABS visualization for the currently selected source is displayed in the right detail window.

For Complex Demodulation, induced activity around 25 Hz appears in channels ACsL and ACsR in the latency range of 400 ms to 800 ms. The short mono-phasic time-locked activity of the sources ACpL and ACpR is revealed in the latency range of 50 ms – 200 ms. Wavelet Transform shows induced activity in a narrower time window from 550 ms to 740 ms.

15. Press **Finish** to save and close this time-frequency project. Please enter **StOn AC9D** as **Selected Project** name and press **Save** to store the project and go back to the start-up screen.

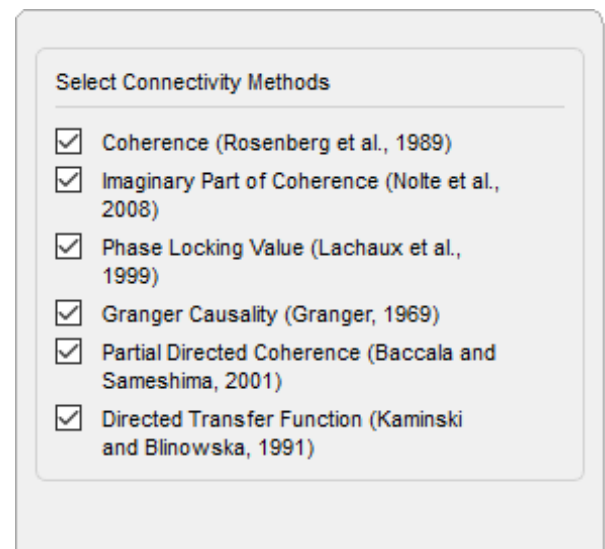


F. Connectivity Analysis with Simulated Data

1. Press **Connectivity Analysis** to start a new connectivity analysis workflow.



2. The first work step provides an overview of all connectivity methods that are available. selected folder. Well-established methods like Coherence, Imaginary Part of Coherency and Phase Locking Value are supported, as well as state-of-the-art methods like Granger Causality, Partial Directed Coherence and Directed Transfer Function. Please select all methods to enable a comprehensive comparison of all options.



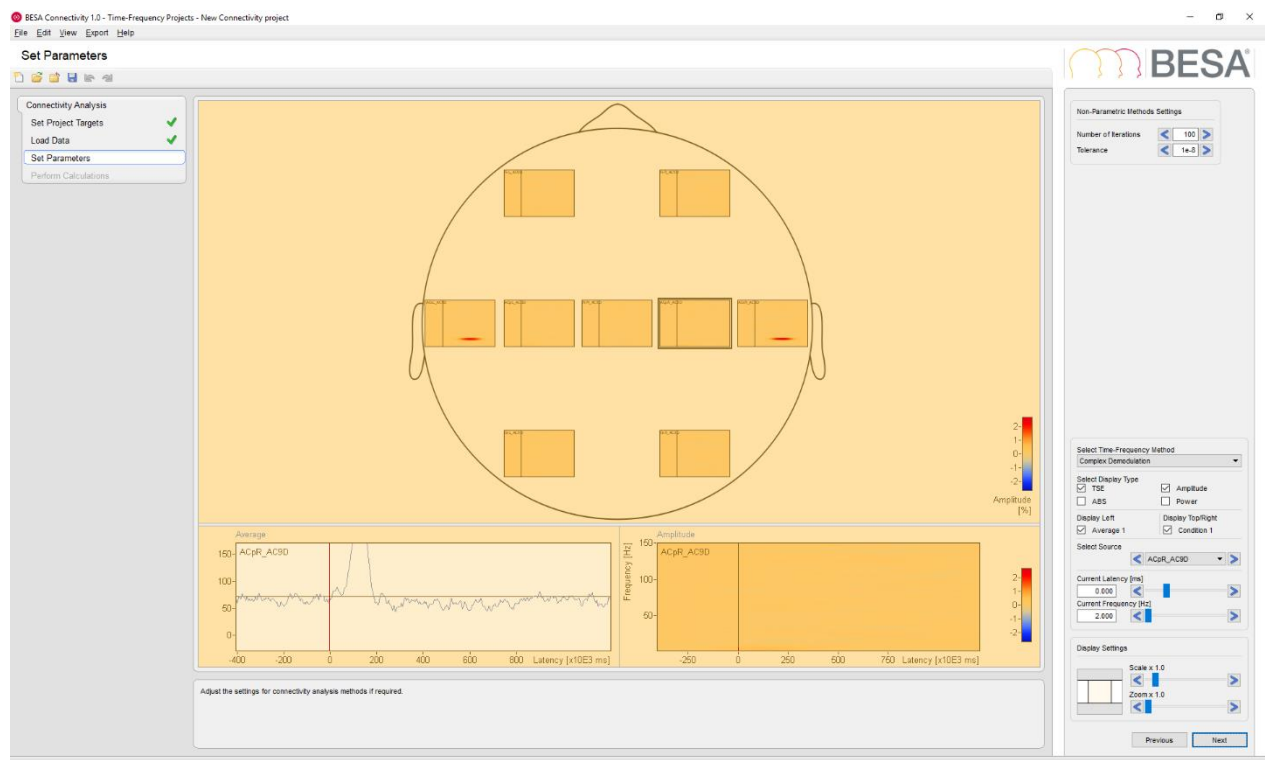
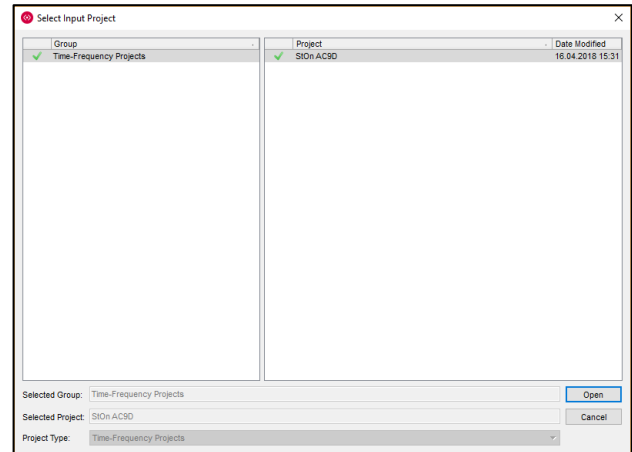
Press **Next** on the bottom right (or hit the space bar) to get to the next work step.

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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

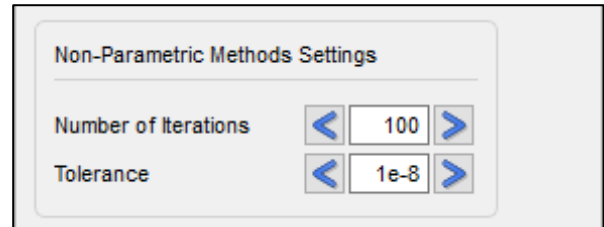
3. Press **Select Time-Frequency Input Project** to load the currently saved time-frequency results for the **StOn** condition. A summary of the loaded data file is shown in the main window.

Press **Next** or hit the space bar to continue.



4. Results from the selected time-frequency project are loaded and displayed in the **Set Parameters** work step.

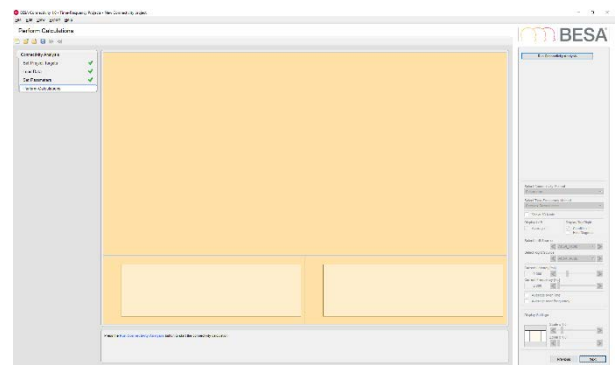
5. The **Non-Parametric Methods Settings** section provides parameters for the calculation of the non-parametric methods (Granger Causality, Partial Directed Coherence or Directed Transfer) and is only available if one of them was selected.



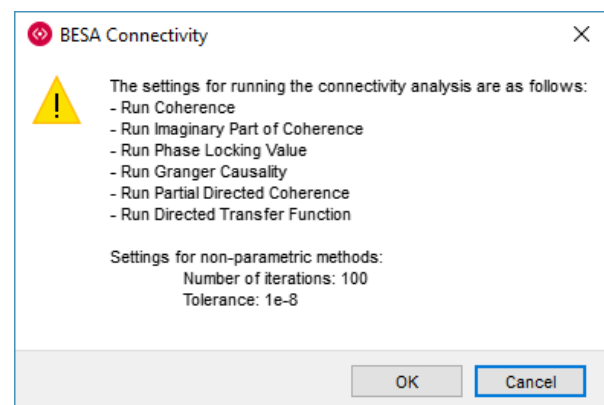
The parameters **Number of Iterations** and **Tolerance** are required during the factorization of the cross-spectral density matrix. For every iteration, the estimation error of the spectral factors is recomputed. If the estimation error is lower than the **Tolerance** threshold, the computation is terminated.

Press **Next** or hit the space bar to continue.

6. Press **Run Connectivity Analysis** to start the connectivity analysis using the selected methods and defined settings.



7. An information window appears summarizing the selected connectivity methods as well as the specific settings. Press **OK** to continue. Please note that the following calculations can be time-consuming, particularly if one or more non-parametric methods have been selected.



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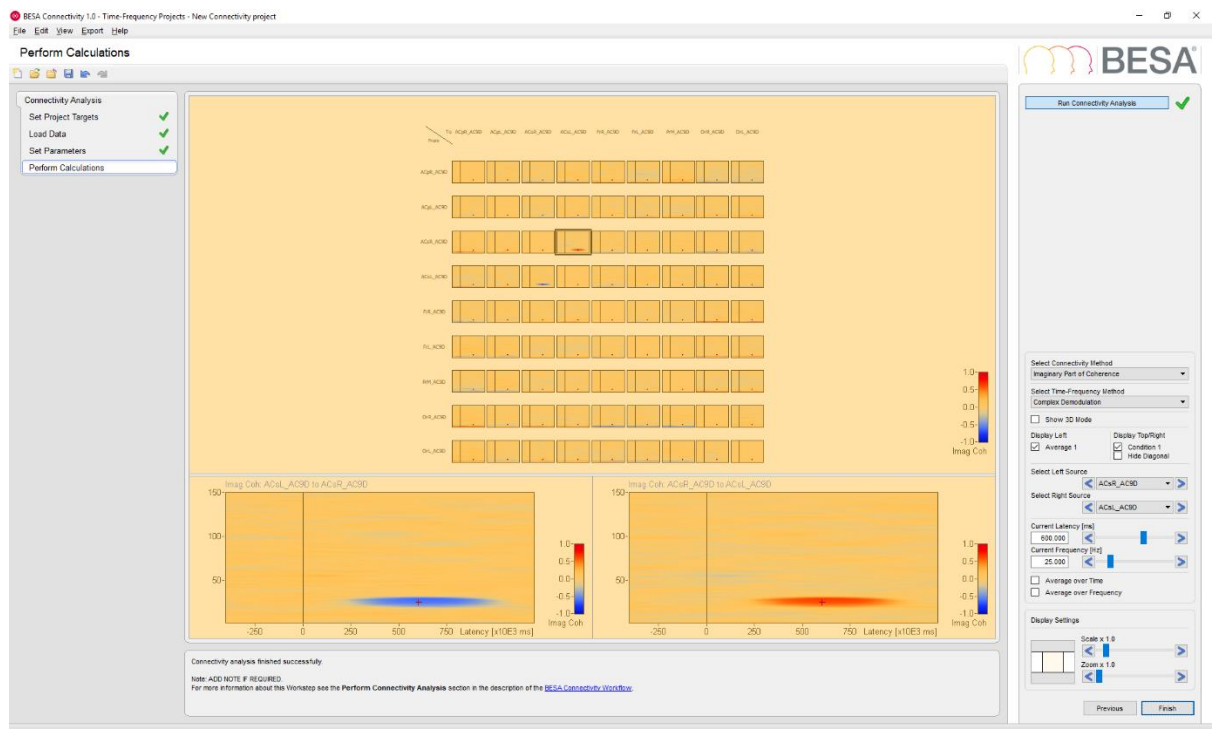


8. After all calculations are completed, the results of Coherence based on Complex Demodulation are displayed as a matrix view. Normalized power spectral densities are displayed on the diagonal of the matrix.

The detail windows show the connectivity between the selected pair of sources. Since Coherence is a symmetric measure, it does not provide information regarding the direction of information flow between any pair of signals. Therefore, the displayed matrix is also symmetric.

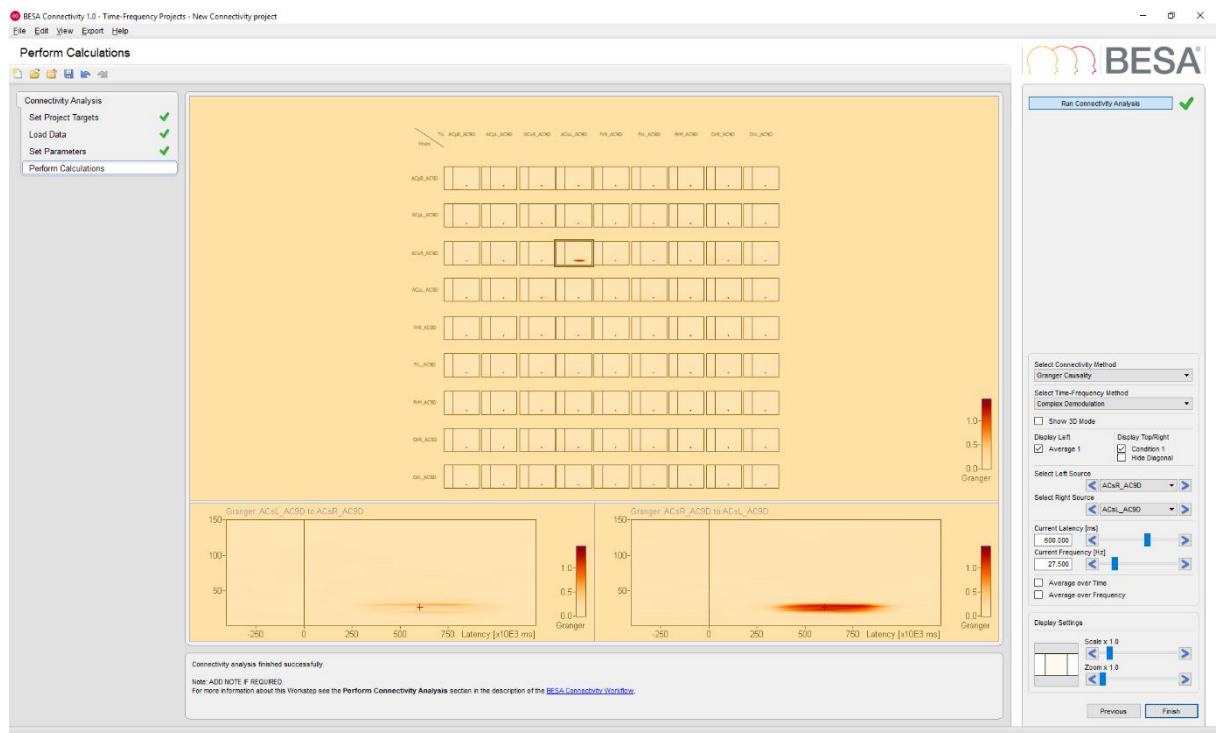
Choose ACsR in the **Select Left Source** drop-down box and ACsL in the **Select Right Source** drop-down box. As expected from the simulation, high correlation between the two channels is shown from 400 ms to 800 ms at a frequency of 25 Hz. There is practically no coherence with all other channels.

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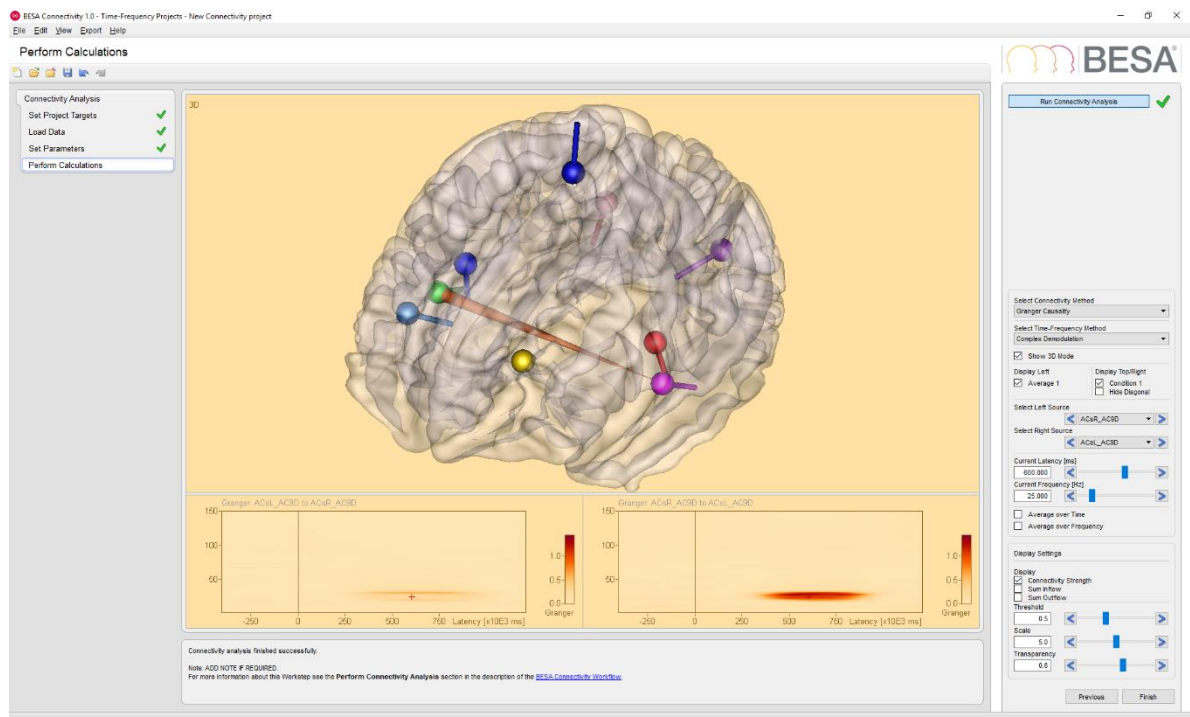
9. Select Imaginary Part of Coherency in the **Selected Connectivity Methods** drop-down box. This method is able to determine the direction of information flow and returns positive values to indicate information is flowing from source ACsR to ACsL.

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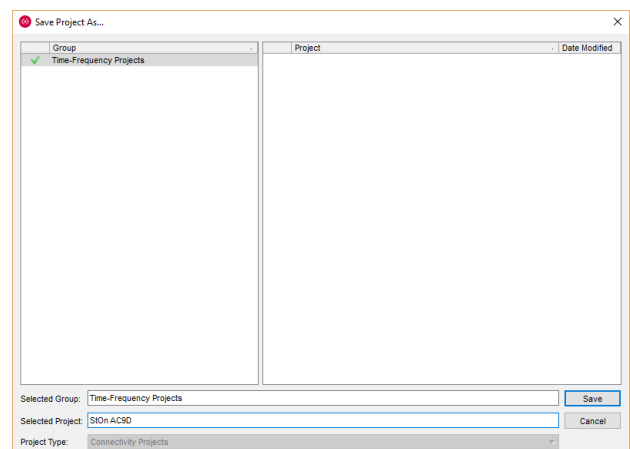
10. Select Granger Causality in the **Selected Connectivity Methods** drop-down box. Granger Causality is rather insensitive to noisy signals and will provide stable and reliable results even for poor signal-to-noise ratios. Furthermore, Granger Causality results show less spurious connectivity among all sources.

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11. Select **Show 3D Mode** in the interaction window. The main window will switch to a 3D view of a transparent brain with all sources and arrows between connected sources. Select a current latency of 600ms and current frequency of 25 Hz to visualize the Granger Causality for the simulated induced activity. To increase the size of the arrows, please use the **Scale** slider in the **Display Settings** sections. There is only one prominent arrow indicating the information flow from source ACSr (green dipole) to source ACSl (pink dipole).

12. Press **Finish** to end and save the current project. Save it under an appropriate name.



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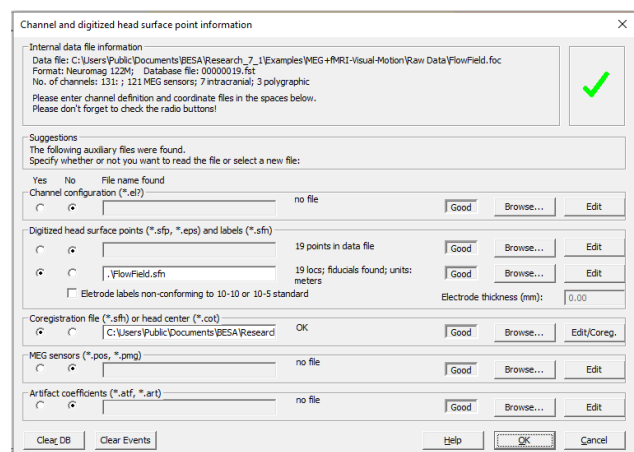
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G. Time-Frequency Analysis using an atlas beamformer virtual sensor montage

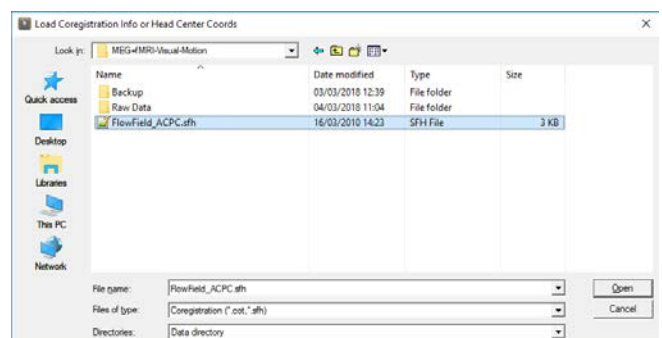
We will now move to a real data set. Since it is not always easy to come up with a robust and accurate dipolar source model, we can use the approach of atlas-based source montages instead. To improve sensor specificity, this can be combined with beamformers (cf. Hillebrand et al., NeuroImag 59:4, 3909-3921, 2012). Our data set is the previously used Visual Motion example.

We have already created an Atlas Beamformer source montage for this data set in Tutorial 9. We will now use this source montage to proceed further to time-frequency analysis.

1. In BESA Research, select **File / Open** and browse to the folder **./Examples/MEG+fMRI-Visual-Motion/Raw Data**. Open the data set **FlowField.foc**. If you had not opened it before, the **Channel and digitized head surface information** dialog appears. Otherwise, please press **CTRL-L** to open it.



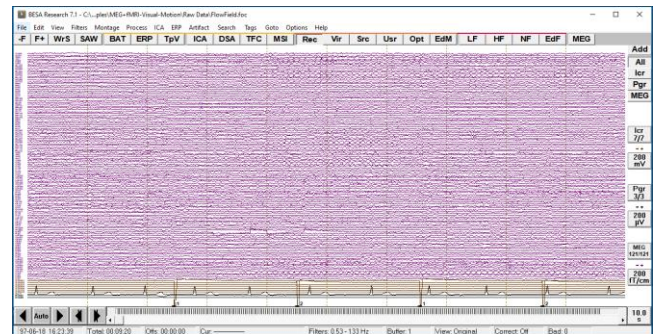
2. In the section **Coregistration**, click the **Browse** button. In the dialog that appears, go up one folder, and select file **FlowField_ACPC.sfh**.



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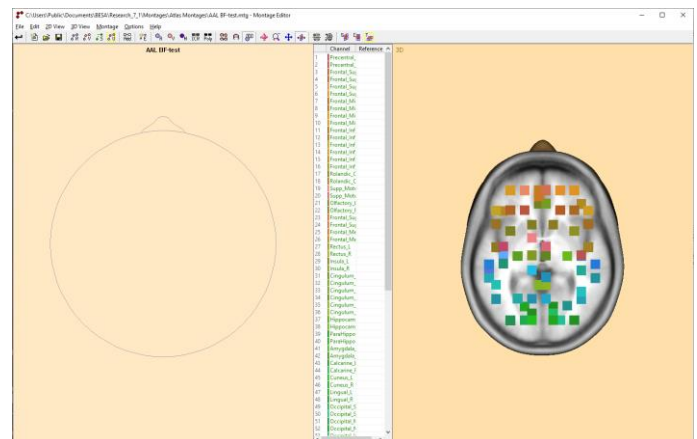
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

3. Press **OK** to close the **Channel and digitized head surface information** dialog. The file opens.


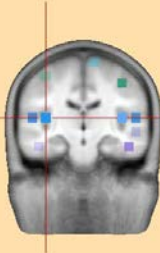





4. Click the **Usr** button and select the source montage **AAL_BF-test.mtg** that we saved in Tutorial 9 (if the montage is not there, then please go back to Tutorial 9 E and repeat the steps of this section).

5. We will now reduce the number of channels in the source montage to the ones that are relevant for visual processing. **Close** the Source Analysis window. In the Review window, press the **EDM** button. The Montage Editor opens.



Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

- | | Channel | Reference | Sag | Cor |
|----|----------------|-----------|--|--|
| 1 | Calcarine_L | |  |  |
| 2 | Calcarine_R | | | |
| 3 | Cuneus_L | | | |
| 4 | Cuneus_R | | | |
| 5 | Lingual_L | | | |
| 6 | Lingual_R | | | |
| 7 | Occipital_Su | | | |
| 8 | Occipital_Su | | | |
| 9 | Occipital_Ml | | | |
| 10 | Occipital_Ml | | | |
| 11 | Occipital_Inf | | | |
| 12 | Occipital_Inf | | | |
| 13 | Fusiform_L | | | |
| 14 | Fusiform_R | | | |
| 15 | Postcentral_L | | | |
| 16 | Postcentral_R | | | |
| 17 | Parietal_Sup | | | |
| 18 | Parietal_Sup | | | |
| 19 | Parietal_Inf_L | | | |
| 20 | Parietal_Inf_L | | | |
| 21 | SuperMarger | | | |
| 22 | SuperMarger | | | |
| 23 | Angular_L | | | |
| 24 | Angular_R | | | |
| 25 | Precuneus_L | | | |
| 26 | Precuneus_R | | | |
| 27 | Paracentral_L | | | |
| 28 | Paracentral_R | | | |
| 29 | Heschl_L | | | |
| 30 | Heschl_R | | | |
| 31 | Temporal_Sc | | | |
| 32 | Temporal_Sc | | | |
| 33 | Temporal_Pt | | | |
| 34 | Temporal_Pt | | | |
| 35 | Temporal_M | | | |
| 36 | Temporal_M | | | |
| 37 | Temporal_Po | | | |
| 38 | Temporal_Po | | | |
| 39 | Temporal_In | | | |
| 40 | Temporal_In | | | |
| | | | A | P R |
| | | | 3D | Tra |
| | | |  |  |
| | | | | |
| | | | R | L |

- 

-

Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

- Press the **ERP** button. Go to the **Epoch** tab and select condition **Motion**. Since connectivity analysis is quite time-consuming, we will shorten the interval for this tutorial: In the boxes for the Averaging Epoch, enter **-100 ... 400 ms**. Then press the button **Assign to Selected**.

Paradigm

Trigger	Condition	Epoch	Filter	Artifact	Average	Coherence
		Averaging Epoch	Baseline Definition	Artifact Rejection	Stimulus Artifact	Delay
Start Position		-100 ms	-100.0 ms	-100.0 ms	0.0 ms	0.0 ms
End Position		400 ms	0.0 ms	400.0 ms	0.0 ms	ms

Assign to All Assign to Selected Undo Changes

Condition	Averaging Epoch	Baseline Definition	Artifact Rejection	Stimulus Artifact	Delay
Motion	-100..400 ms	-100..0 ms	-100..400 ms	0..0 ms	0 ms
Static	-400..800 ms	-100..0 ms	-400..800 ms	0..0 ms	0 ms

File Load Save As

OK Cancel Help

- Go to the **Artifact** tab and re-run the artifact scan. Then move to the **Coherence** tab, and select the condition **Motion** as the target condition. Also, select **All Traces** in the Regional Sources section. Then press the **Start Connectivity** button.

Paradigm

Important note: Time-Frequency Analysis is for research use only. Results may not be used for diagnostic purposes!

☒ Time Frequency Analysis Target Condition: Motion ☐ Use Control Condition: Static

Settings

Frequency and Time Sampling: 2.0 Hz, 25 ms

Lower Frequency Cutoff: 4.0 Hz

Higher Frequency Cutoff: 60.0 Hz

Regional Sources

☐ Radial Orientation ☒ All Traces ☐ First Orientation

Scan for Artifacts Start Connectivity Start Time-Frequency Analysis

OK Cancel Help

- In BESA Connectivity, select Wavelet transform and un-select Complex demodulation. Press Next.

Select Time-Frequency Method

☐ Complex Demodulation ☒ Wavelet Transform ☒ Wavelet Morlet ☐ Wavelet Mexican Hat

Define Number of Conditions

Number of Conditions: 1

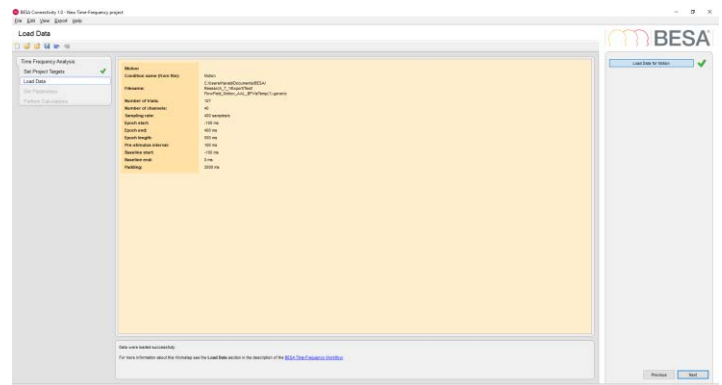
Define Condition Names

Condition 1: Motion

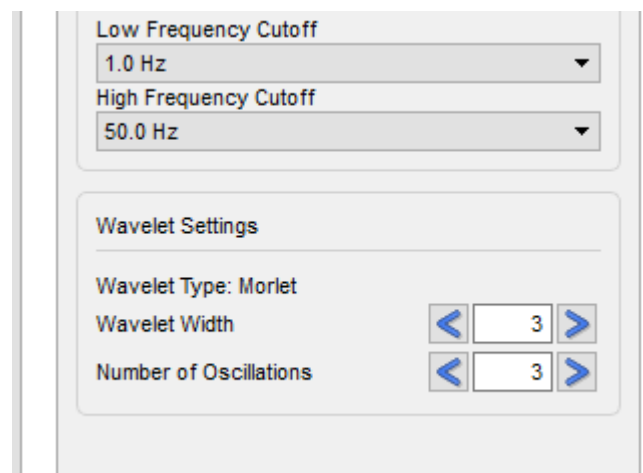
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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

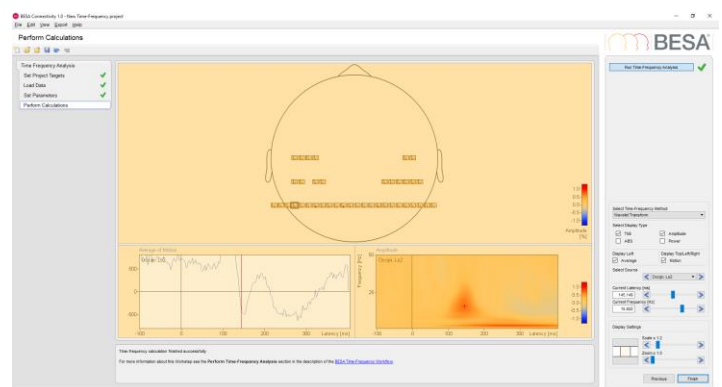
12. Press the **Enter** key twice to walk through the next steps until the data set is loaded.



13. Press **Next** again. In the settings for the wavelet transformation, use 3 oscillations, and then an interval of 1Hz – 50 Hz.



14. Press **Next** and then run the Time-Frequency analysis. Then cycle through the channels using the **left-right arrows** in the section **Select source**. There is some beta band synchronization in the lateralized occipital regions.

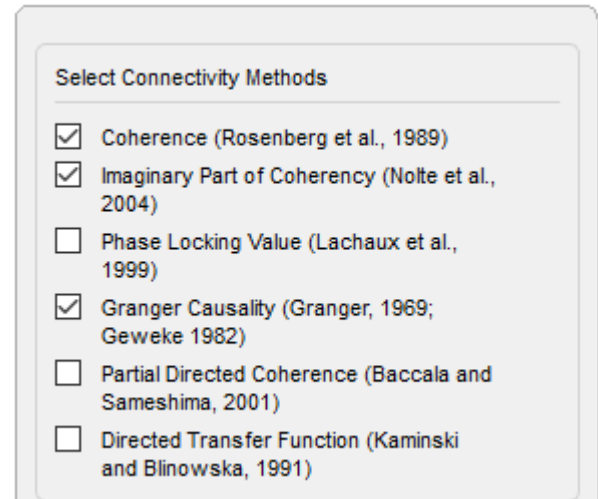


15. Click the **Finish** button and save the project to a new folder (e.g. folder name **Visual**, project name **Motion-AAL_BF-wvlt_1-50Hz**).

H. Connectivity analysis using atlas-based beamformer virtual sensors

Now let us analyze connectivity using this time-frequency decomposition in source space.

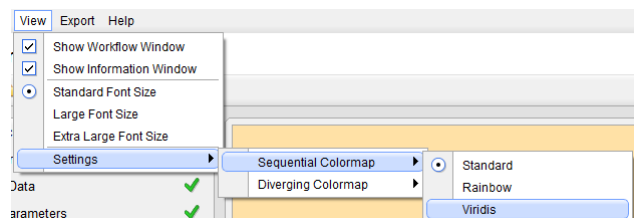
1. In BESA Connectivity, start a Connectivity workflow. In the work step Set Project Targets, check three methods: Coherence, Imaginary Part of Coherency, and Granger Causality. Then press **Next**.



2. Pressing Enter three times will load the previous data set that we just saved. Press **Next** (or Enter) again to show the previous time-frequency result, and the non-parametric method settings. We will not change the settings. Press Next again and then start the computation of the Connectivity analysis. This will take some time.



3. The display now shows a large matrix, with 20 channels having two orientations each. There is a large amount of coherence, but some of it will be due to noise modelling artifacts in the inverse processing. Check the **Hide Diagonal** check box to get a better orientation in the matrix. In the View menu,

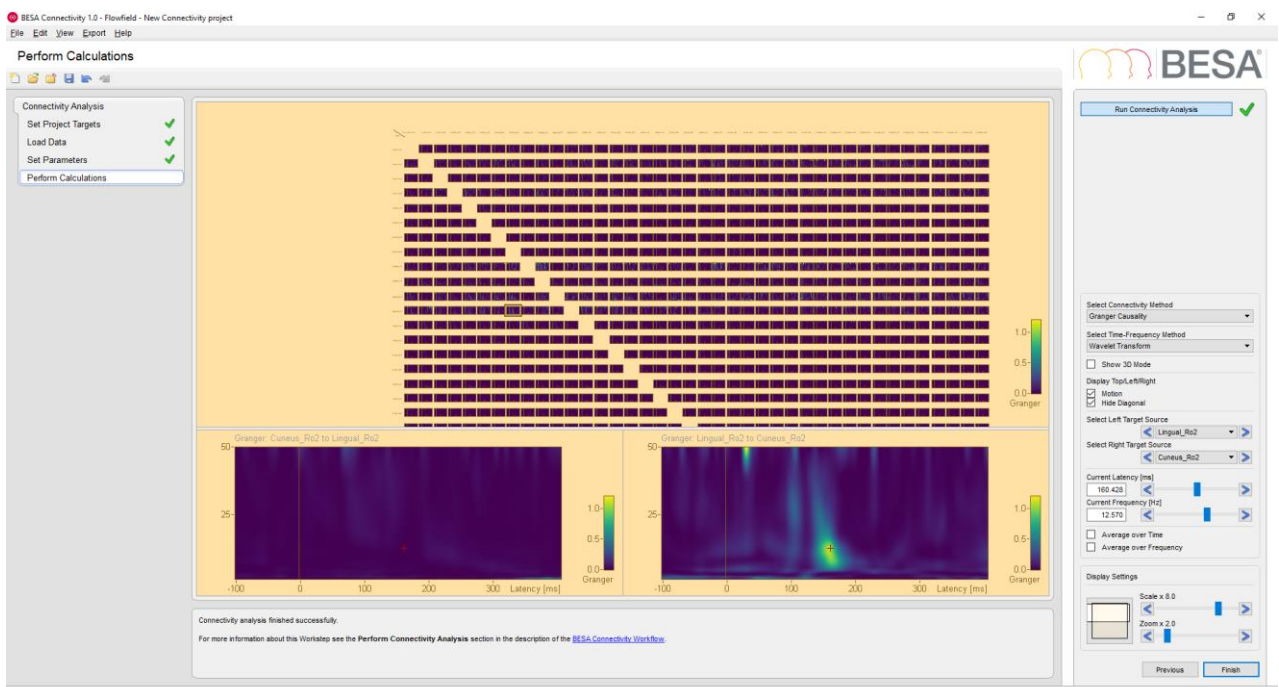
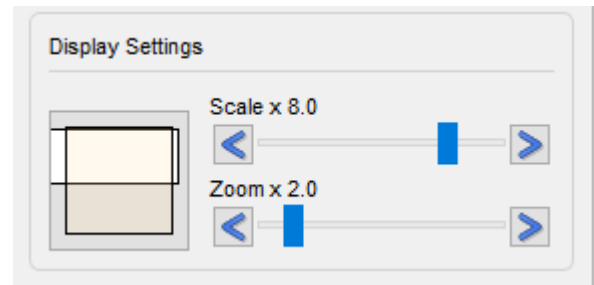


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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

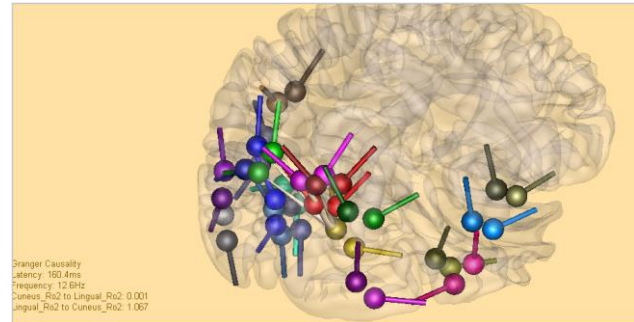
open Settings, then Sequential Colormap and select the map Viridis.

4. Switch to the Connectivity Method Granger Causality, and scale up to a factor of 8. Zoom the display to a factor of 2. Then drag the sliding rectangle beside the zoom control so that you can see the top rows. In the 12th row, select the 8th column. This will bring up the Granger Causality between Lingual R (orientation 2) and Cuneus R (orientation 2).

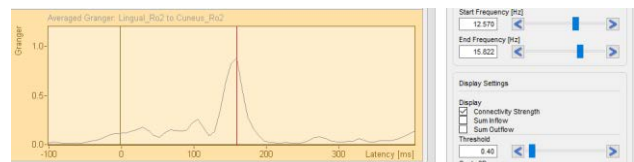


Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

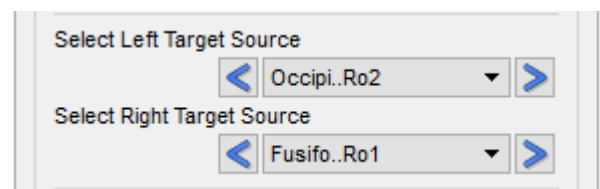
- Click onto the peak at about 160 ms, and 12.5 Hz. Then check Show 3D mode. This will show that the lingual area passes information to surrounding areas at this time and frequency.



- Check Average over Frequency and set an interval of approximately 12Hz-15Hz. You can see that in this interval, the peak information transfer from the lingual area is at around 150 ms.



- Adjust the threshold to 0.3 and change latencies. It becomes apparent that there is also connectivity between temporal areas and occipital areas. You can hover over any channel in the 3D plot to see the channel label, and then change the channel in the target source plot.



8. Also, check the Imaginary Part of Coherency - this shows different connections, which are strongest for lower frequencies. But when looking at Coherence, the rise in connectivity between Lingual R (orientation 2) and Cuneus R (orientation 2) is also visible, if somewhat less pronounced compared to Granger Causality. Press the Finish button to save the project, and close BESA Connectivity.



In summary, Atlas-based beamformer virtual sensor montages are a potential solution if no clear source model is available for the conditions. In MEG in particular, beamforming provides a reliable estimate of activity at a location of interest; the beamformer spatial filter successfully suppresses activity from other locations.

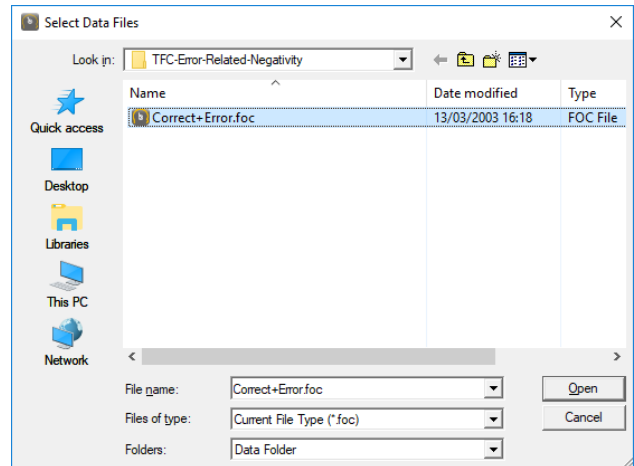
I. Optional - Time-Frequency Analysis with Error-Related-Negativity Data

We will now move to a real data set of an experiment on error-related negativity. It consists of a 128-channel EEG recording where bilateral visual stimuli were presented to the subject with a specific discrimination task. The subject was supposed to respond with a mouse click as fast as possible. Right and left hand response trials were mixed to obtain a large number of ERN trials (cf. Luu P, Tucker DM. Clin. Neurophysiol. 2001, 112:1295-1306).

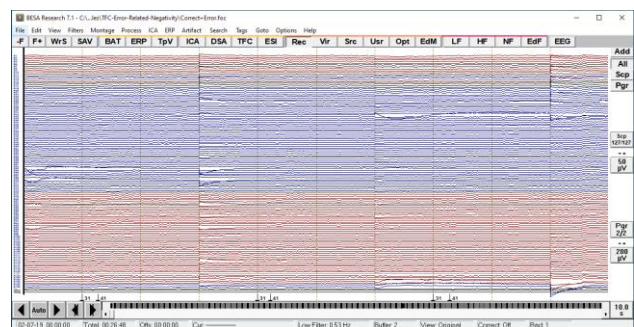
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Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

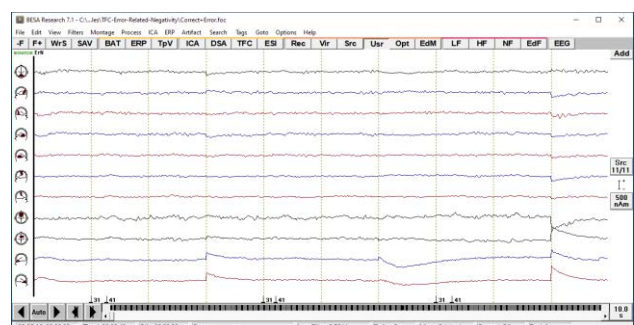
9. Go back to BESA Research and open the data set **Correct+Error.foc** in subfolder TFC-Error-Related-Negativity of the Examples folder. This data set was converted from concatenated ASCII segments with intervals of 1s before and 2s after each visual stimulus.



10. The first block of the file contains correct responses (stimulus trigger 31, response trigger 41), the second block the erroneous responses (triggers 32 and 42). If you don't see these trigger numbers, then go to **Options/Display** and switch off **Show Internal Trigger Names Instead of Codes**. The concatenation of different segments without segment markers causes jumps and trailing artifacts from the boundaries when filtering the data. We will adjust this filter in the paradigm definition.



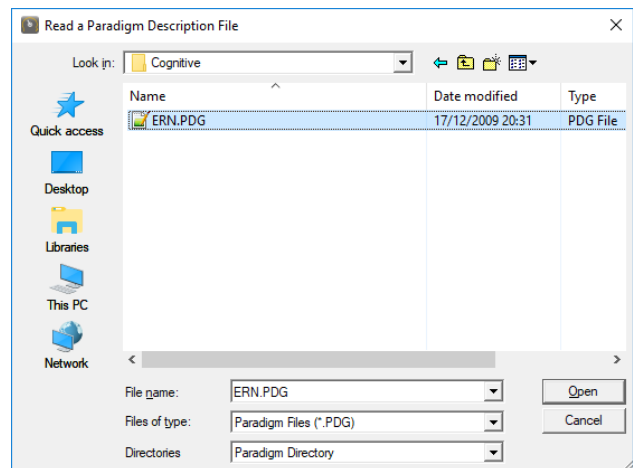
11. Press the **Utr** button in the control ribbon and select the source montage **ErN**. Data are transformed to 11 sources, which model the following brain areas:
 - Visual cortex (Vi) – 3 sources
 - Basal temporal lobes (Tb) - 2 sources
 - Motor cortices (MC) – 2 sources



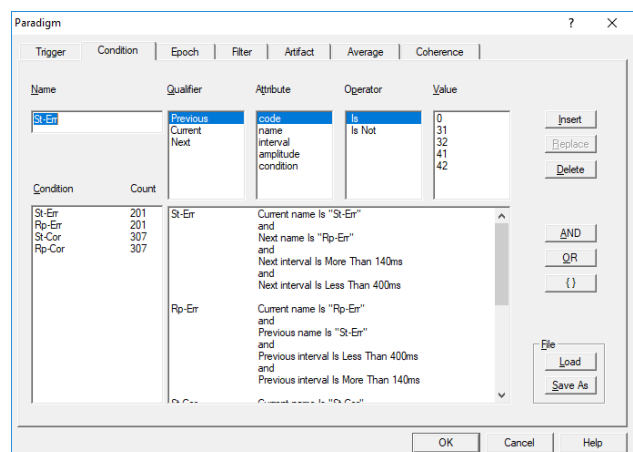
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

- Cingulate gyrus (Cg) – 2 sources
- In addition, two dipoles were modeled in the left and right eye to account for blink artifacts in the data.

12. Select **ERP/ Open Paradigm** and open the predefined paradigm definition file **Cognitive\ERN.pdg**. This will open the Condition tab of the ERP menu.

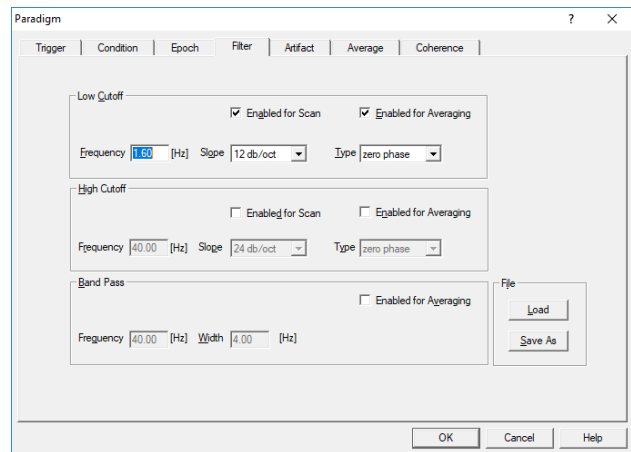


13. The Condition tab shows four predefined conditions: correct and erroneous responses (Rp-Cor & Rp-Err, mouse clicks), and the preceding visual stimuli (St-Cor & St-Err). By appropriate logical expressions, contingent stimuli and responses have been selected which have a reaction time window of 140 to 400 ms. 201 error trials and 307 correct trials fulfill these conditions.

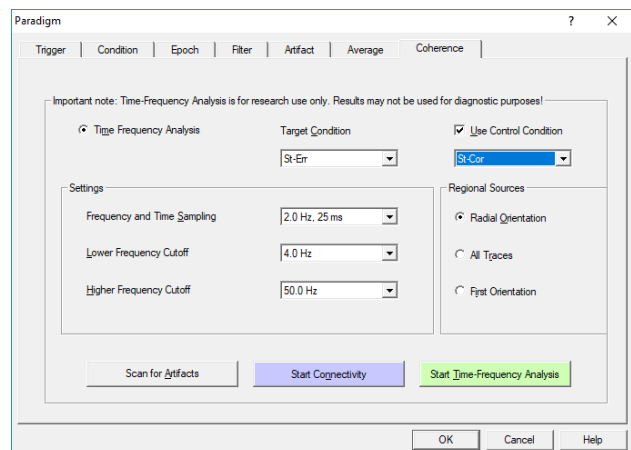


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14. Go to the **Filter** tab. The slow background activity and these artifacts can be sufficiently reduced by switching on a zero phase low-cutoff filter of 1.6 Hz. As we are interested in activity > 4 Hz, the slow frequency artifacts will not cause a problem in downstream analysis.



15. Switch to the 'Coherence' tab. In the 'Condition' drop down menu, select St-Err if not yet preset. Check the box for **Use Control Condition** and select **St-Corr** for this condition. Thus, we will analyse the correct responses as well as the erroneous responses. Press the **Start Connectivity** button.

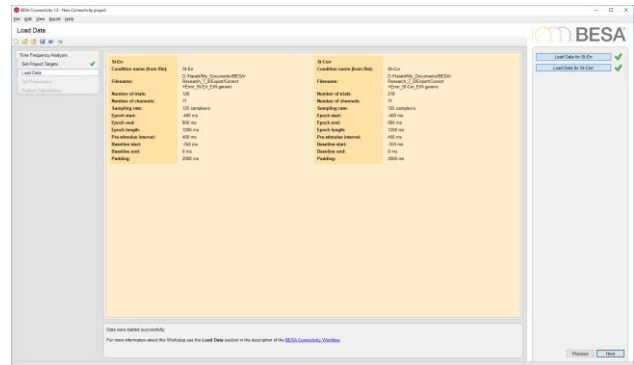


16. BESA Connectivity starts if not already open, and automatically launches the Time-Frequency workflow. Check the boxes for Complex Demodulation and Wavelet (Morlet) and define the condition names St-Err and St-Corr. Then press **Next**.



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- 17.** Now load the data for St-Err (filename **Correct+Error_St-Err_ErN.generic**) and St-Corr (filename **Correct+Error_St-Cor_ErN.generic**). The information for both data sets is shown.

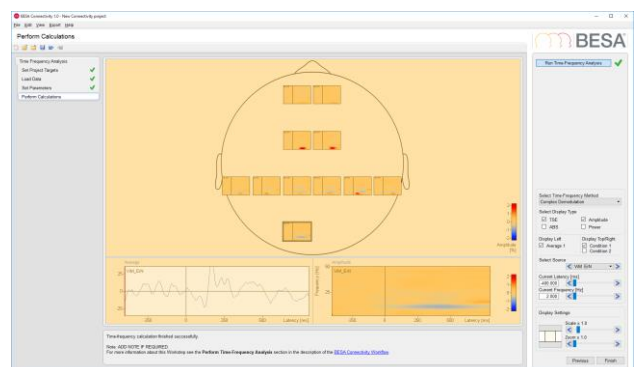


18. Condition 1 data is shown. Adjust the high frequency cutoff to 50 Hz to remove effects of the mains frequency at 60 Hz. Change number of oscillations to 5.

Note: You can click into the Selected Trials field and view individual trials. If you select a trial in the lower half of the display, and then click one below the current trial, you can quickly toggle through all without having to adjust the mouse position. No major artifacts can be seen as we have removed them from analysis.

Press **Next**.

- 19.** Run time-frequency analysis. The TSE display of the first condition (error condition) is shown.



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- 20.** Scale up the display to 1.5. You can notice the strong desynchronization in the visual cortex. Select channel CgP. This has the largest ERN amplitude at low frequencies.



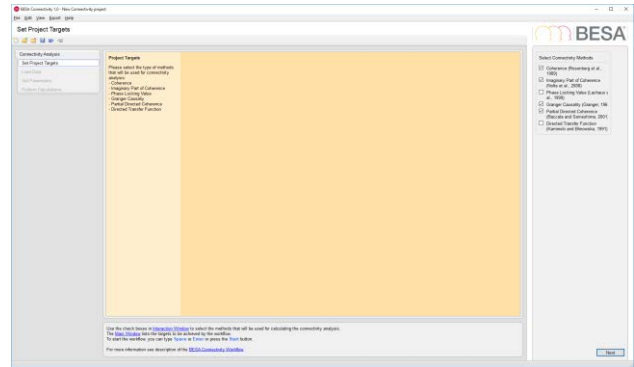
- 21.** Switch condition. The ERN is much less pronounced in the correct response condition. Switch from Complex Demodulation to Wavelet and select channel MCR (right motor cortex). There is synchronization at 6.5 Hz, and a desynchronization at 11-12 Hz. A similar pattern is found in the right visual cortex channel ViR.



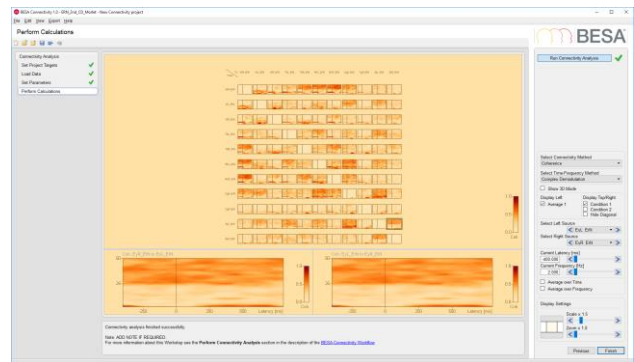
- 22.** Press the **Finish** button and save the project: Create a group ERN and save the project under the name **ERN_2cnd_CD_Morlet**

J. Optional - Connectivity Analysis with Error-Related-Negativity Data

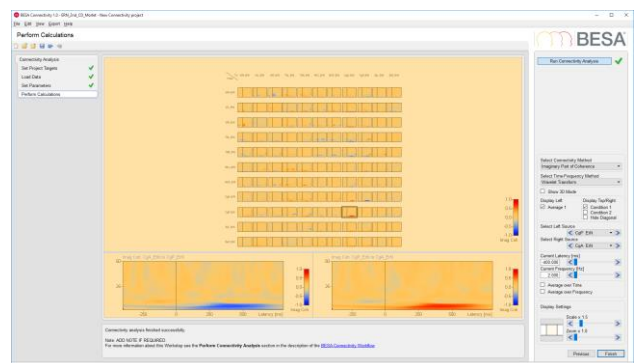
1. Start the Connectivity workflow. Select the following connectivity methods: Coherence, Imaginary Part of Coherency, Granger Causality, Partial Directed Coherence. Press **Next**.



2. In the next work step, select the project **ERN_2cnd_CD_Morlet** that you stored a minute ago (it should be automatically suggested). It will display the TSE display of the first condition (error condition) again. Press **Next** and then run the calculation with the default parameters. After finishing the calculations, it will show the matrix plot for coherence of the first condition, using complex demodulation. We can see a lot of pre-stimulus alpha-band coherence.



3. Switch to **Imaginary Part of Coherency**. Switch to **Wavelet transform**. Then click on the channel CgA to show its connectivity with CgP. There is a strong theta band coherence between these channels, from anterior to posterior cingulate. Double-click into the right display to set the cursor at the maximum around 5 Hz and 350 ms.

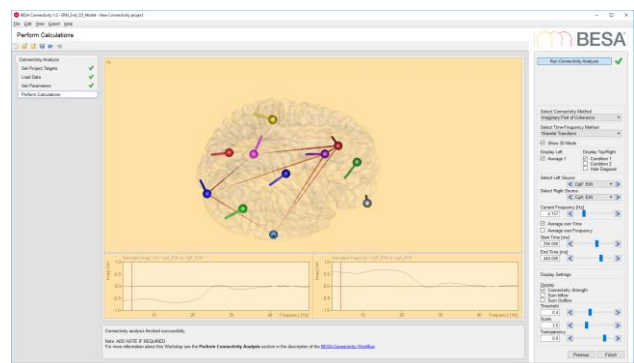


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4. Start the 3D mode by checking the **Show 3D Mode** box. Using the sliders at the bottom, change the threshold to 0.4, the scale to 3, and the transparency to 0.9. Adjust current latency and current frequency to 356 ms and 4.8 Hz. (Note that with wavelets, the frequency steps are non-linear – the resolution is finer for low frequencies than for higher ones.) You can see varying network associations when changing the latencies and frequencies, but a very strong coupling between the cingulate sources is predominant, as well as connections to the temporal and visual areas. Rotate the brain using left mouse drag; use Shift-Ctrl plus mouse drag to zoom the brain in or out.



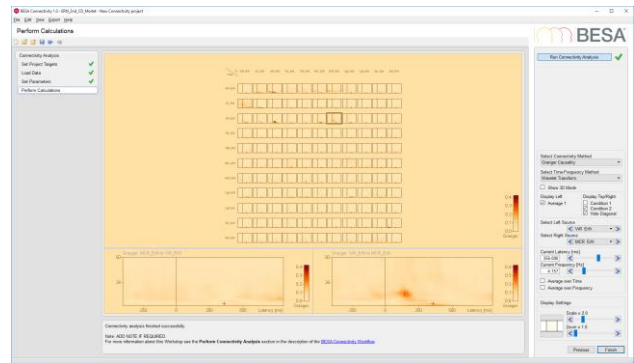
5. Now we want to average over the time interval of interest. Check the **Average over Time** box. Two new sliders appear. Adjust the time interval for averaging from 296 ms to 440 ms. Now, for 4.1 Hz, the network shows very clearly the connectivity between cingulate, temporal, and visual areas. The motor cortices are not involved at these frequencies.



6. Switch to Condition 2. For this condition with correct responses, only very little cingulate coupling is visible.



7. Un-check the **Show 3D Mode** and the **Average over Time** boxes again. Then change Connectivity Method to Granger Causality. Peaks are less prominent now. Scale up to 2.0, and check the box Hide Diagonal to hide the auto-spectrum. There is some higher frequency coupling that now becomes apparent, but not in the cingulate areas. Select the channel ViR where it connects with MCR.



8. The selection window shows a peak from ViR to MCR at approximately 13-14 Hz around 150ms after the stimulus. Switch to condition 1 – interestingly, in the error condition, this connection is almost non-existent. Switch back to condition 2. Double-click on the peak in the right selection window, then switch on 3D mode to visualize this connection. Lower the threshold to 0.2 and scale up to 6.0. The Granger causality connection only shows this one link; also, the ViR area clearly

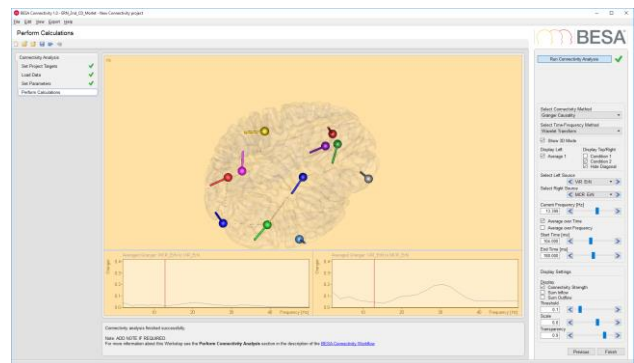


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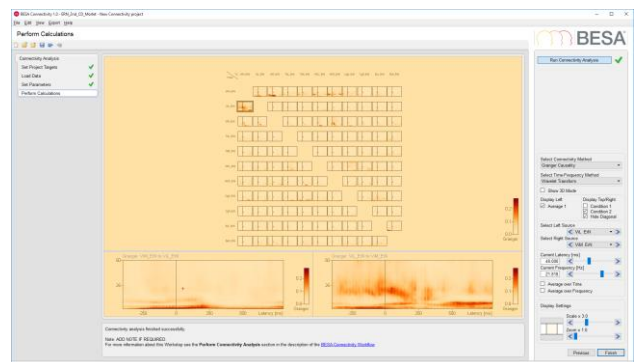
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drives the motor cortex (indicated by the cone that is wider at the ViR end).

- To summarize the activity in the time range where the Granger causality appears, check the box for Average over Time again, and select a time window of 104 to 188 ms. Lower the threshold to 0.1. Again, at 13.4 Hz, the connection from ViR to MCR is apparent, as is some coupling within the visual areas (ViR, ViM, ViL).



- Quit 3D mode again and click on the first channel in the second row to show Granger Causality between ViL and ViM. Scale up to 3.0. It is apparent that there is beta and low gamma band activity before and shortly after the stimulus, flowing from ViL to ViM.



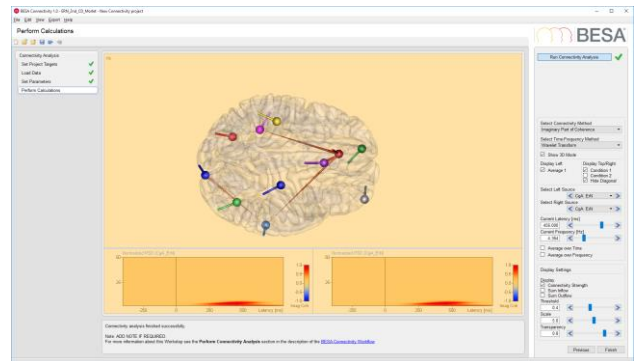
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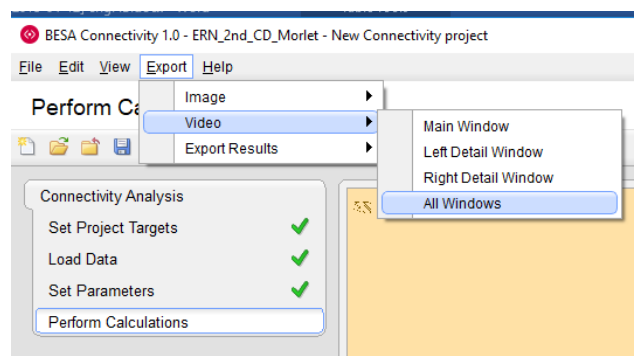
11. Switch back to condition 1. Again, the high frequent activity is less pronounced in this condition.



12. We now want to export the connectivity data for the error condition in a video. Change the method back to Imaginary Part of Coherency and enable the 3D Mode. Select a frequency of 4.1 Hz, set the threshold to 0.4, scale to 5.0, and transparency to 0.8.



13. From the menu, select **Export / Video / All Windows**.

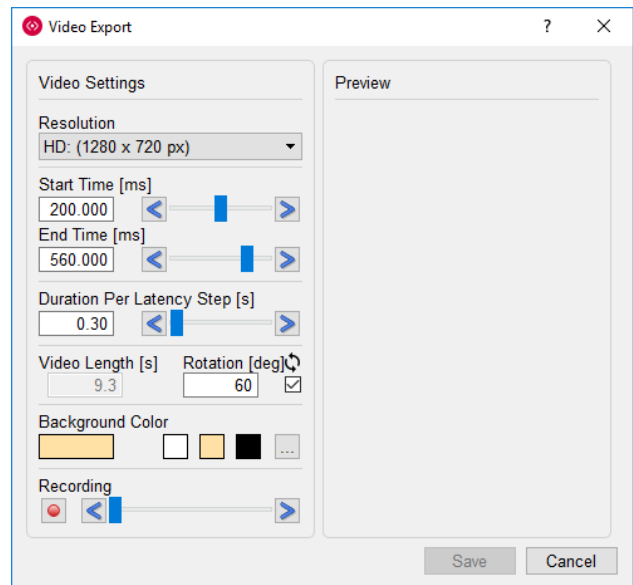


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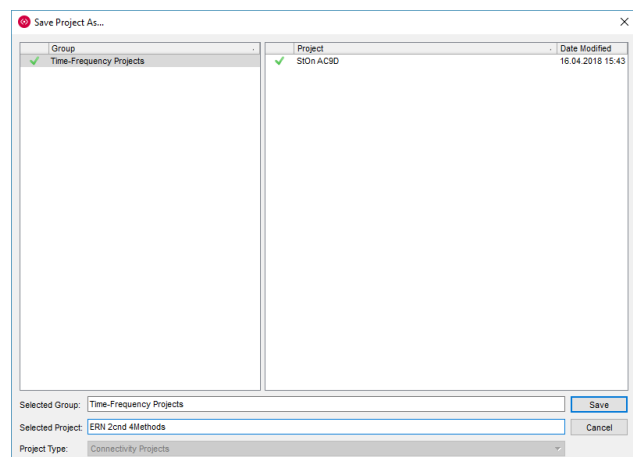
14. In the dialog, adjust parameters as follows:

Choose HD resolution and select a time interval for the recorded video from 56ms to 656ms. Decrease the duration per latency step to 0.3s.



15. Press the **Recording** button. Then press **Save** to store the video to a file on the desktop. Open the video to play in the Media player.

16. Back in BESA Connectivity, finish the project and save with the name **ERN_2cnd_4Methods**.

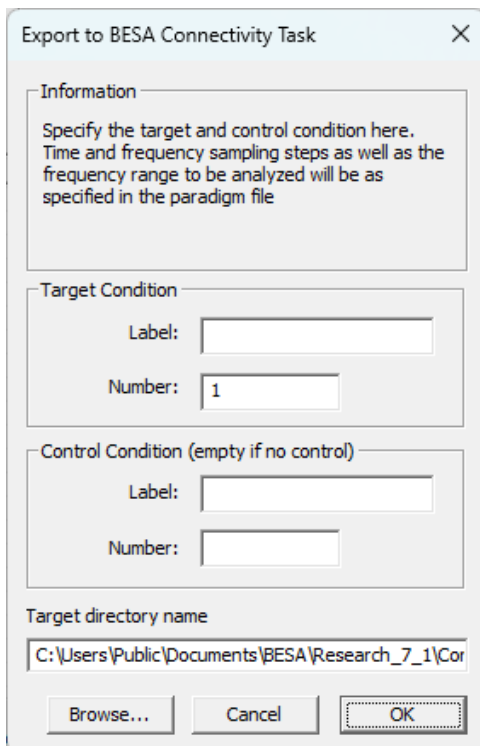


K. Multi-subject analysis in BESA Connectivity

In group studies, it is desirable to perform the same analysis on all subjects and conditions, and also to visualize the grand average. This is possible by selecting all relevant data at the beginning of the Time-Frequency workflow.

As a pre-requisite, the epoched raw data need to be prepared for all subjects and conditions. In BESA Research, this can be achieved in the following way:

1. Define the experimental paradigm and save it in the **/Paradigm** sub-folder.
2. Use the batch command **Paradigm** to load this paradigm (optionally, also add a batch command to run an artifact scan).
3. Use the batch command **ExportToBESAConnectivity** in BESA Research to export the conditions of choice. Enter the label of the condition as it is defined in the paradigm, or the number of the condition.



For this tutorial, we will work with the pre-defined example data set (Connectivity_GoNoGo). This data set is a sub-set of a publicly available Go-NoGo experiment data (<https://openneuro.org/datasets/ds002680/versions/1.2.0>). Electrode coordinates were added according to the original publication by Delorme et al. (*Cognitive Brain Research* 19, 103–113, 2004). In the animal categorization task that is analyzed here, participants were shown

Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

a set of 100 pictures in each run, of which 50% contained animals. They had to respond by lifting a finger from a button whenever there was an animal in the picture.

A source montage was created in order to extract activity in the brain areas of interest. First, two symmetric dipoles were fitted to the main activation of the grand average data. This was then augmented by the source montage of the Fronto-Parietal Task Network. Finally, two dipoles were added to account for the eye fields.

1. In BESA Connectivity, start the **Time-Frequency workflow**.

Select the following time-frequency methods: **Wavelet**, **Multitaper**. De-select **Complex Demodulation**. Set **Number of Conditions** to 2. Name the conditions **Target** and **Distractor**. Press **Next**.

Select Time-Frequency Method

☐ Complex Demodulation

☒ Wavelet Transform

☒ Wavelet Morlet

☐ Wavelet Mexican Hat

☒ Multitaper

Define Number of Conditions

Number of Conditions: 2

Define Condition Names

Condition 1: Target

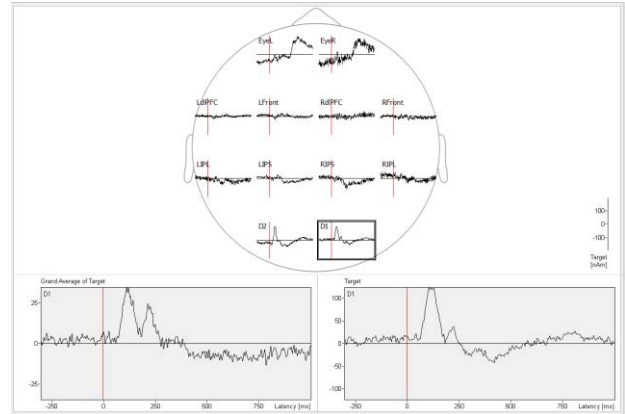
Condition 2: Distractor

2. In the next work step, click the button **Load Data for Target**. Browse to the folder into which you unzipped the Connectivity Examples, and then into the sub-folder **Target**. Drag the mouse pointer over the file names to select all, or press **CTRL-A** on your keyboard. Then press **Open**. Repeat this step for the **Distractor** sub-folder. All data are loaded, and the number of accepted trials for each subject and condition are shown. Note that the montage contains 12 (source) channels. Press **Next**.

Condition name	TargetCon	DistractorCon
Number of trials (per file)	12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12	12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12 / 12
Number of channels	12	12
Sampling rate	1000 samples	1000 samples
Epoch start	-300 ms	-300 ms
Epoch end	1000 ms	1000 ms
Epoch length	1300 ms	1300 ms
Pre-stimulus interval	300 ms	300 ms
Baseline start	-200 ms	-200 ms
Baseline end	-100 ms	-100 ms
Padding	2000 ms	2000 ms
Folder	C:\Users\hans\Documents\BESA_Research_7.1\Examples\Connectivity\TargetCon	C:\Users\hans\Documents\BESA_Research_7.1\Examples\Connectivity\DistractorCon
Files	sub-001_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-002_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-003_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-004_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-005_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-006_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-007_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-008_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-009_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-010_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-011_aveest1_run10_TargetCon_SMO_2075secCH2.meg sub-012_aveest1_run10_TargetCon_SMO_2075secCH2.meg	sub-001_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-002_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-003_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-004_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-005_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-006_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-007_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-008_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-009_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-010_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-011_aveest1_run10_DistractorCon_SMO_2075secCH2.meg sub-012_aveest1_run10_DistractorCon_SMO_2075secCH2.meg

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3. In the **Set Parameters** workstep, you see the Grand Average as well as subject averages for the channels. The channel set consists of two dipoles (D1 and D2) fitted to the visual response, two virtual eye channels that pick up eye activity, two channels for the dorsolateral prefrontal cortex, two for the frontal cortex, two in the Inferior parietal lobule, and two in the Intraparietal sulcus. For the latter 8 channels, radial orientations were used in the paradigm settings.

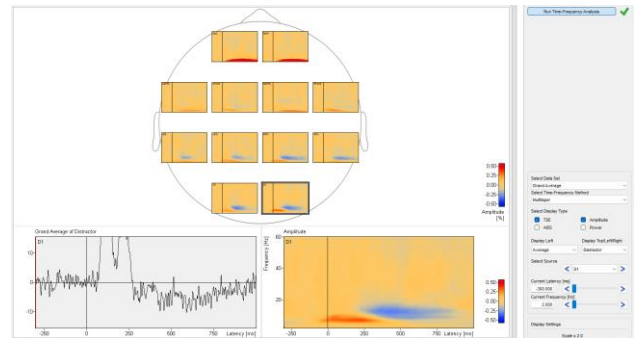


4. Toggle through the files using the list on the top right, and notice the variability in the data. Then adjust the parameters: Set **High Frequency Cutoff** to 60 Hz¹⁴, and **Number of Oscillations** to 4. Then press **Next**.

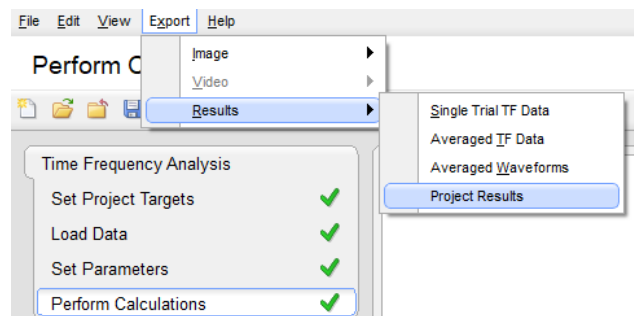
The figure shows the parameter settings for the analysis. The 'Low Frequency Cutoff' is set to 2.0 Hz. The 'High Frequency Cutoff' is set to 60.0 Hz. Under 'Wavelet Settings', the 'Wavelet Type' is set to Morlet, 'Wavelet Width' is set to 3, and 'Number of Oscillations' is set to 4. Under 'Multitaper Settings', the 'Frequency Smoothing' is set to 0.4.

¹⁴ Note that for wavelet and multitaper, the re-sampled time spacing and thus the memory allocation depends on the high cutoff frequency: For higher frequencies, better time resolution is possible with these methods, which in turn means higher (re-)sampling rates and higher memory needs.

- Run the time-frequency computation, which will most likely run for a few minutes. When the result appears, scale it up to 2. Toggle the displays between **Wavelet** and **Multitaper**, and between **Target** and **Distractor** conditions. For Multitaper, there is a clear difference between the two conditions in the de-synchronization at around 10 Hz following the stimulus.¹⁵ For both methods, a synchronization is visible at earlier latencies, and lower frequency around 7 Hz.



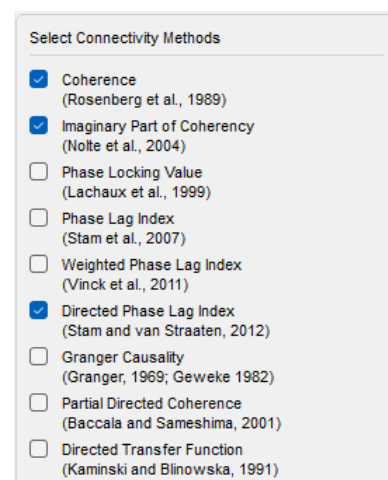
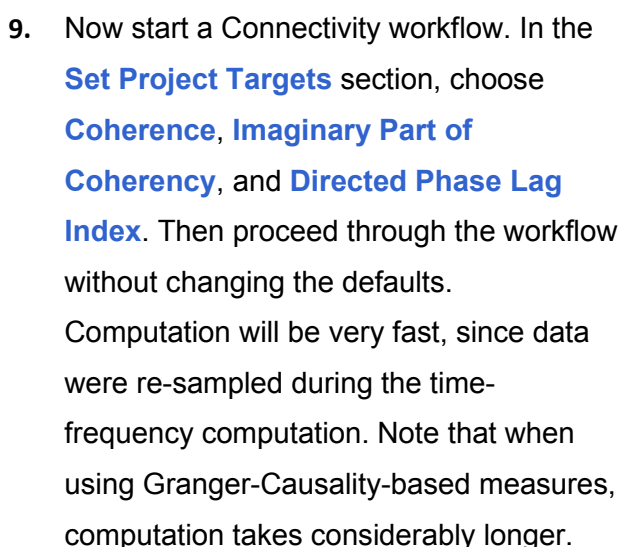
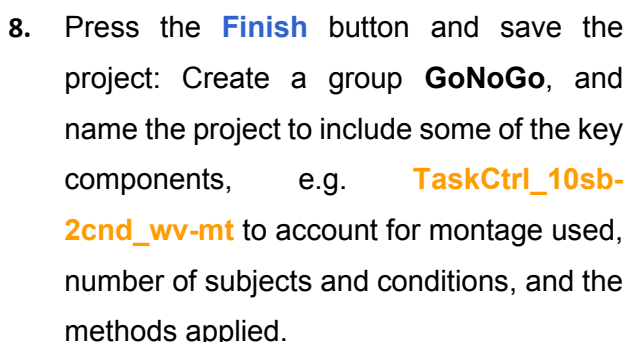
- With the display type set to **TSE** and **Amplitude**, use the menu **Export / Results / Project Results**. When the dialog comes up, create a new folder **GoNoGo**. Then press the button **Select Folder**. This will trigger the writing of the data.



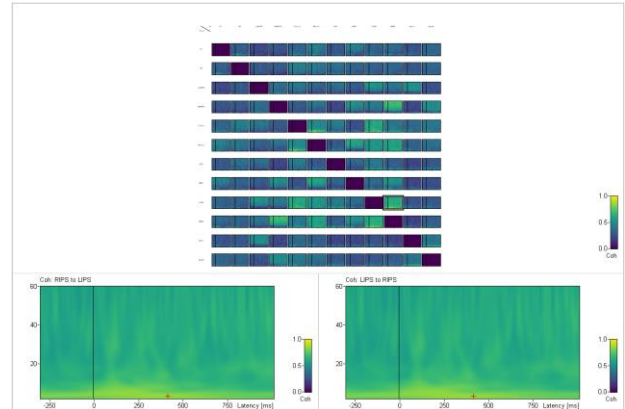
¹⁵ It turns out that when analyzing this further in BESA Statistics, this difference is significant at least for the RIPL channel.

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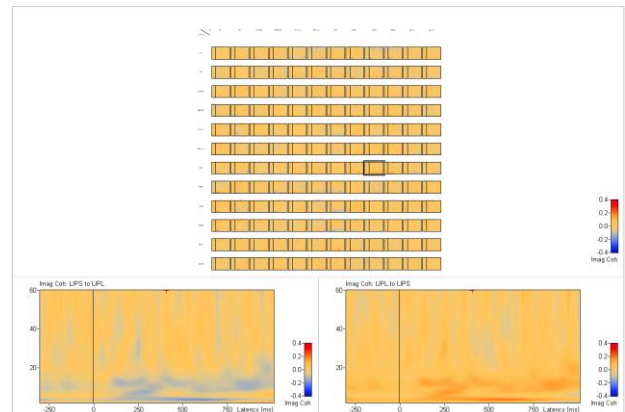
- /Documents/BESA/Research_7_1/Results** folder). You will see another folder inside it with today's date. Clicking on it will reveal sub-folders for the two methods, which in turn contain the conditions and finally the data. In each data folder, the source configuration is also present, in case that the data is read into BESA Statistics later.



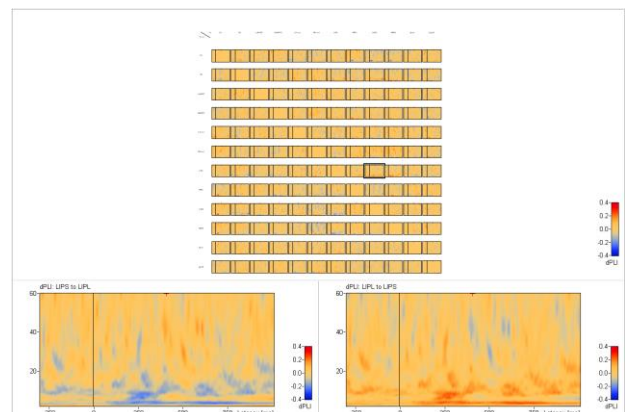
10. You may want to switch the color map to **Viridis** using the menu **View / Settings / Sequential Colormap**. In the Coherence display, there is considerable connectivity at high frequencies, which is most likely due to noise amplification by the spatial filtering.



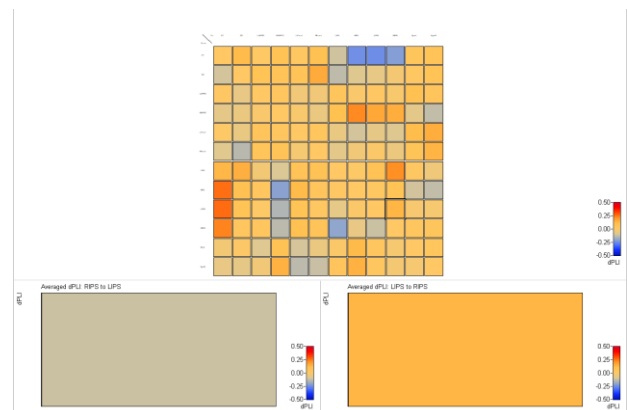
11. Change the connectivity method to **Imaginary Part of Coherency**. You will need to scale up to see some connectivity showing up now.



12. Change the method again to **Directed Phase Lag Index**. Now the pattern emerges a little bit clearer.

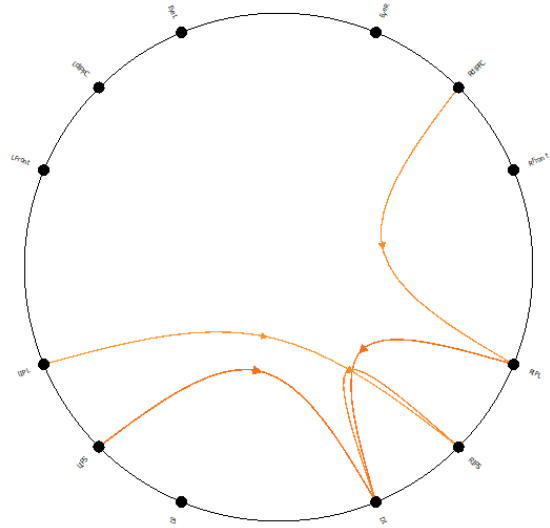


13. We will now focus on a particular window in the time-frequency range. You may remember that there was a relatively strong synchronization in some channels between 100–200 ms after stimulus, at around 7–8 Hz. We will now focus on this range. Check both boxes for **Average over Time** and **Average over Frequency**. Then, in the edit boxes that appear, double-click to mark the whole entries, and replace them with: Start Time 100, End Time 200, Start Frequency 7, End Frequency 8.
14. Scale the display up to 2.0. You now see a tile pattern, with just one time-frequency value per channel pair.

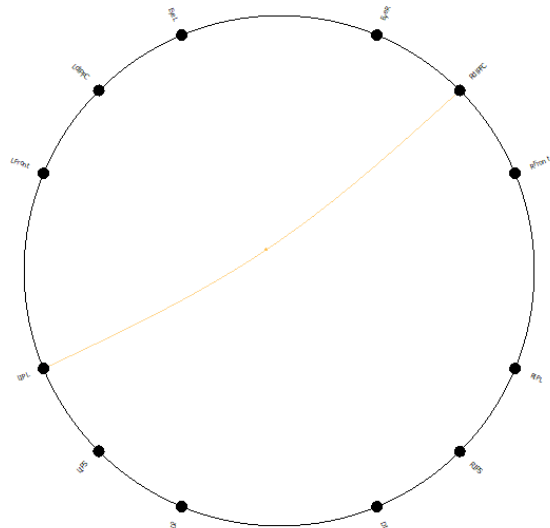


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15. Switch to **Circular Graph View**. A **Threshold** slider appears below. Set the threshold to 0.2. The graph view now shows the connectivities (and directions) with at least a value of 0.2. You can see that connectivity is strongest in the posterior channel network. Switch conditions to see the difference between Target and Distractor. Also, you may want to switch to 3D view to see the anatomical locations of the connections. Note that the threshold for the 3D view can be adjusted separately at the bottom right section.



16. Now we can also check on the de-synchronization pattern that we observed for the distractor. Change the time and frequency to 400–600 ms, and 10–15 Hz. Note that connectivity is much less pronounced for this case – you will need to lower the threshold to 0.1 to see any effect at all. So, apparently there is no connectivity between brain regions for this de-synchronization phenomenon.



17. This concludes our data exploration. Note that you also have the option here to export the whole project data with all methods applied, for later reading into BESA Statistics, using the menu **Export / Results / Project Results**. Press **Finish** to save and close the project.

L. Multiple Source Beamforming in time-frequency domain

In discrete multiple source analysis, the best source model (i.e. source amplitudes, locations and orientations) is one that minimizes a cost function (basically the residual variance).

Beamforming takes a different approach to image brain activity: Here, the whole brain is scanned point by point. The brain activity at each voxel is estimated by applying a spatial filter to the data. This spatial filter is designed to be fully sensitive to activity from the target voxel, while being as insensitive as possible to activity from other brain regions. This is achieved by constructing the spatial filter in an adaptive way, i.e. it takes into account the recorded data.

The BESA beamformer is a modified version of the linearly constrained minimum variance vector beamformer in the time-frequency domain as described in Gross et al., "Dynamic imaging of coherent sources: Studying neural interactions in the human brain", PNAS 98, 696-699, 2001. The beamformer operator is computed using the cross spectral density matrix (the time-frequency equivalent of the data covariance matrix) computed from the single-trial data. This allows to image evoked as well as induced oscillatory activity in a user-defined time-frequency range, where time is taken relative to a triggered event.

The output power $P(\mathbf{r})$ of the beamformer for a specific brain region at location \mathbf{r} is then computed by the following equation:

$$P(\mathbf{r}) = \text{tr}'[\mathbf{L}^T(\mathbf{r}) \cdot \mathbf{C}_r^{-1} \cdot \mathbf{L}(\mathbf{r})]^{-1}$$

Here, \mathbf{C}_r^{-1} is the inverse of the regularized cross spectral density matrix \mathbf{C} in the time-frequency range of interest; \mathbf{L} is the leadfield matrix of the model containing a regional source at target location \mathbf{r} and, optionally, additional sources, whose interference with the target source is to be minimized; $\text{tr}'[\]$ is the trace of the $[3 \times 3]$ (MEG: $[2 \times 2]$) submatrix of the bracketed expression that corresponds to the source at location \mathbf{r} .

In BESA Research, the output power $P(\mathbf{r})$ is normalized by the output power in a reference time-frequency interval $P_{\text{ref}}(\mathbf{r})$:

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$$q(\mathbf{r}) = \begin{cases} \sqrt{\frac{P(\mathbf{r})}{P_{\text{ref}}(\mathbf{r})}} - 1 = \sqrt{\frac{\text{tr}'[L^T(\mathbf{r}) \cdot C_r^{-1} \cdot L(\mathbf{r})]^{-1}}{\text{tr}'[L^T(\mathbf{r}) \cdot C_{\text{ref},r}^{-1} \cdot L(\mathbf{r})]^{-1}}} - 1 & \text{for } P(\mathbf{r}) \geq P_{\text{ref}}(\mathbf{r}) \\ 1 - \sqrt{\frac{P_{\text{ref}}(\mathbf{r})}{P(\mathbf{r})}} = 1 - \sqrt{\frac{\text{tr}'[L^T(\mathbf{r}) \cdot C_{\text{ref},r}^{-1} \cdot L(\mathbf{r})]^{-1}}{\text{tr}'[L^T(\mathbf{r}) \cdot C_r^{-1} \cdot L(\mathbf{r})]^{-1}}} & \text{for } P(\mathbf{r}) < P_{\text{ref}}(\mathbf{r}) \end{cases}$$

P_{ref} can be computed either from the corresponding frequency range in the baseline of the same condition (signal-to-noise ratio) or from the corresponding time-frequency range in a control condition. The beamformer image is constructed from values $q(\mathbf{r})$ computed for all locations on a specified grid.

Traditional single-source beamformers are known to mislocalize activity if several brain regions have highly correlated activity. The BESA beamformer tries to overcome this problem by extending the traditional single-source beamformer. The BESA beamformer can implicitly account for activity from possibly correlated brain regions. This is achieved by using a multiple source beamformer calculation that contains not only the leadfields of the source at the location of interest \mathbf{r} , but also those of possibly interfering sources. As a default, BESA Research uses a bilateral beamformer, where specifically contributions from the homologue source in the opposite hemisphere are taken into account (the matrix L thus being of dimension $N \times 6$ for EEG and $N \times 4$ for MEG, respectively, where N is the number of sensors). This allows for imaging of highly correlated bilateral activity in the two hemispheres that commonly occurs during processing of external stimuli.

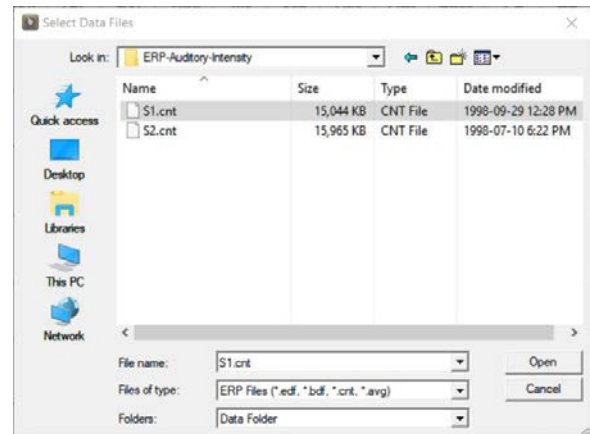
In addition, the beamformer computation can be performed taking into account possibly correlated sources at other specified locations by including them in the leadfield matrix L .

The following chapters illustrate the different properties and application examples of the BESA beamformer.

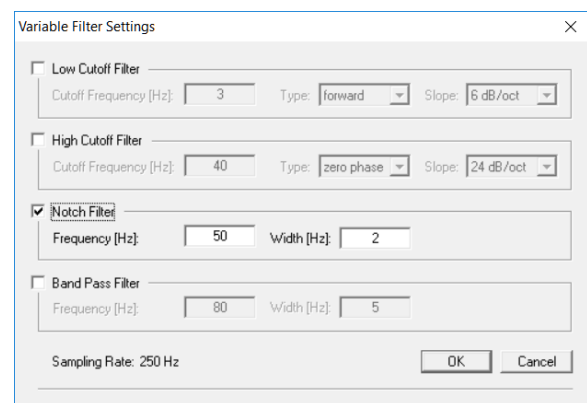
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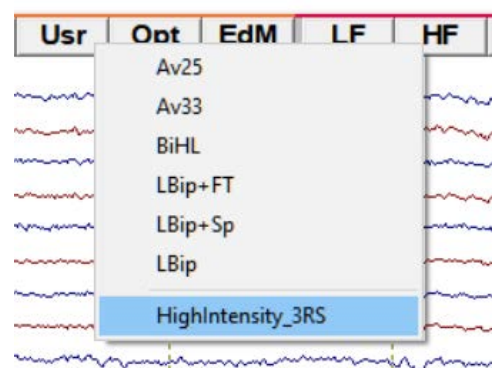
1. **Open** file **S1.cnt** in subfolder ERP-Auditory-Intensity of the Examples folders.



2. Press the **EdF** toolbar **button** to edit the filter settings. **Disable** all but the notch filter that should be set at 50 Hz to reduce mains interference.



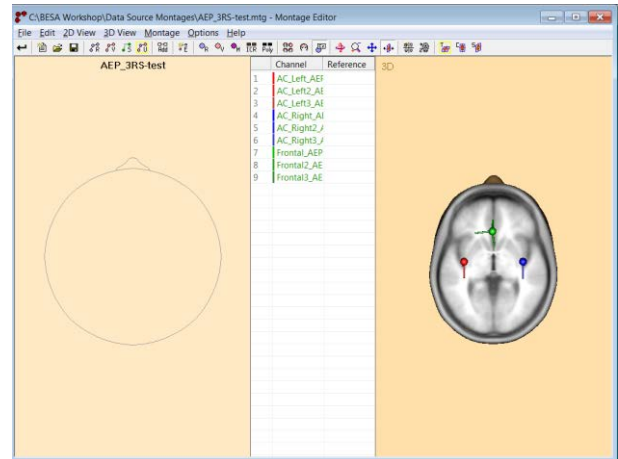
3. Press the **Usr** **button**. Select montage **HighIntensity_3RS-test** from the list of predefined user-montages that are available for this file. Press the **EdM** button to remind us of the details about the current montage again.



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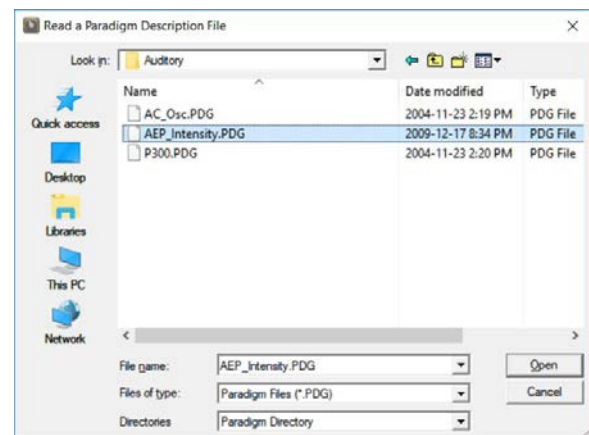
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- The montage consists of the sources we fitted earlier on: 2 auditory regional sources and a frontal source, which have been converted to single dipoles. **Close** the montage editor.

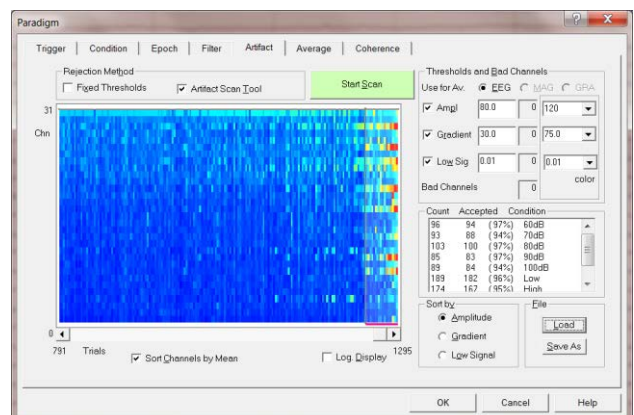


- In a first step, we will perform time-frequency analysis for all sources of the selected montage.

Press **ERP / Edit Paradigm**. The paradigm-file **AEP_Intensity.PDG** should still be available.

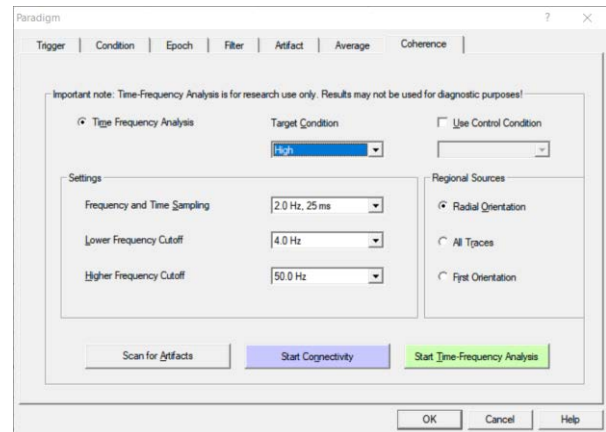


- Move to the **Artifact** tab and press **Start Scan** to re-run the automatic artifact scan with artifact correction switched on.

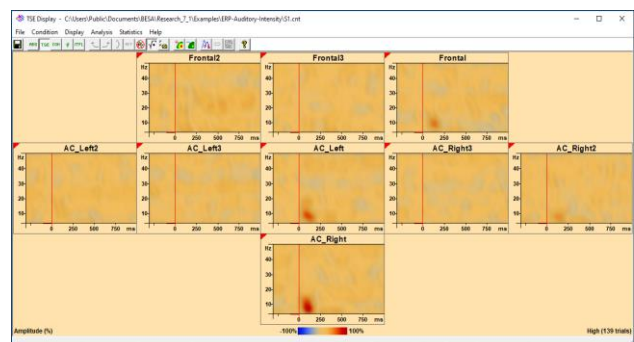


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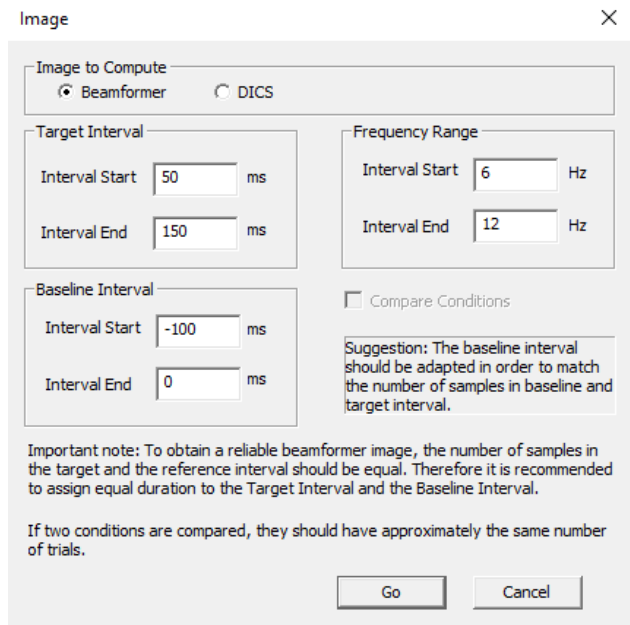
- Switch to the **Coherence** tab. In the **Target Condition** drop down menu, select condition **High**. To start time-frequency analysis with the default sampling of **2.0 Hz, 25 ms** in the frequency range of **4–50 Hz**, press the **Start Time-Frequency Analysis** button.



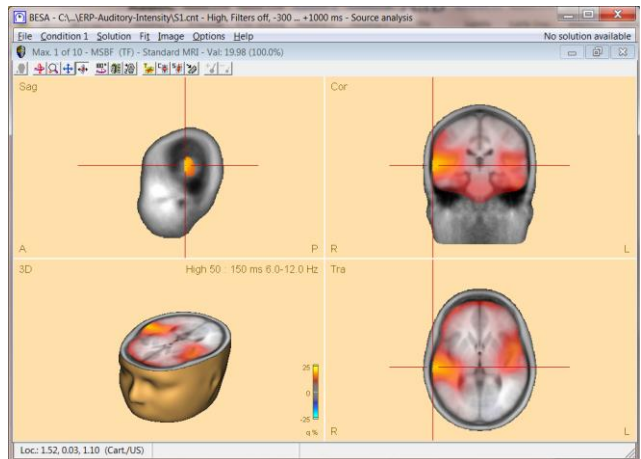
- After the calculations of the time-frequency decomposition is finished, the temporal-spectral evolution for all sources of the montage is displayed. The main activity in the first frontal and in the first and second auditory components are most prominent.



9. As a next step, we will fit the prominent activity in the **High** condition. **Left-drag** a window around the strongest activity in the left-hemispheric auditory source. When **releasing** the left mouse-button choose the option **Image**. If necessary, change the Target interval to **50 to 150 ms** and the Frequency Range to **6 to 12 Hz**. It is very important to choose approximately the same length between the Target and the Baseline interval ¹⁶. Otherwise, Beamforming results can be unstable. Press **Go**.



10. Scale up the image to **+/- 25%**. Use the **Max** button to view the different maxima. The first maximum localizes in the right auditory cortex, the second and third maxima indicate activity in bilateral frontal areas, while the fourth maximum shows activity in the left supra-temporal area. **Close** the source analysis window.

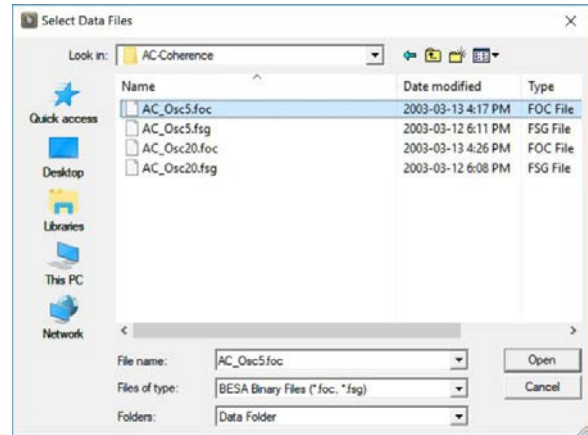


¹⁶ It is also possible to compute beamforming images of the difference between conditions. Tick the box 'Compare Conditions' for this purpose. Instead of using the baseline as reference interval, the same time-frequency range as specified in the target interval will be used in the control condition as a reference.

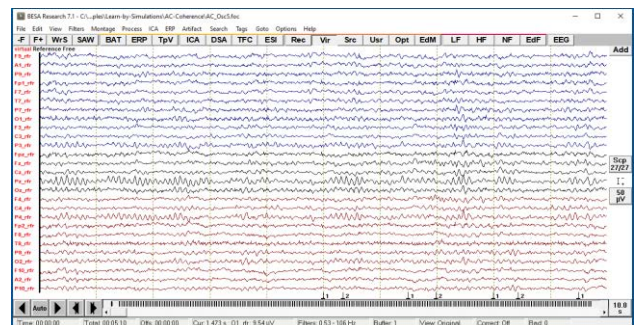
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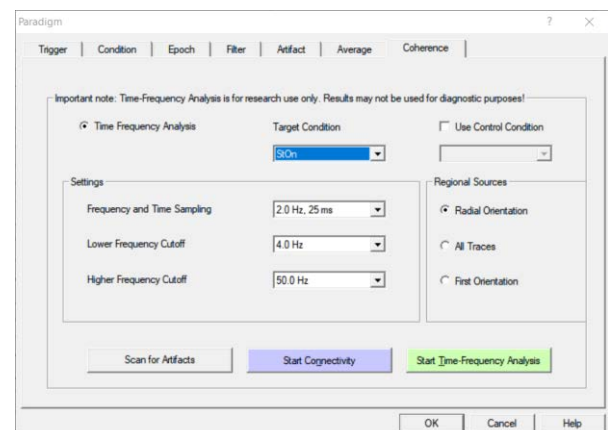
11. BESA Research uses a multiple source beamformer by default. It is also possible to choose a classic single-source beamformer. We will have a look at our model coherence data to see the difference between the multiple source and the single beamformer. Back in the **main window** open file **AC_Osc5.foc** which is located in the examples subfolder **Learn-by-Simulations**.



12. Change to the **virtual reference-free** display using the **Vir** button and selecting the top-most option.



13. Press **ERP / Coherence** to **Start Time-Frequency Analysis** of condition **StOn** using the default settings.

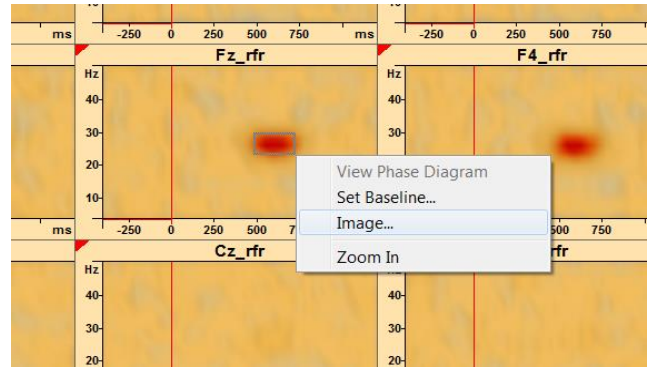


14. Subtract the evoked signal by pressing the



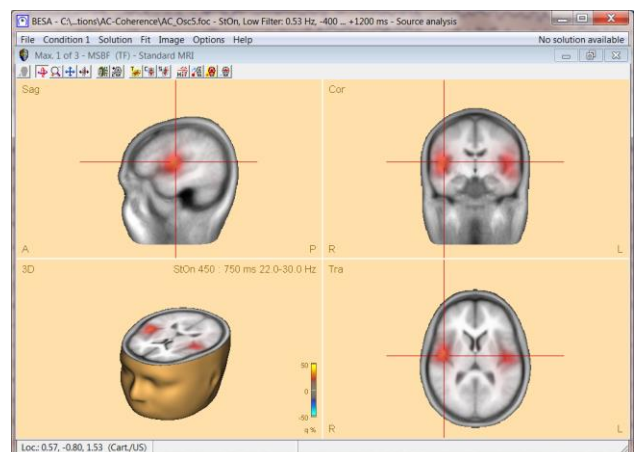
button and selecting **Subtract Average**

Signal. Now we only see the induced activity that is not present in the evoked potential. We want to fit this induced activity by marking a window around the most prominent activity.

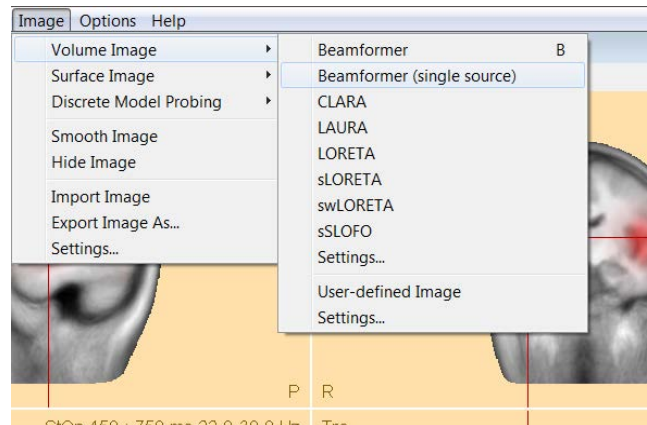


15. In the Image setting dialog box specify a time-range of **450 to 750 ms**, a baseline interval from **-300 to 0 ms** and a frequency range from **22 to 30 Hz**. Press **Go**.

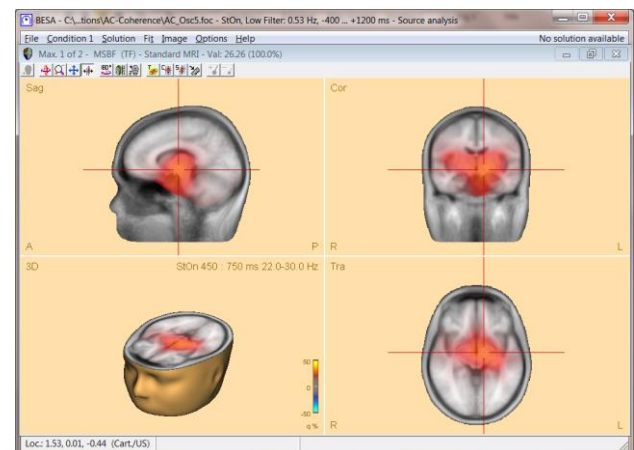
16. Scale up the image to **+/- 25%**. Observe the bilateral auditory activity. We know the maxima are at the correct location from the simulation.



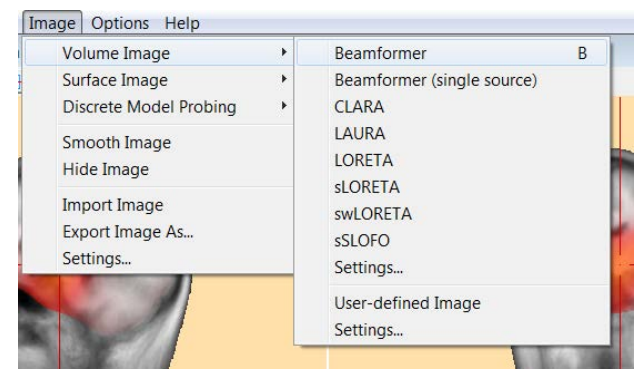
17. Change the type of beamformer by pressing **Image / Volume Image** and select **Beamformer (single source)**. The beamformer image is re-calculated.




18. The single source beamformer mis-localizes the bilateral auditory activity to the middle of the head. The reason is that single-source beamformers produces faulty results if activation in two brain regions is highly correlated.

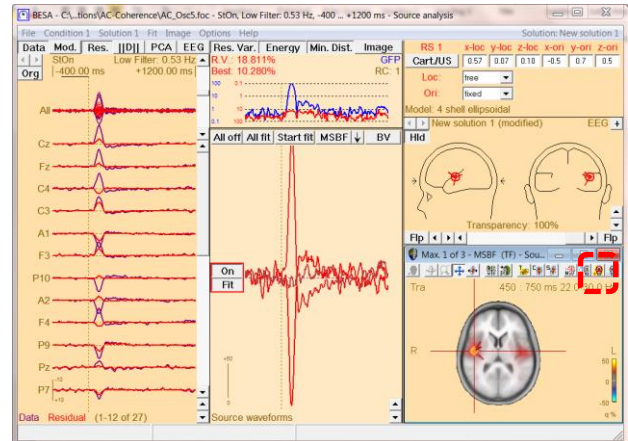


19. Return to the multiple source beamformer by pressing **Image / Volume Image / Beamformer**.

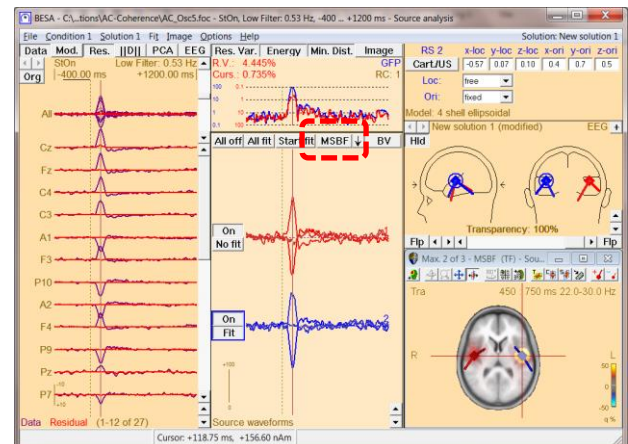


20. **Minimize** the MRI view by pressing the 

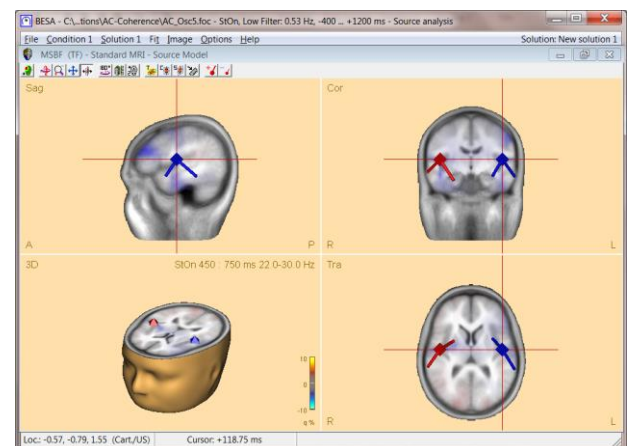
button in the top-right corner. We now want to use the beamformer image to seed dipoles. Select the first maximum and press the  button. Move to the next maximum and place another source.



21. We want to use the beamformer to see, whether there is still some unexplained activity if we model the auditory activity with two regional sources. Press **MSBF** to recompute the beamformer on the residual activity.



22. We need to scale up the image to **+/- 10%** to start seeing some patchy left-over desynchronization that is not modeled by the regional sources. This activity is very weak, so we can neglect it.



M. Dynamic Imaging of Coherent Sources (DICS) – a short introduction

Dynamic Imaging of Coherent Sources (DICS) is a sophisticated method for imaging cortico-cortical coherence in the brain or coherence between an external reference (e.g. EMG channel) and cortical structures. DICS can be applied to localize evoked as well as induced coherent cortical activity in a user-defined time-frequency range.

DICS was implemented in BESA Research closely following Gross et al., "Dynamic imaging of coherent sources: Studying neural interactions in the human brain", PNAS 98, 696-699, 2001.

The computation is based on a transformation of each channels single trial data from the time domain into the frequency domain. This transformation is performed by the BESA Research Coherence module and results in the complex spectral density matrix that is used for the construction of the spatial filter similar to beamforming.

DICS computation yields a 3-D image, each voxel being assigned a coherence value. Coherence values can be described as a **neural activity index** and do not have a unit. The neural activity index contrasts coherence in a target time-frequency bin with coherence of the same time-frequency bin in a baseline.

DICS for cortico-cortical coherence is computed as follows:

Let $L(r)$ be the lead field in voxel r in the brain and C the complex cross-spectral density matrix. The spatial filter $W(r)$ for the voxel r in the head is defined as follows:

$$W(r) = (L^T(r) \cdot C^{-1} \cdot L(r))^{-1} \cdot L^T(r) \cdot C^{-1}$$

The cross-spectrum between two locations (voxels) r_1 and r_2 in the head are calculated with the following equation:

$$C_s(r_1, r_2) = W(r_1) \cdot C \cdot W^{*T}(r_2)$$

where *T means the transposed complex conjugate of a matrix. The cross-spectral density can then be calculated from the cross spectrum as follows:

$$c_s(r_1, r_2) = \lambda_1\{C_s(r_1, r_2)\},$$

where $\lambda_1\{\}$ indicates the largest singular value of the cross spectrum. Once the cross spectral density is estimated, the connectivity¹⁷ (CON) between the two brain regions r_1 and r_2 are calculated as follows:

$$CON(r_1, r_2) = \frac{c_s^{sig}(r_1, r_2) - c_s^{bl}(r_1, r_2)}{c_s^{sig}(r_1, r_2) + c_s^{bl}(r_1, r_2)},$$

where c_s^{sig} is the cross-spectral density for the signal of interest between the two brain regions r_1 and r_2 , and c_s^{bl} is the corresponding cross spectral density for the baseline or the control condition, respectively. In the case DICS is computed with a cortical reference, r_1 is the reference region (voxel) and remains constant while r_2 scans all the grid points within the brain sequentially. In that way the connectivity between the reference brain region and all other brain regions is estimated. The value of $CON(r_1, r_2)$ falls in the interval [-1 1]. If the cross-spectral density for the baseline is 0 the connectivity value will be 1. If the cross-spectral density for the signal is 0 the connectivity value will be -1.

DICS for cortico-muscular coherence is computed as follows:

When using an external reference, the equation for coherence calculation is slightly different compared to the equation for cortico-cortical coherence. First of all, the cross-spectral density matrix is not only computed for the MEG/EEG channels, but the external reference channel is added. This resulting matrix is C_{all} . In this case, the cross-spectral density between the reference signal and all other MEG/EEG channels is called c_{ref} . It is only one column of C_{all} . Hence, the cross-spectrum in voxel r is calculated with the following equation:

$$C_s(r) = W(r) \cdot c_{ref}$$

and the corresponding cross-spectral density is calculated as the sum of squares of C_s :

$$c_s(r) = \sum_{i=1}^n C_s(r)_i^2,$$

¹⁷ Here, the term *connectivity* is used rather than *coherence*, as strictly speaking the coherence equation is defined slightly differently. For simplicity reasons the rest of the tutorial uses the term *coherence*.

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where n is 2 for MEG and 3 for EEG. This equation can also be described as the squared Euclidean norm of the cross-spectrum:

$$c_s(r) = \|C_s\|^2.$$

The power in the voxel r is calculated like in the cortico-cortical case:

$$p(r) = \lambda_1\{C_s(r, r)\}.$$

At last, coherence between the external reference and the cortical activity is calculated with the equation:

$$CON(r) = \frac{c_s(r)}{p(r) \cdot C_{all}(k, k)},$$

where $C_{all}(k, k)$ is the (k, k) -th diagonal element of the matrix C_{all} .

DICS is particularly useful, if coherence is to be calculated without an a-priori source model (in contrast to source coherence based on pre-defined source montages). However, the recommended analysis strategy for DICS is to use a brain source as a starting point for coherence calculation that is known to contribute to the EEG/MEG signal of interest. For example, one might first run a beamformer on the time-frequency range of interest and use the voxel with the strongest oscillatory activity as a starting point for DICS. The resulting coherence image will again lead to several maxima (ordered by magnitude), which in turn can serve as starting points for DICS calculation. This way, it is possible to detect even weak sources that show coherent activity in the given time-frequency range.

The other significant application for DICS is estimating coherence between an external source and voxels in the brain. For example, an external source can be muscle activity recorded by an electrode placed over the according peripheral region. This way, the direct relationship between muscle activity and brain activation can be measured.

In the following, we will first examine cortico-cortical coherence in the model dataset `AC_Osc5.foc` in the subfolder **Learn-by-Simulations\AC-Coherence** of the BESA Research Examples folder. For a full description of the model data see chapter B of the present tutorial.

Second, we will estimate cortico-muscular coherence in an MEG dataset kindly provided by Dr. Jan-Mathjis Schoffelen and Dr. Robert Oostenveld (Donders Institute). The dataset is also

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available in the fieldtrip tutorial (<http://www.fieldtriptoolbox.org/tutorial/coherence>), the results of the experiment were published in Science in 2005 (Schoffelen, Oostenveld, Fries; Science 2005). This is the description of the experiment:

The dataset used in this example has been recorded in an experiment in which the subject had to lift her hand and exert a constant force against a lever. The force was monitored by strain gauges on the lever. The subject performed two blocks of 20 trials in which either the left or the right wrist was extended for about 10 seconds. A trial started as soon as the subject managed to get his force output within a specified range from 1 to 2 N. If the force was not kept constant during the course of a trial, the trial was terminated prematurely.

The bipolar EMG signal was recorded from the right extensor carpi radialis longus muscle in the lower arm. MEG signals were recorded with a 151 sensor CTF Omega System (Port Coquitlam, Canada). In addition, the EOG was recorded to later discard trials contaminated by eye movements and blinks. The ongoing MEG and EOG signals were lowpass filtered at 300 Hz, digitized at 1200 Hz and stored for off-line analysis. To measure the head position with respect to the sensors, three coils were placed at anatomical landmarks of the head (nasion, left and right ear canal). While the subjects were seated under the MEG helmet, the positions of the coils were determined before and after the experiment by measuring the magnetic signals produced by currents passed through the coils. Magnetic resonance images (MRIs) were obtained from a 1.5 T Siemens system. During the MRI scan, ear molds containing small containers filled with vitamin E marked the same landmarks. This allows us, together with the anatomical landmarks, to align source estimates of the MEG with the MRI.

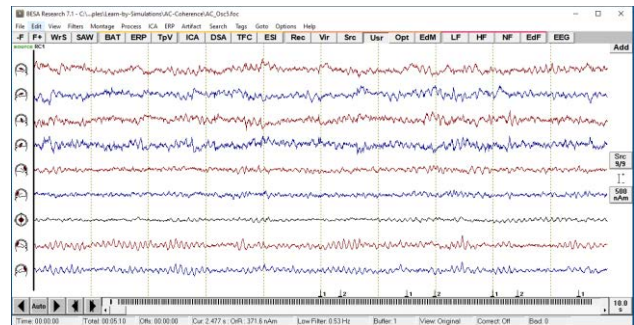
Our data example (Cortico-Muscular_DICS.foc) consists of the data for the left EMG condition, exported and compressed to a BESA binary (*.foc) file. Triggers with code 99 were added to the data at 1 s intervals. A paradigm file (Cortico-Muscular_DICS.pdg) defines 1 s epochs around these triggers. An artifact scan using an amplitude threshold of 3400 fT leaves 115 out of 192 epochs for analysis.

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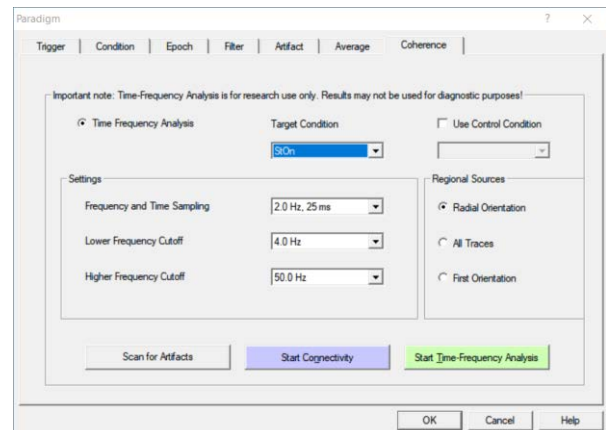
Tutorial 12 – Time-frequency Analysis, Connectivity Analysis and Beamforming

N. Cortico-cortical coherence with DICS

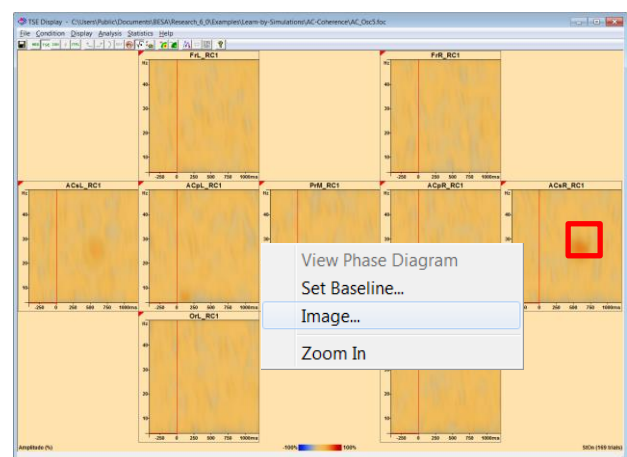
1. Please open file **Learn-by-Simulations\AC-Coherence\AC_Osc5.foc** in the BESA Research Examples folder. Please press the **Usr** button from the button menu and select the source montage **RC1**.



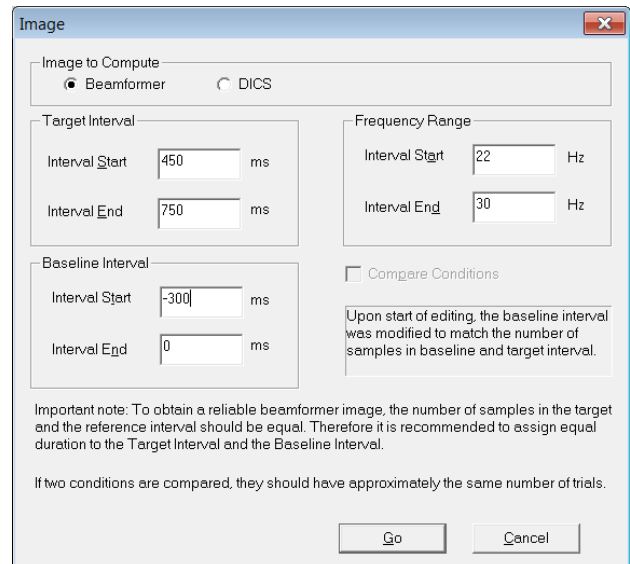
2. Run time-frequency analysis by pressing **ERP / Coherence**. Leave all settings at default and press **Start Time-Frequency Analysis**.




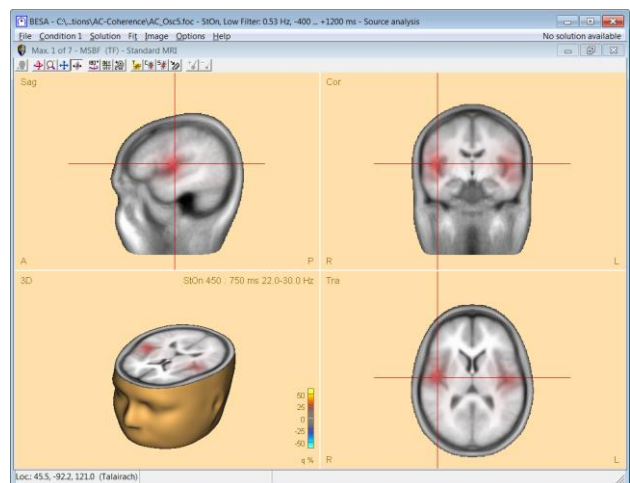
3. **Left-drag** a window over the induced activity in the source **ACsR_RC1**, **release** the left mouse-button and select **Image**.



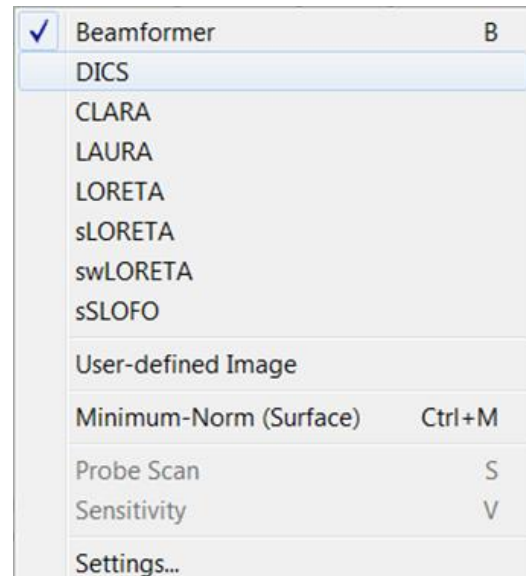
4. Select the Image to Compute to **Beamformer**. Set the **Target Interval** to **450 to 750 ms**, the **Baseline Interval** to **-300 to 0 ms** and the **Frequency Range** to **22 to 30 Hz**. Press **Go**.



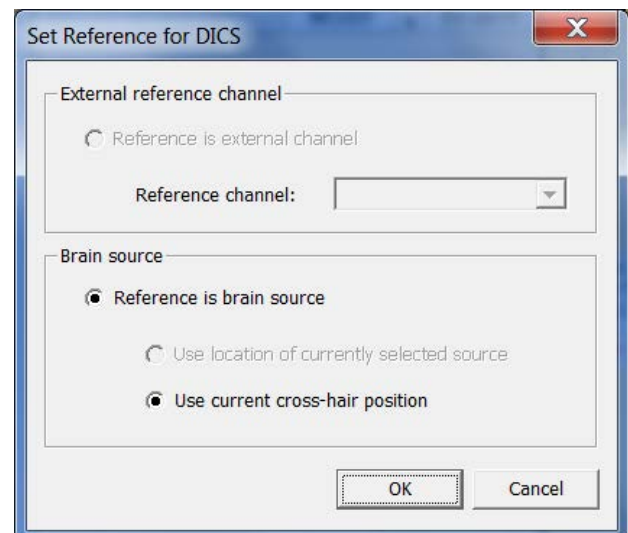
5. **Scale up** the resulting image by pressing the  button several times. The first maximum of the beamformer is located in the right auditory cortex. We will use this maximum (voxel) to probe coherence with all other voxels in the brain.



6. In the middle panel of the source analysis window, press the **arrow key** and select **DICS**.




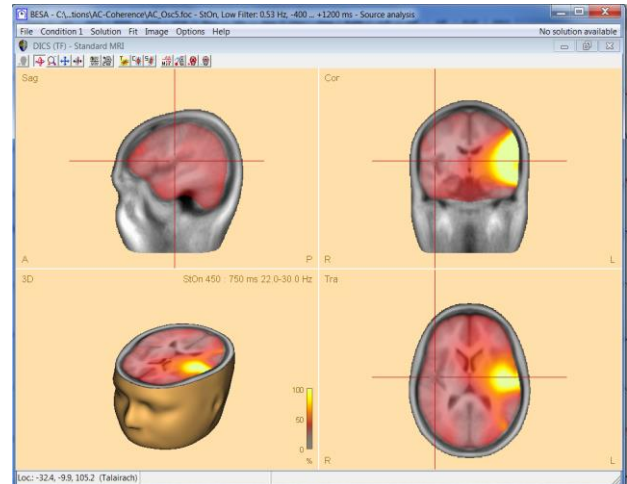
7. In the **Set Reference** dialogue check the option **Use current cross-hair position**. Please note that it is also possible to select a dipole or regional source as the reference in case one is working with a discrete source model. Press **OK**.



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8. The resulting image suggests strong coherence between the right and left auditory cortices. You can use the  button to jump through the DICS maxima and use them as new starting points for further DICS calculations.

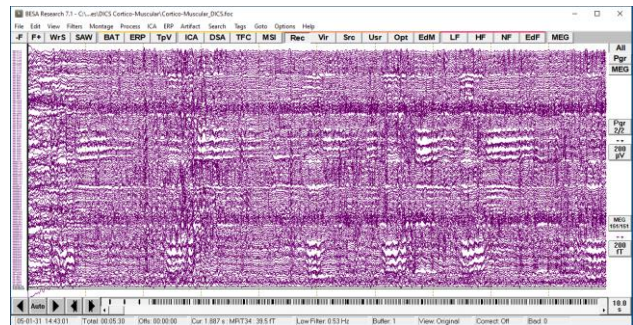


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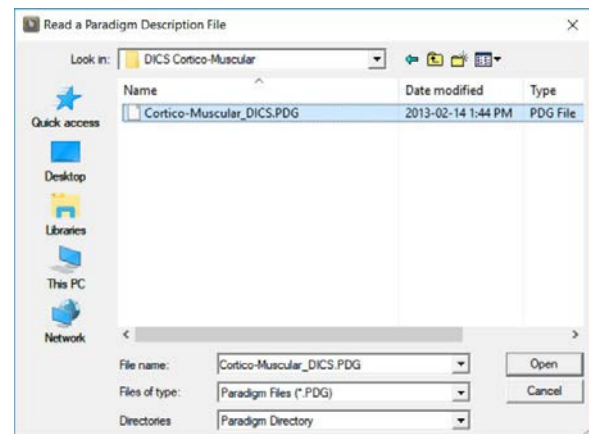
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O. Cortico-muscular coherence with DICS

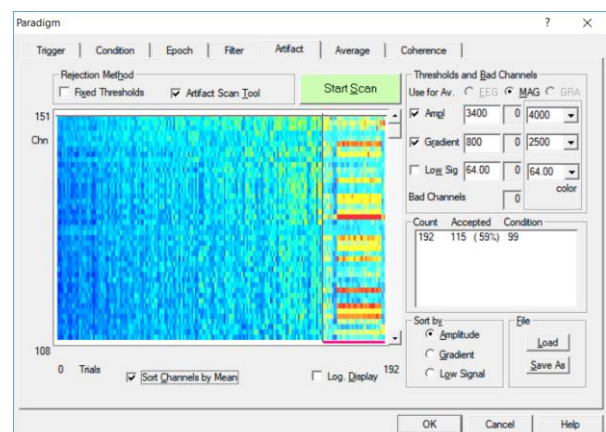
1. Please open file **Examples\DICS Cortico-Muscular\Cortico-Muscular_DICS.foc** in the BESA Research Examples folder. This dataset contains 151 axial gradiometers and 2 polygraphic channels used for recording the bilateral EMG signal.



2. Select **ERP / Edit Paradigm** to auto-load the file **Cortico-Muscular_DICS.PDG** from the data folder. The paradigm file specifies a condition containing the triggers with code 99 that were added to the data at 1 s intervals. Epochs are defined to last 1 s epochs around these triggers.



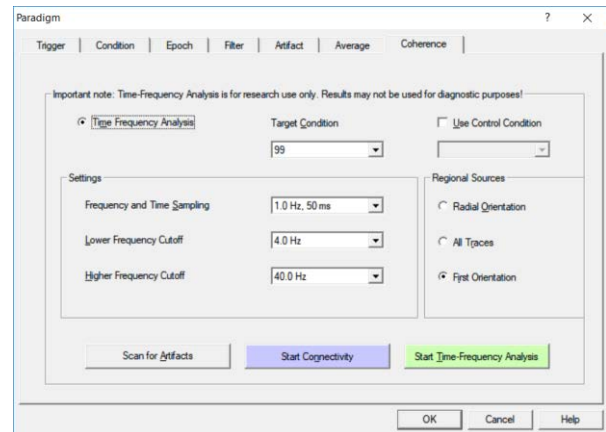
3. Move to the **Artifact** tab and run the artifact scan by pressing **Start Scan**. Using an **amplitude** threshold of **3400 fT** and a **gradient** threshold of **800 fT** leaves 115 out of 192 epochs for analysis.



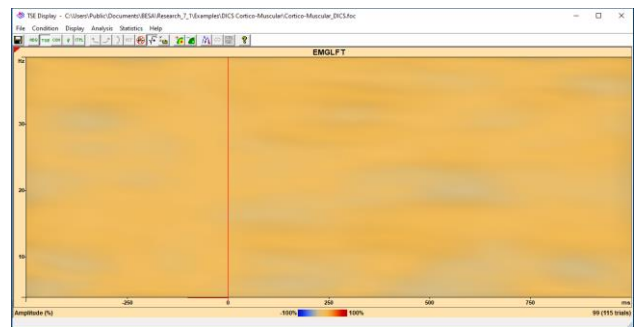
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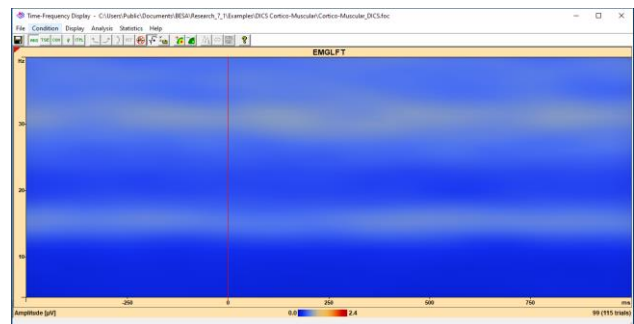
4. Move to the **Coherence** tab and make sure the Frequency and Time Sampling to be **1.0 Hz, 50 ms**, the Low Frequency Cutoff to be **4.0 Hz** and the High Frequency Cutoff to be **40.0 Hz**. Start Time-Frequency Analysis.



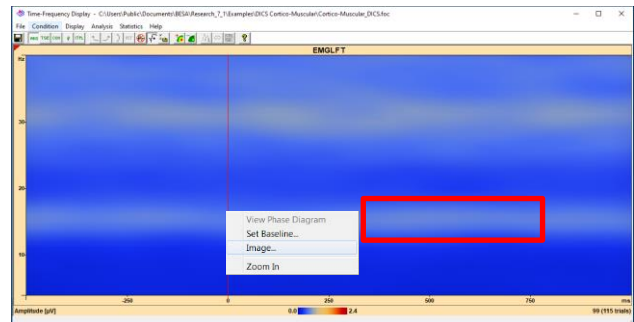
5. In the resulting TFC window, please locate the **EMGLFT** channel, **right-click** and specify **Show only this channel** (this might take a few seconds!)



6. Press the **ABS** button to display the absolute amplitude in the given time-frequency range. **Scale up** the image by pressing the **+** button until the scale ranges from **0.0 to 2.4 µV**. It becomes apparent that there is an increase in amplitude around 15 Hz.



7. **Left-drag** a window over the 15 Hz activity, and select **Image** from the popup menu.



8. Select **DICS** under the section **Image to Compute**, a Target Interval from **0 to 500 ms**, a Baseline Interval from **-500 to 0 ms** and a Frequency Range from **10 to 20 Hz**. Press **Go**. Please note that the baseline interval is relevant only for cortico-cortico DICS computations. It is not used in the cortico-muscular computations, as the one shown in the following points.

The 'Image' window is shown with the 'DICS' radio button selected under 'Image to Compute'. The 'Target Interval' is set from 0 to 500 ms, and the 'Baseline Interval' is set from -500 to 0 ms. The 'Frequency Range' is set from 10 to 20 Hz. A 'Go' button is visible at the bottom.

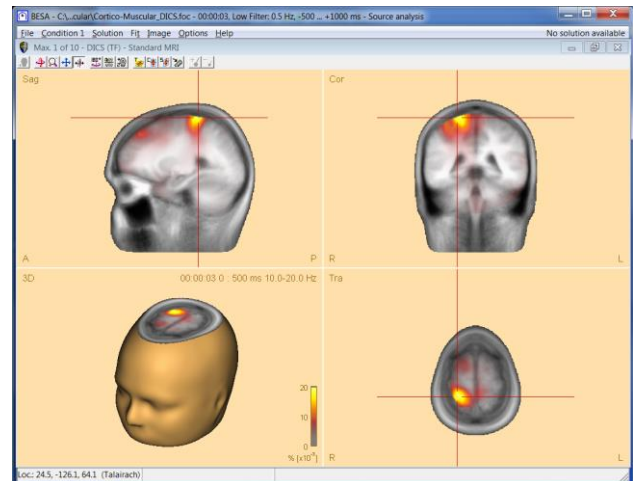
9. After calculating the cross-spectral density matrix in the given time-frequency range, the **Set Reference for DICS** window pops up. Select the option **Reference is an external channel** and choose channel **EMGLFT** to calculate coherence between the left EMG channels and all brain voxels. Press **OK**.

The 'Set Reference for DICS' window is shown. The 'Reference is external channel' radio button is selected, and 'EMGLFT' is chosen in the 'Reference channel' dropdown. The 'OK' button is highlighted.

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10. The resulting image indicates the maximum coherence between the left EMG channel and the right somato-motor area. This is to be expected as the subject was pressing a lever with the left hand, which is represented in the right motor/somatosensory area.



Tutorial 13 – Cross-subject Statistics

What does BESA Research provide?

- ✓ Export of individual results from BESA Research via batch scripting
- ✓ Cross-subject statistics using BESA Statistics
 - ERP / ERF data
 - Source Waveforms
 - Image Data
 - Time-Frequency / Coherence Results

In a previous step (Tutorial 4), we created a source model for conditions high and low based on the grand average data. We now want to compare conditions **high** and **low** statistically. I.e. we want to know, whether a particular source is more or less active in the high compared to the low condition. For this purpose, we will first create a batch that applies our source model to the individual datasets and extracts the source waveforms per person. We will then export the individual source waveforms and analyze them statistically with BESA Statistics.

We will also investigate the differences between more than two conditions in the same experiment, and apply statistics to a different experiment where we look at correlations between measured MEG data and an external covariate of interest.

A. Applying a source model to individual datasets using batch scripting

The grand average model explains the data variance in all conditions. Therefore, it can serve as a master model to calculate the source activity of each individual subject in all 5 conditions. The hypothesis is that the mean source location of the grand average provides a sufficiently good model for each individual data set since a change in source location of 1-2 cm has little effect on the temporal course of the source waveforms. Generally, fitting in individual data results in a large uncertainty of source location, especially in depth, due to poorer signal-to-noise ratio. We therefore want to stabilize the individual solutions by using

- a) a model with fixed sources and individual orientations (locations from grand average or mean Talairach coordinates, cf. Hoenes et al., Neuroreport 11: 2461, 2000)
- b) a model with fixed sources and orientations (same as grand average model)
- c) a model with fixed regional sources (same as grand average model, calculating mean amplitude of each regional source as an orientation-independent measure (cf. Weissner et al., Neuroreport 12:3303, 2002))

The orientation of the different components (N100, N150 and frontal source) differs considerably between subjects according to individual gyral anatomy and functional representation. Since orientation differences have a larger effect on the EEG scalp topography than small changes in location (in the order of 1-2 cm) we should try to define the individual orientation of each component to obtain robust source waveforms (cf. Scherg, M. and von Cramon, D. Evoked dipole source potentials of the human auditory cortex. Electroenceph. Clin. Neurophysiol. 65: 344-360, 1986).

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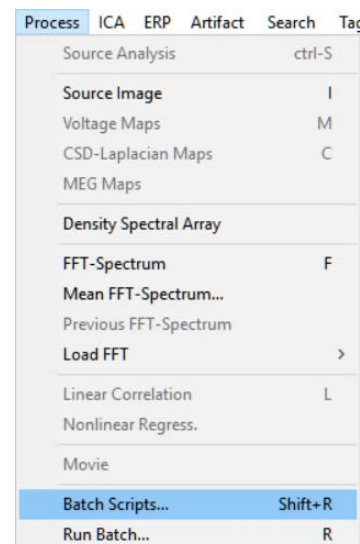
Tutorial 13 – Cross-subject Statistics

Therefore, we will use strategy a) with the mean sources defined by the grand average model and set the orientations of the 3 regional sources individually for each subject in order to obtain appropriate source waveforms. These individual source waveforms will then be used to perform cross-subject statistics. Strategies b) and c) are alternatives for more noisy data.

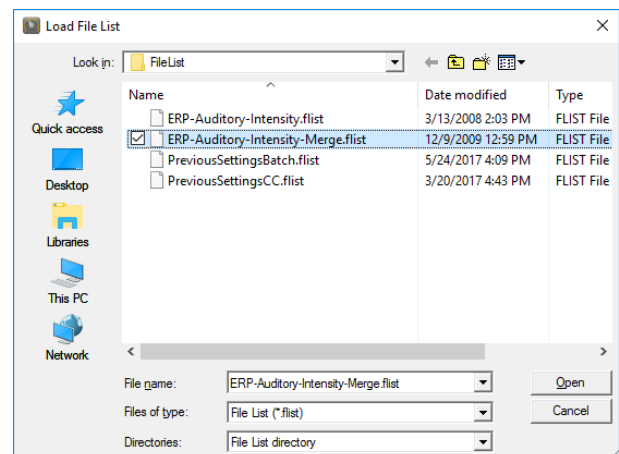
We could apply all required steps manually to each individual data file. This is not necessary, however, and it saves a lot of time to use the source analysis batch functions. In the following, we will create a script that performs all steps automatically.

We will then use BESA Statistics to quickly and conveniently analyze our source waveform results across all 10 subjects.

1. Select **Process / Batch Scripts** in the main window to open the Batch processing window. We will now create a batch that applies the grand average master model to all individual datasets, orients the regional sources individually and exports the individual source waveforms for further statistical analysis.



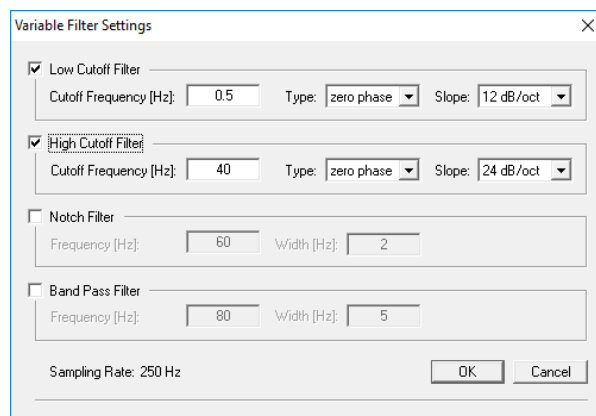
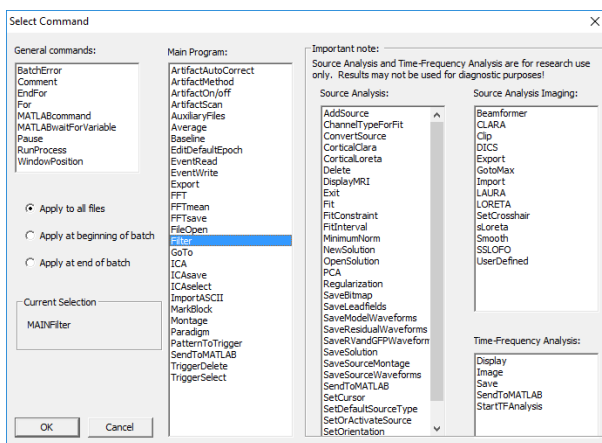
2. In the **File List** tab, click on **Load File List**, select **ERP-Auditory-Intensity-Merge.flist** and press **Open**. This file list has already been used in Tutorial 3 Step B to create the grand average. It specifies individual average files of all subjects.



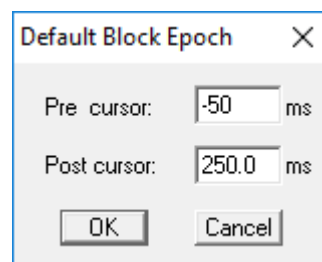
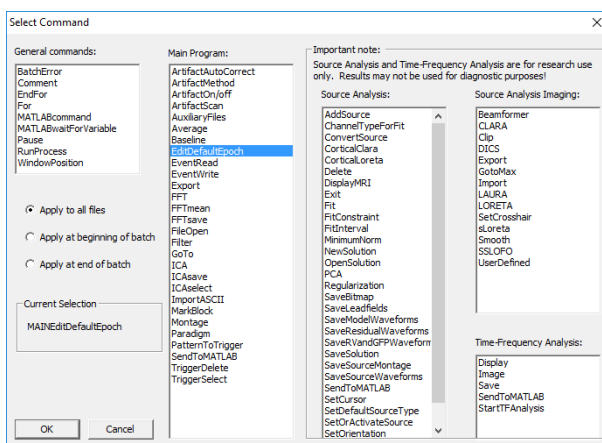
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- Switch to the **Batch** tab. As a first command in this batch, apply appropriate filters to each data set. Press **Add Command** and select **Filter** (Main Programs group). Select a **low cutoff** filter of **0.5 Hz, zero-phase, 12 dB/oct**, and a high cutoff filter of **40 Hz, zero-phase, 24 dB/oct**. Click **OK** twice to confirm these filter settings.



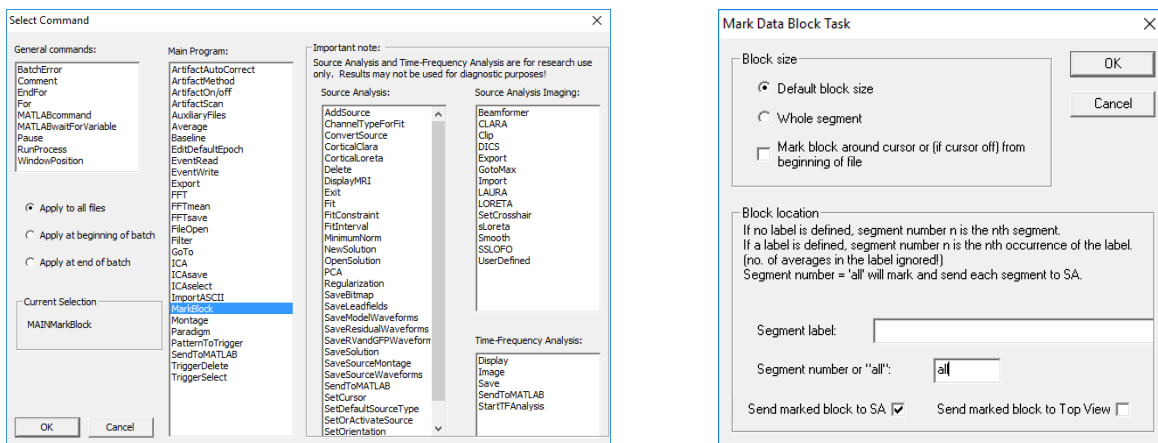
- As a next command, specify the epoch that will be sent into the source analysis window to extract the source waveforms. Press **Add Command** and select **EditDefaultEpoch** (Main Programs group). Specify an interval from **-50 to 250 ms**.



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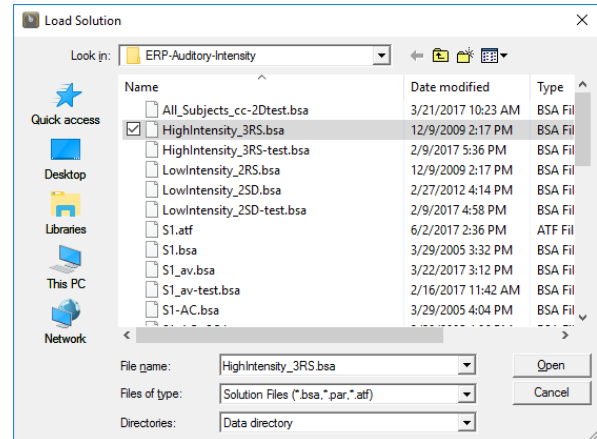
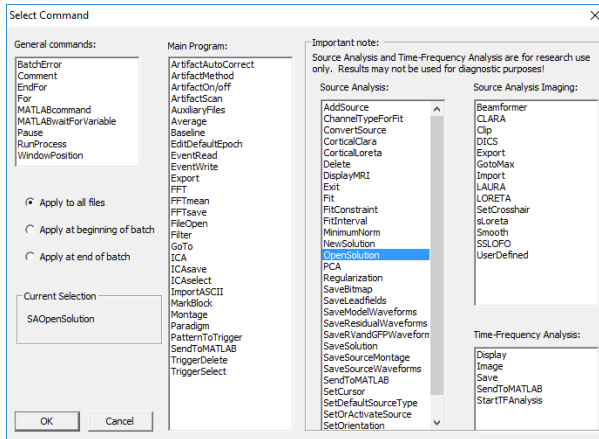
- The next command marks the default block in all 8 conditions, and sends these data blocks into the source analysis window. Press **Add Command** and select **MarkBlock** (Main Programs group). In the upcoming window, select **Default block size**. Instead of specifying a single segment label or segment number, write **all** in the entry Segment number. Note that this will automatically set the checkmark behind **Send marked block to SA** at the bottom of the window. Thus, all conditions from 60dB to All will be loaded in the source analysis window simultaneously.



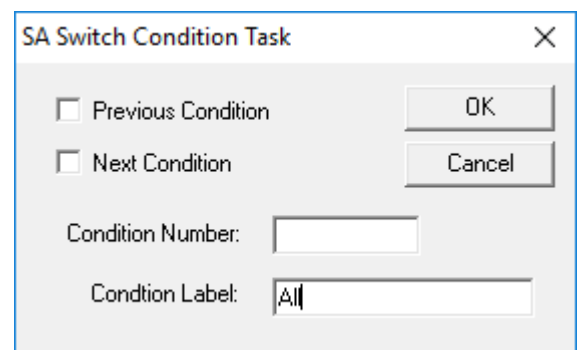
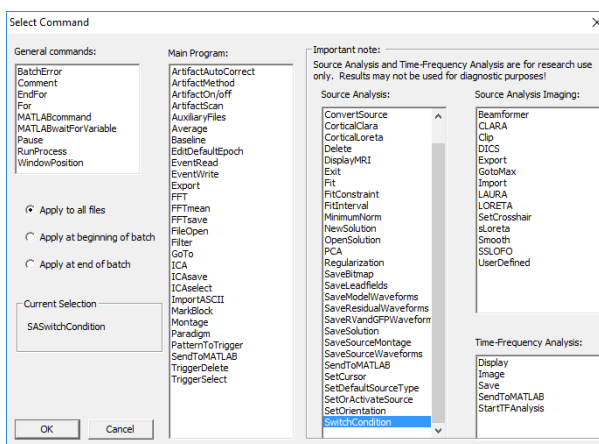
- Now apply the master model that was generated from the grand average. Press **Add Command** and select **OpenSolution** (Source Analysis group). Select file **HighIntensity_3RS.bsa** that contains the two regional sources in the auditory cortex and the frontal source. Press **Open** and **OK**.

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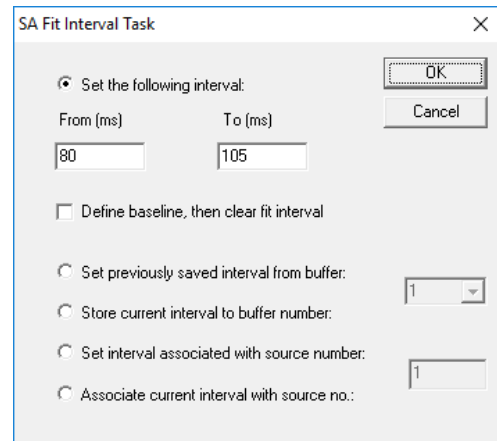
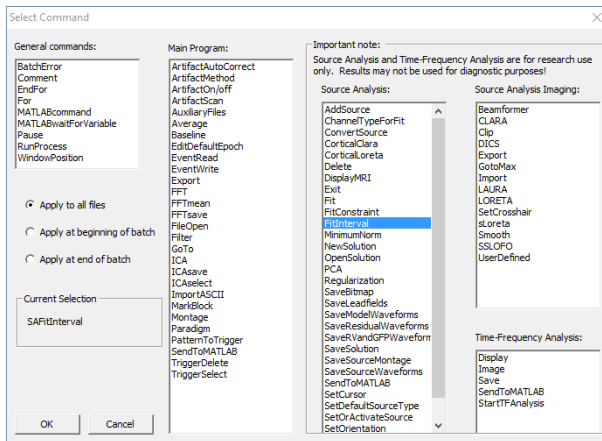
- To obtain correct source waveforms for each individual subject, adjust the master model to each subject's cortical folding by adjusting the orientations of the regional sources. First, we will reorient the auditory cortex sources in condition All that contains the average of all five conditions. Press **Add Command** and select **SwitchCondition** (Source Analysis group). As Condition Label, enter **All**. Press **OK**.



- To adjust the N100 orientation, we need to specify the corresponding latency. Since N100 latencies will differ slightly from subject to subject, we define a time range rather than a fixed latency. Press **Add Command** and select **FitInterval** (Source Analysis group). Specify a latency range of **80 to 105 ms**. Leave all other options unchanged and hit **OK**.

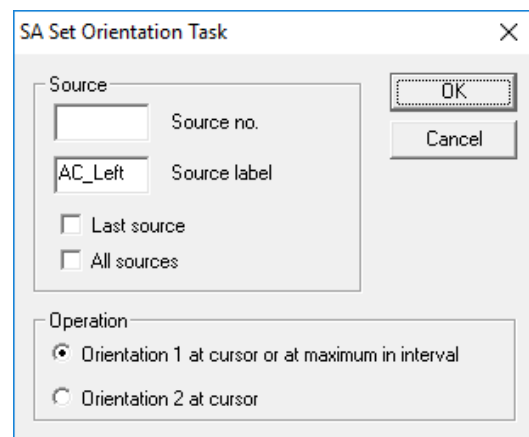
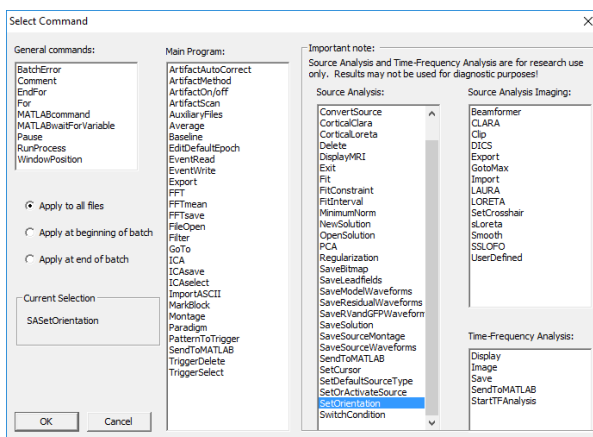
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Note: At this point in the batch, we could insert a Pause command (General group). It would cause the batch to interrupt at this stage and allow us to modify the marked fit interval to match each subject's data before it continues on our OK. In this tutorial we pass this step, but generally it is recommended to keep an eye on what the batch is doing when working with your own data.

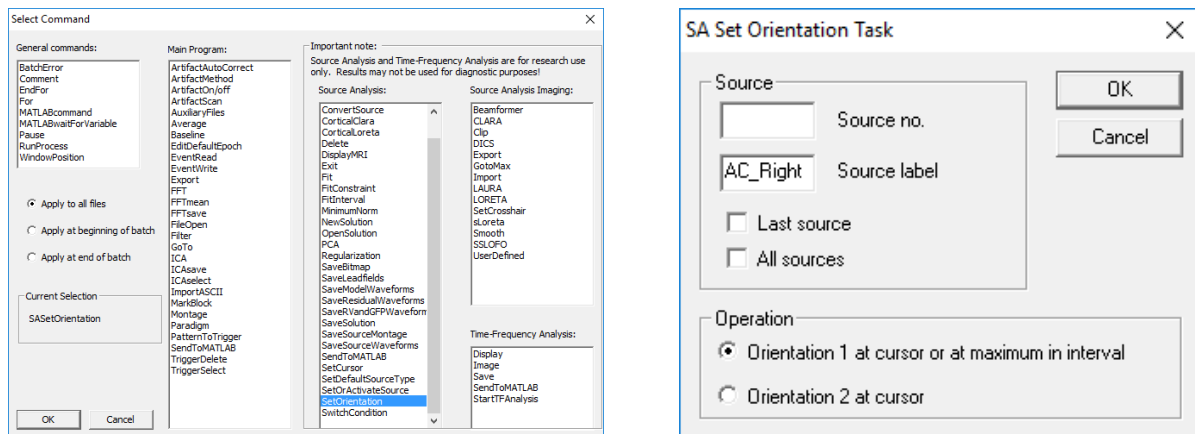
- Now the first and second regional source in the model (representing the bilateral auditory cortices) can be oriented. **Add Command** and select **SetOrientation** (Source Analysis group). In the upcoming parameter window, specify **Source label AC_Left**. As operation select **Orientation 1 at cursor or at maximum in interval**. BESA will automatically determine the latency within the fit interval at which the total power of the regional source is maximal and perform source orientation at this latency. Confirm with **OK**.



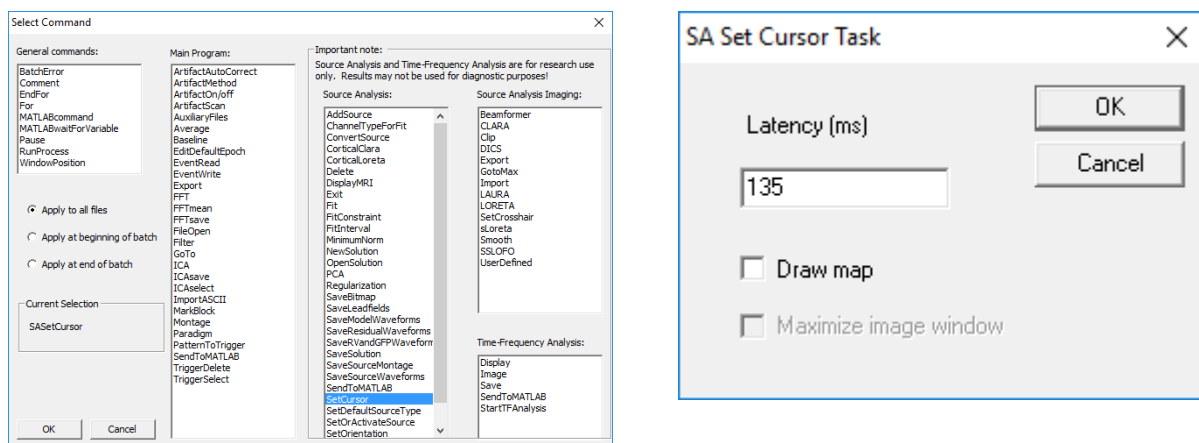
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10. Repeat the previous command **SetOrientation** with **Source label AC_Right**, the auditory cortex source in the other hemisphere.



11. To set the second orientation to account for the N140 component, press **Add Command**, select **SetCursor** (Source Analysis group) and specify a latency of **135 ms**.

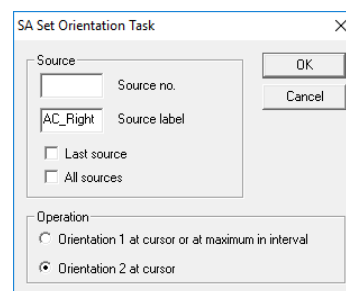
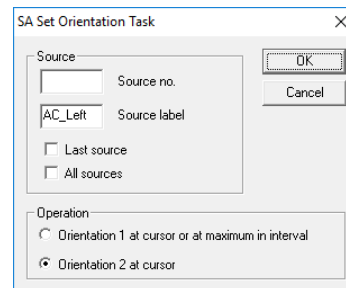
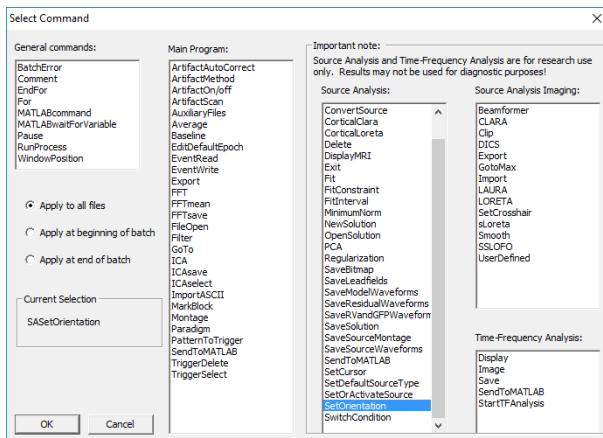


Note: Again, at this stage it could be advisable to insert a Pause command (General group) to adjust the cursor position to the individual N140 latency, if required, before the batch continues.

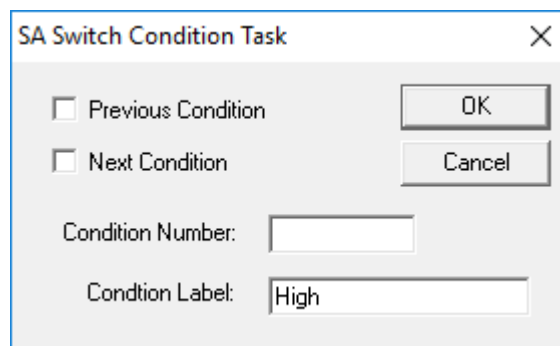
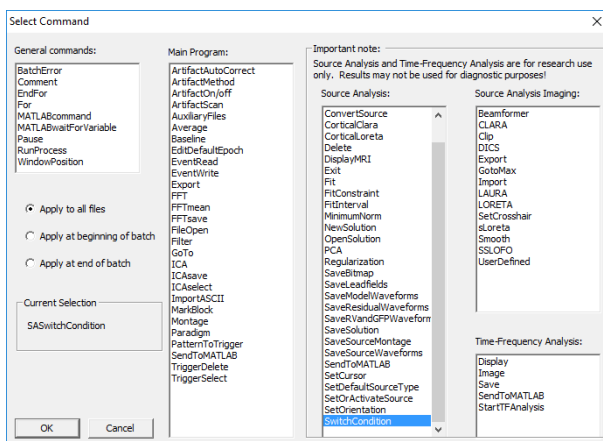
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12. As in steps 10 and 11, add the command **SetOrientation** twice. First, specify **Source AC_Left** and select **Orientation 2 at cursor** as operation. Then repeat the command and specify **Source AC_Right**, again with operation **Orientation 2 at cursor**.



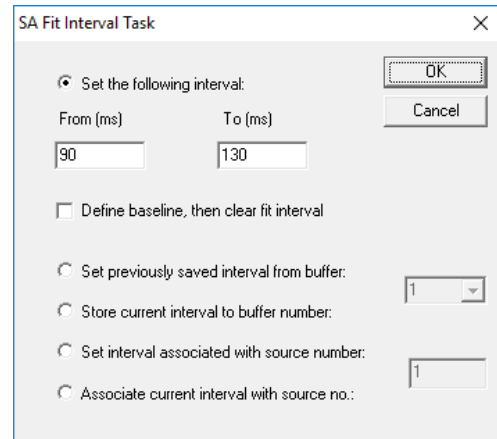
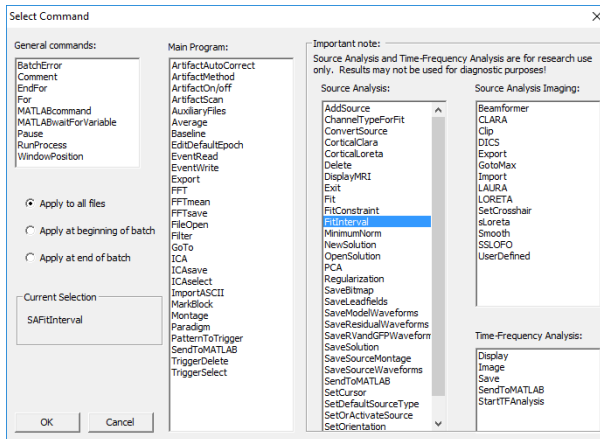
13. Finally, we need to set the orientation of the frontal source. Its amplitude is largest in condition High. Therefore, add a command **switchCondition** (Source Analysis group) and specify condition label **High**.



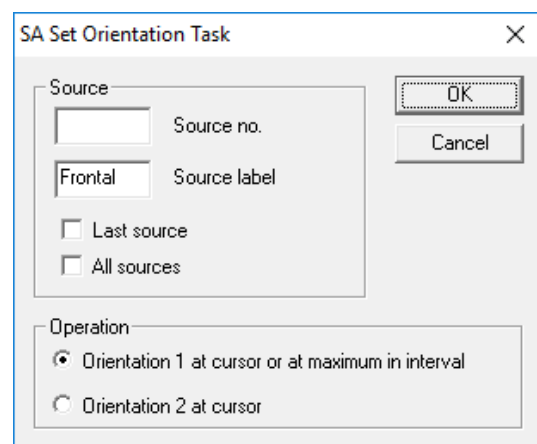
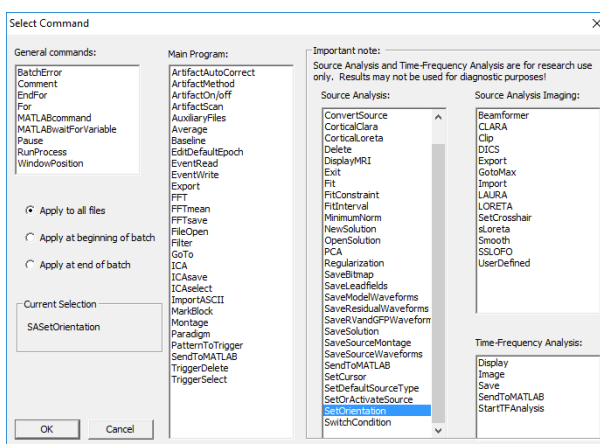
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14. To orient the frontal source, we will again mark a fit interval that includes its maximum activity. Add command **FitInterval** (Source Analysis group). Specify a latency range of **90 to 130 ms**. Leave all other options unchanged and hit **OK**.



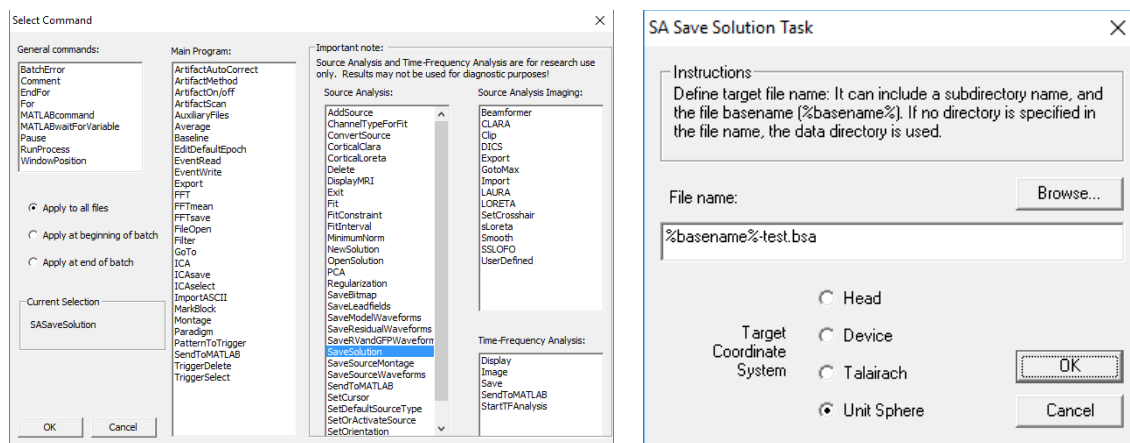
15. Add the command **SetOrientation** (Source Analysis group). This time specify source **Frontal** and **Orientation 1 at cursor or at maximum in interval**. Because no cursor is set anymore, BESA Research orients the source at the latency of maximum source power. This completes the adjustment of the master model to the individual subjects' brain gyration.



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16. We will now save this model for later re-use. Add the command **SaveSolution** (Source Analysis group). As a file name, specify **%basename%-test**. The string %basename% will be replaced by the basename of the individual data file. This makes sure that the solution is saved under different names for each subject and is not overwritten during the repeated execution of this command with different datasets. Note that you can specify the coordinate system in which the solution is to be saved. If the solution is opened with the same data set later on, the coordinate system is irrelevant. However, for comparison of different solutions across subjects, a standardized coordinate system like Talairach or Unit Sphere is recommended.



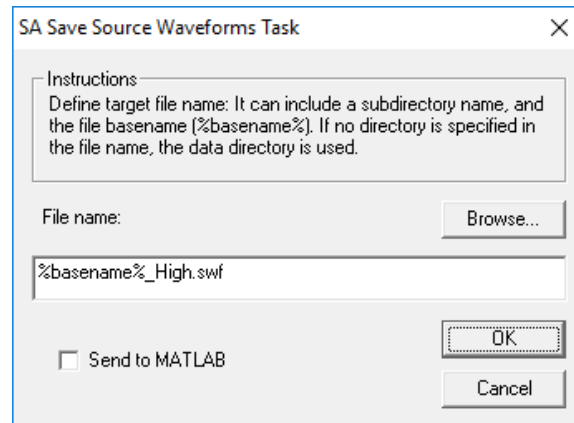
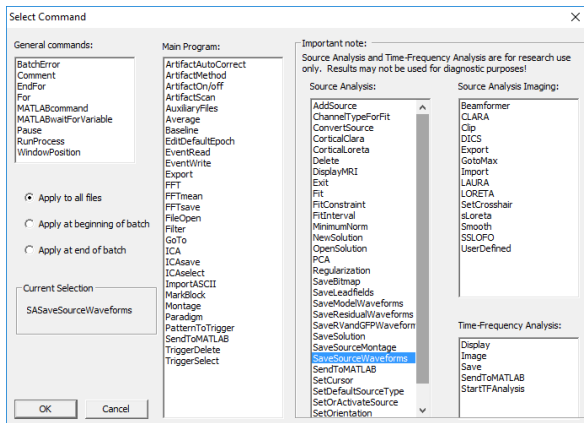
B. Exporting individual source waveforms via batch scripting

Next, we want to save the individual source waveforms of conditions High and Low, which we will later load in BESA Statistics.

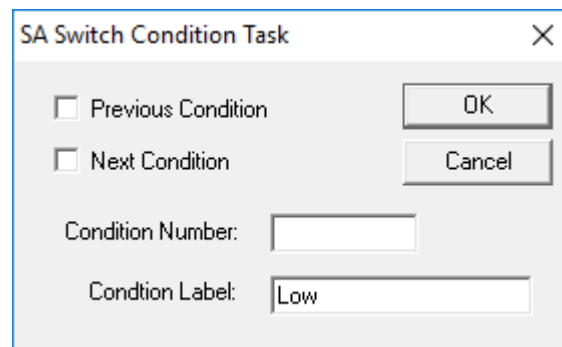
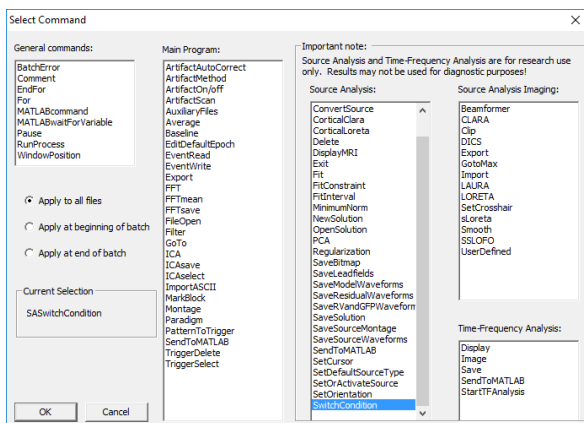
1. Add the command **SaveSourcewaveforms** (Source Analysis group) to save the source waveforms to an ASCII file (*.swf). In the file name include **%basename%** as a placeholder for the datafile, and add the extension **"High"** in order to be able to associate each *.swf file with the corresponding subject and condition.

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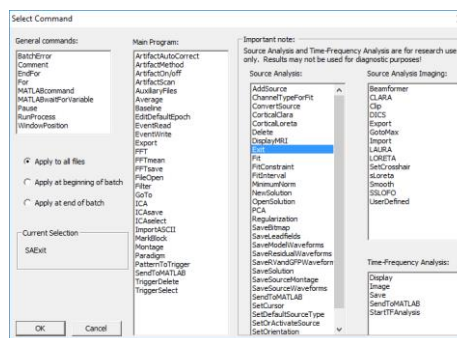
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2. Add a command **SwitchCondition** (Source Analysis group). As Condition Label, enter **Low**. Hit **OK**.



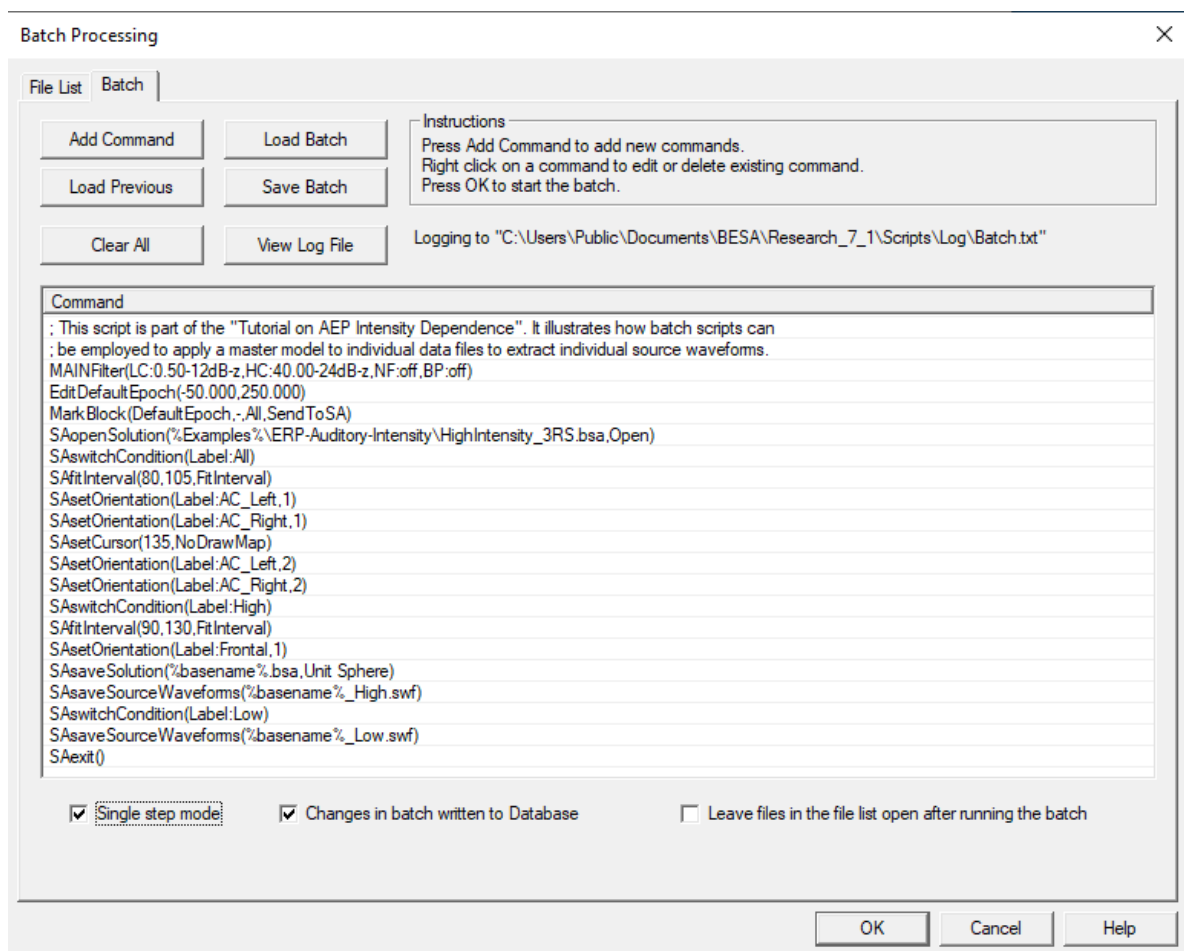
3. Repeat Step B1 for condition “Low”.
4. Add command **Exit** (Source Analysis Group). This will close the source analysis window after each subject to prevent data remaining when processing the next subject.



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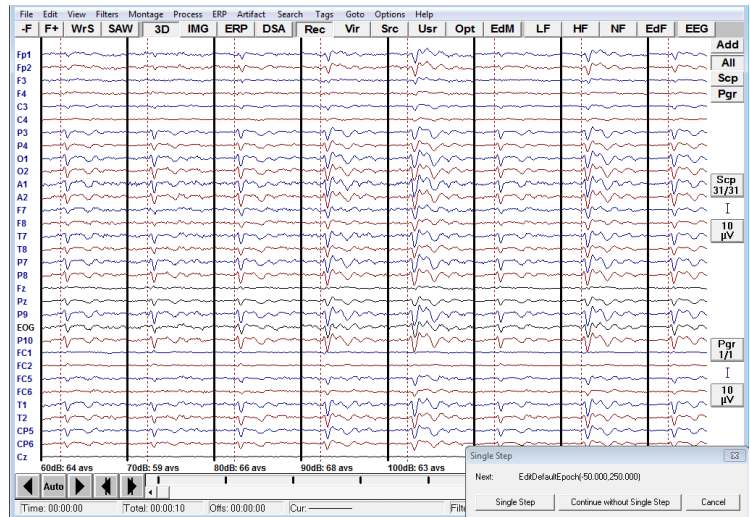
5. The script is now ready to be applied to all data files in the file list. You may save the script to disc for later reuse by pressing the **Save Batch** button. At this point you may open the predefined batch script **AudIntensity-SWFs-for-BESA-Statistics.bbat** using the button **Load Batch** (then navigate to folder **Auditory**). This script contains all commands as described above. In addition, a script comment has been added in the first lines using the command **Comment**. These lines (preceded by a semicolon) are not evaluated during script execution. Note that the batch scripts are stored in ASCII files (*.bbat) that can also be edited with a standard text editor.



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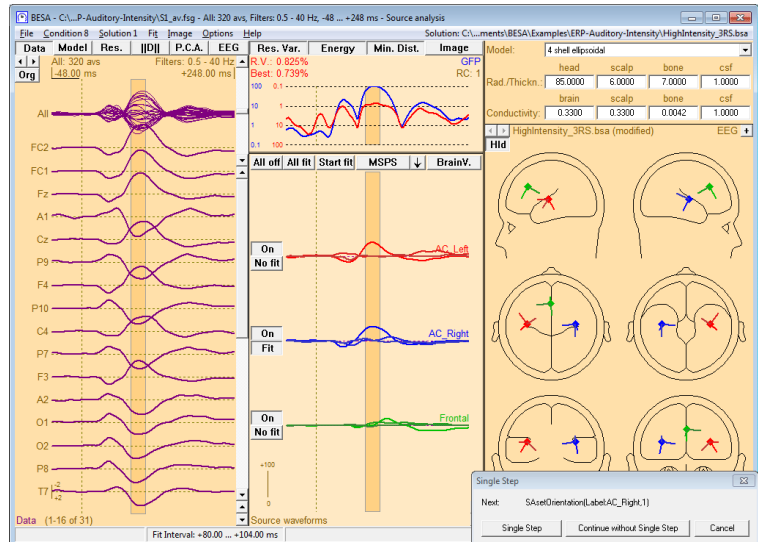
6. Select the option **Single step mode** at the bottom right – this will cause the batch to pause after every single command. This helps us in this tutorial to visually follow the processing steps and understand how the batch works. Press **OK** to start the batch.
7. BESA Research starts applying the batch commands to the first data file in the file list (S1_av.fsg). It loads the file and applies the specified filters. At the bottom right, a small window appears that indicates the next batch command to be executed. Proceed step by step by hitting the **Single Step** button and observe how BESA Research processes the different commands



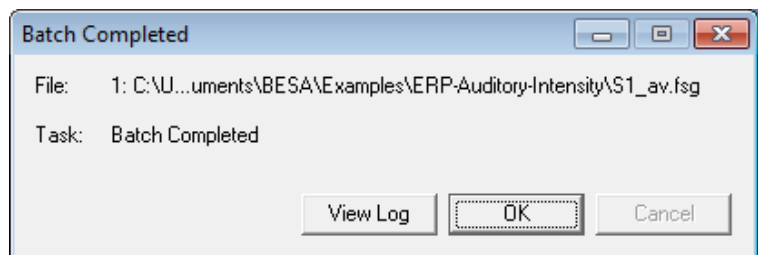
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8. Note for example how the orientation of the N100 components (the first components of AC_Left and AC_Right) takes place in the marked fit interval. If the marked fit interval would not include this subjects N100 latency, we could manually adjust the fit interval while the batch pauses before continuing. For the data in this tutorial, the fit intervals have been defined appropriately for each subject, therefore you can hit **Continue without single step** at any time to make the batch proceed automatically without interruption.



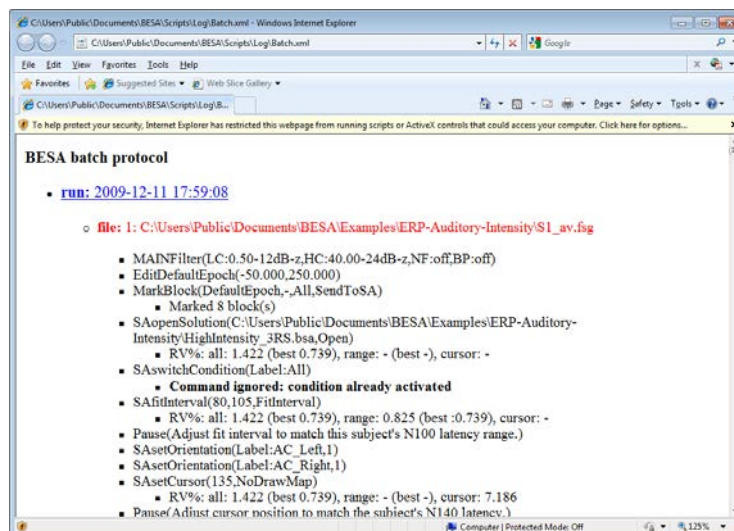
9. When the batch processing has completed, a notification window will appear.



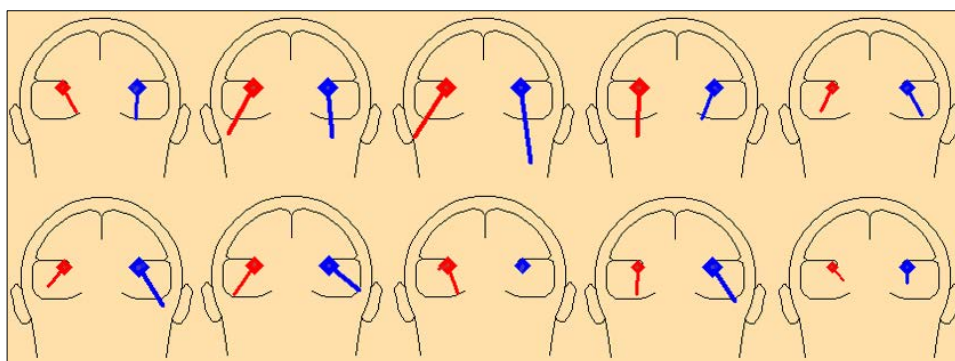
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10. BESA Research keeps track of all steps that have been carried out and documents them in a log file. After completion of the batch, you can press **View Log** in the **Batch Completed** window to view this log file. Then press **OK** to close the **Batch Completed** message window.



Batch scripts like the one shown above allow for simple and fast analysis of a complete EEG or MEG study. Output of our example script are individually adjusted source model files (*.bsa) and individual source waveforms for each condition, containing the brain responses to the different auditory stimuli in each subject.



The plot above illustrates the necessity to model the orientations individually. Shown are the ten different orientations obtained for the N100 component as stored in the individual solution files (*.bsa). The large variation of the N100 orientation between subjects is a correlate of the inter-subject variability in the orientation of the auditory cortex. Without adjusting the orientations individually, the first components of **AC_Left** and **AC_Right** would not optimally reflect the individual N100 component.

C. Introduction Cluster Permutation Statistics

Before we get started with BESA Statistics, it is important to understand the background of cluster permutation statistics. The following paragraphs will give a brief overview.

Preliminary parametric test

The preliminary parametric test is the first step in the analysis of data in BESA Statistics. The type of test that is applied depends on the experimental design that was chosen.

t-Test: Comparing two groups or conditions

For the comparison of two groups or two conditions, as a first step, BESA Statistics calculates a preliminary Students t-test (Hays 1988) between groups / conditions per data point. A t-test is computed to determine whether there is a significant difference between the mean of two groups / conditions. A t-test is associated with a t-value and a corresponding p-value which indicates the significance of an effect. P-values smaller than 0.05 are generally considered significant. The p-value becomes smaller if the t-value becomes larger. t-values are influenced by the size of the difference between the group / condition means and the size of the variance in both groups / conditions. Generally speaking, the difference between two group / condition means can be small for the test to become significant if the variance in both groups is also small. On the other hand, a large difference between two group / condition means does not automatically imply a significant effect. It is also required that the variance in both groups / conditions is not too large. Apart from the t-value, the p-value is influenced by the degrees of freedom (DF) for the specific test computed. DF are dependent on the number of subjects. The more subjects constitute the groups / conditions, the larger the DF. Larger DF are more likely to be associated with a significant test result, as variance can be estimated more precisely with a larger number of subjects.

A t-test can be paired or unpaired. A paired t-test is appropriate when there is a dependency between the two conditions that are compared. This is generally the case if two conditions in the same set of subjects are compared (e.g. subjects listening to high intensity vs. low intensity tones) or if the same subject is measured twice for the same task (e.g. listening to 1000 Hz tones before and after a training period). An unpaired t-test is appropriate when there is no dependency between the two groups that are being compared. This is generally the case if two different groups of subjects are compared for the same condition (e.g. motor response in left-handed

subjects vs. right-handed subjects). The selection of the correct type of t-test is important: in a paired t-test smaller differences between conditions are necessary for the test to become significant in comparison to an unpaired t-test.

Generally speaking, the likelihood of obtaining significant results is higher if a specific hypothesis about the data is tested. When there is no specific hypothesis as to whether one group / condition has higher or lower values than the other group / condition, a two-tailed t-test should be selected. When there is the hypothesis that the first group / condition has higher values than the second group / condition, a one-tailed-right t-test should be calculated. When there is the hypothesis that the second group / condition has higher values than the first group / condition, a one-tailed-left t-test should be calculated.

F-Test: Comparing more than two groups or conditions

If more than two groups or conditions need to be compared, the t-test is no longer feasible. For this scenario, the preliminary test of choice is the F-test. Here, an F-value is computed that corresponds to a p-value. The F distribution is not symmetric – there are no negative F values - and so there is no scope for choosing a one-tailed or two-tailed test as in the t-test scenario. Similarly to the t-test, the p-value is a measure for the likelihood that all groups / conditions were drawn from the same underlying distribution, and are thus interchangeable. In other words, a significant p-value (e.g. $p < 0.05$) points to a high probability that at least one of the groups / conditions differs from at least one of the other ones. It is, of course, also possible, that more than one pair of conditions differs from each other.

Permutation Test (non-parametric)

When computing a large number of t-tests or F-tests, the probability of obtaining a significant result by chance is high. Typically, an α -error of 5% ($p\text{-value} = 0.05$) is assumed when calculating statistical tests. Thus, if a significant result is achieved, there is a 5% chance that this result is considered significant although in truth it is not. The more tests are computed, the higher the probability those statistically significant results are obtained by chance.

Statistically analyzing EEG / MEG data usually involves computing a large number of tests, as two conditions are compared for a large number of electrodes over a time interval containing

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many data samples. Therefore, the multiple comparisons problem is particularly prominent when running statistics on EEG / MEG data.

There are different ways to address the multiple comparisons problem. The easiest is to apply the Bonferroni correction (Abdi 2007), in which the significance level (e.g. $p = 0.05$) is divided by the number of tests computed and only those tests are assumed to be significant with p-values smaller than the corrected value. For example, if 100 tests are computed, the corrected p-value would be $0.05 / 100 = 0.0005$. This approach is very conservative and the chance is high that significant results are wrongfully rejected.

BESA Statistics uses an alternative approach to deal with the multiple comparisons problem: Permutation testing in combination with data clustering. The main idea is that if a statistical effect is found over an extended time period in several neighboring channels, it is unlikely that this effect occurred by chance. Thus, the initial step is to define data clusters that show a significant effect between groups / conditions. For each cluster, a cluster value can be derived consisting of the sum of all t-values of all data points in the cluster. Then it is tested if the initial data clusters survive permutation. Permutation means that the data of subjects (i.e. unpaired tests were used for t-test, or between-group measures were taken for F-test) or conditions (i.e. paired t-tests, or repeated measures within the same group were used) get systematically interchanged. Depending on the number of subjects per group / condition and the type of test, a certain number of permutations are possible. For example, if 10 subjects are compared for two conditions using a paired t-test, 1024 (2^n , where n is the number of subjects) permutations are possible. If 10 subjects are compared with another set of 10 subjects for the same condition using an unpaired t-test, 184756 ($\binom{n+k}{k}$, where n is the number of subjects in the larger group, and k is the number of subjects of the smaller group; NB: in this example, the groups are the same size!) permutations are possible. For each of the calculated permutations (default: 1000¹⁸), a new test is computed and a new cluster value is derived for each of the initial clusters. Thus, a new distribution of cluster-values is determined for each of the initial clusters. Based on this new distribution, the significance of the initial cluster value can be determined. For example, if only 2% of all cluster values are larger than the initial cluster value, the initial cluster can be considered significant with

¹⁸ Drawn randomly without repetitions from all possible permutations. If there are not enough subjects to select 1000 permutations, the number is automatically adjusted to the maximum possible number of permutations.

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a p-value of 0.02. Thus, based on the computed cluster-value distributions, the significance of each initial cluster can be determined directly (see the following Figure C-1).

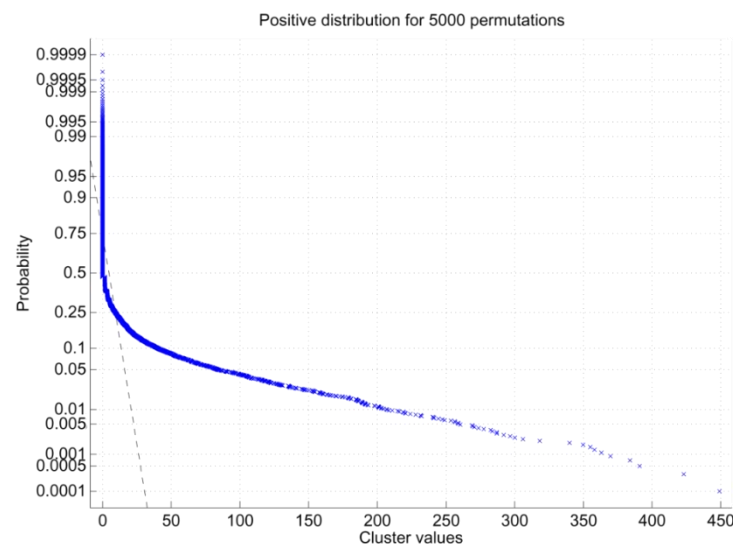


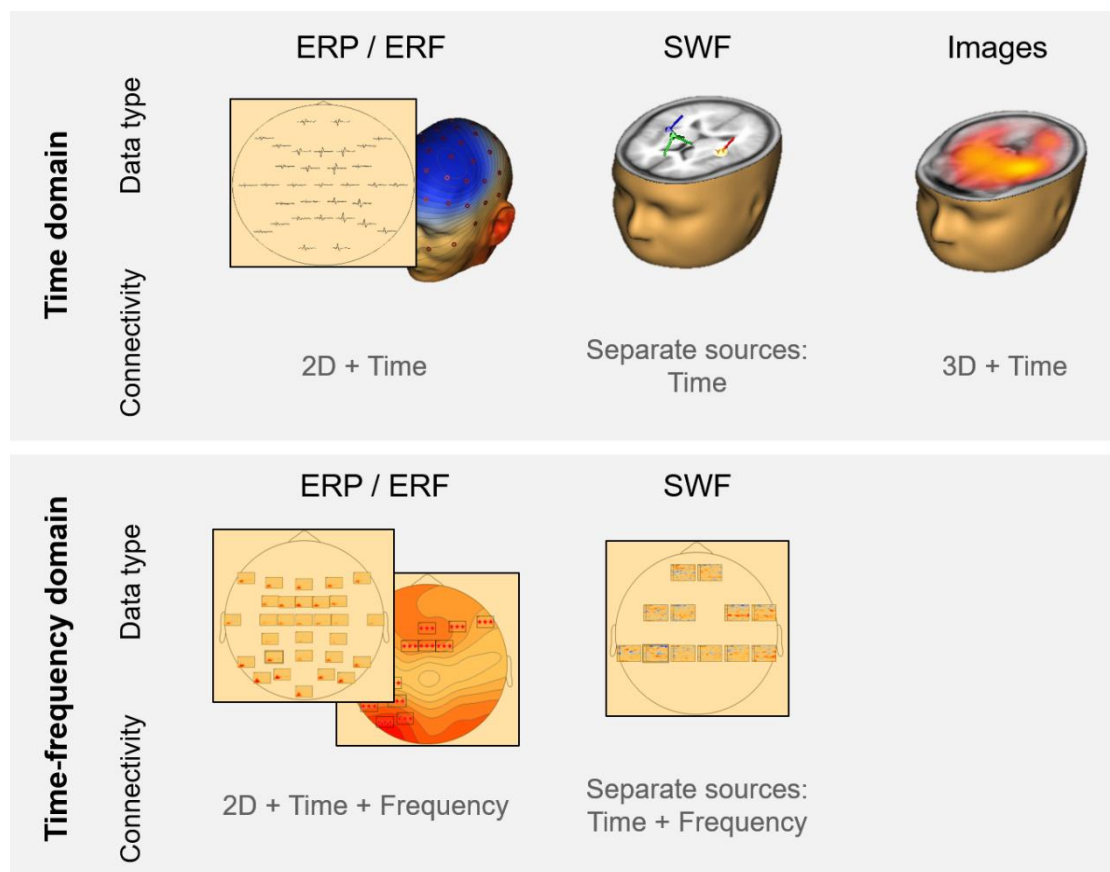
Figure C-1: A realistic distribution of cluster values based on 5000 permutations is displayed. The figure indicates that a cluster value of 200 is associated with a probability value of $p=0.01$, meaning that only 1% of all clusters have values larger than 200.

Depending on the direction of a statistical effect (i.e. condition 1 can have larger or smaller values than condition 2), negative and positive clusters can be found. If a negative cluster is tested for significance, it will survive permutation testing if the initial cluster value is more negative than 95% of all cluster values generated by permutation.

Since in permutation testing the distribution of cluster values is computed from the input data, and p-values are derived directly from the computed distribution, permutation testing is considered non-parametric, or parameter-free. This is a great advantage, since it is not required that data are normally distributed, as would be the case if classic parametric tests were used.

For more details on the implementation of the permutation test as implemented in BESA Statistics please refer to the following publications: (Bullmore, Suckling et al. 1999; Maris and Oostenveld 2007; Ernst 2004).

Cluster neighborhoods depend on the type of data: The figure below shows an overview of neighborhood connectivity with the data types supported by BESA Statistics.



Post-hoc testing

In the case of F-tests used in univariate ANOVA, it is highly desirable to investigate which pairs of conditions / groups were responsible for the significant effect. For this purpose, a post-hoc test is available. BESA Statistics uses a Scheffe test with subsequent Bonferroni-Holmes correction - after all, the problem of multiple testing applies for post-hoc tests as well: If, for example, 4 conditions are part of the test, 6 different combinations of pairwise comparisons need to be made. The Scheffe test ensures that the pairwise clusters do not grow outside the boundaries of the previously established F-test clusters. The Bonferroni-Holmes correction is less conservative than the pure Bonferroni correction but still provides a valid correction for multiple comparisons.

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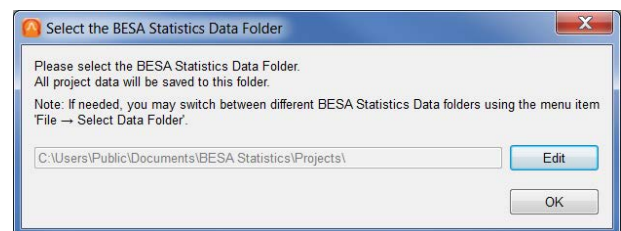
D. Analyzing source waveforms statistically using BESA Statistics

In the following, we will load the source waveforms we created in BESA Research and run a cluster permutation test in order to identify time-regions and sources, which show reliable differences between conditions High and Low across all subjects.

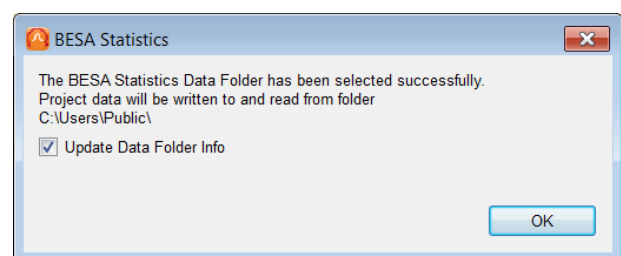
1. **Start** BESA Statistics by double-clicking its icon on your desktop.



2. When BESA Statistics is opened for the first time, the project folder needs to be defined. This is the folder where BESA Statistics stores and reads all project and result data. A dialog box appears. Press **OK** to confirm the pre-selected folder.



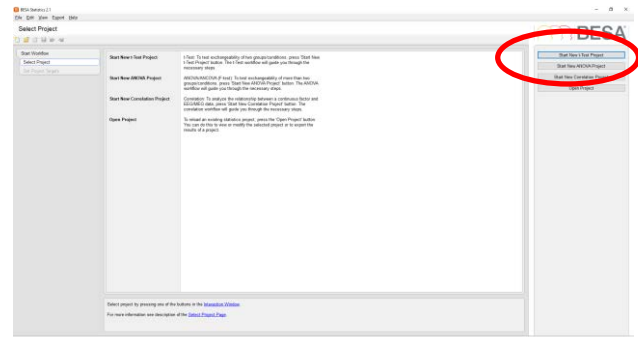
3. Please close the notification box by pressing **OK**. We can now start with setting our project targets.



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- Press **Start New t-test Project** in the interaction window on the right-hand side.



- As we want to analyze the source waveforms we created in the previous steps, please select **SWF** in the interaction window. Press **Start**. We will use a **paired t-test** for preliminary statistics as we compare two dependent samples, i.e. two conditions within the same set of subjects. We will use a **two-tailed t-test** as we do not want to test a specific hypothesis.

Select data type for which statistics shall be performed

☐ TFC

☐ Image

☒ SWF

☐ ERP / ERF

☐ Connectivity

Select statistical test

☒ t-Test

☒ Paired t-Test

☒ Two-tailed

☐ One-tailed-left

☐ One-tailed-right

☐ Unpaired t-Test

- Press **Next** or hit the **space bar** to continue to the next workstep.



- Press **Load Data for Condition 1** in the interaction window. (Please note: Had we selected an un-paired t-test, we would be prompted to load data for Group 1.)

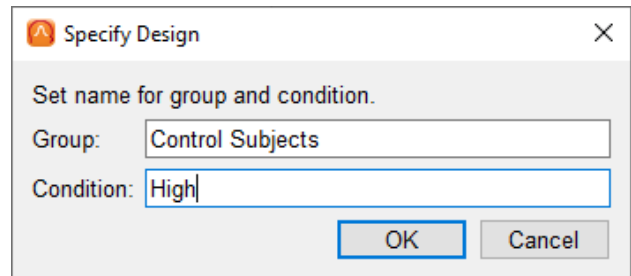
Load Data for Condition 1

Load Data for Condition 2

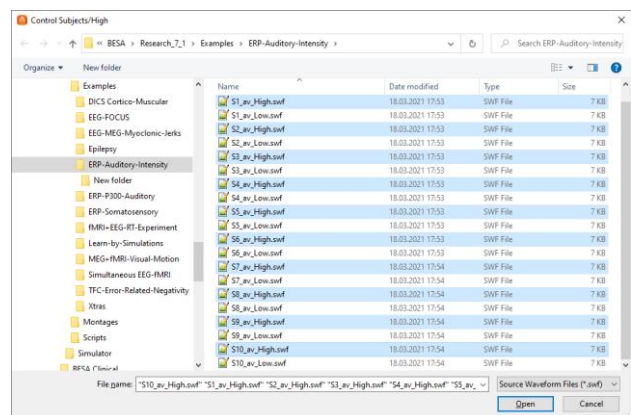
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- Specify the Group name to be “Control Subjects” and the Condition name to be “High” and press **OK**.

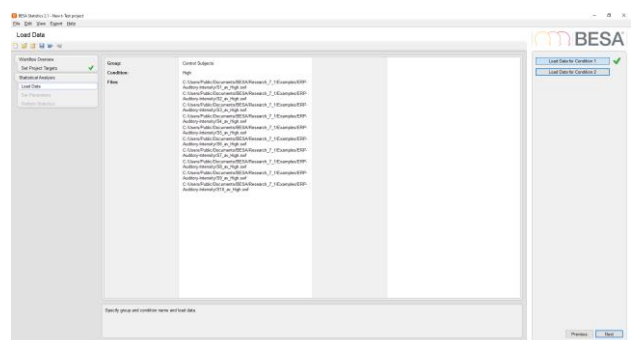


- Please browse to the folder **C:\Users\Public\Documents\BESA\Research_7_1\Examples\ERP-Auditory-Intensity** and select the **10 swf-files** we previously created for condition “High”. Press **Open**.



Note: Depending on the data selection under Set Project Targets, Files of Type will be automatically set to the expected file format.

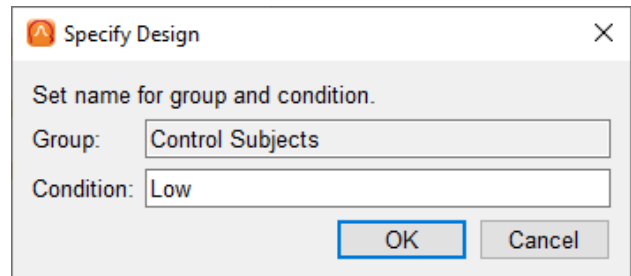
- A summary of the files we selected will be displayed in the main window and a green tick-mark will appear next to the first load-button. Press **Load Data for condition 2** (or press Next or hit the space bar).



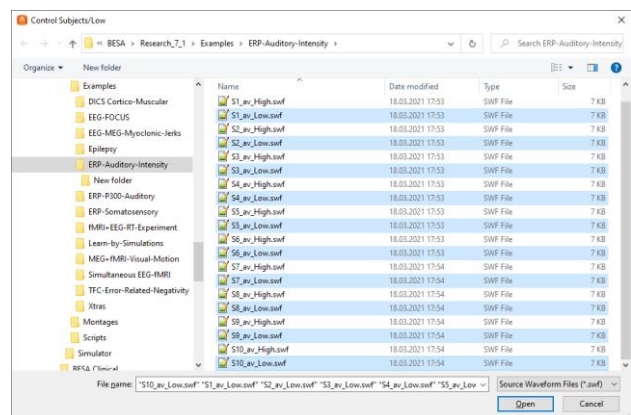
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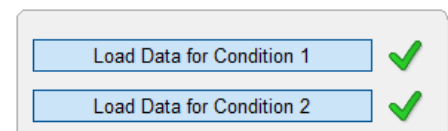
11. Specify the second Condition name to be “**Low**”. Note that Group cannot be edited anymore, as the paired t-test expects two different conditions the **same** set of subjects. Press **OK**.



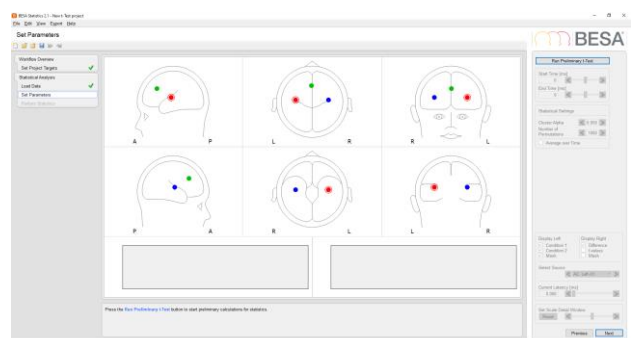
12. Now **select all 10 swf-files** with the extension “**_Low**” and press **Open**. **Important note:** If a paired t-test was selected under Set Project Targets, the number of files loaded in both conditions needs to be **identical**. This is not the case for un-paired t-tests.



13. Again, a summary of all files loaded for the second condition will be displayed in the main window and a green tick-mark will appear next to the second load-button. Press **Next** or hit the space bar to continue.



14. The three sources that are part of our source model are now displayed in the main window. They have the same colors as in the source analysis window in BESA Research. Press **Run Preliminary t-Test** or **Next** to see point-wise t-test results.



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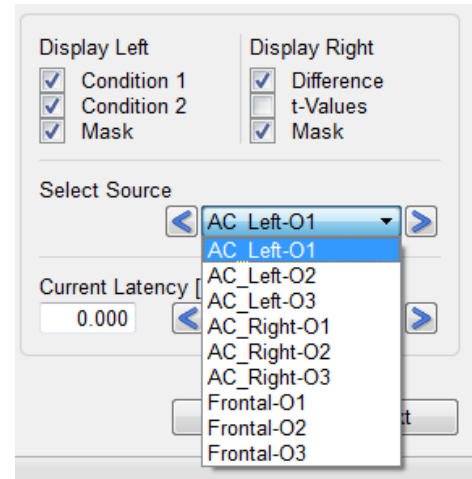
15. Results for the first orientation of the first source in the source model (AC_Left) are displayed in the detail windows. It appears that “Low” has smaller amplitudes than “High” in the baseline, and “High” has smaller amplitudes than “Low” over an extended time-range starting roughly at 150 ms.

Important note: These are preliminary results that are not corrected for multiple comparisons! They should not be interpreted. They only serve as an initial orientation for what is in the data and for defining regions of interest.

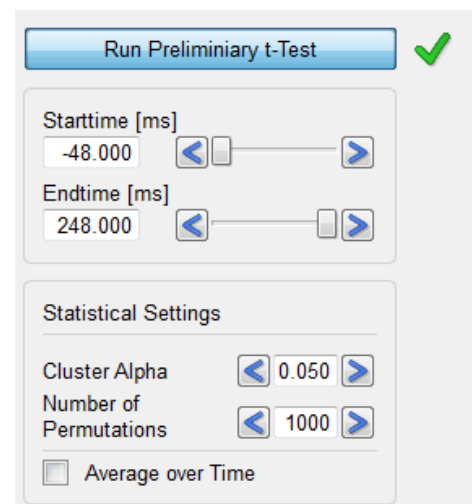
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16. Different sources and orientations can be selected in the drop-down menu of the interaction window. Under “Display Right” a selection can be made between Difference (i.e. in this case “High” minus “Low”) or t-values (point-wise). The according selection will be displayed in the right detail window. A mask indicating significant time-periods can be switched on or off for both detail windows.



17. It is possible to restrict further analysis to a region of interest by changing the Starttime and Endtime. This can increase the chance that a cluster survives permutation as the distribution of cluster values is estimated based on a restricted sub-set of data-points. For example, one might only include the post-stimulus period in the calculations. We will not restrict the time-window now but see what happens to the cluster in the baseline after permutation.



Under the section “Statistical Settings”, a Cluster Alpha value needs to be set. This value refers to the significance level that is the threshold for a data-point to enter a cluster. The default value – which we will use now – is **p = 0.05**. However, it can also be a value larger or smaller than 0.05, larger p-values leading to larger clusters. **Please note that the Cluster Alpha value does not equal the significance level of the permutation statistic!**

The number of permutations also needs to be set. The default level – which we will be using – is **1000** in order to get a reliable estimate for a significance level of $p = 0.05$, i.e. if the test is run multiple times, the same clusters will stay significant. The possible number of permutations is restricted by the number of subjects and the type of preliminary t-test (paired

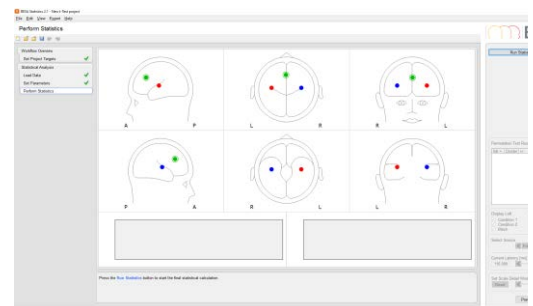
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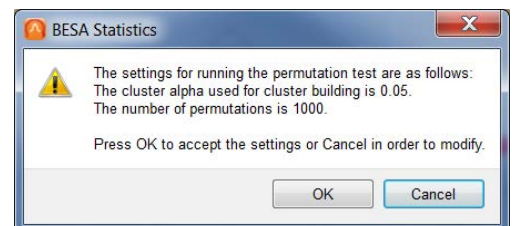
or unpaired, see above). If 1000 exceeds the number of possible permutations, BESA Statistics will automatically reduce the value to the number of possible permutations.

Press **Next** or hit the space bar to continue.

18. Press **Run Statistics** to start the permutation process and all according calculations necessary for determining the probability of our initial clusters.

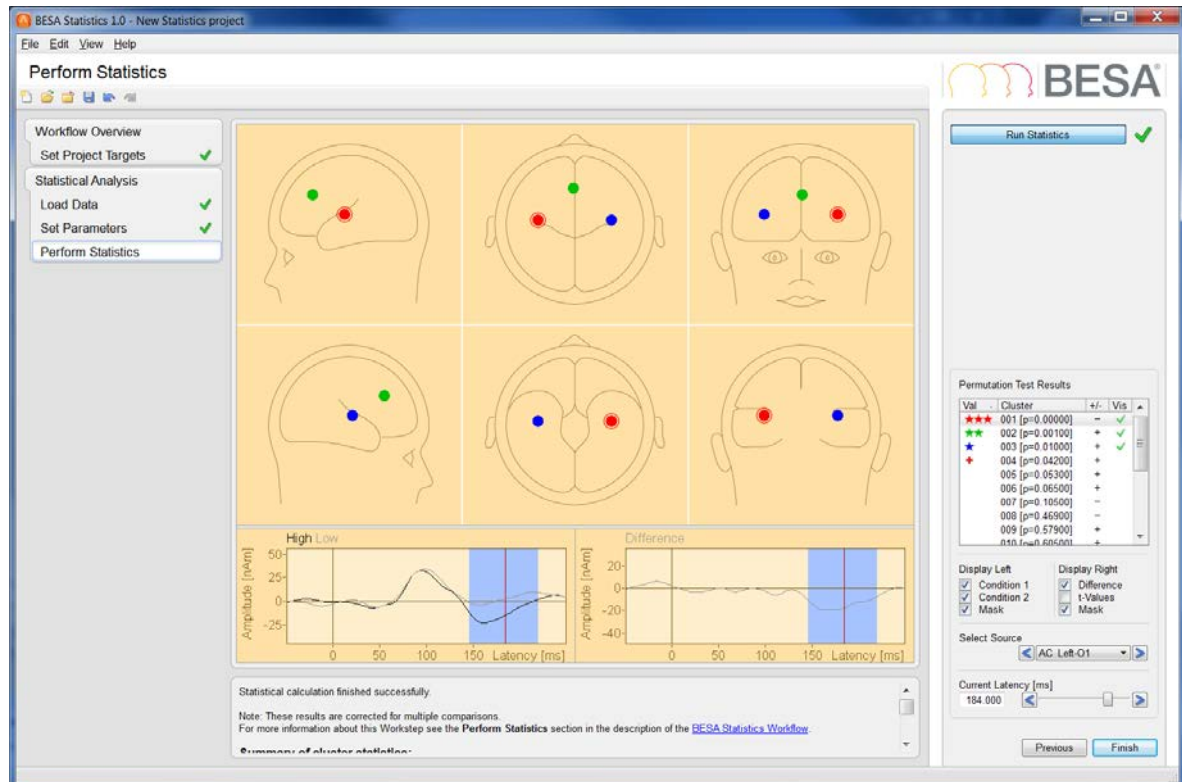


19. An information window appears summarizing the settings for the cluster permutation test. Press **OK** to continue. Please note that the following calculations can be time-consuming depending on the type of data and the number of data-points.



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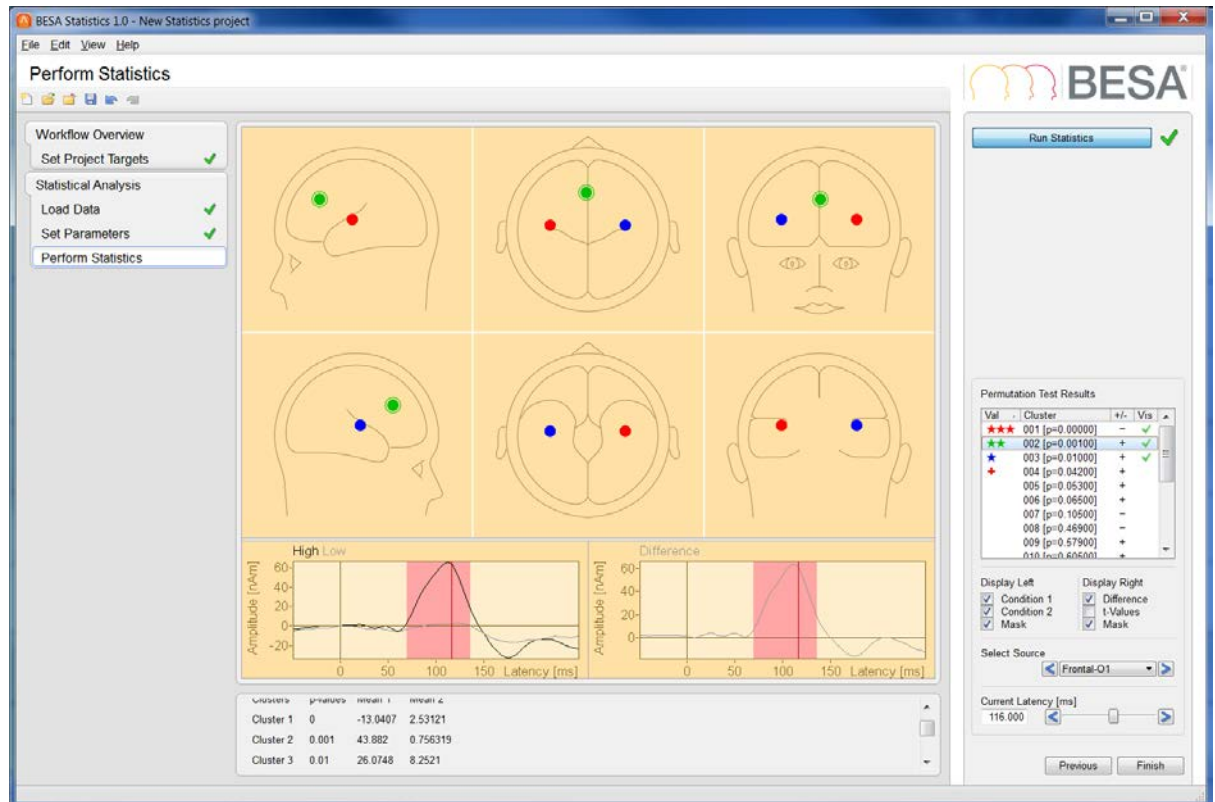


20. Once permutation statistics are computed, the cluster with the largest cluster value (and smallest p-value) is automatically selected and displayed. Up to 100 clusters are displayed in the interaction window and significant clusters are marked with stars according to their significance level. Clusters that do not reach $p = 0.05$ but are smaller than $p = 0.1$ are marked with a “+”.

The biggest cluster is the one we saw previously (see step C 15) in source AC_Left in the first orientation. We can now be certain that “High” does indeed lead to a more negative amplitude than “Low” in an area of the left auditory cortex associated with tangential activity. This effect lasts from 144 ms to 216 ms. It is noteworthy that the preliminary cluster that could be seen in the baseline did not survive permutation!

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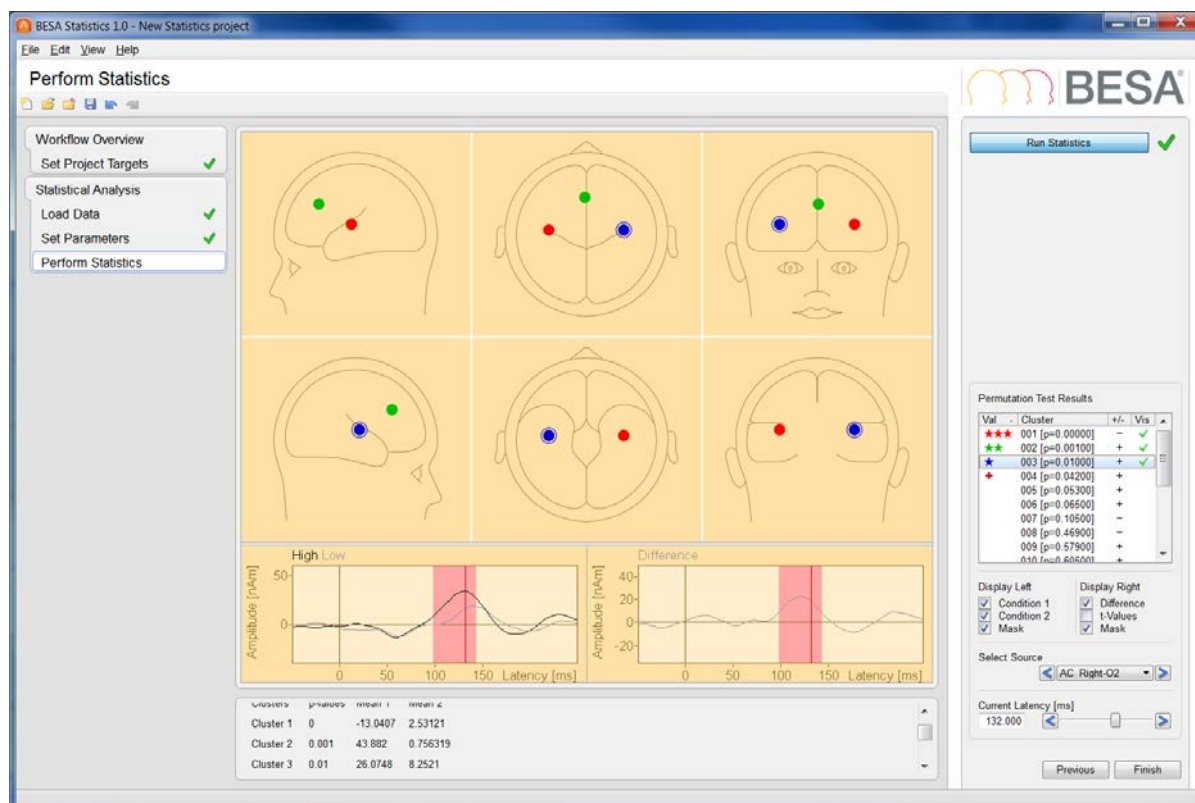
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21. The second significant cluster is found in the first orientation of the frontal source. “High” leads to larger amplitudes than “Low”. This effect starts at 68 ms and ends at 136 ms.

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22. The last significant cluster can be found in the second orientation of AC_Right, i.e. the auditory cortex region associated with radial activity. Again, “High” has larger amplitudes than “Low” from 100 ms to 144 ms.

23. A summary of cluster statistics containing the cluster p-values and the condition means are displayed¹⁹ in the information window below the main window.

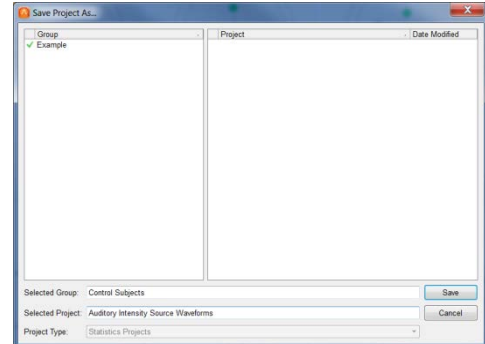
Summary of cluster statistics:			
Clusters	p-values	Mean 1	Mean 2
Cluster 1	0	-13.0407	2.53121
Cluster 2	0.001	43.882	0.756319

¹⁹ It is also possible to export all statistical results as well as group/condition and individual means as csv-files. Likewise, it is possible to export all images as png or eps-files.

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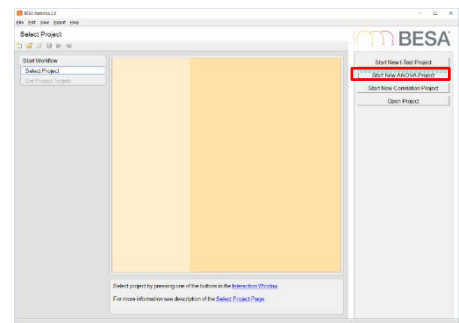
24. Press **Finish** to end and save the current project. Save it under an appropriate name.



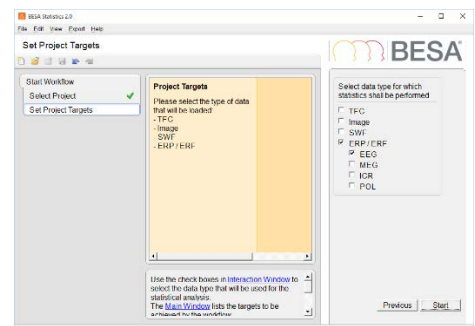
E. Comparing more than two conditions or groups with BESA Statistics

In the following, we will explore the possibility to compare more than two conditions or groups using the ANOVA workflow. We will continue using our auditory intensity data set, however this time we will work with scalp data and will be asking if there is a significant difference between the conditions: 60dB, 70dB, 90dB and 100dB. Additionally, we will consider a variable of no interest, in this case the number of trials per average per condition per subject, and will thus be using the ANCOVA workflow.

1. Start BESA Statistics by double-clicking its icon on your desktop. Then start a new ANOVA project by selecting the Start ANOVA project button.



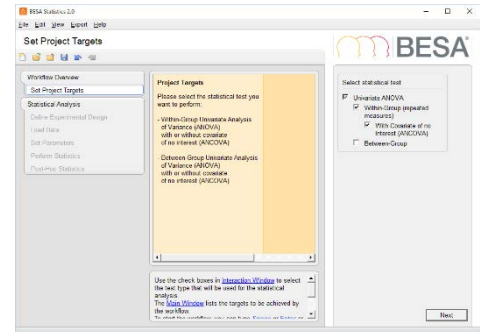
2. Please select the data type to be analyzed. In this case it will be an ERP/ERF experiment and we will be looking at EEG data directly. Press **Start** to proceed to the next step.



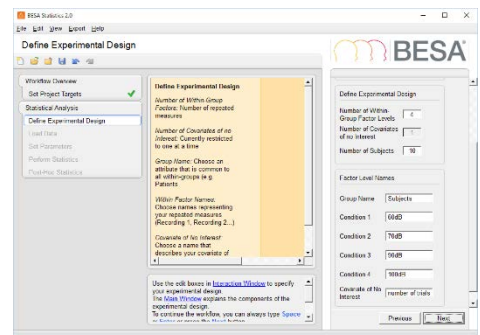
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- As we are dealing with different conditions within one group of subjects we select the **Within Group (repeated measures)** option. We wish to consider the number of trials per condition per subject as a covariate of no interest and thus select the option **With Covariate of no Interest (ANCOVA)**. Please press **Next**.



- Our example auditory intensity experiment has **10** subjects and we are considering **4** conditions (**60dB**, **70dB**, **90dB** and **100dB**) and our covariate of no interest is the **number of trials**. Please enter the values in the respective fields and press **Next**.

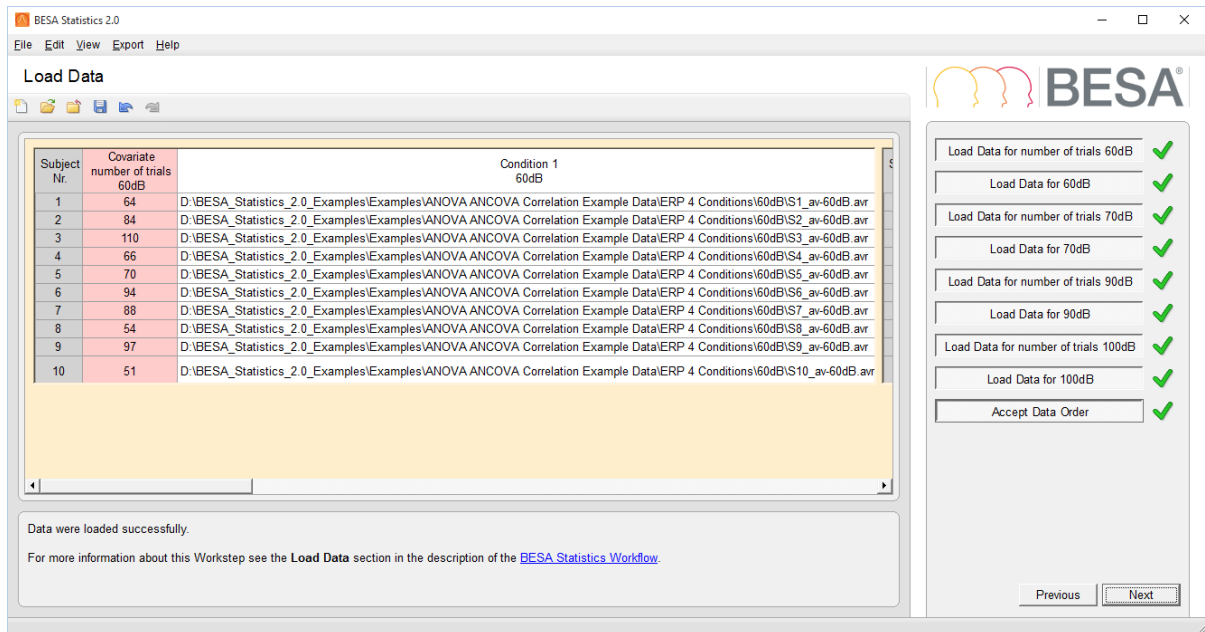


- Load all covariates of no interest and conditions for all subjects. The respective files are located in the BESA examples folder:
..\BESA_Statistics_2.0_Examples\Examples\ANOVA ANCOVA Correlation Example Data\ERP 4 Conditions\... Please note that as we will be permuting over the conditions (whose difference we are probing) the order of the subject files must be the same for all conditions. If this was an in-between group case instead, the order of the subject files would not matter. Check that the order is indeed the same. In case that it is not, the order can be changed by clicking into the respective cell and using the arrow button that appears. When

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Tutorial 13 – Cross-subject Statistics

you have confirmed the order please select **Accept Data Order** and press **Next**.

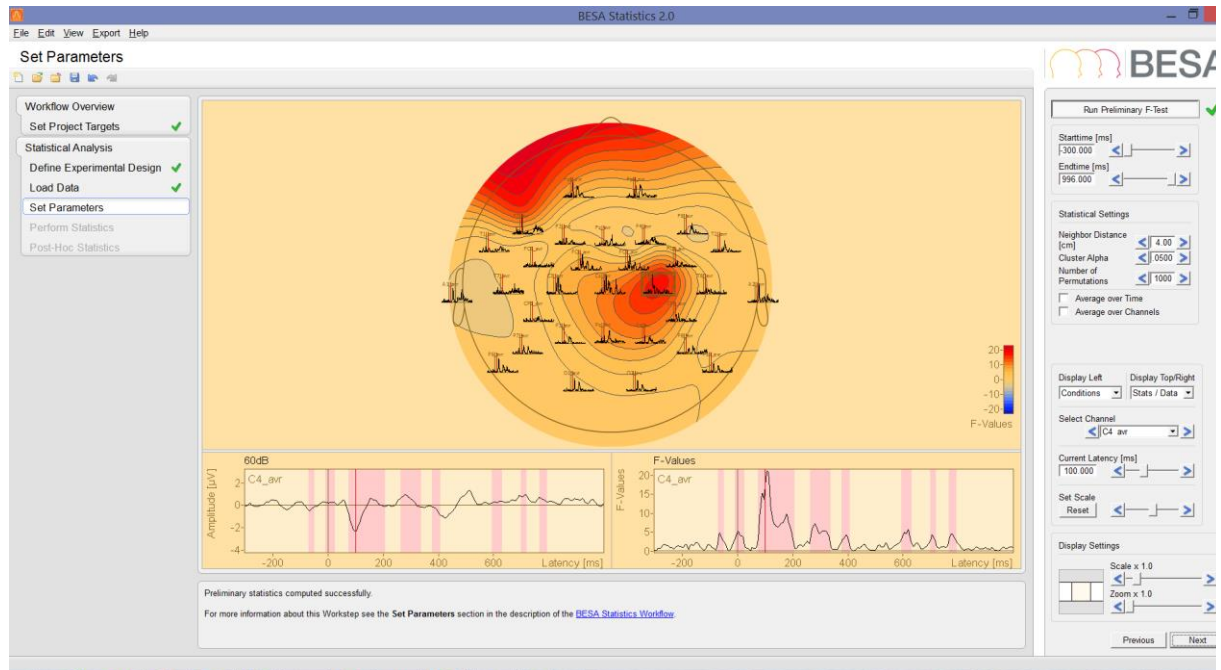


- Once you pressed **Run Preliminary F-Test** you can recognize several regions where significant results were found. Change the **Current Latency** to 100 ms. Using the map of F-values you can pick the channel with the peak of the map (C4). Click on this channel in the Top View to see the F value and amplitude distribution displayed in the selection window. You can choose to visualize each of the conditions via the **Display Top/Right** drop down menu. Note the maximum around the C4_avr channel that corresponds to a preliminary cluster as is evidenced by the red shading in the right display window. In the left detail window, the amplitude plot for the 60dB condition is shown. The **Display Left** drop down

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menu can be used to display the other conditions including an overlay of several conditions.



- In the menu **Statistical Settings**, we should choose a neighborhood relation for the channels. Please select 6 cm for **neighbor distance**. Larger values would produce more spatially extended clusters. The **cluster alpha** should be set to 0.01. Please note that, as previously mentioned, the cluster alpha is not the significance level of the permutation test. Instead, it determines the threshold for which points will be part of the same cluster in each permutation. The **number of permutations** should be set to 1000.

Statistical Settings

Neighbor Distance [cm]
6.00

Cluster Alpha
0.01

Number of Permutations
1000

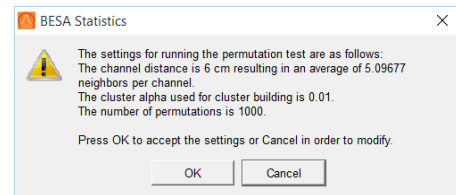
☐ Average over Time

☐ Average over Channels

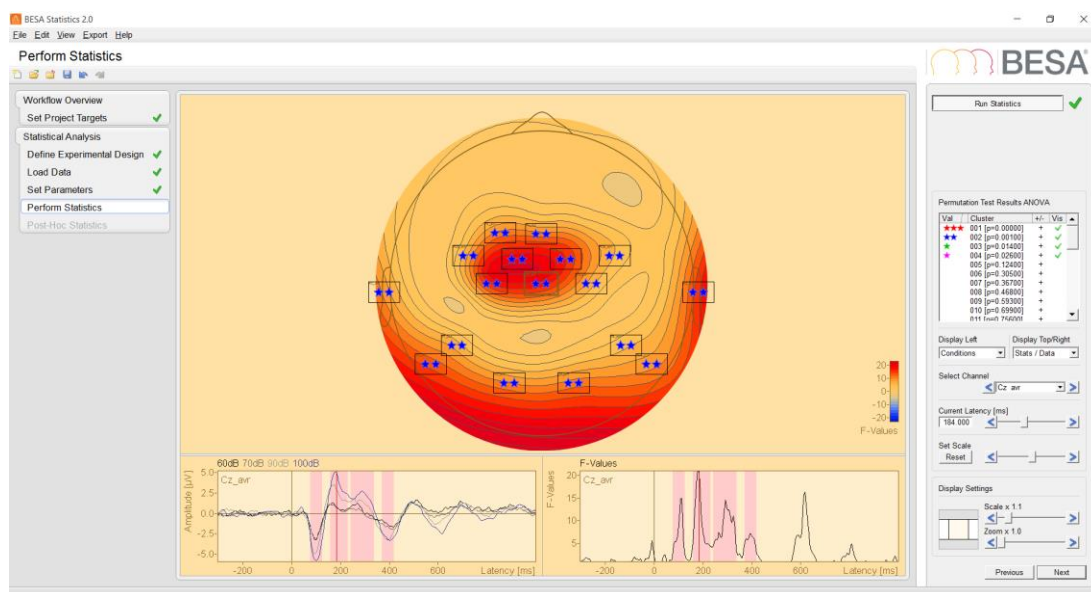
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- Please click on **Next** and on the ensuing screen press **Run Statistics**. A dialog will pop up requesting to confirm the statistical settings. Press **Ok** to proceed with the computations.



- On the **Permutation Test Results ANOVA** list the clusters, that now also have a spatial dimension, are shown in order of smallest p-value first. The clusters marked with stars or plus signs (the latter is not present in the screenshot) have p-values smaller than 0.05. Note that contrary to our previous source waveform example the interpretation of the clusters of scalp recordings might be more challenging. Different clusters might actually be due to the same physiological effect and as such should be interpreted together.



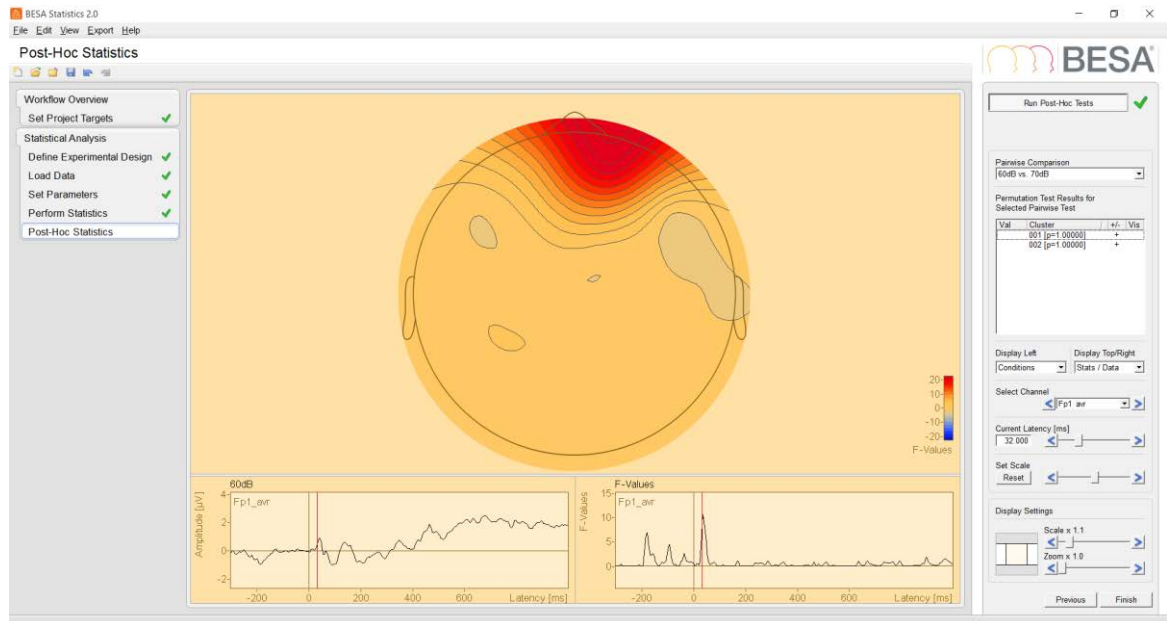
- While browsing through the clusters we might already recognize that the signal from the green source we analyzed earlier in section D is part of one of the star marked clusters. Press **Next** to proceed to the post hoc evaluation.

- In the post hoc workstep we can determine which pairs of conditions actually differ from each other. Select the **Run Post-Hoc Tests** button to start the computations. In the **Pairwise Comparison** menu choose which two conditions are to be compared. By default we start with the first conditions 60dB vs 70dB. The **Permutation Test Results for**

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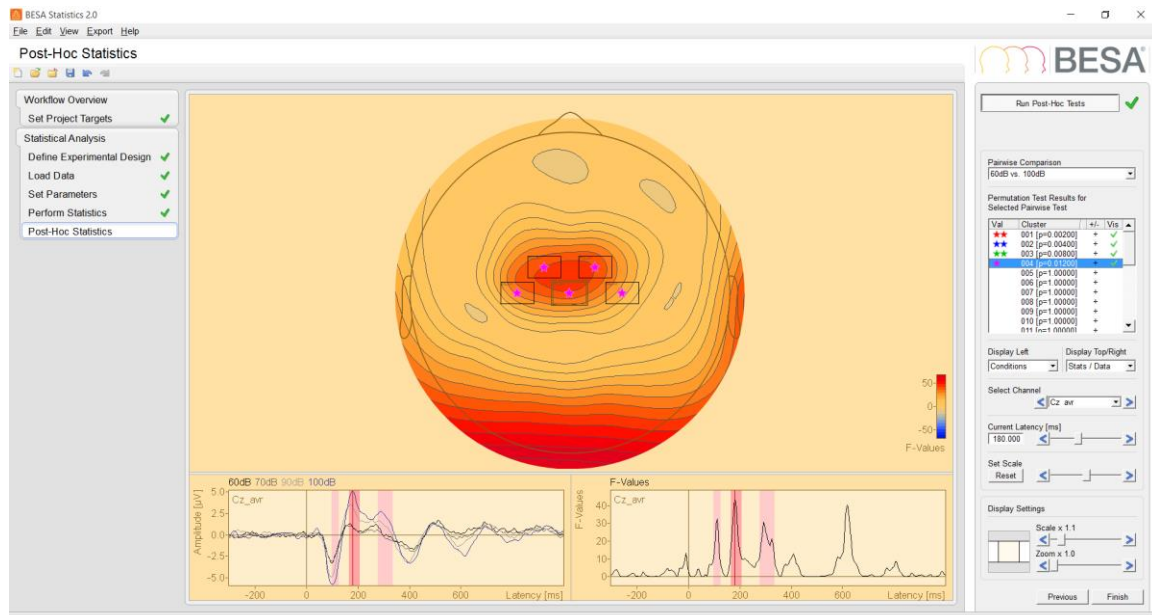
Selected Pairwise Test menu shows that all clusters were discarded by the post-hoc test. Hence we conclude that the conditions 60dB and 70dB are interchangeable. Note that all clusters that were discarded by the post-hoc test are set to p-value = 1.0.



12. When comparing 60dB to 100dB instead a number of clusters survive the post-hoc test. These conditions are therefore significantly different. This goes in line with our earlier findings with the source space data set where we find a frontal activity at high intensities to be significantly different from that at low intensities. The cluster highlighted below as well as the third cluster suggests the same interpretation for early latencies. The clusters 1 and 2 are active at later latency ranges.

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F. Analyzing the correlation between physiological response and a covariate of interest

The data we will use for the following example were kindly provided by Peter Schneider, University of Heidelberg, Germany. Part of the data was used in a publication by Schneider et al. (2005) in Nature Neuroscience²⁰.

The experiment involved measuring MEG data while playing tones (instrumental sounds) to professional musicians. Subjects listened passively. Between 500 and 1000 stimuli were recorded and averaged for each subject.

For each subject, a musicality index was also established using the AMMA test for musical aptitude (Advanced Measurement of Music Audiation by E.E. Gordon, 1989). The tonal score was used for this experiment. It can lie in a range between approx. 20 points (random guessing) and 40 points.

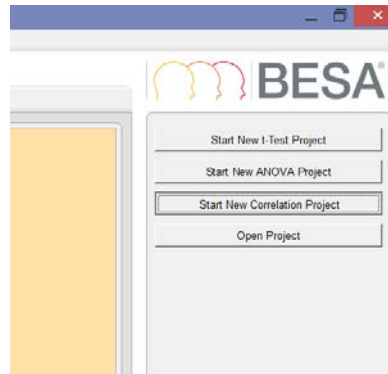
²⁰ P. Schneider, V. Sluming, N. Roberts, M. Scherg, R. Goebel, H.J. Specht, H. G. Dosch, S. Bleeck, C. Stippich & A. Rupp (2005). Structural and functional asymmetry of lateral Heschl's gyrus reflects pitch perception preference. Nature Neuroscience 8:9, 1241-1247

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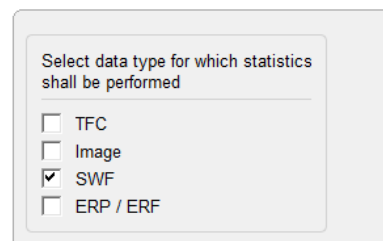
Tutorial 13 – Cross-subject Statistics

We want to find out whether there is a correlation between the strength of source activation following the musical stimulus and the musical aptitude.

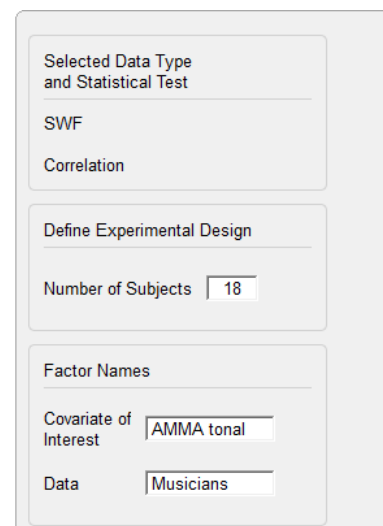
1. Start BESA Statistics by double-clicking its icon on your desktop. Then start a new Correlation project by selecting the **Start New Correlation Project** button.



2. Select type **SWF**. Press the **Start** button.

This is a dialog box titled 'Select data type for which statistics shall be performed'. It contains four checkboxes: 'TFC', 'Image', 'SWF' (which is checked), and 'ERP / ERF'.

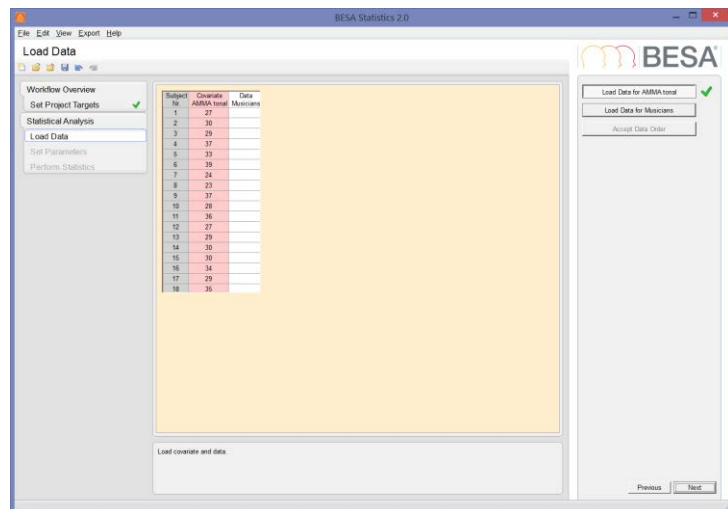
3. Enter the Number of Subjects: 18, and names for the covariate of interest and data (AMMA tonal and Musicians). Then press the **Next** button.

This is a multi-section dialog box. The first section, 'Selected Data Type and Statistical Test', shows 'SWF' and 'Correlation'. The second section, 'Define Experimental Design', has a 'Number of Subjects' field with the value '18'. The third section, 'Factor Names', has two fields: 'Covariate of Interest' with the value 'AMMA tonal' and 'Data' with the value 'Musicians'.

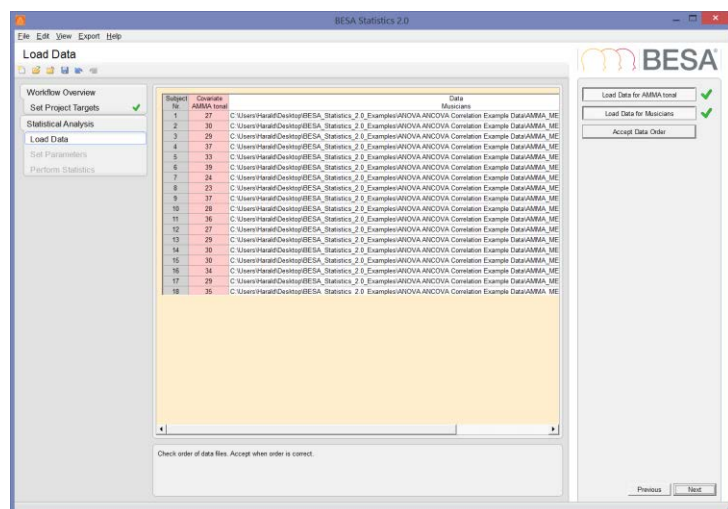
BESA® Research 7.1

Tutorial 13 – Cross-subject Statistics

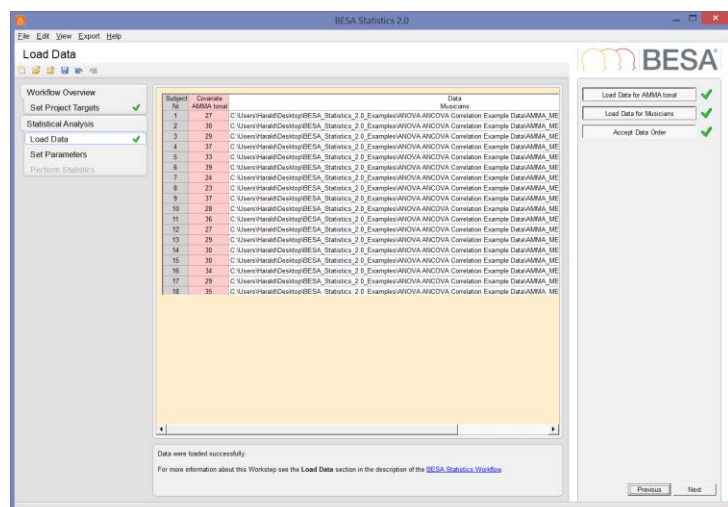
- The next step is loading the data for the covariate. Press the **Space** key on the keyboard or the button **Load Data for AMMA tonal**. Then browse to the file **AMMA_MusAlphabetical.txt** in the folder **AMMA_MEG** that should be on your desktop. Open the file.



- Now load the MEG data. Press the second button or the **Space** key on the keyboard. Browse to the folder **Mus_SWF300** and select all files in the dialog box. Then press **Open**.



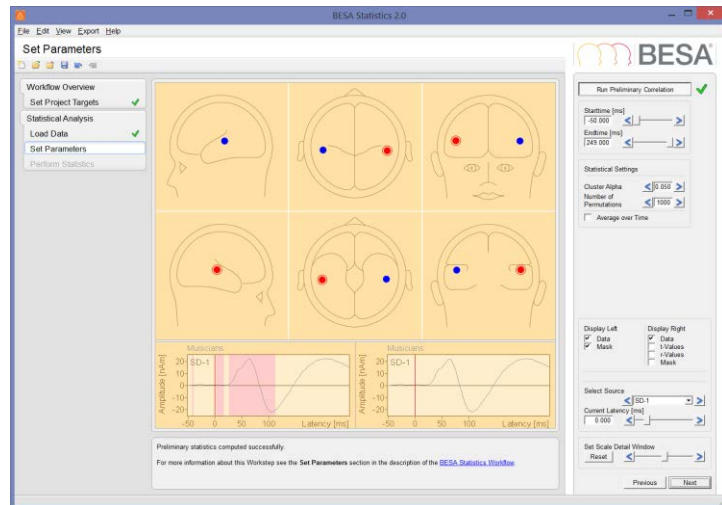
- Check that the files are sorted alphabetically (the AMMA scores were given in alphabetical order). If not, click into a row to re-sort using the arrows that appear. Once finished, press the button **Accept Data Order**. Then press **Next**.



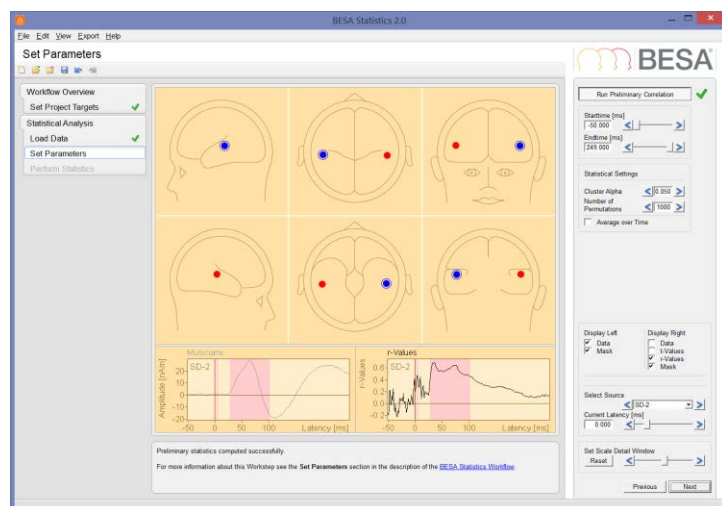
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Tutorial 13 – Cross-subject Statistics

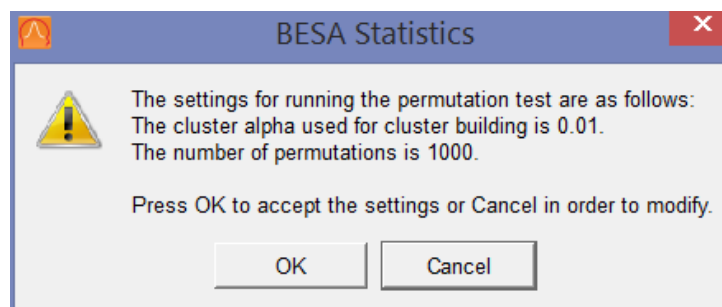
- The plot shows the approximate position of the dipoles. Press the button **Run Preliminary Correlation**. The widgets below the head symbols show the zones where an initial correlation was found for source SD-1 in the right auditory cortex.



- Select the source SD-2 and change the display of the right widget to show **r-Values** and the **Mask**. The oscillations of r values in the baseline and early post-stimulus and a more steady behavior at later latencies are apparent. Note that for SD-1, there is some significant correlation in the baseline, too.



- Change the **cluster alpha** to 0.01. Leave the number of permutations and the time interval unchanged. Press **Next**, then **Run Statistics**. Press **OK** when the dialog box appears.

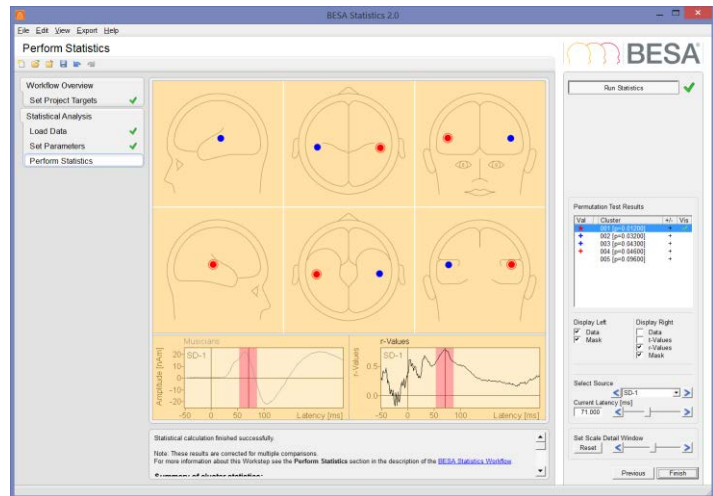


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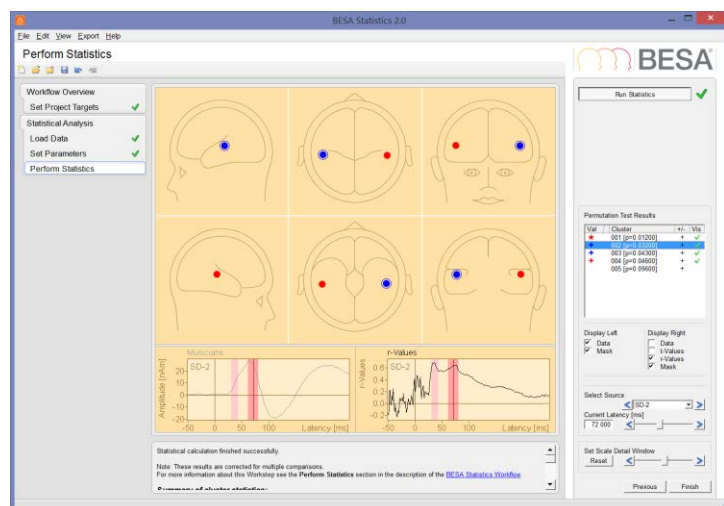
Tutorial 13 – Cross-subject Statistics

10. The Correlation test finds one significant cluster in SD-1, and three trends. (Note that the trends have p-values < 0.05, but are not deemed significant since we can have positive or negative correlation, i.e. we are running a two-sided test).

The right-hemispheric cluster starts just after 50ms post-stimulus, and extends to about 85 ms. It ends well before the N100 response takes place.



11. Select cluster 2. This cluster is in the left hemisphere, and is in a similar interval between approximately 60 and 80 ms.
12. The other trends also appear in early processing intervals.
13. Press Finish and save the project.



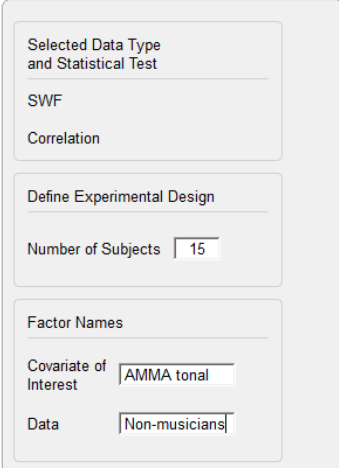
This experiment shows that for professional musicians, there is a (positive) correlation between the auditory response and the musical aptitude, which manifests itself in the early auditory processing stages between 50 and 90 ms after a tonal stimulus. There is no significant correlation at later stages of the processing (N100, N150).

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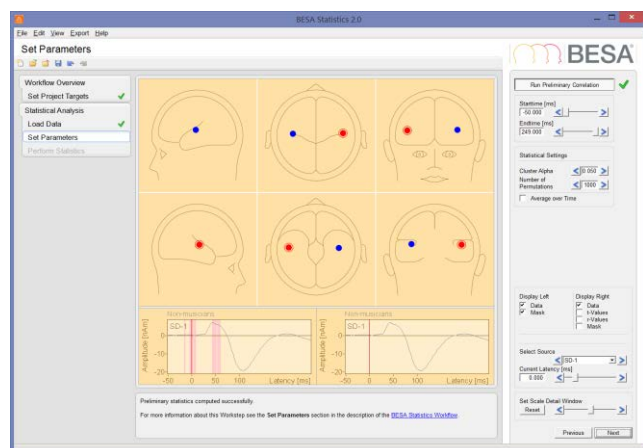
Now let us see if we can get similar results for non-musicians. We will follow the same steps.

14. Start a new Correlation project by selecting the **Start Correlation Project** button. Then select **SWF** as data type. Press **Start**. In the step **Set Project Targets**, set **Number of Subjects** to 15, and name the factors as AMMA tonal and Non-musicians. Press **Next**.



15. Load the data. The covariate is in the text file **AMMA_NonmusAlphabetical.txt**.

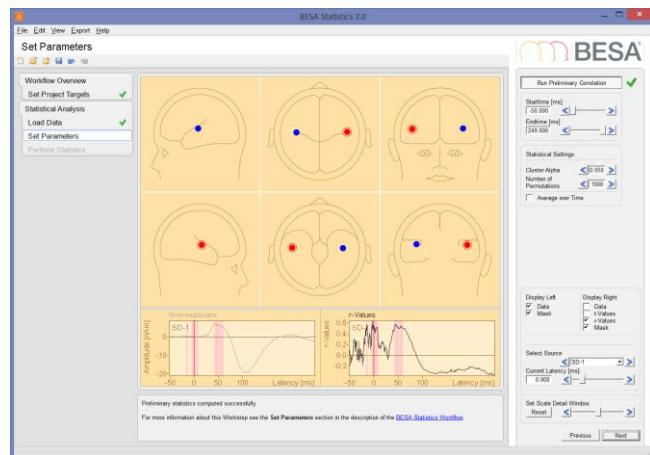
The SWF data are in folder **NonMus_SWF300**. Select all files and open. Then accept the data order and press **Next**. On the **Set Parameters** workstep, press the button **Run Preliminary Correlation**. The initial significance plot appears.



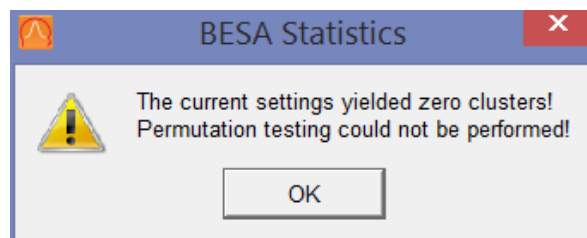
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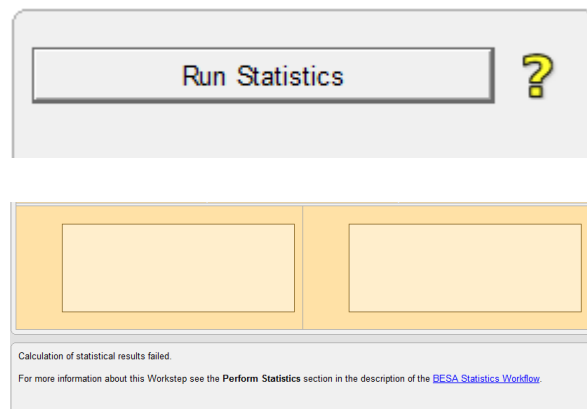
16. Switch to **r-Values** for the right widget and activate the mask. Toggle between the two sources. We can see that there is some preliminary correlation around the P50 latency similar to the previous example, and also around the stimulus latency.



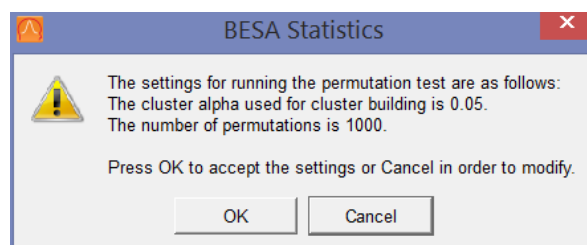
17. Let us proceed as before. Set the cluster alpha value to 0.01. Then press **Next** and **Run Statistics** on the next screen. Accept the settings in the dialog.



A message box appears to inform that no clusters emerged. The result is a question mark beside the **Run Statistics** button, and a notification at the bottom that the calculation failed.



18. The reason for this is the problem that not a single cluster could be built with the stronger condition of a 0.01 alpha value. Press the **Previous** button to go back to the workstep **Set Parameters**. Increase the alpha



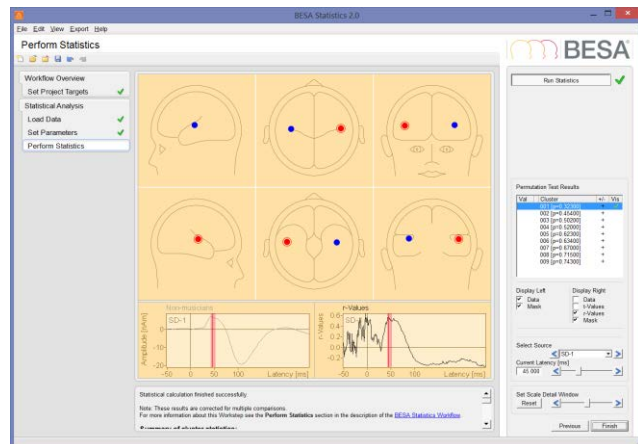
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value back to the original of 0.05.

Then advance and re-run the Statistics.

19. With this setting, clusters are found. However, none of them is significant or shows even a trend.



We can conclude that contrary to professional musicians, for non-musicians, there is no significant correlation between the tonal musical aptitude and the amplitude of the auditory response to musical tones in the primary auditory cortex.

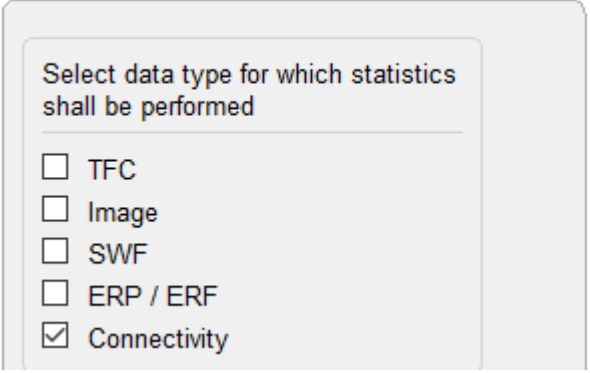
G. Analyzing connectivity data in BESA Statistics

Cluster permutation statistics can also be performed on connectivity data saved by BESA Connectivity. BESA Connectivity calculates the connectivity values in a channel-by-channel matrix, resulting in $(N_{\text{channel}} * N_{\text{channel}} - 1)$ channel pairs (for some connectivity measures like Granger causality, the order in the pairing of channel 1 and channel 2 is not interchangeable). For connectivity measures, clusters are always calculated within the channel pair; they can not spread from one channel pair to another one. However, this still leaves the time and frequency dimensions for clusters to grow in.

The present example was kindly provided by Michael Johnson, University of Utah, USA. It consists of 10 subjects who underwent a guided meditation exercise. The question is whether long-range connectivity increases with a deeper meditation state, and if so, at which frequency ranges.

Data were pre-processed using a Default Mode Network source montage, and trigger events were inserted at regular intervals at the beginning of the meditation exercise in a period of 5 minutes, and also towards the end (approximately 1 hour later), also in a period of 5 minutes. Noise sources were removed from the source montage, in order to focus on the default mode network only. Overlapping epoched data were exported to BESA Connectivity, and the coherence between all source channels with all orientations was then calculated in a frequency range between 1 Hz and 30 Hz. The final data were exported from BESA Connectivity for statistical analysis (manuscript in preparation). These are the data we will now evaluate.

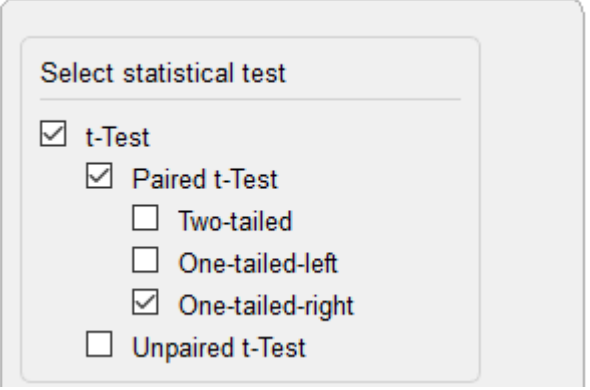
1. In BESA Statistics, start a new t-test project. Then select the box Connectivity.



Select data type for which statistics shall be performed

- ☐ TFC
- ☐ Image
- ☐ SWF
- ☐ ERP / ERF
- ☒ Connectivity

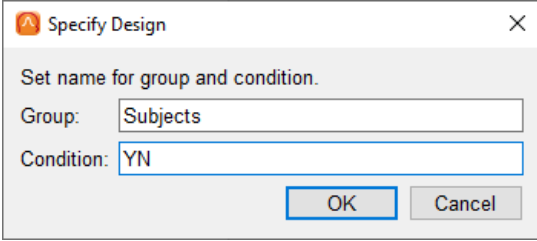
2. Select a paired t-test and choose the option One-tailed right.



Select statistical test

- ☒ t-Test
 - ☒ Paired t-Test
 - ☐ Two-tailed
 - ☐ One-tailed-left
 - ☒ One-tailed-right
 - ☐ Unpaired t-Test

3. Provide names for the group and the condition. First we will load the final (Yoga-Nidra or YN) phase.



Specify Design

Set name for group and condition.

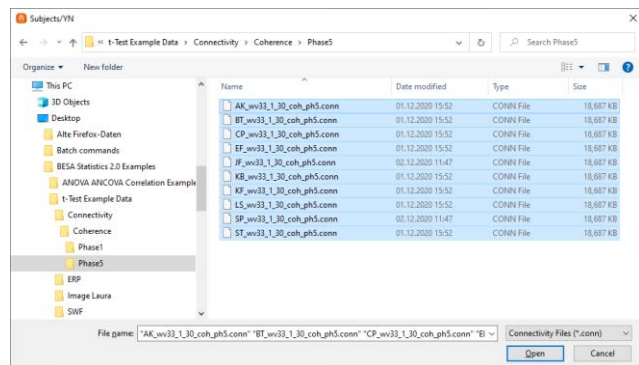
Group:

Condition:

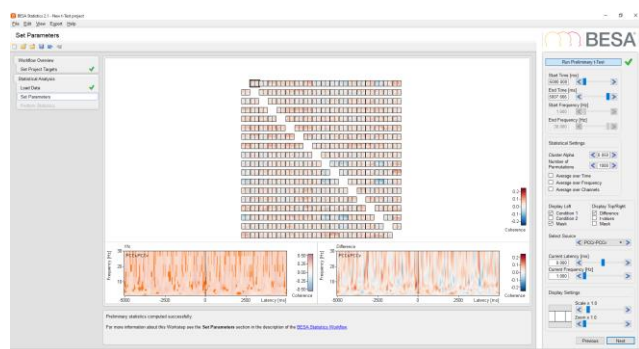
BESA® Research 7.1

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4. Browse to the Statistics example data and into the sub-folder t-test Example Data, and then Connectivity. In sub-folder Coherence / Phase5, select all files.



5. Do the same for the files in Phase1. Check that the file order matches. Then press Next to advance to the Set Parameters work step.
6. Press the button Run Preliminary t-Test. The matrix containing 18 x 18 channels (6 DMN source channels with 3 orientations each) is shown.



- Run Preliminary t-Test

Start Time [ms]
3.833

End Time [ms]
5007.666

Start Frequency [Hz]
1.000

End Frequency [Hz]
30.000

Statistical Settings

Cluster Alpha
0.050

Number of Permutations
1000

☒ Average over Time

☐ Average over Frequency

☐ Average over Channels

-
- The screenshot shows the BESAP Performance Statistics window. The main area contains a table of performance metrics for various simulation runs. The table has columns for 'Run Time', 'CPU Time', 'Memory', and 'Performance'. The rows represent different simulation runs, with the first row being the 'Baseline' run. The table is sorted by 'Run Time' in ascending order. Below the table are two heatmaps: 'Performance vs. Run Time' and 'Performance vs. CPU Time'. The heatmaps show the performance of the simulation runs across different parameters. The right sidebar contains a 'Parameters Test Results' section with a tree view of simulation parameters and their values.

The frequency range is shown on the right, and is from 2-7 Hz, so in the theta spectrum range. The two trends that did not reach significance are between Left angular gyrus and left lateral temporal region, and posterior cingulate gyrus and left lateral temporal region.

Appendix A – List of Error and Warning Messages

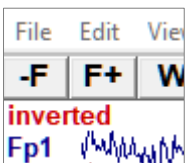
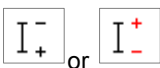
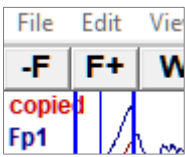
A. Error messages

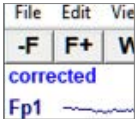

Window	Message text / Symbol	Description
Review	Sentinel LDK Protection System No valid license detected. Please attach a BESA HASP dongle in your local network. Make sure that the HASP driver is installed. Also ensure that your HASP is up-to-date and that you own a license for this version of BESA Research (contact sales@besa.de). (H0007)	If a dongle with a valid license is not found or the license driver is not correctly installed, this message is shown.
Review	Error in BESA-Matlab interface setup! BESA is set up for Matlab #.#. Besa.ini specifies 32-bit, but there appears to be a path to a 64-bit Matlab in the PATH environment string:	This message indicates a platform mismatch between MATLAB setting in BESA.ini (<i>Platform=32</i>) file and the installed MATLAB (<i>64-bit MATLAB</i>). The platform of both is required to be the same. BESA.ini file is usually located in the following folder: C:\Users\Public\Documents\BESA\Research_7_1\
Review	Error in BESA-Matlab interface setup! BESA is set up for Matlab #.#. Besa.ini specifies 64-bit, but there appears to be a path to a 32-bit Matlab in the PATH environment string:	This message indicates a platform mismatch between MATLAB setting in BESA.ini file (<i>Platform=64</i>) and the installed MATLAB (<i>32-bit MATLAB</i>). The platform of both is needed to be the same. BESA.ini file is usually located in the following folder: C:\Users\Public\Documents\BESA\Research_7_1\
Review	An error occurred... The marked block is empty or too narrow. Please increase the marked block size. The BESA Source Analysis module cannot be started.	This message is shown when the <i>ESI</i> (or <i>MSI</i>) button in the control ribbon is clicked without setting a proper data block.
Review	No Triggers in Data file There are no triggers in the data file. Please import triggers or create triggers using the ERP menu commands before editing the paradigm.	If no trigger events exist in the data file, this message is shown after selecting the <i>ERP / Edit Paradigm</i> menu entry or clicking the <i>ERP</i> button in the control ribbon).
Review	Batch Interrupt	This message is shown when an error occurs during a batch process.





	Batch interrupted on file 1: [file_name]: Task [task_name]. Stop batch? ('No' continues batch will next data file) <input type="checkbox"/> Closing with 'Yes' in ## seconds	Detailed error messages can be checked in the <i>Batch Log</i> dialog after closing the dialog.
Review	BESA Batch Unable to run more than one batch at a time!	If this message shows, it is possible that a previous instance of BESA Research has not shut down correctly and there may still be a process of BESA Research running in the background. You can check for this by closing BESA Research and then open the "Task Manager" of Windows. If BESA Research is still running, either log off and on again or close the BESA Research background processes in the Task Manager (by right-click on the corresponding row in the Task Manager display). Then, re-start BESA Research.
Source Analysis	An error occurred. There was a problem with neighborhood calculation. Please lower the voxel size in the image settings.	SESAME: This error message is shown when the number of neighbors of a source location is too small in neighborhood calculation.
Source Analysis	An error occurred. There was a problem with neighborhood calculation. Please increase the voxel size in the image settings.	SESAME: When the voxel size in Talairach space is set too small (e.g. 3 or 4 mm) in the <i>General</i> tab of the <i>Image Settings</i> dialog, neighborhood calculation may be failed.
Source Analysis	Image Error Image error: probably due to lack of sufficient memory <input type="checkbox"/> closing with 'OK' in # seconds	This error message may be shown after aborting a source imaging computation or if a memory allocation issue occurred.

B. Warning messages and symbols

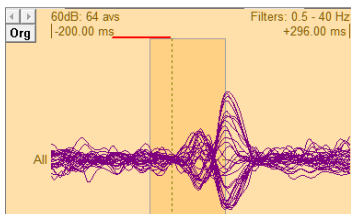
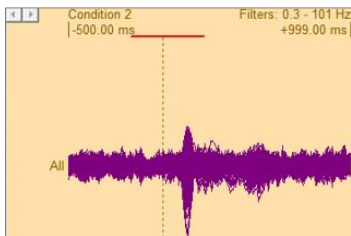
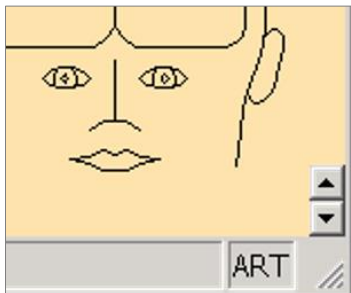
Window	Message text / Symbol	Description
Review	WARNING: Edit Channel Configuration Editing the channel configuration will change the channel assignment of your EEG data file. You should make changes only if channels have been incorrectly assigned or not defined during data acquisition. Do you want to proceed?	This message is shown after selecting the <i>Edit / Channel configuration</i> menu entry.

Review	Warning Warning: This selection causes the data to be inverted when they are read. Any files, e.g. averages, that are generated from the data file will also be inverted! Use only if you need to correct data that have the wrong polarity!	This message is shown after selecting the <i>View / Inverted data</i> menu entry.
Review		The “inverted” text appears in the top-left corner of the review window after selecting <i>View / Inverted data</i> menu entry to warn that the data is inverted.
Review		When the <i>View / Show negativity up</i> menu entry is unchecked, the color of the + and - symbols on the right side of the review window is changed to red to warn about the changed setting.
Review		The “copied” text appears in the top-left corner of the review window to note that at least one of the displayed average buffers (<i>View / Average Buffers</i>) was copied from another data file.
Review	Open Source analysis module Warning: At least one average buffer was copied from another data file.	If at least one of the displayed average buffers was copied from another data file, this warning message is shown when source analysis starts (<i>Process / Source Analysis</i>). After pressing the “OK” button of this warning dialog, source analysis is aborted.
Review	No Averaged Segment Found No averaged segments were found in the data file. Please mark a block to indicate the data you want to view.	This message is shown when the <i>View / Top view of data...</i> menu entry is selected (or the <i>TpV</i> button in the control ribbon is clicked) without marking a data block or opening averaged segments.
Review	BesaExport High cutoff filter set to 35% sampling rate to avoid aliasing. Press Filter button to adjust filters if necessary. If your data are sufficiently low-pass filtered, you may uncheck ‘Current filters’.	<i>Export data</i> dialog If export without filters is selected or if the current high cutoff filter is set to a value that is higher than 1/3 of the sampling rate, BESA Research sets the filter and shows this warning message. The filters can be adjusted by pressing the “Filters...” button in the <i>Export data</i> dialog.
Review	WARNING Please select a valid tag pattern (pattern 1-5) for search/average	This message is shown if no valid pattern (Pattern 1–5) is selected in the context menu for search/average.
Review	Processing Please mark a latency or a block	This message is shown when the <i>Process / Source Image</i> menu entry is selected without marking a block.

Review		The “corrected” text appears in the top-left corner of the review window after applying artifact correction.
Review		<p>Artifact correction state is shown in the status bar of the review window. It indicates whether artifact correction is turned on or off.</p> <p>If artifact correction is turned off:</p> <ul style="list-style-type: none"> • “Correct: Off” <p>If artifact correction is turned on:</p> <ul style="list-style-type: none"> • “Correct: PCA”: Principal component analysis (PCA) is used for artifact correction. • “Correct: Surr”: Surrogate method is used for artifact correction. • “Correct: SSP”: Subspace projection (SSP) is used for artifact correction.
Review	<p>High Cutoff Filter Switched On</p> <p>The High Cutoff Filter has been enabled. You retain more information if High Cutoff is off during averaging.</p> <p>Do you want to switch the High CutoffFilter off now?</p>	<p><i>Paradigm dialog - Filter tab</i></p> <p>If high pass filtering is set for averaging and the user switches the tab, this warning message shows to warn there is a potential risk of loss of data.</p>
Review	<p>Filter Settings Change</p> <p>The artifact scan was performed on this data using a different setting.</p> <p>Do you want to keep the current selection of accepted trials?</p>	<p><i>Paradigm dialog - Filter tab</i></p> <p>If the filter setting is changed after finishing the artifact scan and the user switches to another tab, this warning message shows to warn that the filter settings were changed, and no longer match the settings which were used for the artifact scan.</p>
Review	<p>Scan Exists</p> <p>A scan has already been performed.</p> <p>Assignments of bad channels which were done in this editing session will be lost if you scan again.</p> <p>Do you want to scan again?</p>	<p><i>Paradigm dialog - Artifact tab</i></p> <p>When the <i>Start Scan</i> button is clicked again after finishing the artifact scanning, this message is shown to inform about a possible loss of previous changes.</p>
Review	<p>Set beamformer intervals</p> <p>One of the intervals is too small</p>	<p><i>Paradigm dialog / Average tab / Set beamformer interval dialog - Beamformer interval section</i></p> <p>If any of the noise or signal intervals holds less than 2 sampling points, this warning message is shown because the computation of the covariance matrix is not possible.</p>
Review	<p>Cancel Paradigm Definition</p>	<p><i>Paradigm dialog</i></p> <p>When the “Cancel” button of the Paradigm dialog is clicked after changing settings, this message is</p>

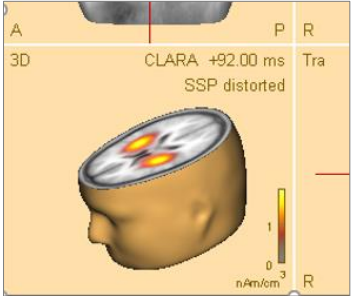

	You have made changes to the paradigm. Are you sure you want to cancel the changes?	shown to warn that the changed settings are not saved.
Review	Channel and digitized head surface point information  or 	<i>Channel and digitized head surface point information</i> dialog The symbol located at the top-right of the dialog indicates whether the current setting is correct (green check mark) or not (red exclamation mark).
Review	Use spherical electrode locations? The electrode locations in the file are currently defined on a sphere For MRI coregistration, we recommend that you use digitized coordinates. Press 'OK' to retain the spherical coordinates, or 'Cancel' to abort coregistration	If there is no information on digitized coordinates for electrodes, this warning message is shown after selecting <i>File / MRI coregistration</i> menu entry.
Review	Coregistration with MRI Your data use standard electrode without digitization (or MEG headshape information is too sparse)! Coregistration in BESA source module may be inaccurate.	<i>Coregistration with MRI</i> dialog - <i>Coordinate Information</i> section BESA Research presents a warning message, saying that for MRI coregistration realistic electrode coordinates produce better results.
Review	Coregistration with MRI  or 	<i>Coregistration with MRI</i> dialog - <i>Coregistration files</i> section The symbol located top-right of the dialog indicates whether the current file setting is correct (green check mark) or not (red exclamation mark).
Review	Warning No EEG recording reference is defined! Artifact-corrected data are always average referenced in this case! <input type="checkbox"/> Do not show this message again <input type="checkbox"/> Closing with 'OK' in ## seconds	This warning message is shown when the <i>Artifact / Automatic...</i> menu entry is selected for the data without reference channels.
Review	Starting fMRI Artifact Correction Warning: fMRI artifact correction may be used for RESEARCH PURPOSES only. Warning: fMRI artifact correction may be used for RESEARCH PURPOSES only.	This warning message is displayed when the <i>Artifact / fMRI artifact...</i> menu entry is selected. The user has the choice to accept or to cancel and return to the review module. The user can opt for only displaying this warning once in this session.

	<p>Press OK to continue, Cancel to return to the review window.</p> <p><input type="checkbox"/> Do not show this information again in this session.</p>	
Review	<p>Starting Source Analysis</p> <p>Warning: Use of the Source analysis module for diagnostic purposes may only be performed by experienced neurologists with profound knowledge of the methods used in the module.</p> <p>Only the following methods may be used for diagnostic purposes by the user group listed above, with the restrictions stated in the Intended Use:</p> <ul style="list-style-type: none"> - Equivalent Dipole Modelling - CLARA <p>Press OK to continue, Cancel to return to the review window.</p> <p><input type="checkbox"/> Do not show this information again in this session.</p>	<p>This message box appears when starting Source Analysis.</p> <p>This message box will not be shown again in the current session if the check box “Do not show this information again in this session” is checked.</p>
Review	<p>Using Source Analysis in batch</p> <p>Warning: Use of the Source Analysis module for diagnostic purposes – restricted methods:</p> <ul style="list-style-type: none"> - Equivalent Dipole Modelling - CLARA <p>may only be performed by experienced neurologists with profound knowledge of the methods used in the module.</p> <p><input type="checkbox"/> Do not show this message again</p>	<p>This message box shows when users start a batch process that will use Source Analysis features.</p> <p>This message box will not be shown again in the current session if the check box “Do not show this message again” is checked.</p>
Source Coherence	<p>DataWindow</p> <p>Only few samples were selected for time-frequency imaging. This may compromise the results. Do you want to continue?</p>	<p><i>Image</i> dialog</p> <p>When the time or frequency intervals is too small, data dimensionality may be reduced. In this case BESA Research shows this warning message.</p>
Source Coherence	<p>DataWindow</p> <p>One of the values you entered is outside the range. Please correct the values.</p>	<p><i>Image</i> dialog</p> <p>When one of the values for the time and frequency intervals is outside the range, BESA Research shows this warning message.</p>
Source Analysis	<p>Calculating image</p> <p>For the beamformer image, covariance information is</p>	<p>This message indicates that the current condition does not have covariance information. For preparing covariance information for a beamformer image, the ERP (time-domain beamformer) or</p>

	required, but the current condition does not contain it.	Source Coherence (time-frequency domain beamformer) modules need to be used.
Source Analysis	BESA – Source analysis Please mark a fit region before starting SESAME.	For SESAME computation, a fit region is needed to be defined first.
Source Analysis	Warning... Cursor is lying outside the brain volume of the current head model.	<i>Set Reference for DICS dialog</i> This warning message is shown if the current cross-hair in the 3D window is located outside of the brain (source space) and the following option in the dialog is selected: Reference is brain source / Use current cross-hair position.
Source Analysis		The line that indicates the baseline interval above the butterfly plot of the Channel box is changed to red when the baseline overlaps with the fitting interval. In this case, the baseline may be incorrect.
Source Analysis		The line that indicates the baseline interval above the butterfly plot of the Channel box is changed to red when a signal power of more than 50% of maximum global filed power (GFP) is contained in the baseline. In this case, the baseline may be incorrect.
Source Analysis		The text “ART” at the right of the status bar in the Source Analysis module indicates that artifact corrected data is currently used in source analysis and subspace projection (SSP) is switched on.
Source Analysis	Warning... This is an artifact-corrected data set. In order to ensure correct discrete source localization, BESA performs a subspace projection (SSP) on the data and the source leadfields. The SSP removes the artifact topography from the data. Due to this fact, the 3D maps and distributed sources in the Source Analysis module will be distorted. This will be indicated by the additional text “SSP distorted” in	This warning message is shown when an artifact-corrected data is used for source imaging in the Source Analysis module.

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Appendix A – List of Error and Warning Messages

	the header line of the 3D window.	
Source Analysis		The text “SSP distorted” is shown in the 3D view of the Source Analysis module to warn that an artifact-corrected data is used for source imaging.
Source Analysis		The text “Volume-based image only” is shown in the 3D window of the Source Analysis module when a volume-based source image is computed and the toggle button for Glass brain is pressed.

Appendix B – Range, accuracy and precision of displayed values

A. Range, accuracy and precision of displayed values

The following table lists the tasks that the user may perform during a data analysis procedure in a clinical context. For these tasks, the measured quantity, the range within the software, the accuracy and precision where known are listed.

Task	Measured quantity	Range	Accuracy	Precision
Fast Fourier transformation of EEG or MEG data	Dominant frequency in Hz	Typical range: 1–30 Hz. The permitted range lies within 0.001 Hz and 2,000,000 Hz	0.2 Hz	0.1 Hz
Amplitude measurements of displayed EEG or MEG data	Maximum and minimum amplitudes of a channel in a defined interval, in μV (EEG), fT (MEG magnetometers or axial gradiometers), or fT/cm (MEG planar gradiometers)	Typical range: 1–200 μV (EEG). Permitted range: 0–1 V (EEG);	2 μV	0.2 μV
		0–100 nT (MEG magnetometers or axial gradiometers);	23 fT	5 fT
		0–100 nT/cm (MEG planar gradiometers)	2 fT/cm	2 fT/cm
Dipole localization	Position in the brain (Talairach units)	Typical range: -85 mm ... +85 mm Permitted range: -128 mm ... +127 mm (relative to the brain centre)	Accuracy depends on many factors, the strongest being the head model used and the depth of the source. In a spherical model scenario with 64 electrodes and noise, accuracy was found to be approximately 1–3 mm in each direction. However, head model and co-registration errors enlarge it in real scenarios (cf. Lantz et al. 2003; Duez et al. 2019).	Precision is a function of signal-to-noise and is calculated and displayed for each dipole fit separately. In a typical noise scenario (SNR approximately 10), it is in the order of 5–10 mm in each direction.
Measurement of latencies of amplitude peak activations relative to stimulus	Peak latency in ms	Typical range: -400 ms ... +1200 ms Permitted range: -1,800,000 ms ... +1,799,990 ms	± 1 ms	± 5 ms

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The CE marking certifies that this product fulfills the essential requirements of the Medical Devices Directive MDD 93/42/EEC. The number 0197 represents the identification number of the Notified Body.

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