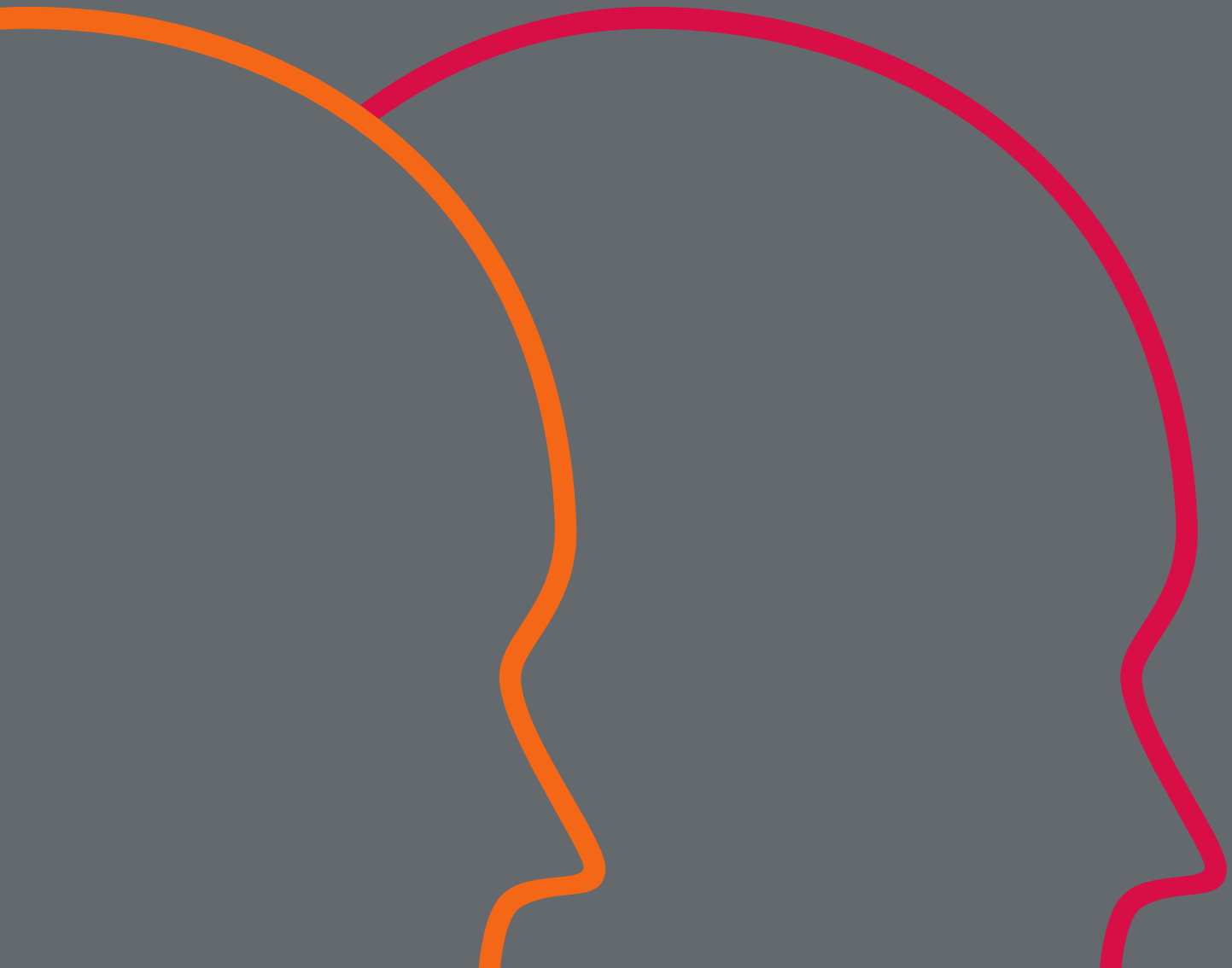
BESA Workshop Tutorial



BESA®

BESA Workshop - Tutorial

A tutorial for analyzing interictal spikes and seizure onset using BESA Research

This tutorial is based on “Guideline for Mapping and Localization in LTM” (revision 003) written by Dr. Michael Scherg and “BESA Research 7.1 – Tutorial” (revision 014).

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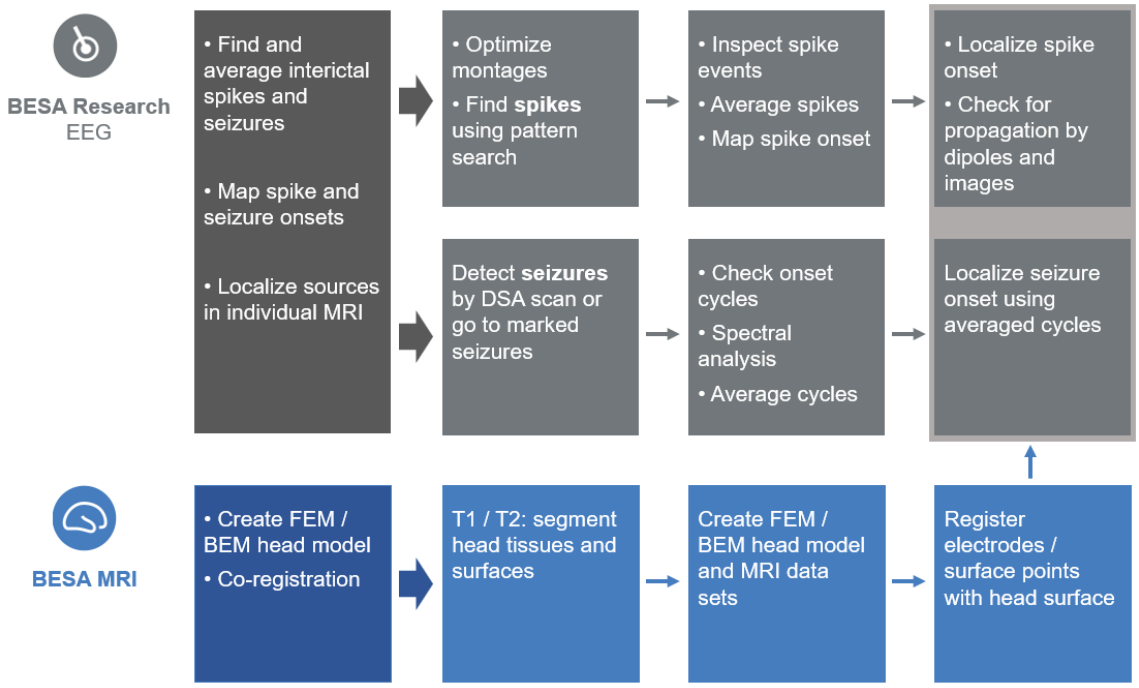
1. Introduction

The evaluation of seizures and interictal spikes in EEG, typically recorded during pre-surgical evaluation of epilepsy patients, is often limited to visual inspection of the EEG data in bipolar montages. However, the advances in computer-assisted processing of digital EEG data offer much more information on the origin and propagation of epileptiform activities in these patients. This information, if properly assessed using the individual MRI, can help to guide further exploration by depth electrodes or even lead to a non-invasive confirmation of the involved brain region outlined by neuro-radiological or other clinical findings.

Using the BESA software, we have created a pipeline for the effective processing of EEG data to save time and gain more information:

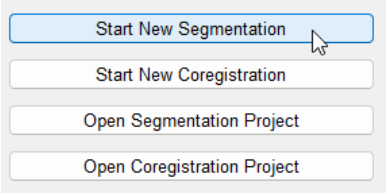


In this tutorial, we will use the **BESA Research** and **BESA MRI** software to learn the essential steps for the mapping and localization of interictal spikes and seizure onset.

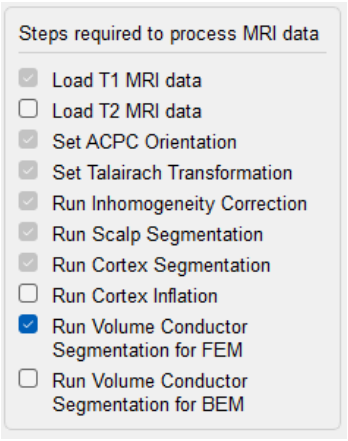
2. BESA MRI: MRI segmentation

MRI data must be segmented in order to co-register the electrodes in the EEG data with an MRI image and to create individual head models. The segmentation in BESA MRI is fully automatic after setting up anatomical landmarks.

1. Start **BESA MRI**, then press **Accept** on the welcome screen.
2. Press the **Start New Segmentation** button in the interaction window.

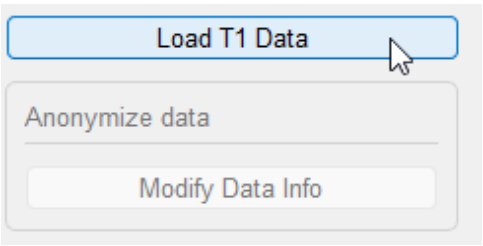


3. In the next screen additional features can be added, like Cortex Inflation or Volume Conductor Segmentation.
   Select the check boxes for **volume conductor segmentation for FEM**.
   Press **Next** button to proceed to the next screen.



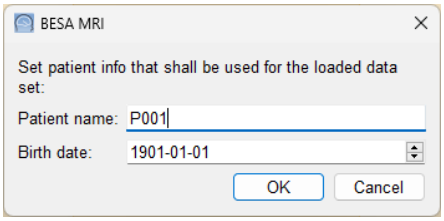
Tip: A T2 sequence can be also added to improve the quality of segmentation. Please read the BESA MRI manual for more details.

4. Press **Load T1 Data** in the Interaction window. A new dialog box will be opened.
5. Navigate to folder *C:\Users\Public\Documents\BESA\Research_7_1\Examples\Epilepsy\LTM-Tutorial\Spikes\Temporal_Basal+Polar\MRI*
6. Select the **MRISeg_MRI_T1_TAL.vmr**, then press **Choose**.



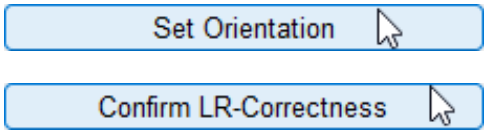
Note: The MRI file has already been transformed to Talairach space. However, we will consider it as the original MRI data in this tutorial.

7. Change the Patient name to **P001**, then press **OK**.
   Click **Yes** in the message dialog to remove the file path of the loaded data set for anonymization.

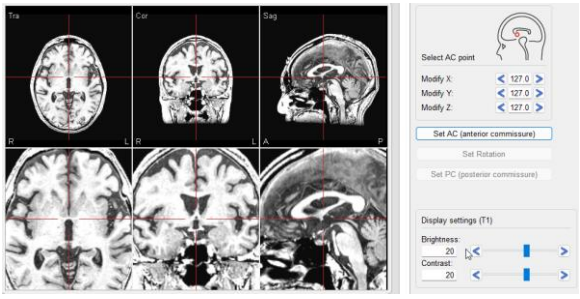


8. Press **Next** to continue.

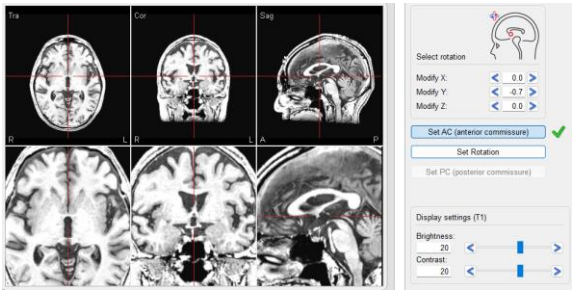
9. Press **Set Orientation**, then press **Confirm LR-Correctness**.
   Press **Next** to continue.



10. **Mark** the **anterior commissure (AC)** point on the MRI slices using the crosshair. This is a fiber bundle that connects the hemispheres, located just inferior of the corpus callosum.
    • The bottom views provide higher detail for easier navigation to the correct location. You can use the **mouse scroll wheel** in the left bottom view to slice through the brain until the fiber bundle appears.
    • Note the head schematic image in the interaction window that shows the rough location of AC.
    Press **Next** to continue.

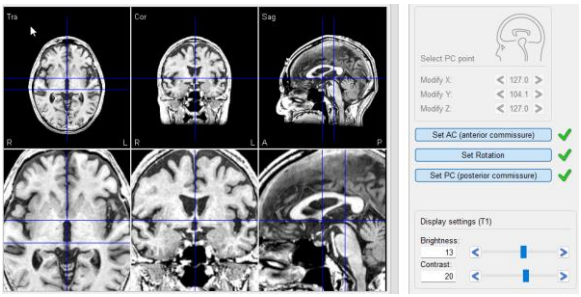


11. **Set rotation** of MRI slices by placing the mouse in the bottom views and dragging the cursor to the desired position while the left mouse button is pressed.
    • Start with the left view (coronal) to align left and right hemisphere. The rotation should be set such that axial and coronal view 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.

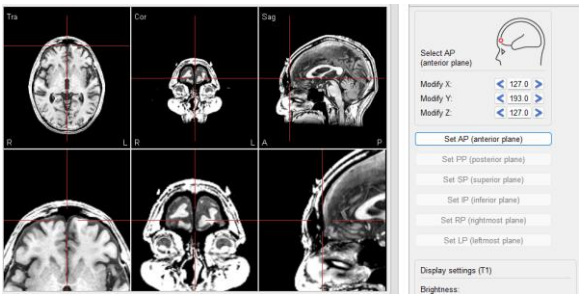


12. **Mark** the **posterior commissure (PC)** point on the MRI slice using the crosshair.
    Press **Next** to continue.

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

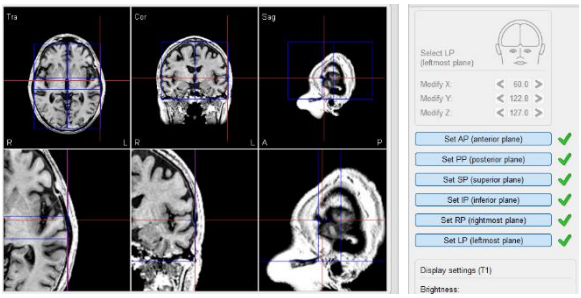


14. **Mark the anterior point (AP)** on the MRI slices using the crosshair.
    Note the head schematic image in the Interaction window that shows roughly where the AP is located.
    Press **Next** to continue.



15. Repeat the previous step for **posterior point (PP), superior point (SP), inferior point (IP), rightmost point (RP), left most point (LP) anterior point (AP)** on the MRI slices using the crosshair.
    Press **Next** to continue.

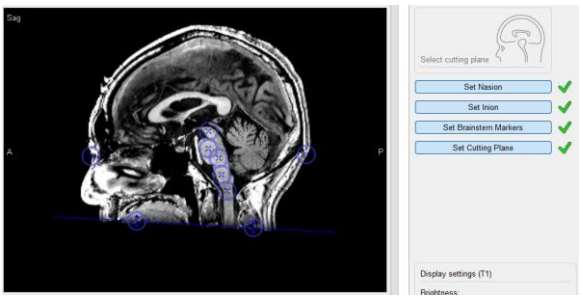
16. When all points are defined you can again review them. The brain should be inscribed in a blue box.
    Press **Next** to continue.



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

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

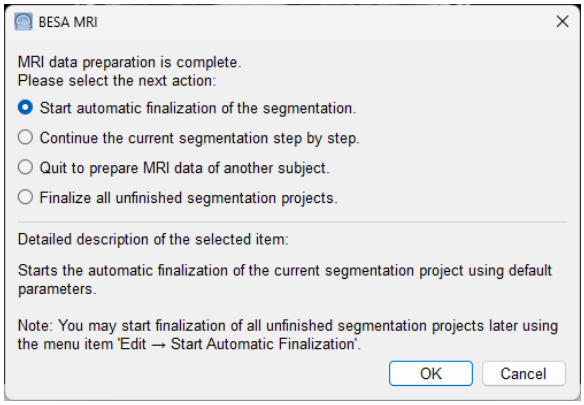
19. **Mark 3–5 brainstem markers** on the sagittal slice as indicated in the head scheme.
    • The markers have to be located within the brainstem, but there is no rule about exactly where to place them.
    Press **Next** to continue.



20. 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.

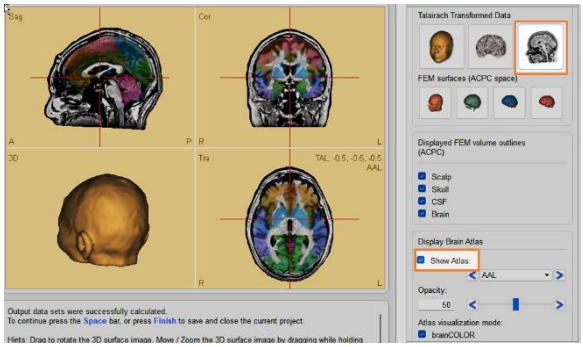
21. When all points are defined you can again review them.
    Press **Next** to continue.

22. A new window will pop up. Here you can decide whether you want to do. By default, the first option "**Start automatic segmentation**" is selected.
    Press **OK** to start segmentation.



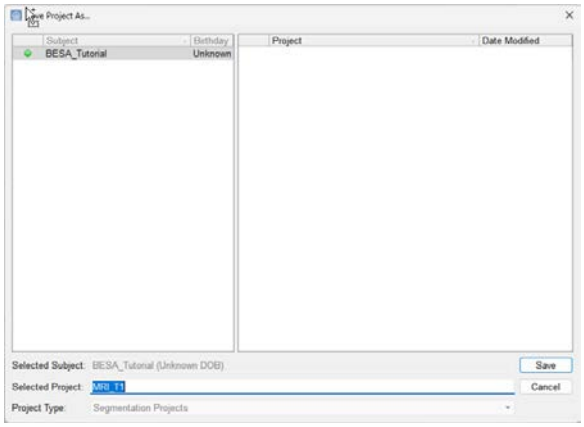
Note that this process may take a while. During segmentation, the current step and overall progress is presented on the screen.

23. When segmentation is finished the results (ACPC transformed data, Talairach transformed data, head model surfaces, atlas, etc.) can be reviewed by pressing buttons in the Interaction window at the right.



24. Press the **Finish** button to save it.

25. 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.



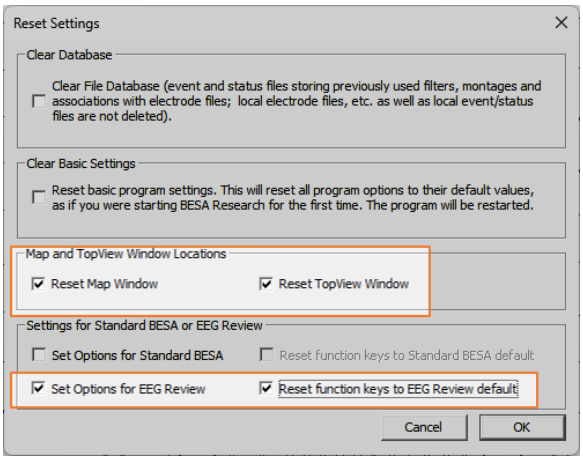
26. Close BESA MRI.

3. Getting started: Data review, filters, and montages

3.1. Setting up BESA Research to analyze epilepsy data

This section serves to show the special settings used in BESA Research for working with epilepsy data: Maps will be shown upon single click and special epilepsy settings become available for the function keys F2–F12.

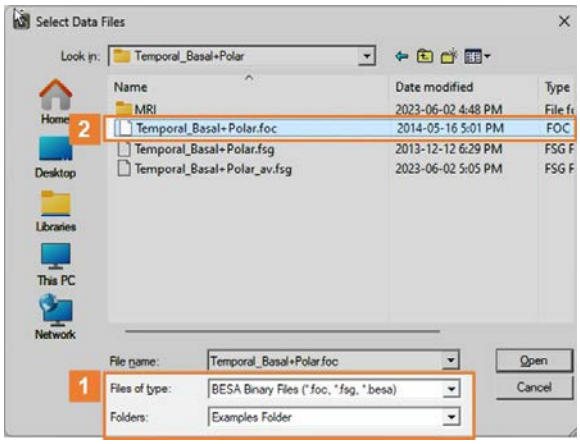
1. Start **BESA Research.**
2. To reset the special settings for epilepsy, select **Options | Open "Reset Settings" Dialog...** from the main menu.
3. Select the following options:
   - Reset Map Window
   - Reset TopView Window
   - Set Options for EEG Review
   - Reset function keys to EEG Review default
4. Press the **Ok** button.
5. Select **Options | Top View** from the main menu, then uncheck the **Enable Top View by Single Click**.



3.2. File open and navigation

1. From the main menu, select the **File | Open** menu item. In the *Select Data Files* dialog, select:
   - Files of type: **BESA Binary Files**
   - Folders: **Examples Folder**

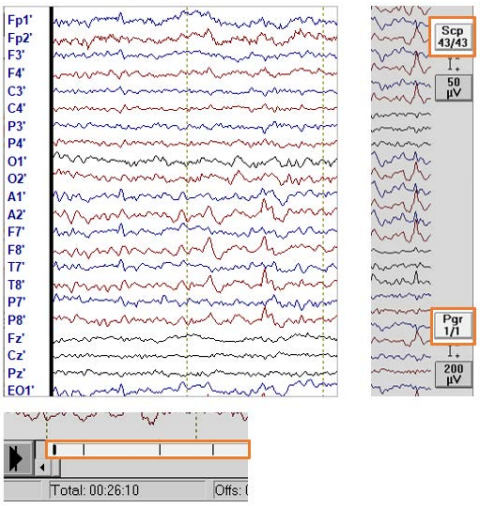
   C:\Users\Public\Documents\BESA\Research_7_1\Examples
2. Select folder "*.\Epilepsy\LTM-Tutorial\Spikes\Temporal_Basal+Polar*", then open file **Temporal_Basal+Polar.foc**.



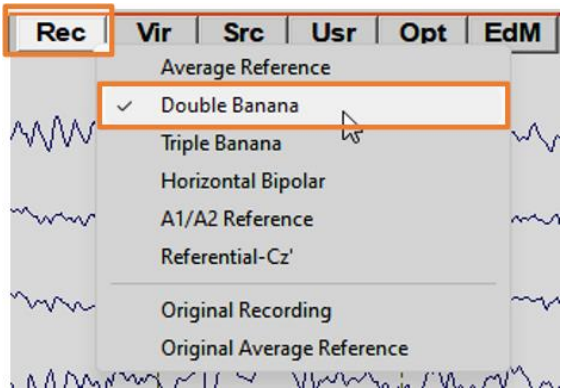
When opening an EEG file for the first time, BESA Research shows the original channels as recorded. Here, you will see 43 scalp channels (**Scp**) and 1 polygraphic channel (**Pgr**, EKG).

The waveforms of the left channels are displayed in blue and those of the right channels are displayed in red. The waveforms of the midline channels are displayed in black.

Triggers are coded as vertical black bars at the bottom of the screen.



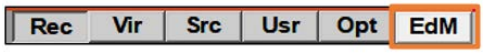
3. Press **Rec** (montage button to use channels as recorded) from the control ribbon, then select **Double Banana**, the commonly used longitudinal bipolar montage.

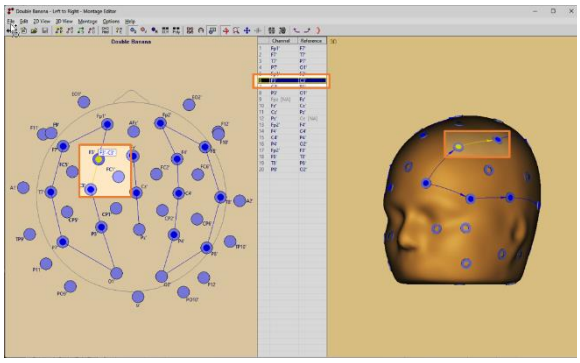


The symbol **'** after an electrode label (e.g., T7**'**), indicates that electrodes have digitized or modified coordinates.

Tip: Montage can be also changed using the **Montage** menu.

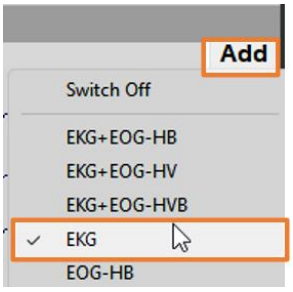
4. Press **EdM** from the control ribbon to inspect the **Double Banana** montage using the **Montage Editor** window.



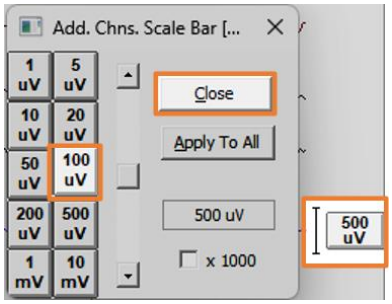


5. Click onto the diagram on the left or onto the label index in the montage list to view the different bipolar channels.
6. Close the Montage Editor window.

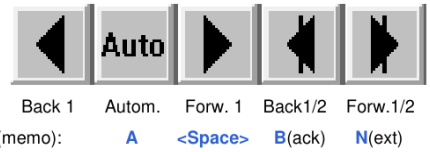
7. We will add the EKG channel at the bottom to be seen together with all montages. Thus, we can check if a spike is coincident with the R-wave of the EKG.
   Press **Add** on the upper right to select **EKG**.



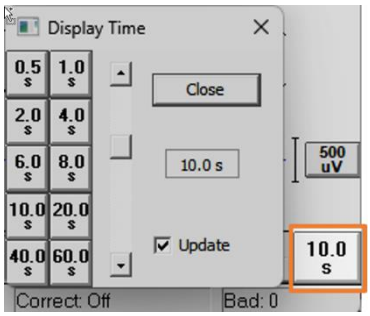
8. Press the **amplitude-scaling button** on the right side of the ECG channel (showing 500 uV) to set voltage scale to **100 uV**.
9. Press **Close** to close the scaling window.



10. To navigate in the EEG for review, you can either press the **space bar** or use the **arrows button** 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.
    You may also use the **mouse scroll wheel** to page forward and backward.
    Press the **Home** key or drag the **scroll bar** in the time bar at the bottom to the left to return to the beginning of the EEG data.



11. 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.

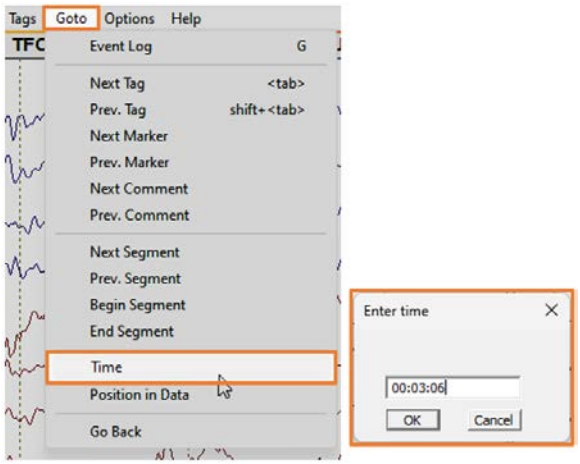


3.3. Filters

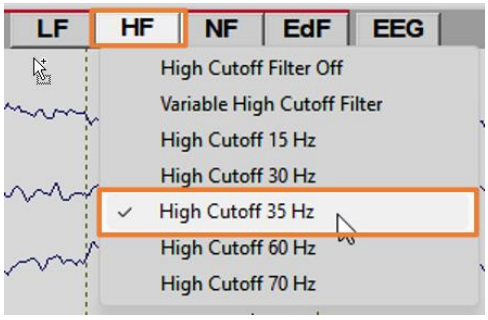
Spike perception can be improved by using appropriate filters. When opening an EEG file, the time constant is set to **0.3 s** – the typical clinical review setting. This time constant filter is equivalent to a low cutoff forward filter of 0.53 Hz with a slope of 6 dB/octave. The high cutoff filter is off by default.

The filter buttons are on the right side of the control ribbon.

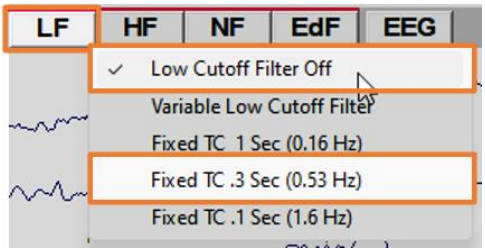
1. Select the **Goto | Time** menu item, then enter **00:03:06** to go a page with spikes and artifacts.
   An event marker, **TL bas**, shows the presence of a temporal left basal spike not seen in this montage.



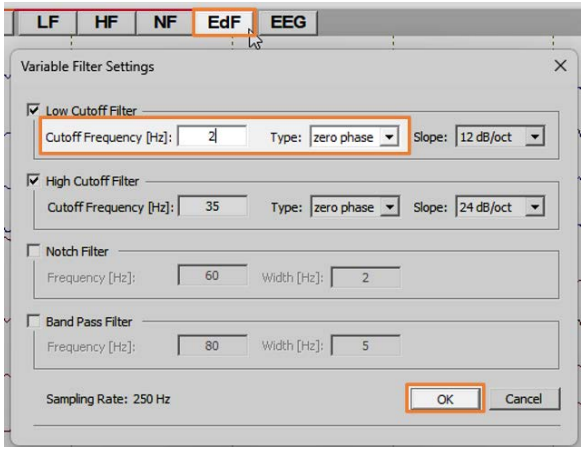
2. Press **HF**, then select **High Cutoff 35 Hz**. Now, EMG artifacts are reduced.



3. Press **LF**, then select **Low Cutoff Filter off** to switch the low filter off. Slow EEG activity is larger now.
4. Press **LF**, then select **Fixed TC .3 Sec (0.53 Hz)** to restore the filter. Slow EEG activity is slightly reduced.



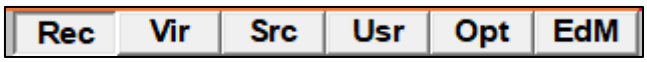
5. Press **EdF** to edit the filter using the *Variable Filter Settings* dialog. For the **Low Cutoff Filter**, select:
   • Cutoff Frequency of **2 Hz**
   • Type: **zero-phase**
   Press **OK** to set.



Slow EEG is suppressed more effectively by the steeper cutoff of the zero-phase-shift filter. However, spikes are still hard to recognize.

3.4. Recorded, virtual and user montages

In the middle of the control ribbon, you can find the buttons for quickly switching between montages:



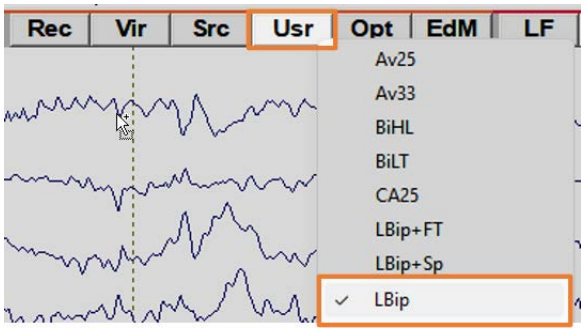
- **Rec**: Recorded montages: preset montages using the recorded electrodes, e.g., in the original sequence
- **Vir**: Virtual montages: preset montages using standard 10-10 electrodes based on spline interpolation
- **Src**: Source montages: based on equivalent sources in 25 brain regions, different regions are highlighted, etc.
- **Usr**: User montages: some convenient standard montages (e.g., Av33) and montages created by user
- **Opt**: Options for setting the sequence of channels and display mode of virtual and source montages
- **EdM**: Open Montage Editor

Note: When the Rec button is pressed and the current montage is no recorded montage, the last displayed recorded montage becomes the current montage. When the Rec button is pressed while a recorded montage is displayed or if there is no last displayed recorded montage, the popup menu opens to select a recorded montage. The same applies to the Vir, Src and Usr buttons.

For more details on these montages, select **Help | Help Topics**, then see **Montage Editor / Standard Montages**.

1. On the lower left the status bar should show Time: **+00:03:06**. Otherwise, select the **Goto | Time** and enter **00:03:06**.

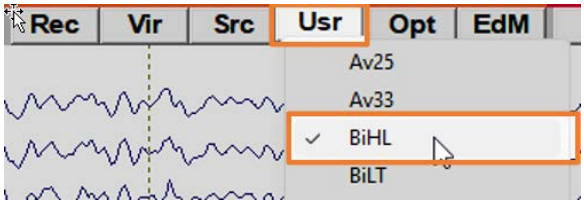
2. Press **Usr** from the control ribbon, then select **LBip**, longitudinal bipolar montage with added midline channels and a convenient sequence.



3. Press **Rec** to switch back to the **Double Banana** montage.
   Then, press **Usr** to switch back to the **LBip** montage.

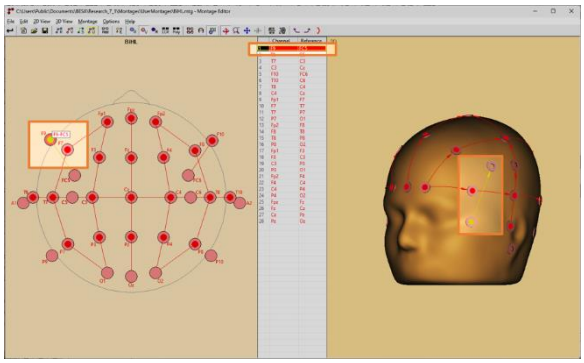
Tip: You can switch between different types of montages (**Rec**, **Vir**, **Src**, **Usr**) by pressing one of these buttons to get back to the previously chosen montage with the category defined by the button.

4. Press **Usr** again to obtain the list of available user montages. Now select **BiHL**, a virtual montage that first displays 4 horizontal (vertical / transverse) channels on each side of the head prior to the typical longitudinal bipolar channels.

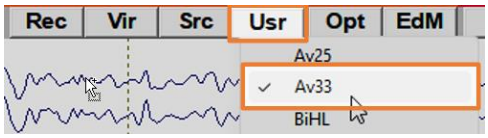


The **BiHL** montage includes inferior electrodes to render basal and polar temporal spikes with upward polarity, presents left and right groups symmetrically, and uses 20% distances to have the same distance scaling as the longitudinal channels.

5. Press **EdM** to inspect the **BiHL** montage. Click onto the diagram on the left or onto the label index in the montage list to view the different bipolar channels.
   Close the Montage Editor window.



6. Press **Usr** and select **AV33**, the standard average reference montage using virtual, interpolated electrodes.



Av33 montage

The **Av33** montage helps to understand the spike topography since the voltages at each of the 33 virtual standard electrodes are referenced to the mean over all 10-10 electrodes calculated by spherical spline interpolation. The voltage values of this montage are very close to the reference-free values seen in the maps.

The spline interpolation works well, even if electrodes are bad or missing. Local artifacts are slightly smoothed which reduces local superficial signals, e.g., EMG.

The average-referenced electrodes are arranged in groups with left preceding right hemisphere. Groups go from inferior to lateral and superior (as in BiHL). The larger number of electrodes in the longitudinally arranged groups helps identifying spikes (e.g., Fp2-F8-FC6-T8-CP6-P8-O2).

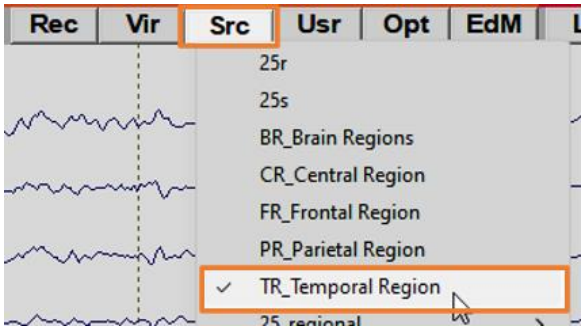
3.5. Source montages

Source montages (Scherg et al., 2019, 2004, 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 faster and more precise epilepsy assessment (Beniczky et al., 2016a; 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).

1. Press **Src** to select the **TR_Temporal Region** source montage.

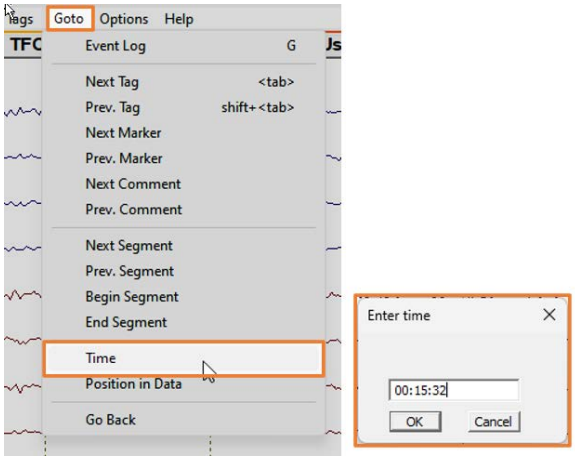


Now, several spikes appear very clearly and separated in the left temporal (upper 4) and right temporal (next 4) channels.

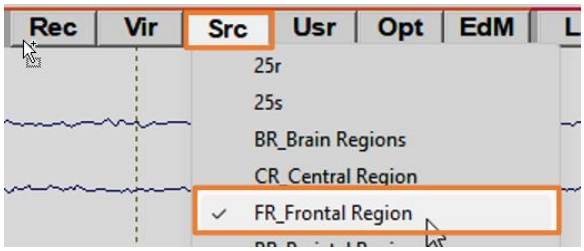
Most spikes on this EEG page are predominant in the 1st or 5th trace, i.e., the reconstructed basal temporal activity (e.g., at comment **TL bas**). Several smaller spikes are seen as well at the left temporal basal trace that were not conspicuous before.

2. Press **Usr** and **Src** in alternation to compare.

3. Select **Goto | Time** and enter **00:15:32** to see another page in this EEG with several spikes. The left basal spike signal appears leading in time over the polar and lateral anterior traces (2nd and 3rd traces).

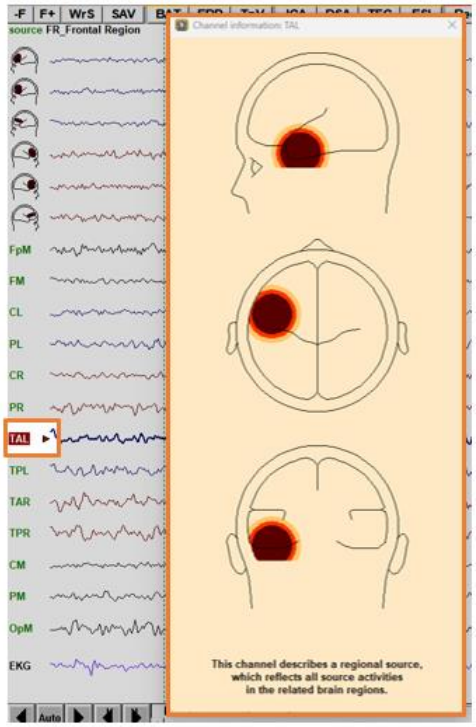


4. Press **Src** and select **FR_Frontal Region** to see the 3 activities (radial, horizontal vertical) of the left and right frontal sources. They are quite flat and show only little crosstalk from the temporal sources (slow wave activity maximal in the regional sources TAL, TPL, and TAR of the temporal lobe).

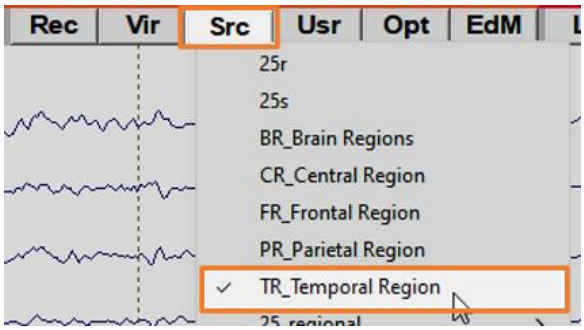


Similarly, you may check the other regions (**CR_Central Region**; **PR_Parietal Region**) for which standard source montages are available.

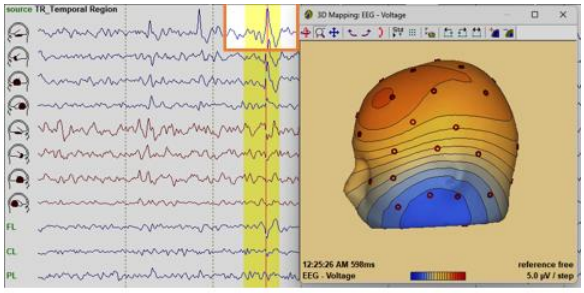
5. **Double click** the label **TAL** to show the source location in the Channel Information window.
   Close the Channel Information window.
   If the TAL label is selected, click the TAL label to deselect it.



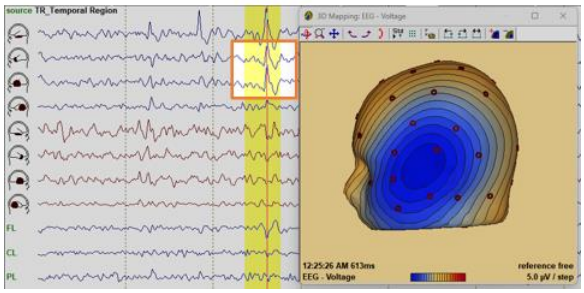
6. Press **Src** and select **TR_Temporal Region** to reset to the temporal lobe source montage.



7. **Click** the left basal spike (1st trace) to see the typical temporal basal map.
   Adjust cursor with the **mouse scroll wheel**.



The basal spike in the left basal channel (1st trace) is leading in time over the polar and lateral spikes (2nd and 3rd traces).

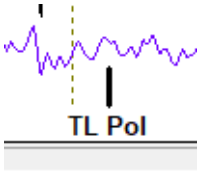


Tip: The Map window can be saved as a bitmap image file by pressing **Shift + S**.

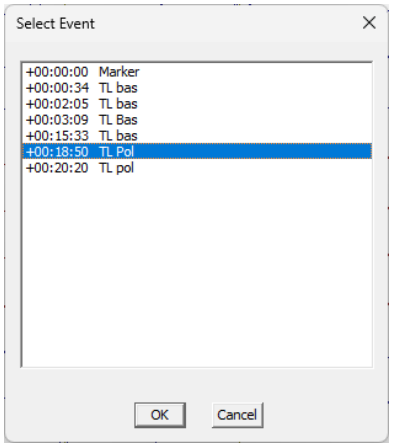
8. Press **Esc** to remove the cursor and close the Map window.

9. Select **Tags | All** from the main menu.

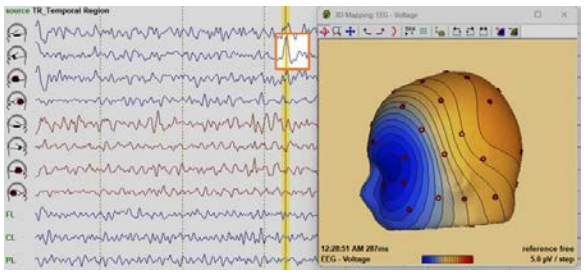
10. Press **<Tab>** to go to the next comment (**TL pol**) or select **Goto | Time** and enter **00:18:47**.



Tip: The most convenient way to go to an event is to type **G** (**Goto | Event Log**) and select from the pop-up list of events, if there are just some event markers and comments in the file.



11. **Click** onto the polar slow wave seen in the 2nd trace to map. The spike signal in the left temporal-polar trace is leading over the weak basal and lateral activities. Note the different topographies of the basal and polar 3D maps.

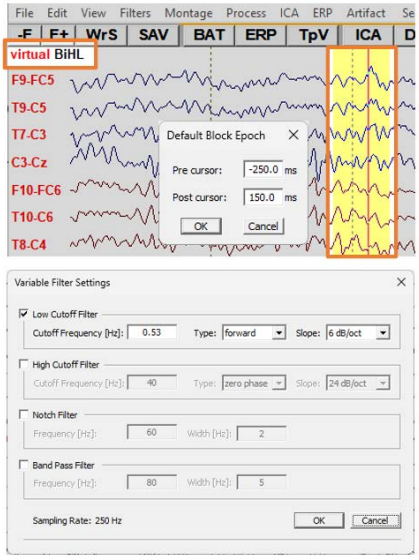


12. Press **Esc** to remove the cursor and close the Map window.

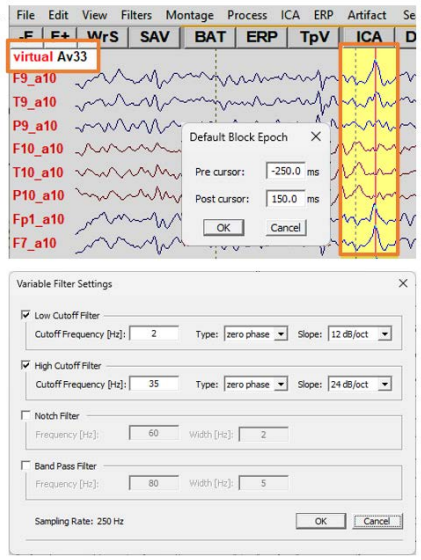
3.6. Function keys and batches for fast settings of filters and montages

For convenient and fast changes of montages and filters, batch functions have been created and associated with the function keys. We will use these function keys for fast setting of specific filters, montages and the default epoch for spike analysis throughout this tutorial. A summary of the function keys and the batch function can be found in section 10.1.

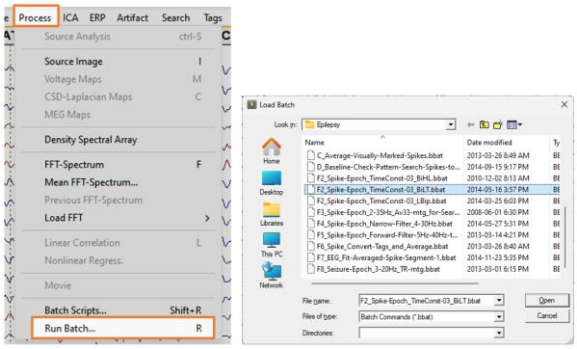
1. Press the **F2** function key to set:
   - **BiHL** montage
   - the standard clinical filter setting – low cutoff filter **0.53 Hz,** forward (time constant: 0.3 s) and high cutoff filter off
   - a default epoch **from -250 ms to +150 ms** around the cursor that is displayed when you click onto a peak in the EEG to map (yellow epoch). This spike epoch is used also for pattern search by default.



2. Press the **F3** function key to set:
   - **Av33** montage, the standard average reference montage
   - filter settings optimized for spike review and pattern search – **2–35 Hz** (zero-phase-shift characteristic)
   - a default epoch **from -250 ms to +150 ms** around the cursor



3. Pressing a function key is the same as selecting the **Process | Run Batch…** menu item (or press **BAT** from the control ribbon, shortcut key: **R**) and choosing the batch file that is associated with the function key (F2–F8).



The function key **F2** is preset to run the batch function **F2_Spike-Epoch_TimeConst-03_BiHL.bbat** (standard clinical EEG viewing mode).

The function key **F3** runs the batch function **F3_Spike-Epoch_2-35Hz_Av33-mtg_for-Search.bbat** (standard setting for spike review and search).

How to associate a function key with a specific batch:

In order to associate a batch function with a function key, press the function key while holding the **<Shift>** key. For example, you can associate the **F2** function key with the montage **BiLT**, if you prefer a standard bipolar montage with a different sequence of the channel group sequence, i.e., longitudinal first, followed by transverse and vertical bipolar channels.

The names of the preset batch files have been chosen to indicate the processes they perform. After pressing **<Shift> + F2**, you will see the list of batch files located in folder:

C:\Users\Public\Documents\BESA\Research_7_1\Scripts\Batch\Epilepsy

- The *Load Batch* dialog also comes up after pressing the key **R** to select a batch function.
- Different options for export and concatenation are available from the batch folder "*.\Export & Concatenate*".
- Batches **1–5** (e.g., *1_EEG_Fit-Averaged-Spike_Sp1.bbat*) are for localization of spike types Sp1, …, Sp5.
- Batches **A–D** (e.g., *Average-All-BESA-Epilepsy-Spikes.bbat*) serve for convenient preprocessing including selected averaging.
- The batches **F2–F8** (e.g., *F2_Spike-Epoch_TimeConst-03_BiHL.bbat*) provide standard settings for clinical review with different default montages.

Notes on bipolar montages:

There are various ways to combine the most frequently used clinical standard montage, i.e., longitudinal bipolar, with additional horizontal or transverse bipolar channels to observe spikes with transverse or vertical orientation of the dipole potential distribution. In BESA Research, we have preset the montage **BiHL** with additional vertical and horizontal channel groups preceding the longitudinal bipolar group. An alternative standard with the longitudinal groups preceding transverse and vertical groups is provided in montage **BiLT**. You can associate the function keys **F2** and **F10** with this montage.

4. Spike mapping in data

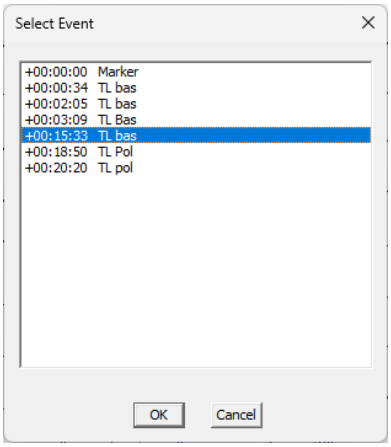
Here, we show how to obtain reasonable spike maps in continuous EEG data by using adequate filters. Spike peak and onset can be mapped most reliably from averaged spikes with specific filter settings. For the interpretation of 3D maps, it is recommended to read the *BESA Quick Guide on 3D maps* and *Learn to interpret voltage maps: an atlas of topographies* (Foged et al., 2022).

Hints for mapping:

- The best way to adjust the latency is to use the **mouse scroll wheel**. You can also use the **arrow keys** or the **arrow buttons** in the Map window.
- The 3D map automatically rotates to the center of the scalp surface potential activation for best viewing of both poles. Use the **rotation buttons** in the Map window to modify the viewpoint quickly.
- After changing the filter setting, press **M** to recalculate the map.
- To have the Map windows at its standard positions on the right, select **Options | Open "Reset Settings" Dialog…** menu entry and then select the **Reset Map Window** check box.

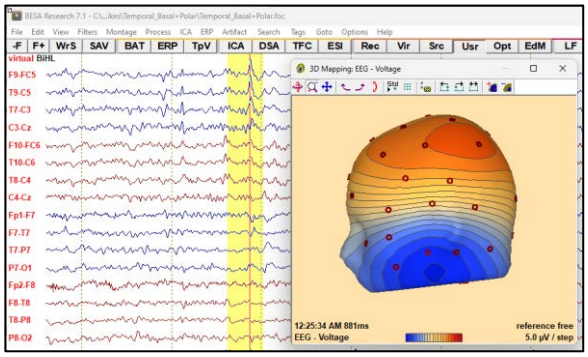
4.1. Spike mapping in continuous EEG data

1. **Open** the EEG file **Temporal_Basal+Polar.foc** if it is not already open.
2. Press **Usr**, then select **LBip** to set the longitudinal bipolar montage.
3. Type **G** to select the event **TL bas** at **+00:15:32**. This leads to an EEG page showing several spikes.



The spikes are not clearly visible in the longitudinal bipolar montage. Therefore, we want to use a montage that combines horizontal or transverse with longitudinal bipolar channels.

4. Press the **F2** function key to activate the montage **BiHL** and to set the clinical filters with a time constant of 0.3 s.



Spikes are now easily recognized in the transverse, vertical channels (3 spikes at the left inferior channels, 1 at the right inferior channel).

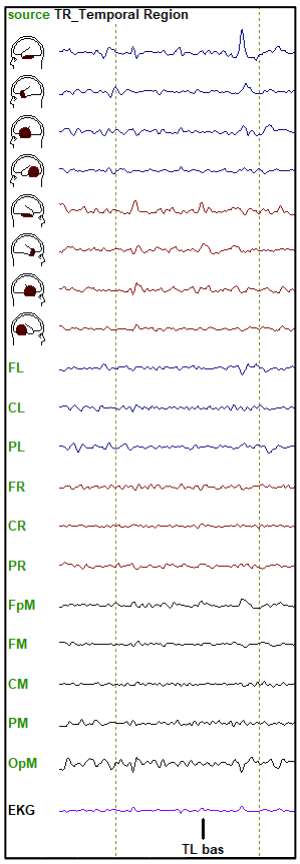
5. **Click** onto the first spike marked by the comment **TL bas** to observe the typical vertically oriented dipole topography of the left temporal-basal region (use the **scroll wheel** to adjust to the peak).

Tip: If needed, press  in the toolbar of the Map window to adjust the mapping step size to 1 or 2 ms.

6. Press **Esc** to remove the cursor and close the Map and Top view windows.

7. The signals are not optimally filtered for spike mapping. Therefore, use the shortcut **F3** to obtain the *optimized spike settings* with filters of **2–35 Hz** and the **Av33** montage.

8. Press **Src**, then select **TR_Temporal Region** to set the temporal lobe source montage.

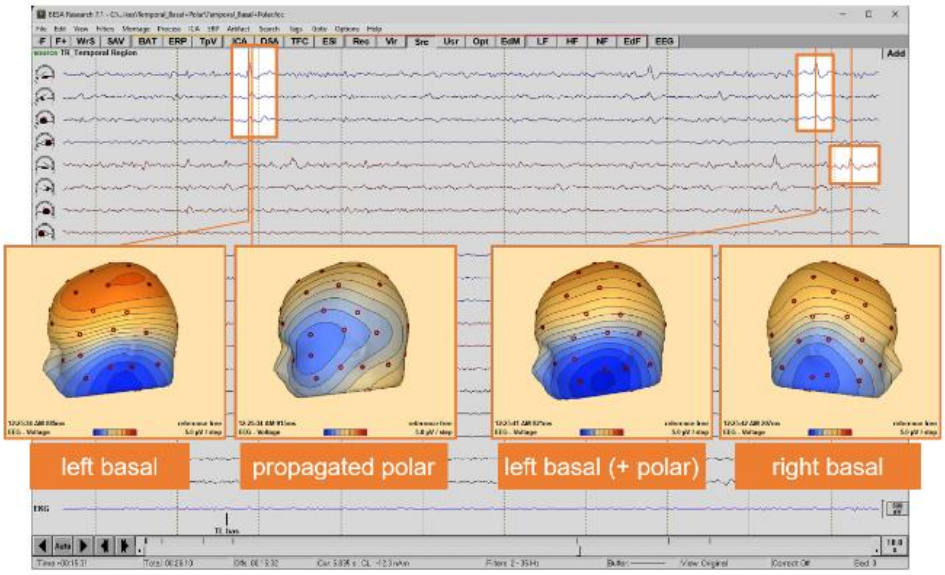


In this montage, the spikes are most conspicuous and prominent. It shows the estimated activities of the basal, polar, antero-lateral and postero-lateral cortical surfaces of the left and right temporal lobes (group of 4 traces each from top).

The 2nd, polar trace shows a later, smaller and smoother peak than the 1st basal trace indicating delayed propagation to polar from mesial structures as compared to the inferior-basal structures.

9. **Click** onto the spike (*left basal*) and move the cursor 30 ms later using the mouse scroll wheel.

4. Spike mapping in data

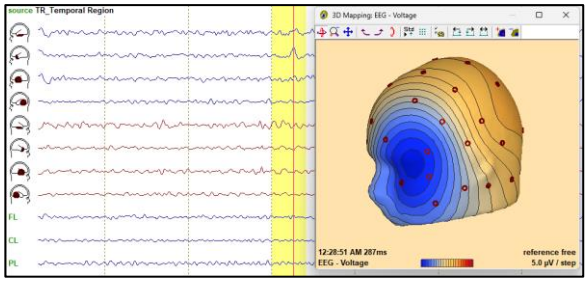


Observe the rotation of the map (propagated polar) due to the overlap of the earlier basal with the later polar activity as well as some intermediate antero-lateral activity. The relative timing of these activities can be seen quite clearly in the first 3 traces of the source montage.

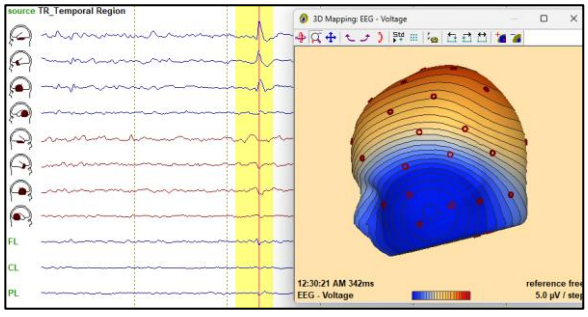
The last left temporal spike on this page is also a basal spike type as seen in the source traces, but with a small polar overlap. Note that the negativity appears more anteriorly (left basal (+ polar)).

About 400 ms after this left basal-temporal spike, you can see a right basal-temporal spike (right basal).

10. Press **Esc** to remove the cursor and close the Map and Top view windows.
11. Press **<Tab>** (or press **G**) to view the event list and select event **TL Pol** (+00:18:50). You will now see the most prominent spike in the 2nd trace (left temporal polar trace).



12. **Click** onto the spike to map.
    This spike shows little propagation to the basal and lateral surfaces as seen in the source waveforms.
13. Press **Esc** to remove the cursor and close the Map and Top view windows.
14. Press **<Tab>** (or press **G**) to go to the next polar spike marked **TL pol** (+00:20:20).



15. **Click** onto the spike peak in the polar trace.
    At this time, also the basal and antero-lateral surfaces start getting active as seen

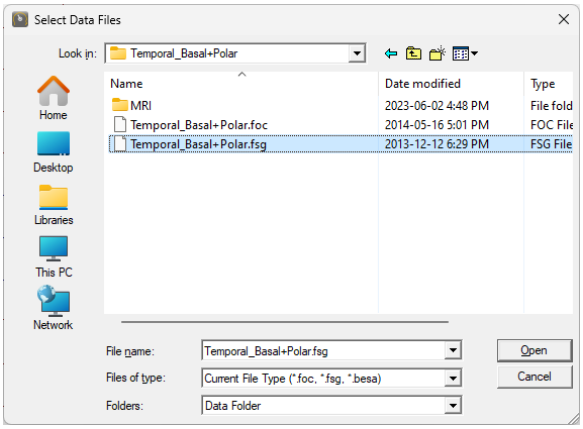
in the source waveforms. The 3D map shows a mixture of all 3 patterns.

All the maps shown above are typical for mesio-basal temporal lobe epilepsy. The spikes seen in the scalp EEG are propagated from the deep mesio-basal structures (e.g., amygdala; hippocampus). However, these do not produce large enough signals to be observed on the scalp (~ 1 µV). For different spikes, the propagation paths may vary, even within a subject.

Exercise: Map and check montages at the other **TL bas** events.

4.2. Spike mapping of onset and peak in averaged data

1. From the main menu, select **File | Open** menu item. Open the averaged data file **Temporal_Basal+Polar.fsg**.

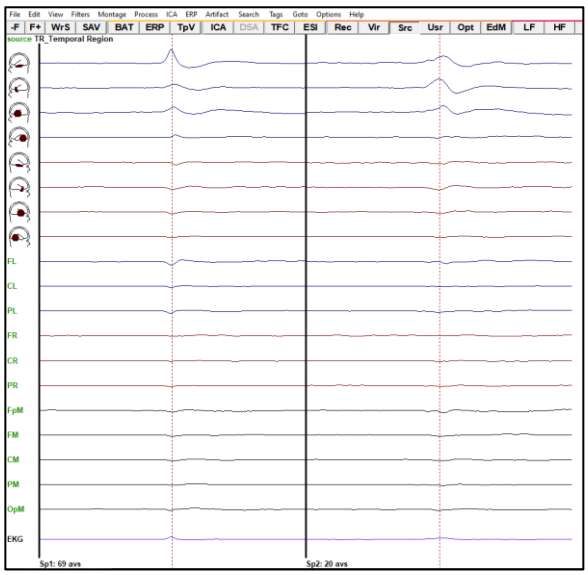


If the file is not present in the Select Data Files dialog, please follow the steps below:

From the main menu, select **File | Open** menu item. In the Selected Data Files dialog, select:
• Files of type: **BESA Binary Files**
• Folders: **Example Folder**
C:\Users\Public\Documents\BESA\Research_7_1\Examples

Select folder "*.\Epilepsy\LTM-Tutorial\Spikes\Temporal_Basal+Polar*", then open file **Temporal_Basal+Polar.fsg**.

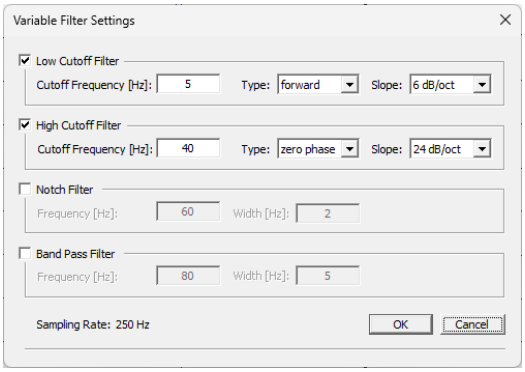
2. Press **Src**, then select **TR_Temporal Region** to set the temporal lobe source montage.



The file shows 2 averaged spike segments:
Sp1 is an average of 69 spikes with *leading or dominant basal activity* (1st trace = left temporal-basal source waveform).

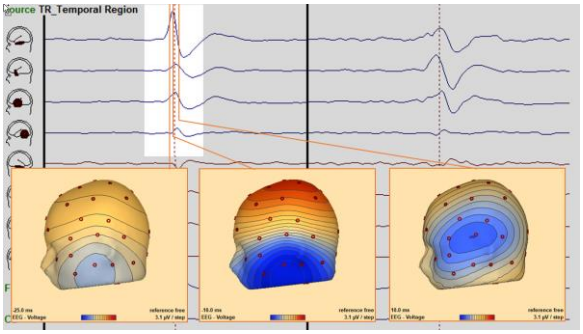
Sp2 is an average of 20 spikes with *leading or dominant polar activity* (2nd trace = left temporal-polar source waveform).

3. Press **EdF** to edit the filter settings
   • Low cutoff filter – **5 Hz, forward, 6 dB/oct** (this forward filter creates a good baseline prior to spike onset)
   • High cutoff filter – **40 Hz, zero-phase, 24 dB/oct.**



4. Use **Scale** button or **arrow key**, ↑**,** to scale to **500** or **400 nAm**.

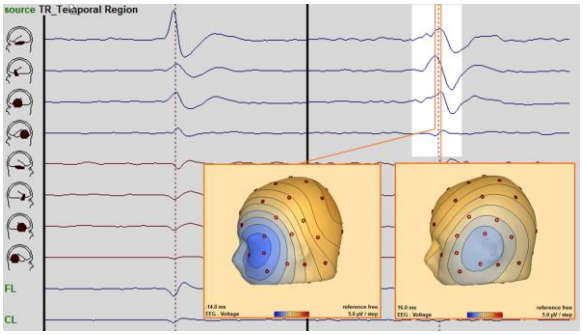
5. **Click** onto the peak of the **Sp1** spike and observe that the basal activity dominates at this time. However, also the polar and antero-lateral source waveforms show rising activities. Thus, the map already exhibits more anterior and superior negativity than basal activity alone would show.



6. Use the **mouse scroll wheel** to move the cursor to an earlier latency, e.g., to **about -23 ms**, and note that there is little change in the map topography since the relative contributions of the basal, polar, and lateral activities to the dipole field do not change much.

7. **Move the cursor** to the zero-crossing after the basal spike and note how the delayed lateral activity dominates the map at **about +9 ms**.

8. **Click** on the peak of the **Sp2** spike and adjust the cursor to **about -15 ms**. Observe that at this time the polar activity dominates. However, also the basal and antero-lateral source waveforms show small rising activities.



9. **Move the cursor** to the zero-crossing after the polar spike at **about +15 ms** and observe how the map now reflects a mixture of lateral and basal activity.

5. BESA MRI: Co-registration of EEG and MRI data and individual head modeling

Co-registration

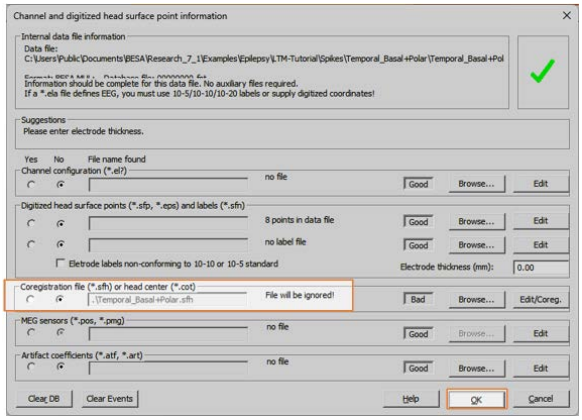
Co-registration of EEG and MRI data allows mapping a source position to an actual cortical area. Without co-registration it can only be roughly estimated, which cortical area a certain x-y-z position corresponds with. Further, individual anatomy can be used for seeding sources or verifying source localizations.

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 **ACPC** (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.

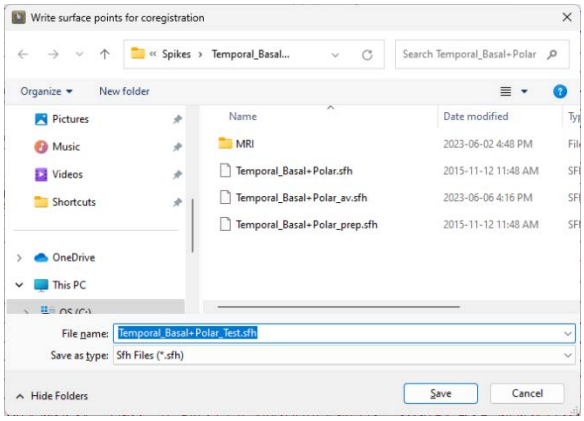
Individual head modeling

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

1. Open the EEG file **Temporal_Basal+Polar.foc** if it is not already open.
2. Select **File | Surface Points and Sensors | Load Coordinate Files…** (shortcut: **Ctrl + L**) from the main menu.
3. In the "*Coregistration file (*.sfh) or head center (*.cot)*" section, **select the second radio button** (No) to ignore the applied coregistration file. Press **OK**.
   We will set a new .sfh file later.

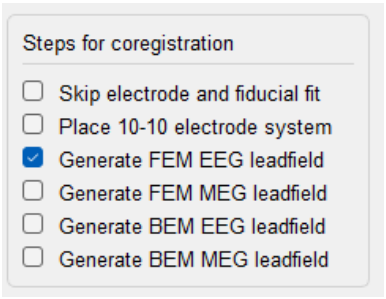


4. Select **File | MRI Coregistration…** from the main menu.



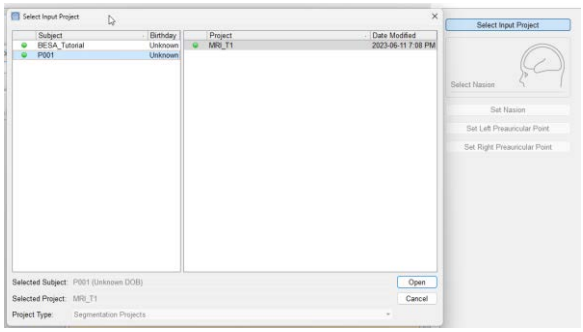
5. You will be prompted to create and save an ***.sfh** file, which will be used to store all coregistration information necessary for the interaction between BESA Research and BESA MRI.
   BESA Research will automatically suggest the filename of the current subject plus the extension **.sfh**. Change the file name to **Temporal_Basal+Polar_Test.sfh**, then pressing **Save**.

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



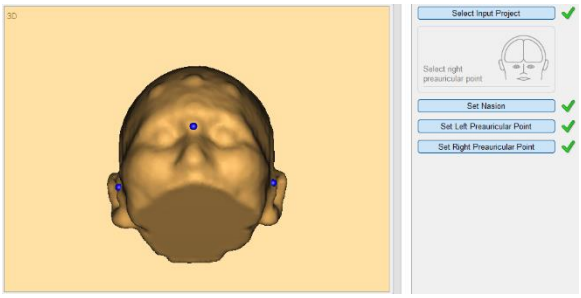
7. A new coregistration project is started.
   Check the check boxes for generate FEM EEG leadfield.
   Press **Next** on the bottom right (or hit the space bar).

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



9. Choose the project **MRI_T1** of subject **P001**. Press **Open**.

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



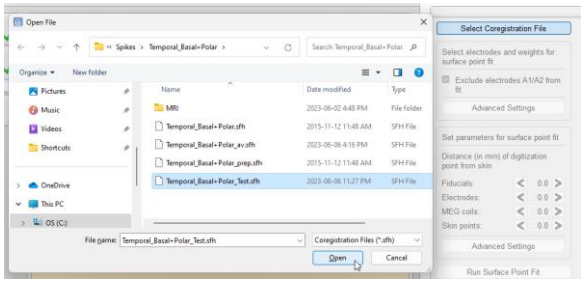
11. Mark **LPA** (left preauricular point), then press **Next** to continue.

12. Mark **RPA** (right preauricular point), then press **Next** to continue.

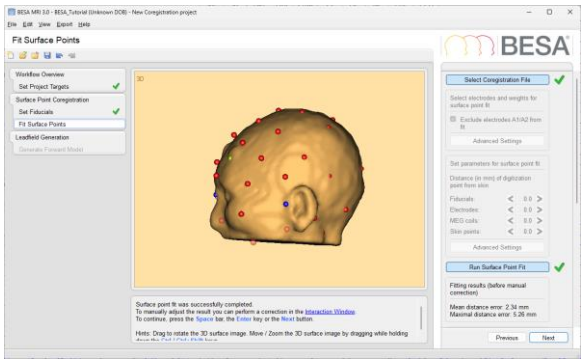
13. All fiducials are now positioned. Press **Next** to continue.

5. BESA MRI: Co-registration of EEG and MRI data and individual head modeling

14. Press **Select Coregistration File** to load the **Temporal_Basal+Polar_Test.sfh** file we saved earlier. Press **Open**.

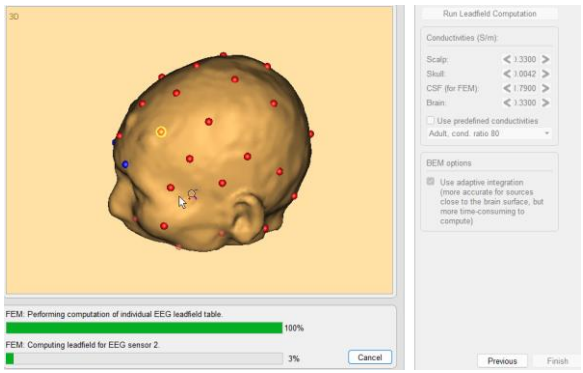


15. The electrode coordinates are loaded to BESA MRI.
16. Press **Run Surface Point Fit** and then press **Next**.

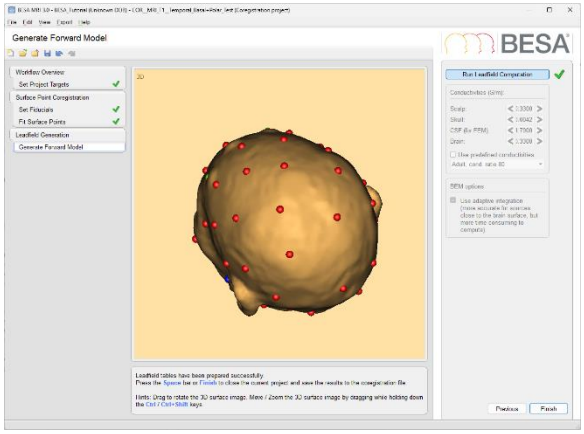


17. Press **Run Leadfield Computation** to start FEM and BEM leadfield computation.

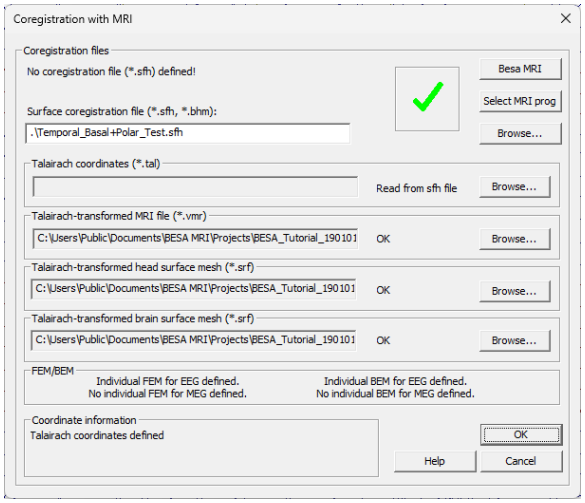
Note: This process may take a while.



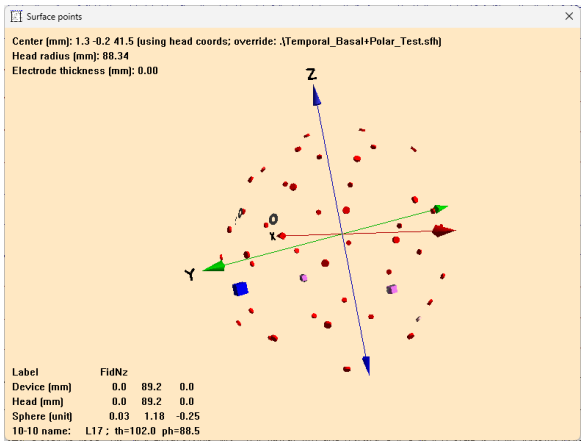
18. Press the **Finish**, button to save it.
19. A popup window for saving will be displayed. Press the **Save** button to save the coregistration project with the suggested name. After saving the coregistration workflow will be closed.
20. Close BESA MRI.



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



22. Press **V** to view the surface point and electrode cloud (i.e., fiducials, electrodes, etc.).
    Close the *Surface points* window.



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

We can co-register the EEG data with an MRI image by following the 10-10 EEG placement rule if individually digitized electrodes information is not available. When "**Place 10-10 electrode system**" option is selected in the *Set Project Targets* workflow step in the coregistration project, electrode coordinates can be automatically generated on the subject's scalp surface by following 10-10 placement rules in BESA MRI. Please see Chapter 6 of BESA Research 7.1 – Tutorial for more details.

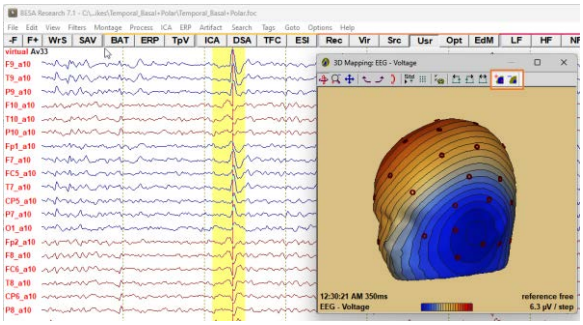
6. Finding and averaging spikes by pattern search

The Search Average View (SAV) function allows for a quick and automatized pattern search and averaging with predefined parameters. The pattern to be used in the search needs to be marked in the BESA Research main window before the SAV button is pressed.

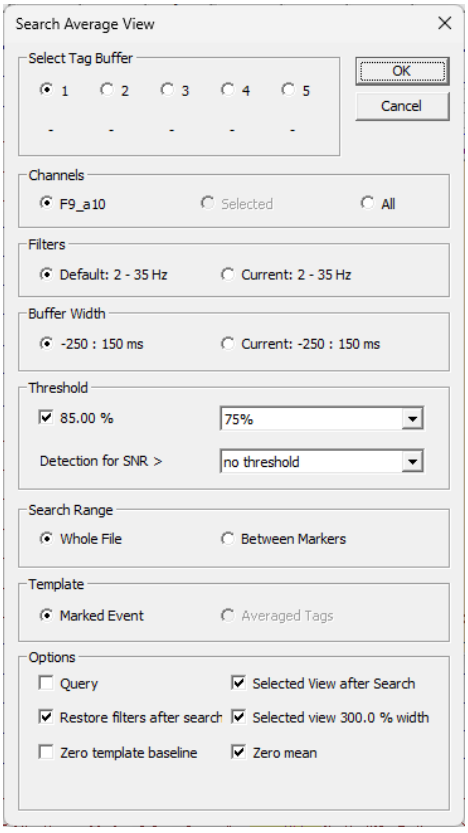
6.1. Single channel and spatio-temporal pattern search

1. Open the EEG file **Temporal_Basal+Polar.foc** if it is not already open.
2. Press the **F3** function key to set for standard spike review.
3. Press the **G** key, then select the event **TL pol** at **+00:20:20.** Press **OK** to move to this event in the EEG.
4. **Click** onto the spike and adjust to peak using the **mouse scroll wheel** while inspecting the 3D map.
5. Press **SAV** (Search-Average-view) from the control ribbon to open the *Search Average View* dialog.
6. For the first pattern search, we will use all preset settings, i.e., the channel having the largest marked pattern is used (**F9_a10**). Default filters and block width will be used with a high correlation threshold (85%) in single channel search.
   Press **OK**.

After the search terminates, the detected epochs are displayed in **Selected View** (menu **View | Select…**; shortcut: **S**) for inspection and deletion of bad epochs. Here, we skip checking each single channel detection to perform a spatio-temporal search using all channels in the Av33 montage.



To better view the map, reduce scale by pressing the button on the right in the Map window.

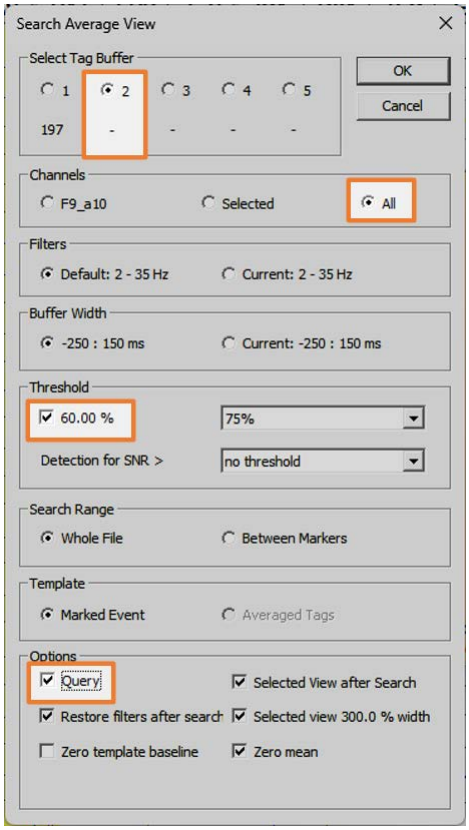


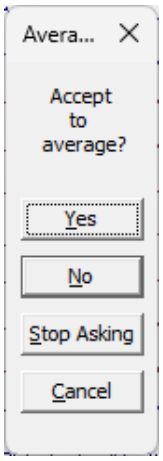
7. Select **View | Original Data** (shortcut: **E**) to return to the EEG view. The previously marked spike block appears again.

8. **Click** onto the same spike and adjust to peak using the **mouse scroll wheel** while inspecting the 3D map.

9. We will use the whole spatio-temporal pattern in the **AV33** montage.
   Press **SAV**. Detections now go into **buffer 2**.

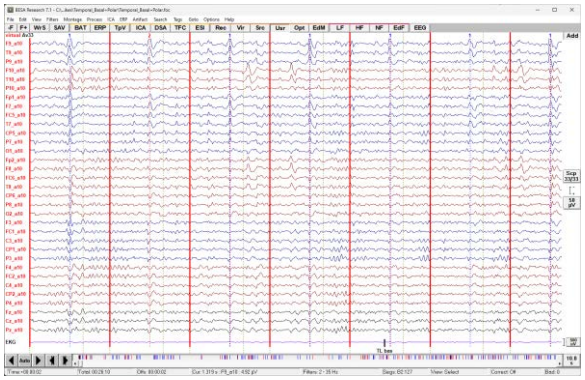
10. • Select the **All** check box.
    • Correlation threshold is set to **60%** for the search using all channels. Search will be more selective if set higher, e.g. to 65% or 70%.
    • By selecting the **Query** check box and then pressing **OK**, you can decide after each detection, whether the signal is clear enough and not contaminated in the preceding epoch.
    • Use the keys **Y** and **N** to decide in the *Average* dialog.
    • After some detections, press the button **Stop Asking** in this tutorial to complete the search.



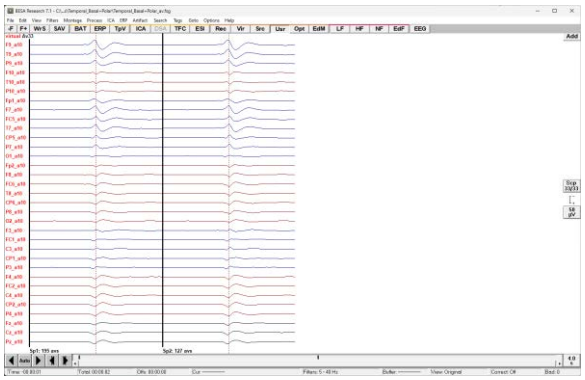


This pattern search will be more selective and the number of detections smaller because the same pattern must be present across all channels. By this spatio-temporal search, only spikes with similar topography and propagation are detected.

6.2. Inspection of detections and averaging

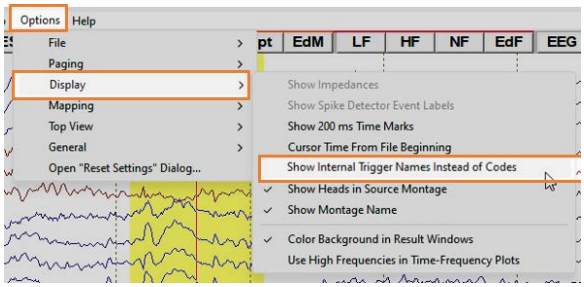


1. After the search is completed, **Selected View** presents the detected epochs (Pattern 2, red, and Pattern 1, blue). You will observe that most epochs have also been detected by the single channel search (Tag1, blue). Press the **Home** key to go to the first detection (or drag the scroll button in the time bar at the bottom to the left).
2. You can now page through the detections using the paging buttons or **<Space>**, **B**(ack), and **N**(ext).
3. If an epoch is contaminated, **click into it near the middle of an epoch**, then press **D** or **<Del>** key to delete.

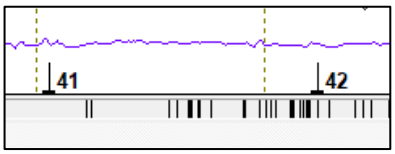


4. After completing the visual check in **Selected View**, press **F6** to run the prepared batch function **F6_Spike_Convert-Tags_and_Average.bbat**.
   • This batch converts the **pattern tags 1–5** into **triggers codes 41–45** and creates an average file with up to 5 spike averages labeled **Sp1–Sp5**.
   • The batch opens with the 2 buffers we have used and the file (**Temporal_Basal+Polar_av.fsg**) contains the spike averages Sp1 from the single channel search (~195 spikes averaged) and Sp2 from the search using all channels (~130).
5. Press the button **–F** to the left in the button bar to return to the continuous EEG file.

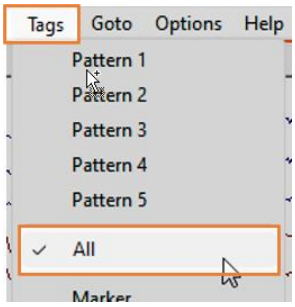
6. Uncheck **Options | Display | Show Internal Trigger Names Instead of Codes** menu entry.
   Note that the tags 1–2 have been converted into triggers 41–42 by the batch associated with F6.



Tip: The trigger events can be saved as an event file (*.evt) using the **ERP | Save Events As…** menu item.

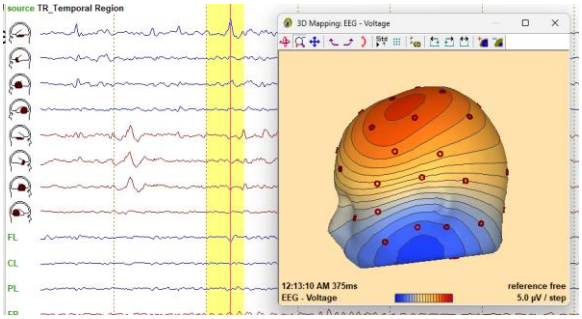


7. Pressing <Tab> takes you from one detected event to the next (<Shift> + <Tab> to previous events).
   For this, the **All** (events) menu entry must be tick marked in the **Tags** menu.



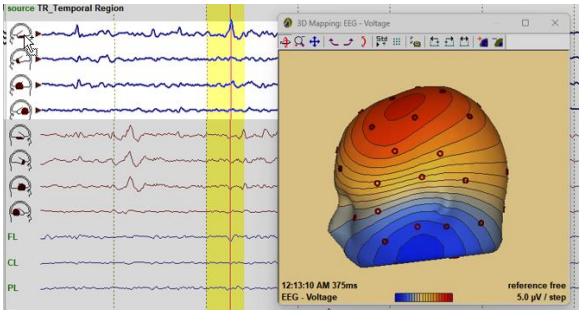
6.3. Pattern search using a standard source montage

1. Press the F3 function key to reset filters to 2–35 Hz for spike review and averaging.
2. Press Src, then select **TR_Temporal Region** to set the temporal lobe source montage (or shortcut F11).
3. Type G and select the event **TL bas** at time **+00:03:09** (or Select **Goto | Time** to go to 00:03:08).
4. **Click** onto the basal spike and adjust to peak.

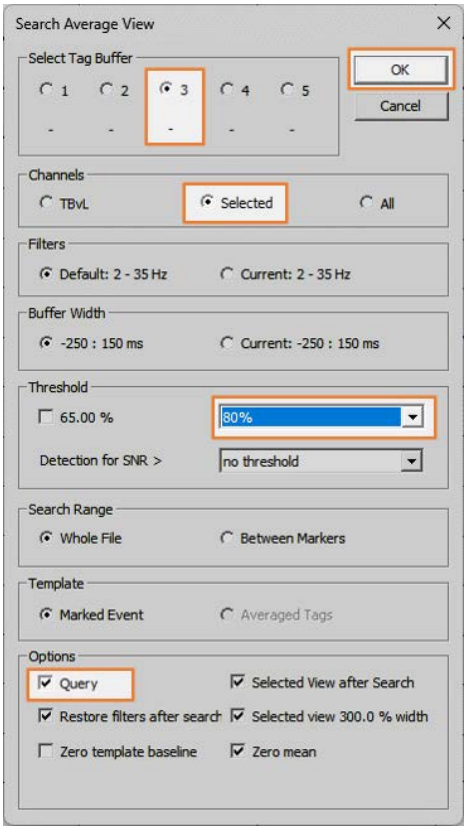


There is a pronounced spike at the left temporal basal (1st trace) at comment **TL bas**. This basal spike has not been detected, because it was not accompanied by polar activity (2nd trace) and showed only little lateral activity (3rd and 4th traces). Therefore, we want to use this specific spatio-temporal pattern of the 4 left temporal lobe traces to search for more left basal spikes.

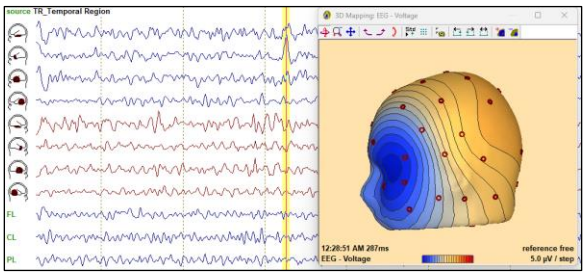
5. Hold the **<Ctrl>** key and **click** onto the channel labels of the first 4 channels to mark this combined selection.



6. Press **SAV** to perform a pattern search using the selected channels.
   • Select **Tag Buffer 3** to avoid overwriting triggers 41 and 42.
   • In Channels mark **Selected**.
   • Click onto the threshold drop down list and select **80%** for higher detection similarity (default 65%).
   • Further below, check the box **Query**.
7. Press **OK** to start searching using the selected combination of source channels. During query, accept only spikes with basal lead and predominance.
   After some detections, press the button **Stop Asking** in this tutorial to complete the search.
8. After completing, press **F6** to average.



9. **Exercise**: Repeat a similar search using the clear polar pattern prior to the **TL pol** marker in EEG (**00:18:50**) as seen in **TR_Temporal Region** montage.
   • Mark the first 3 source montage channels.
   • In the SAV dialog, select **Tag Buffer 4** to avoid overwriting the other triggers, and set threshold to **70%**.
   • Press **OK** to start search
   • In selected view, press **F6** to average.



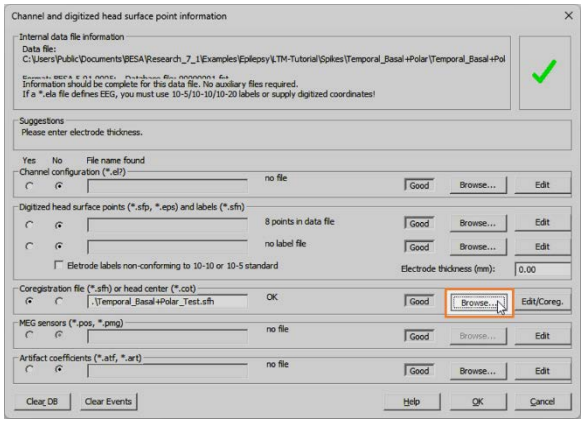
7. Work steps to localize spikes

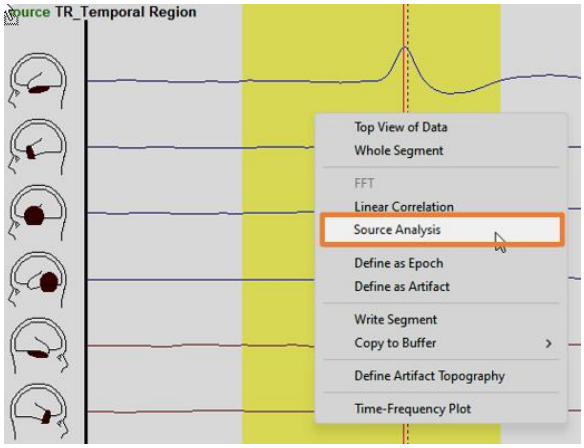
7.1. Prepare data for source localization

The following steps are needed to prepare data for source localization.

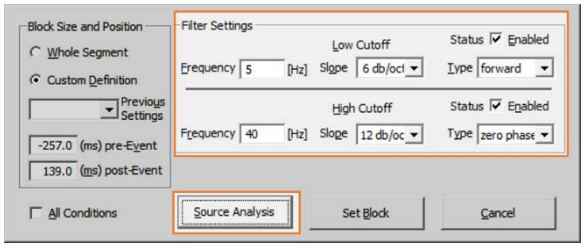
- Define a sufficient default epoch around the spike to obtain a standard view onto the spike and the preceding background signal (suggested: -250 ms to +150 ms around spike peak).
- Mark this epoch in the average data and center around spike peak.
- Set appropriate filters, i.e. a forward low cutoff (5 Hz or event 10 Hz) and a smoothing high cutoff filter (40 Hz).

1. Open the averaged EEG file Temporal_Basal+Polar.fsg if it is not already open.
2. Select **File | Surface Points and Sensors | Load Coordinate Files…** (shortcut: **Ctrl + L**) from the main menu.
3. In the "*Coregistration file (*.sfh) or head center (*.cot)*" section, press **Browse...** and then select the sfh file (Temporal_Basal+Polar_Test.sfh) we saved. Press **OK**.
4. Press **Src**, then select **TR_Temporal Region** to set the temporal lobe source montage (or press **F11**).
5. Select **Edit | Default Block Epoch** to set pre- and post-cursor intervals to **-250 ms** and **150 ms**, then set the low and high cutoff filters as follows:
   • Low cutoff filter: **5 Hz, forward**, 6 dB/oct
   • High cutoff filter: **40 Hz, zero phase**, 12 dB/oct
   (or press **F5**).
6. **Click** on the peak in the **Sp1** average. Use the mouse scroll wheel or arrow keys to adjust the cursor.
7. **Right click** into the marked block and select **Source Analysis** in the context menu.

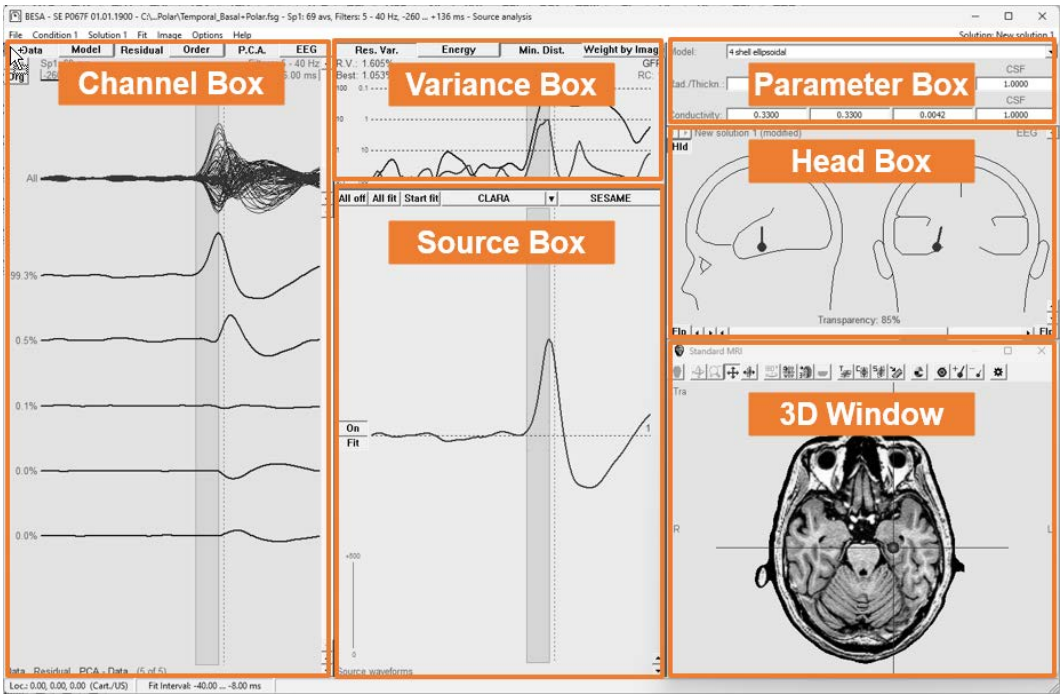




8. In the pop-up box, set the low and high cutoff filters as below:
   • Low cutoff filter: **5 Hz, forward**, 6 dB/oct
   • High cutoff filter: **40 Hz, zero phase**, 12 dB/oct.
   • Keep the custom definition of the block size (post interval is adjusted to the nearest sampling point).
9. Press the **Source Analysis** button.
10. Click **OK** in the *Starting Source Analysis* dialog.



The **Source Analysis** window is subdivided into six main parts (boxes):



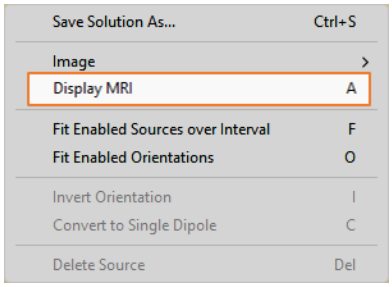
The 3D window will not normally appear automatically (unless specified in the **Options | Preferences** menu), and the head box will take up more space if the 3D window is not displayed.

7.2. Localize a single dipole in the onset-to-peak interval.

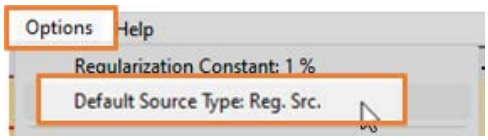
We will first proceed manually to observe each step in detail. Later, we will be using the more convenient semi-automated batch functions.

7. Work steps to localize spikes

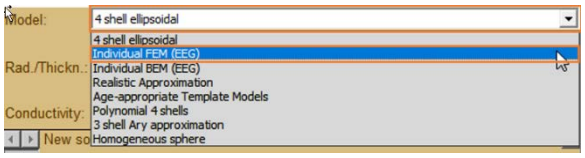
1. **Right click** into the head scheme window and select **Display MRI** (Shortcut: **A**) to show the 3D window (= MRI window).



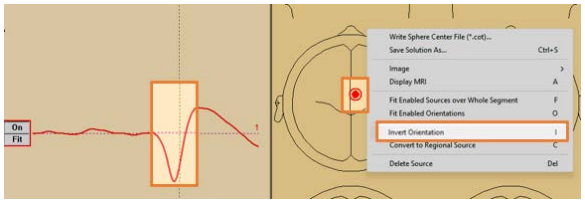
2. Select menu item **Options** and click onto **Default Source Type: Reg. Src**. to change the default source type to dipole source.
   If already showing **Default Source Type: Dipole**, go to the next step.



3. In the Parameter box, select **Individual FEM (EEG)** head model.

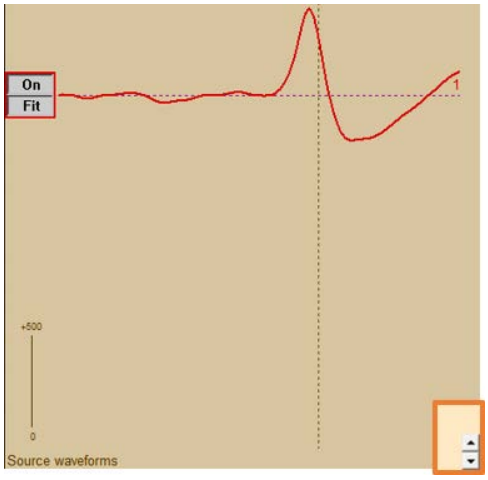


4. **Double click** into the middle of the left head scheme to create a dipole.
5. If the spike peak in the source waveform near 0 ms is pointing downward, **Right click** on it and select **Invert Orientation**. (shortcut: **I**).

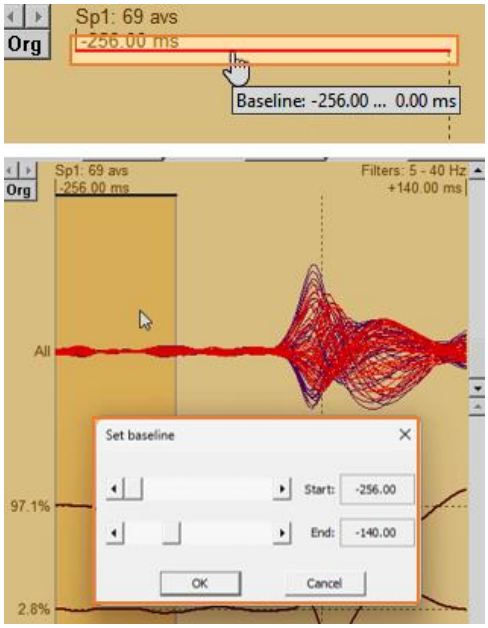


Consistent with spike physiology, we want dipole currents to be cortex negative in order to reflect current flowing from the cortical surface into the brain (dipole arrow indicates positive current direction, if the 0 ms peak in the source waveform is positive).

6. Use the **Scale buttons** at the lower right of the source waveform window to scale.



7. **Click** the red line in the *Channel box* (or select **Condition 1 | Set Baseline: -256.00 … 0.00 ms** from the menu), then set the baseline interval from **-256 ms to -140 ms** using the *Set baseline* dialog.

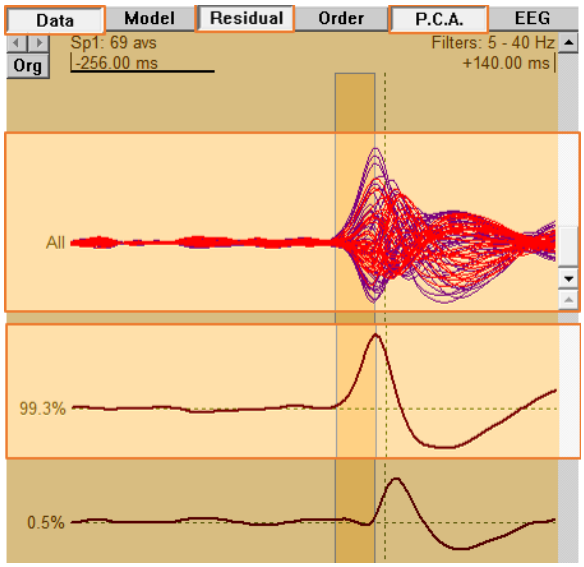


In the upper part of the Channel box, a butterfly plot of the scalp waveforms is displayed. The red waveforms indicate the residual, which is unexplained data.

You can toggle the button **Order** to see data and/or residual waveforms in the sequence as recorded (**Order**) or sorted by the magnitude of the data (**II Data II**) or residual (**II Res. II**).

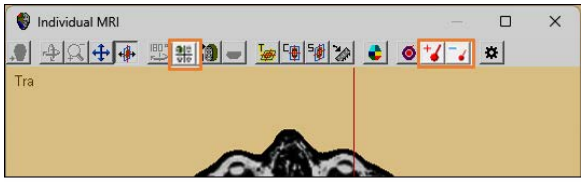
8. Drag the mouse over the onset-to-peak phase of the source waveform to mark an interval from about -40 ms to -8 ms for the fitting of the dipole.

9. Press **P.C.A.** (principal component analysis) on the Channel box to analyze the number of components in the marked onset-to-peak interval.
   The waveforms on the left only display one relevant independent component.

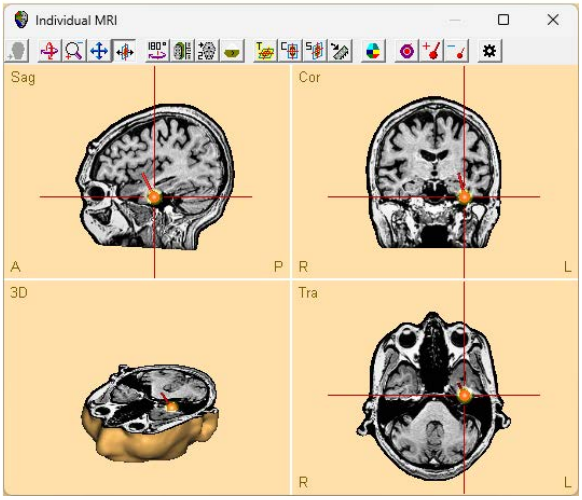


Components may be considered relevant if their variance is large, depending on the noise level in the pre-spike interval.
You may drag the dipole to a different location or modify its orientation by dragging it at the tip of the bar. Observe how the source waveform and residual variance (R.V.) are immediately recalculated with each change of the dipole parameters.

10. Press **Start Fit** to fit the dipole (Shortcut: **F**).



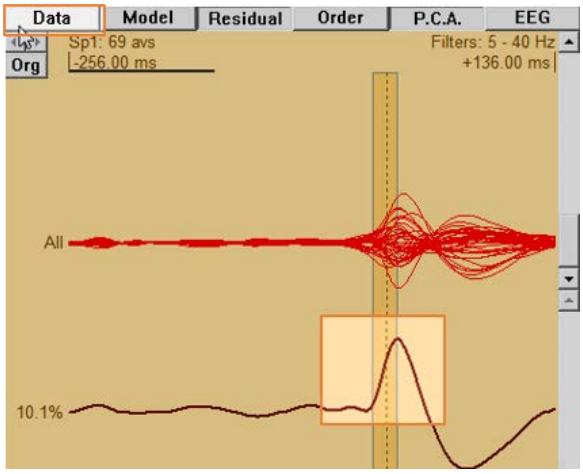
11. **Scale** the source waveform in the Source box.
12. **Toggle** the MRI view to **Multiple view** (by pressing  in the toolbar of the 3D window), then **scale** the dipole size in the 3D window.



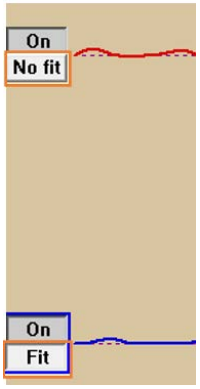
The fitting procedure in BESA Research scans the whole brain in gross steps using a regional source for the best starting point and then performs a single dipole fit initiated at this point. Thus, the dipole is not likely to get trapped in a local minimum.

Tip: By toggling the MRI view () in the 3D window, multiple MR slices can be viewed in the **Slice View**.

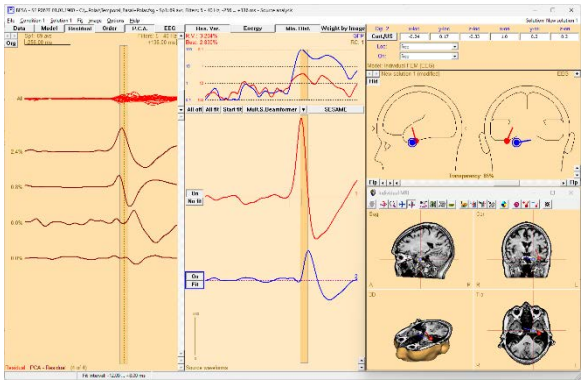
A more physiological approach is to create a model where the onset activity is allowed to continue into and beyond the peak interval of the spike. This is done by keeping the onset dipole fixed in the model and fitting a 2nd dipole to the peak interval. We will follow this approach now.



13. **Double click** into one of the head schemes to add another dipole. This creates a blue dipole (if a regional source has been created with 3 dipoles, press **C** on the keyboard to convert into a single dipole).
14. **Toggle** the **Data** button to show only the residual waveforms.
    Mark an interval of about -16 to +8 ms (from the onset to the peak of the first PCA waveform) for the fitting of the dipole.
    Note that the blue dipole switches into status **Fit** and the red onset dipole into status **No Fit**, thus becoming fixed during the next fit.



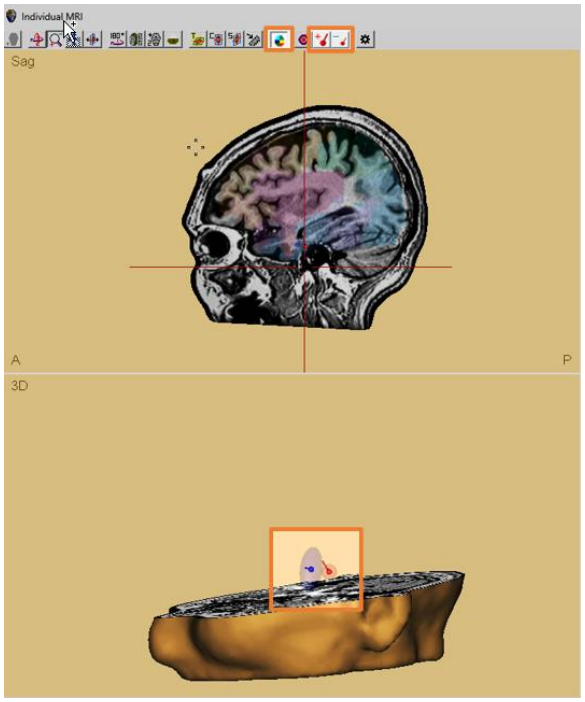
15. Press **Start Fit** to fit the blue dipole (Shortcut: **F**) while the red dipole remains in the model to separate the onset activity.



16. Maximize the 3D window, then adjust source plot size using  on the toolbar to check the confidence ellipsoids of the dipoles.

To understand the limitations, especially in accuracy, of the modeling, it is useful to investigate the confidence limits (95% confidence interval). Confidence limits are only available for co-registered MRI data.

17. Press  on the toolbar to turn on brain atlas overlay (shortcut: **Shift + A**).
    A brain atlas can be overlaid on the MRI in the 3D window.



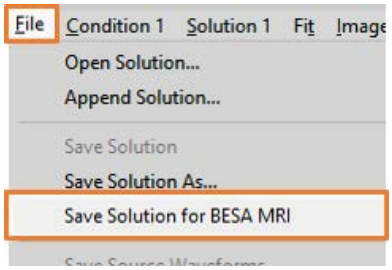
Note that brain atlases were created using either averaged data or post-mortem data from a single subject and may not fully correspond to the individual subject's MRI data.

18. Press  on the toolbar to display the cortex surface in the 3D window.

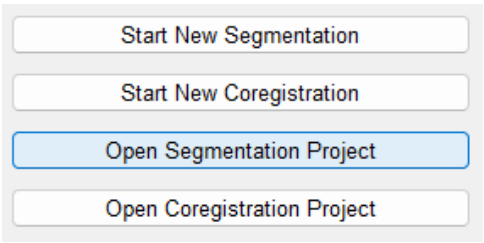
19. Minimize the 3D window.

Tip: The Source Analysis and window can be saved as a bitmap image using **File | Save Source Analysis window as Bitmap…** or **File | Save 3D Window as Bitmap…** menu item.

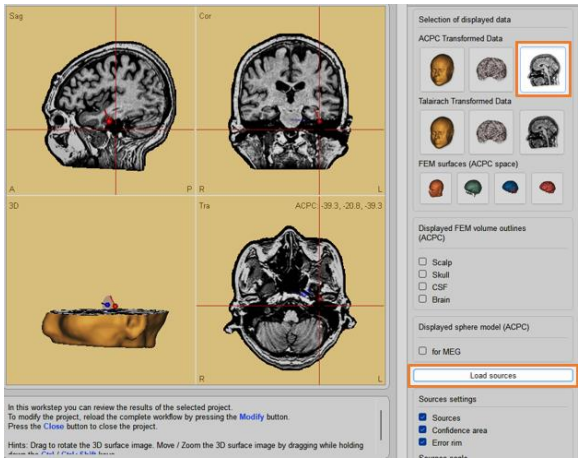
20. Select **File | Save Solution for BESA MRI** from the main menu of Source Analysis window.



21. Start **BESA MRI**, then press **Accept** on the welcome screen.
22. Press the **Open Segmentation Project** button in the interaction window.
23. Select the segmentation project saved previously, then press **Open**.



24. Press the **Load sources** button in the Interaction window.
25. Select the saved solution file (***. bsa**) in the MRI project folder (e.g., *C:\Users\Public\Documents\BESA MRI\Projects\P001_19010101* **Temporal_Basal+Polar-Sp1 69 avs.bsa**). The dipoles and their confidence areas are displayed in the ACPC coordinate system of the subject's MRI.

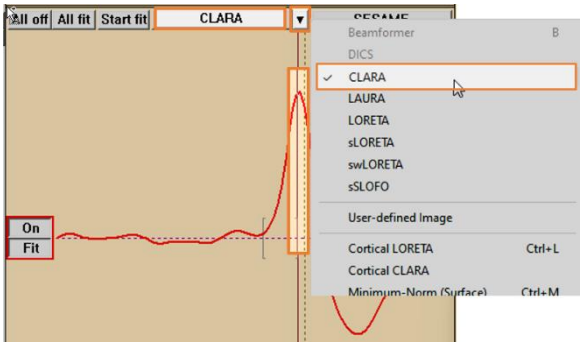


7.3. Compare the dipole solution with CLARA and Cortical CLARA images

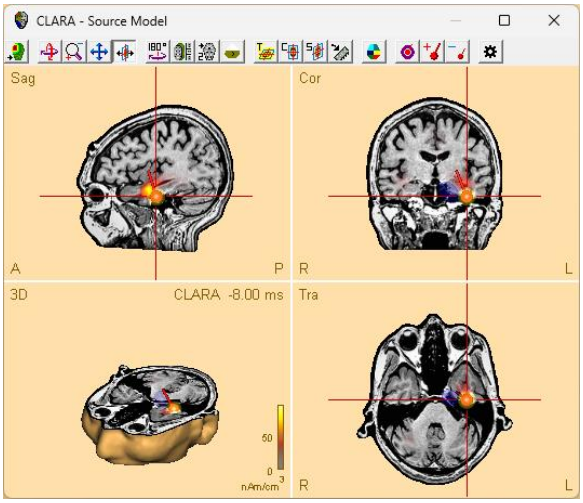
We will now compare the solution obtained by onset and peak dipoles with **CLARA** image (Jordanov et al., 2014; Kovac et al., 2014), an iterative application of the LORETA method that assumes a smoothed current distribution in the brain volume (or cortical surface for **Cortical CLARA**).

7. Work steps to localize spikes

1. **Double click** onto the red source waveform to set a cursor at the onset peak at **-8 ms**.
2. Press the image button (next after **Start Fit**) that should show **CLARA** (otherwise use the **dropdown arrow** button to select **CLARA**).

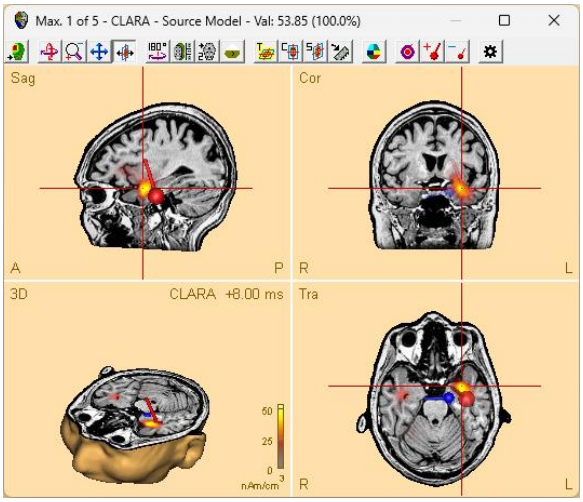


3. The first maximum of the CLARA image can be checked by **clicking** on the  button in the toolbar of the 3D window.

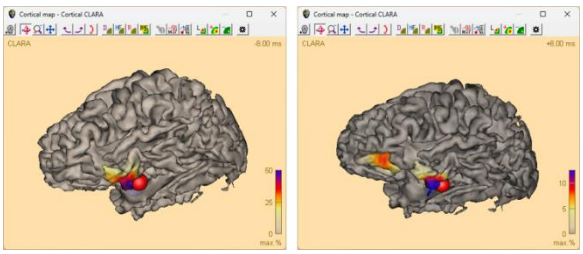


4. **Double click** onto the blue source waveform to set a cursor at the onset peak at **+8 ms**.
5. Press **CLARA** to image at this latency.

Since the CLARA image is not using a cortical constraint, the images of superficial sources may appear deeper in the brain.



6. Set a cursor at **-8 ms** and select **Cortical CLARA** using the **dropdown arrow** button. The reconstructed activity at -8 ms shows near the red dipole.
7. Set a cursor at **+8 ms**, then press **Cortical CLARA**.



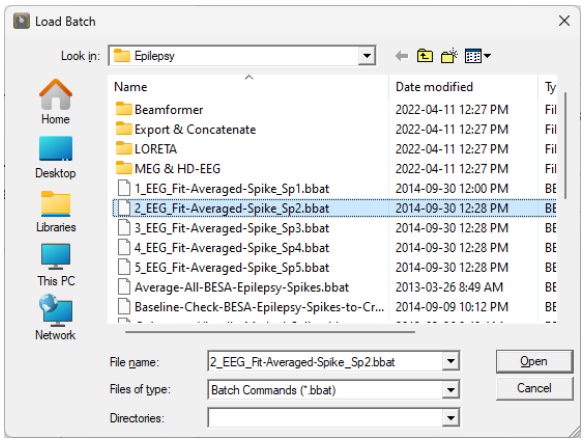
7.4. Use the batch for source localization

We will localize the second segment **Sp2** of the Temporal_Basal+Polar.fsg file using the batch, 2_EEG_Fit-Averaged-Spike_Sp2.bbat. It performs the following steps with user interactions (we did most steps manually before):

1. Spike epoch: Set **from -250 ms to +150 ms**
2. Filters: Set low cutoff filter 5 Hz (forward) and high filter 40 Hz.
3. Load segment into the Source Analysis window.
4. Load and display MRI.
5. **User interaction 1**: Select head model.
6. Fit a regional source into a tentative onset-peak epoch.
7. Calculate and display PCA over this epoch (giving first estimate of no. of components).
8. **User interaction 2**: Drag the boundaries of the marked epoch to optimize onset epoch with one major PCA component.
9. Fit a *regional source* into the *onset* epoch, orient and retain the first dipole (red onset dipole).
10. Fit a *regional source* into the *peak* epoch, orient and retain first dipole (blue peak dipole).
11. Fit a *regional source combined with the fixed onset dipole*, orient and retain (green peak dipole).
12. Store solution as %basename%_Sp2_On+Pk2.bsa.
13. Fit a *regional source* to the *whole epoch*, orient by the user-defined onset epoch and store solution as %basename%_Sp2_RS.bsa (blue, 3 dipole source waveforms).
14. **User interaction 3**: Press **CLARA** (and **Cortical CLARA**) to create images at onset and peak. Compare with dipoles.
15. **User interaction 4**: Switch dipole 3 on and dipole 2 off to check for propagation. Compare multiple dipole solution(s) with regional source solution.

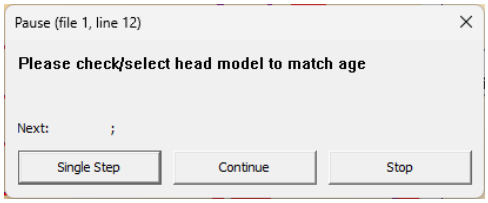
The user first needs to select an adequate head model and define the onset epoch visually. At the end, the pop-up boxes of the batch process serve only as reminders to the user how to evaluate and compare the calculated solutions and images.

1. **Close** the Source Analysis window and make sure that the averaged file Temporal_Basal+Polar.fsg is open.
2. Type R to run the batch function 2_EEG_Fit-Averaged-Spike_Sp2 (in .*Batch**Epilepsy*\). This batch will load segment 2 with adequate spike filtering into SA.



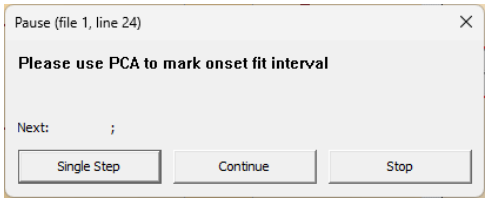
Tip: The same batch function has been provided for all spike types Sp1…Sp5. F7 can be used as fast shortcut for **Sp1** localization.

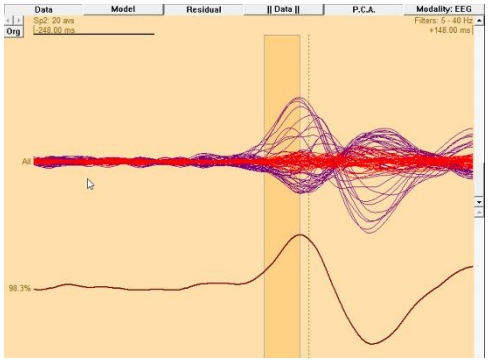
3. When the first pop-up box is displayed by the batch function, select the **Individual FEM (EEG)** from the dropdown list. Then, press **Continue** in the batch box.



Tip: If you press **Single Step**, you can see the effect of each step that is performed by the batch file. Press **Continue** at any time to get to the next user interaction.

4. The PCA waveforms are displayed in the Channel box. We want to isolate the onset component by changing the fit interval of **-40 : -8 ms**.
   The 1st PCA component almost completely explains the onset, while the 2nd has become quite small.



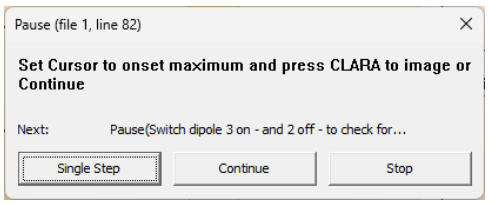


5. **Click** the red line in the Channel box, then set the baseline interval from -248 ms to -140 ms.

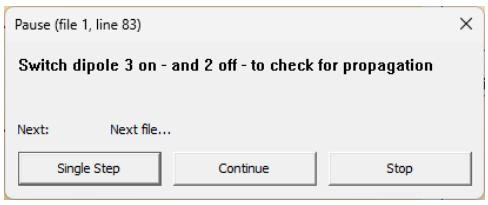
6. With this onset definition, we can now continue the automated fitting. Press **Continue** in the batch box.

Note: If the following warning message is shown, press **OK**: "*Warning: Sources # and # were lying outside the brain volume of the current head. They were moved to the closest inside locations.*"

7. User interaction 3 suggests creating a CLARA image manually at the peak of the onset period. Press **Continue** in the batch box.

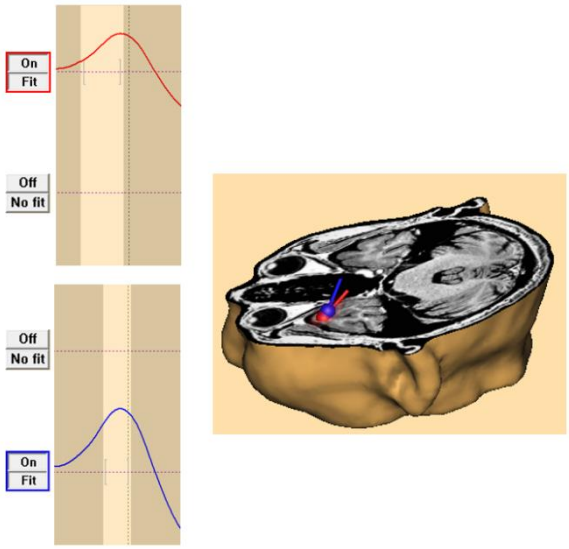


8. The batch terminates after user interaction 4 suggesting to check for propagation. Press **Continue** in the batch box.

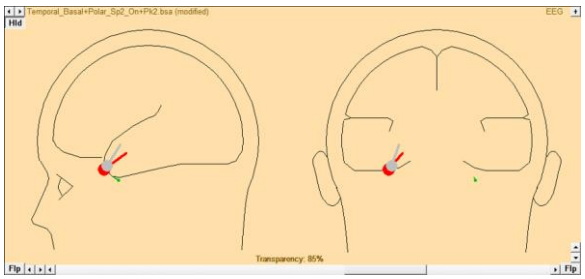


Tip: When the batch box shows '**Set Cursor to onset maximum and press CLARA to image**', automated fitting is completed. Thus, you may stop the batch by pressing **Cancel**, since the next and last user interaction is the suggestion to switch dipole 3 on and 2 off to check for propagation.

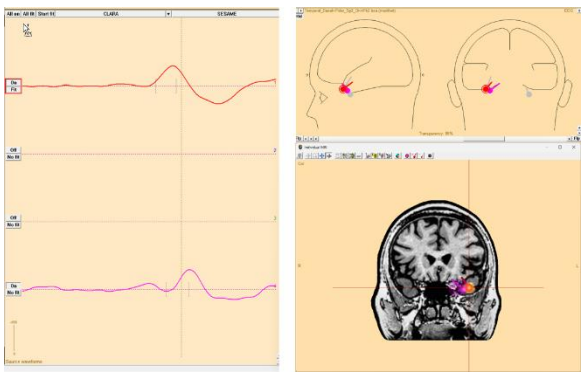
9. First, we will inspect the dipoles. The red (onset epoch) and blue (peak epoch) dipoles are close together but exhibit slightly different orientations. Thus, the activity appears to rotate slightly.



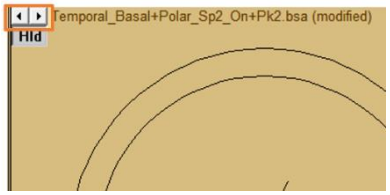
10. Switch **Off** dipole 2, and switch **On** dipole 3. In this solution, the blue dipole was fitted for the peak epoch. On the other hand, the green dipole (peak epoch) was fitted in the presence of red dipole to account for the overlap of the continuing onset activity. The red dipole explains most of activity, but the green dipole only a small additional activity. Thus, the green dipole can be seen as fitted to the small residual.



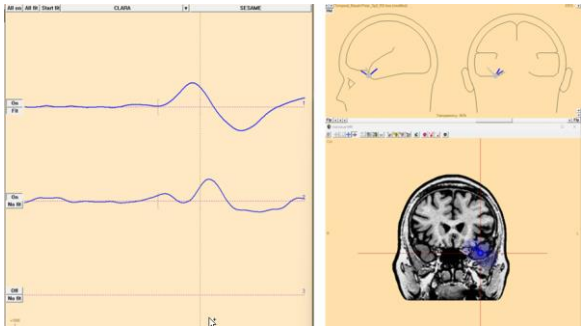
11. Switch **Off** the dipole 3, then toggle the **Data** button in the Channel box to show only the residual waveforms.
12. **Double click** into one of the head schemes to add another dipole (pink). If a regional source has been created with 3 dipoles, press **C** to convert into a single dipole.



13. Mark an interval of about **-24 to +23 ms** for the fitting of the dipole.
14. Press **Start Fit** to fit the pink dipole (Shortcut: **F**) while the red dipole remains in the model to separate the onset activity.
    The red (onset epoch) and pink (peak epoch) dipoles are close together but exhibit slightly different orientations.
15. Toggle the **Data** button in the Channel box to show the data waveforms again.
16. Next, we will inspect the regional source solution. Press the **left arrow button** at the upper left in the Head box to obtain the regional source solution that was fitted to the whole preset onset interval -60 : 0 ms.



17. Switch **Off** the dipole 3 because it explains only a small additional activity.
    The waveforms and orientations of the remained dipoles are similar to the dipole in the previous source solution.



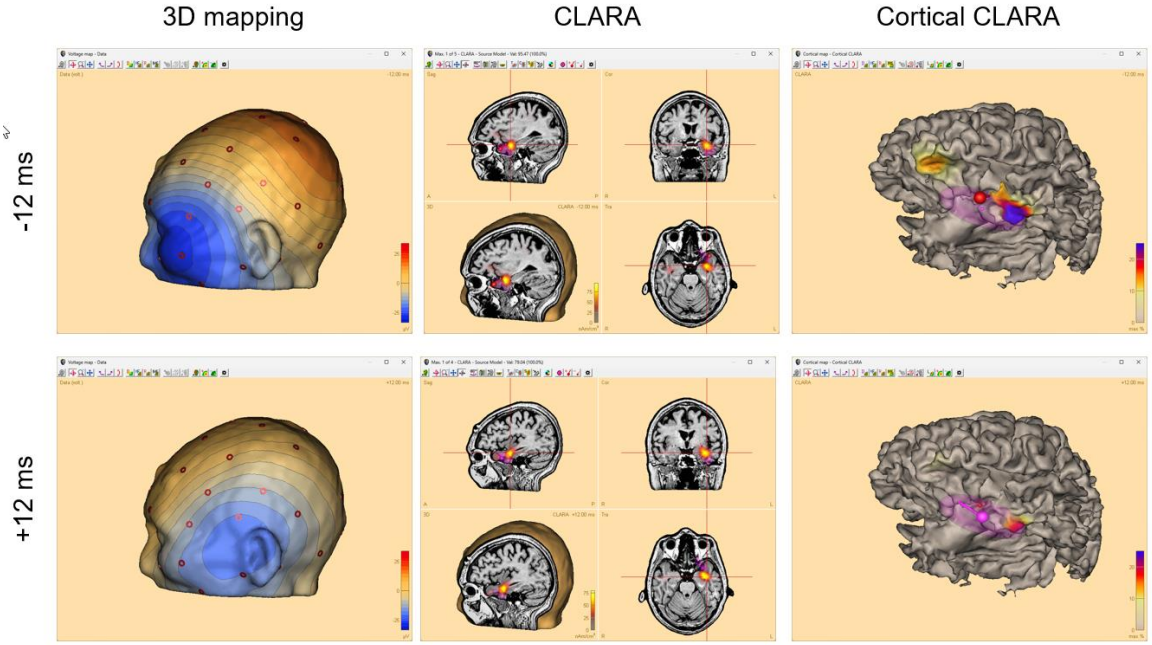
18. Press the **right arrow button** at the upper left in the Head box to obtain the previous source solution.

Note: If the data are noisy (e.g., with few averages or close tangential and superficial activities), a more robust localization can be obtained using a regional source, a source at an equivalent center location with orientations in all 3-dimensions to model both fissural and superficial cortex.

19. Next, as suggested in the User interaction 3, we will inspect the CLARA and Cortical CLARA images. **Set the cursor** at **-12 ms** and press **CLARA** to obtain the onset image (press  to go to the first maxima).
20. Press **Cortical CLARA** to obtain the onset image on cortex surface.
21. Set the cursor at **+12 ms** and repeat the previous two steps to obtain the **CLARA** and **Cortical CLARA** images.

Tip: Press  in the toolbar of the 3D window to show the **3D mapping** at -12 ms.

7. Work steps to localize spikes



These images also demonstrate the difficulty in precise estimation of the depth of EEG sources. Depth depends on many factors: source extent (cannot be estimated by EEG, only amplitude is a certain indicator), tissue thickness (scalp, bone and CSF cannot be precisely segmented using T1-weighted MRI), tissue conductivities (not know sufficiently in individuals), head model assumptions, smoothing parameters in imaging method, electrode placement etc. Therefore, depth needs to be interpreted with caution and the combination of two different methods (e.g., dipoles and CLARA) illustrates the region of spike origin together with the limits of EEG source localization. Thus, over-interpretation by visual bias inherent in images using the individual brain can be avoided.

8. Seizure onset analysis

This chapter is intended to show how to use the BESA Research software to find the earliest oscillatory activity of seizure and to localize the zone of onset using the oscillatory activity (Beniczky et al., 2016b; Kovac et al., 2014; Scherg et al., 2002).

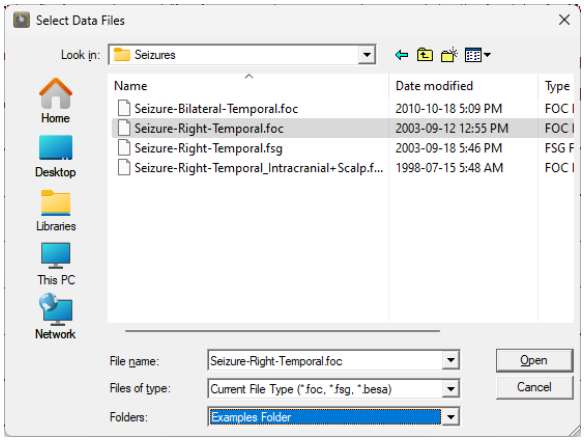
The earliest rhythmic activity at seizure onset can be used to localize the zone of onset, if certain criteria are fulfilled:

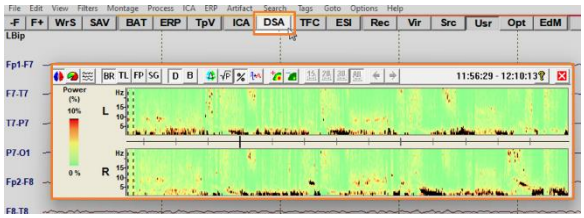
1. An oscillatory activity must be present and recognizable using appropriate montage and filters.
2. The earliest activity must be identifiable prior to propagation.
3. EEG background must not contain too large artifacts or rhythmic activities confounding the onset.

8.1. Find seizure onset by DSA

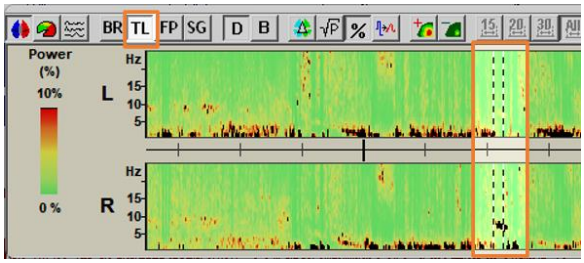
The **Density Spectral Arrays (DSA)** module displays a compressed two-dimensional time-frequency display of the activity in the data file. It focuses on the frequency range of 1–25 Hz which includes the commonly observed oscillatory rhythms in the human brain. This allows for a quick overview of the sections where events of interest occur, e.g., in the analysis of epileptic seizures or in sleep research.

1. **Close** the Source Analysis window, and select **File | Close All** from the main menu.
2. From the main menu, select **File | Open** menu item. In the *Select Data Files* dialog, select:
   • Files of type: **BESA Binary Files**
   • Folders: **Examples Folder**
   C:\Users\Public\Documents\BESA\Research_7_1\Examples
3. Select folder "*.\Epilepsy\Seizures*", then open file **Seizure-Right-Temporal.foc**.
4. Press **Usr**, then select **LBip**, the traditional clinical longitudinal montage.
5. Press **DSA** from the control ribbon to obtain the density spectral arrays of the left and right hemispheric sources.





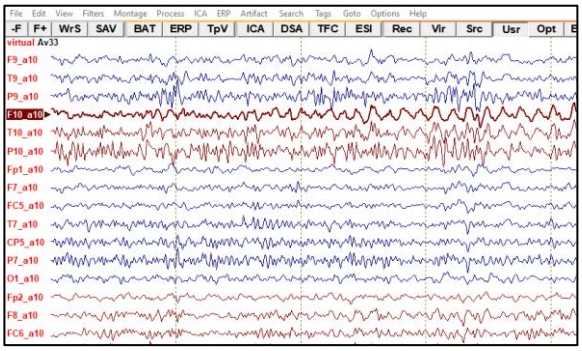
6. Press the TL button in the DSA window to compare right and left temporal lobe spectral activity over the 14-minute recording.



7. **Click** onto the chirp just left of the middle of the DSA window (initial frequency 8.1 Hz). This chirp is clearly lateralized to the right side
   (or select **Goto | Time** and enter **00:02:04** to be exactly at this position).

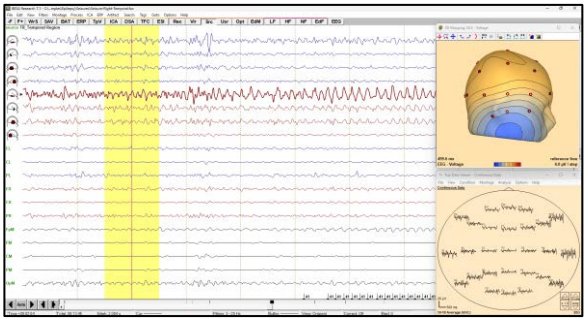
8. **Close** the DSA window.

9. Press the F3 function key to set:
   • **Av33** montage, the standard average reference montage
   • filter settings optimized for spike review and pattern search – **2–35 Hz** (zero-phase-shift characteristic)
   • a default epoch **from -250 ms to +150 ms** around the cursor



Note that the muscle activity is not completely suppressed. The **Av33** montage shows an earlier seizure rhythm at **F10**.

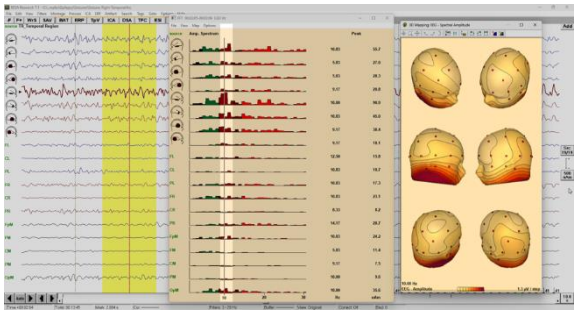
10. Press the F8 function key (shortcut for seizure settings: filters 3-20 Hz, TR-Temporal Region source montage, 1 second epoch).



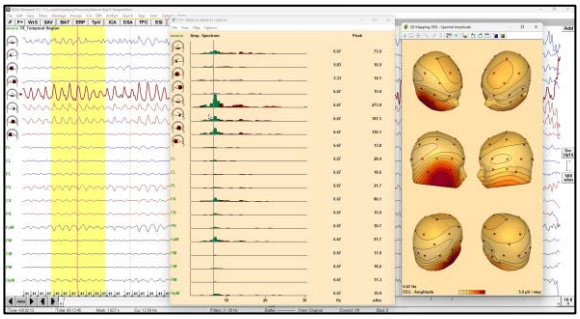
Now, the narrower filters show a clear seizure onset already in the 1st second of the displayed screen emerging in the right temporal basal channel (5th trace).

11. **Click** onto the earliest oscillation and adjust to peak to see the vertical right basal temporal map.

12. **Mark** a few seconds of the oscillation, then press **F** to obtain the FFT.
13. **Click** onto the peak value of **10.00 Hz** in the right temporal basal channel (5th trace) to see the map of spectral amplitude. The right basal temporal region is more active.
14. Press **Esc** to remove the cursor and close the windows.



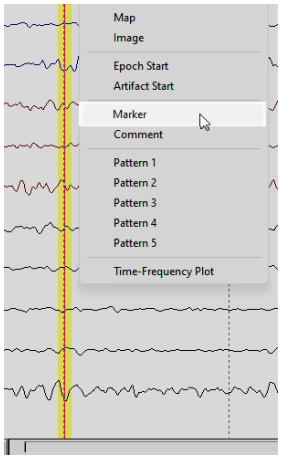
15. Select **Goto | Time** and enter **00:02:12** (to go further into the seizure). **Click** onto the EEG and adjust to a peak to see the map.
16. **Mark** a few seconds of the oscillation, then press **F** to obtain the FFT.
17. **Click** onto the **6.67 Hz** in the right temporal basal channel (5th trace). The polar and lateral regions are more active. This is a sign of increased propagation, but still within the right temporal lobe.
18. Press **Esc** to remove the cursor and close the windows.

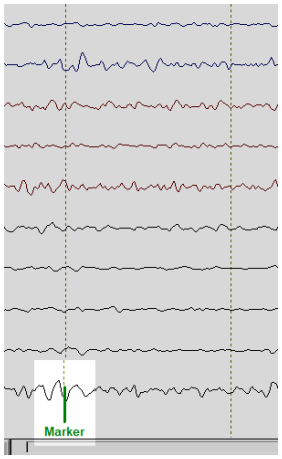


8.2. Localize seizure onset using averaged cycles

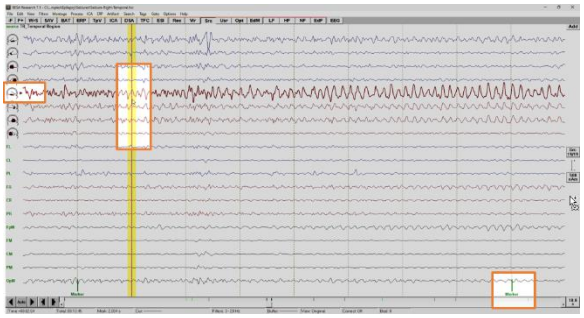
The basic idea is to mark the seizure onset cycles manually and use the average function. Make sure to mark only the earliest cycles before propagation sets in and frequency changes.

1. Select **Goto | Time**, then enter **00:02:04**.
2. Before the earliest oscillation, right click into the data and select **Marker** to add a marker.

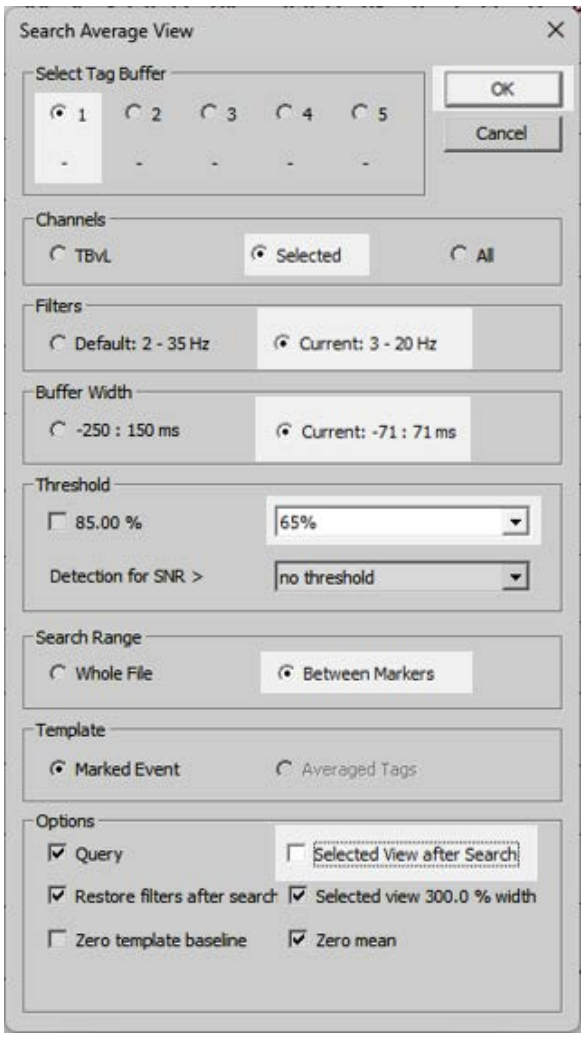




3. Add another **Marker** after 9 s.
4. Select the right temporal basal channel (5th trace).
5. **Drag** the data with the left mouse button over the oscillation, then **adjust** the cursor to the peak using the mouse wheel.



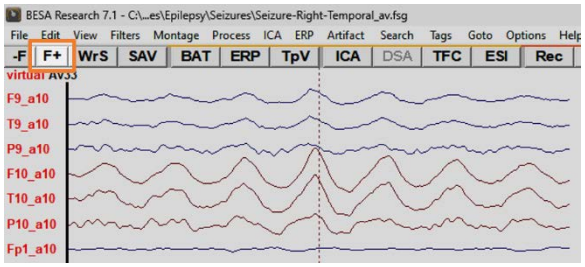
6. Press **SAV** to perform a pattern search using the selected channels.
   - In Channels, mark **Selected**.
   - In Filters, mark **Current**.
   - In Buffer Width, mark **Current**.
   - Click onto the threshold drop down list and select **65%**.
   - In Search Range, mark **Between Markers**.
   - Further below, mark **Query**, and unmark **Selected View after Search.**
7. Press **OK** to start searching the peaks between the inserted markers.



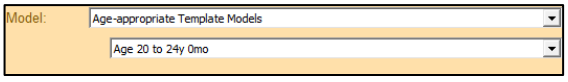
Tip: The peaks can be manually tagged by pressing **a number key 1 (1–5)** at each peak instead of using the Search Average View mode.

Note: If the number of averages is small and the signals are noisy, localization is less reliable as compared to spikes.

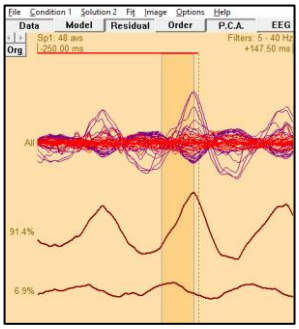
8. Press **E** (**View | Original Data**) to see the original data.
9. Press the **F6** function key to average the cycles using the batch.
10. Press **F+** from the control ribbon to see the averaged data (***.fsg**).



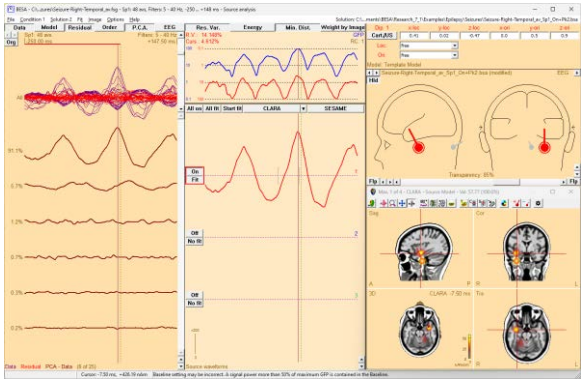
11. Press **F3**, then **F5** to change the montage and filter settings.



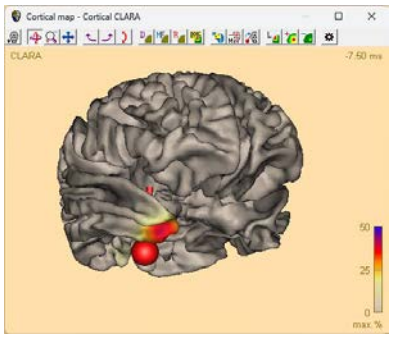
12. Press the **F7** function key to run the batch function for source analysis.



13. *User interaction 1*: In the Parameter box, select **Age-appropriate Template Models, Age 20 to 24y 0mo**
    Press **Continue**.
14. *User interaction 2*: Drag the mouse over the onset-to-peak phase.
    Press **Continue**.
15. *User interaction 3*: **Double click** at the peak, then compute **CLARA** and **Cortical CLARA** images.
    Press **Continue**.



16. *User interaction 4*: Switch dipole 3 on and dipole 2 off to check for propagation.
    • The red and blue dipoles are very close together but exhibit slightly different orientations. Thus, the activity appears to rotate slightly but does not propagate.
    • The red dipole explains most of activity, but the green dipole only a small additional activity.
    Press **Continue**.



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10. Appendix

10.1. Function keys

Batches and montages can be assigned to function keys on the keyboard.

- Function keys **F2 – F8** can be used to store **batches**.
- Function keys **F9 – F12** can be used to store **montages** that are frequently used. The assignment is user specific.
- To set a batch, press **Shift + <Function key>**. A selector box opens from which the batch of choice can be selected.

For clinical use, function keys for batches and montages can be automatically set by following these steps: From the main menu, choose **Options | Open "Reset Settings" Dialog…**, then select the checkbox "**Set Options for EEG Review**" and click the **OK** button in the dialog.

Key	Set montage / Action	Set filter	Set default block around cursor
F2	*BiHL* – bipolar mixed	Low cutoff filter: 0.53 Hz, forward (time constant: 0.3 s)	-250 ms : +150 ms
F3	*Av33* – average ref. a10	Low Cutoff Filter: 2 Hz, zero phase High Cutoff Filter: 35 Hz, zero phase (**narrow-band filters for spikes**)	-250 ms : +150 ms
F4	-	Low Cutoff Filter: 4 Hz, zero phase High Cutoff Filter: 30 Hz, zero phase	-150 ms : +90 ms
F5	-	Low Cutoff Filter: 5 Hz, forward High Cutoff Filter: 40 Hz, zero phase (**optimized filtering for spike onset**)	-250 ms : +150 ms
F6	*Action*: Convert tags to triggers 41–45 and average	-	-
F7	*Action*: Fit sources to 1st spike onset & peak (Sp1)	-	-
F8	*TR_Temporal Region*	Low Cutoff Filter: 3 Hz, forward High Cutoff Filter: 20 Hz, zero phase	-500 ms : +500 ms (**for seizure analysis**)
F9	*AV33* – average ref. a10	-	-
F10	*BiHL* – bipolar mixed	-	-
F11	*TR_Temporal Region*	-	-
F12	*FR_Frontal Region*	-	-

10.2. Keyboard shortcuts

Review window

Paging and navigation	
A	Turn on / off automatic paging
B / N	Page a half page back / forward
Space	Page to next screen, Start / stop of automatic paging if it is on.
Backspace	Page a whole page back
Tab	Go to next event (type as defined in Tab menu)
Shift + Tab	Go to previous event (type as defined in Tab menu)
File	
Ctrl + L	Load coordinate files
W	Write data (export data)
Event handling and viewing	
T	Tag and event (if cursor set)
Ctrl + D or Delete	Delete the current event (if cursor set)
S	Show the selected view (select trigger or tag to view epochs)
E	Return to the EEG view (around cursor)
1–5	Define tag # (if cursor set)
6	Define marker (if cursor or epoch set)
7	Define an artifact epoch (if epoch set) or start / end of artifact epoch (if cursor set)
8	Define an epoch (if epoch set) or start / end of epoch (if cursor set)

10. Appendix

Data analysis and viewing

Ctrl + E	Toggle artifact correction on / off
F	Calculate FFT spectrum of the marked data block
R	Run a batch on the current file
Ctrl + R	Run last-used batch on the current file
V	View coordinates of sensors
Shift + V	View coordinates of sensors including MEG

Mapping

Click onto EEG (or **M** if cursor set)	3D map	center view shown automatically
Scroll wheel	shift cursor	easy to find peak and remap at cursor
Arrow keys: Left / Right	shift cursor	3D map rotates automatically
Arrow keys: Up / Down	scale amplitudes	up / down
ESC	remove cursor and	close map & top view windows
Shift + S (in the Map window)	save as	save the Map window to a bitmap image file

10.3. Useful links

BESA Homepage (https://www.besa.de)

Subscribe to the BESA newsletter: https://www.besa.de/contact/subscribe-to-newsletter/

Support page: https://www.besa.de/support/support-page/

Trial order form : https://www.besa.de/contact/trial-order-form/

BESA Research 7.1 - Download: https://www.besa.de/products/besa-research/downloads/

BESA MRI 3.0 - Download: https://www.besa.de/products/besa-mri/downloads/

Useful documents

BESA Research 7.1 - Getting started: https://www.besa.de/wp-content/uploads/2014/05/BESA-Research-7.1-Getting-Started.pdf

BESA Research 7.1 - Tutorial: https://www.besa.de/wp-content/uploads/2021/11/BESA-Research-7.1-Tutorial.pdf

Quick Guide on 3D Maps: https://www.besa.de/wp-content/uploads/2014/05/BESA-Quick-Guide-on-3D-Maps.pdf

Recommendations for MRI Data in BESA MRI: https://www.besa.de/wp-content/uploads/2014/05/BESA-MRI-3.0-MRI-Data-Recommendations.pdf

BESA Wiki (http://wiki.besa.de/)

BESA file extensions: http://wiki.besa.de/index.php?title=BESA_files_extensions

Supported Data Formats: http://wiki.besa.de/index.php?title=Supported_Data_Formats

BESA YouTube channel (https://www.youtube.com/@BESAGmbH)

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