BESA®

**Research 6.0**

**Epilepsy 1.0**

**MRI 2.0**

# Spike Detection and Localization

# Recipe for MEG using the BESA pipeline

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# Table of Contents

**Table of Contents** ..... 2

**Preliminaries** ..... 3

**1. Prepare individual MRI segmentation and FEM using BESA MRI (BM)** ..... 3

**2. Compress MEEG files and concatenate using BESA Research (BR)** ..... 3

**3. Register the concatenated original MEEG file with the individual MRI** ..... 4

**4. Average EKG for correction and rejection of artifact channels** ..... 4

**5. Create artifact corrected MEG source montage for easy spike scan** ..... 5

**6. Scan MEG source and virtual EEG channels - create templates** ..... 5

**7. Optimized source channels for spike pattern search** ..... 6

**8. Use MEG and/or EEG spike templates for pattern search** ..... 6

**9. Localize and image spike onset automatically with individual MRI** ..... 7

**Summary of function keys and fast operations** ..... 9

# Preliminaries

It is assumed that you have installed the **VIREPA BESA Research version 6.0 (Sept. 2014)** by expanding the self-extracting files into **C:\VIREPA-SA**. This folder contains all files relevant for the BESA-VIREPA tutorial and the BESA program (except for your own data).

In this recipe, we briefly outline all the steps to process a set of MEEG data files recorded during one session.

**Important advices**:

1. For **Neuromag data**, it is mandatory that you have prepared the .fif files with TSSS correction over all files simultaneously. This will result in the same sensor locations for all files. Otherwise registration, spike pattern search and localization can be inaccurate!
2. Before you start on your own data, make yourself familiar with the tutorial located in the documents folder - **BESA - Mapping and Localization - VIREPA Tutorial.pdf** - and run BESA with the provided teaching example. The better you do this job, the more easily you are going to work on your own data!
3. More details on the specific steps for MEEG data, outlined below, can be found in the tutorial **BESA - Spike-Detection-and-Localization-in-MEG – Tutorial.pdf**.
4. The new file export and concatenation batches (Sept. 2014) are designed to ease and speed up working on your own data by exporting in optimized, compressed form to the folder **C:\BESA Data**.
5. Batches for MEG and HD-EEG data processing are in folder **…\Batches\Epilepsy\MEG_HD-EEG**.

# 1. Prepare individual MRI segmentation and FEM using BESA MRI (BM)

- Start BESA MRI (BM) and create a new segmentation project using patient T1 / T2 data. When starting the project, consider anonymization and name convention (see below).
- Prepare MRI as outlined in the **BM** manual (~ 5 min.) and start automatic finalization.
- Anonymize and save the project. Use a systematic name convention by 'location & patient number': LOC, Pxxx (e.g. SZ, P001 for Salzburg, patient 1).
- For saving your own data use a specific BESA MRI Shared folder in **C:\BESA Data** or on your LTM server.

  **Note:** At any time, the MRI projects (i.e. subfolders of your patients) can be copied to a different BM Shared folder (or zipped and transferred, e.g. by FTP).

# 2. Compress MEEG files and concatenate using BESA Research (BR)

- In **BR**, open all EEG / MEG files in original format. Select **Process → Batch Scripts** and press **Batch / Load Batch** to downsample and export each file in compressed BESA format. Preferably export to **C:\BESA Data** using the following batches:

  **…\ MEG_HD-EEG\1_Export-to-C-BESA-Data-at-250Hz_HF82Hz.bbat** or
  **…\ MEG_HD-EEG \1_Export-to-C-BESA-Data-at-250Hz_HF82Hz_Notch50Hz.**

  Notch filter is recommended for most systems. Alternative batches can be found in the subfolder **…Batch\Downsample**.
- In **BR** close all files. Use drag & drop, or the **File →Open** menu, to open the exported and compressed BESA files (.foc) in reverse order.

- Select **Process → Batch Scripts** and check the sequence in the file list to show the right sequence (**Right click** onto a filename to move up or down). Select the **Batch** tab and press **Load Batch** to concatenate the compressed BESA files into one file. using the batch:

  **…\ MEG_HD-EEG\2_Concatenate-Open-Files-to-C-BESA-Data-Pxxx.bbat**

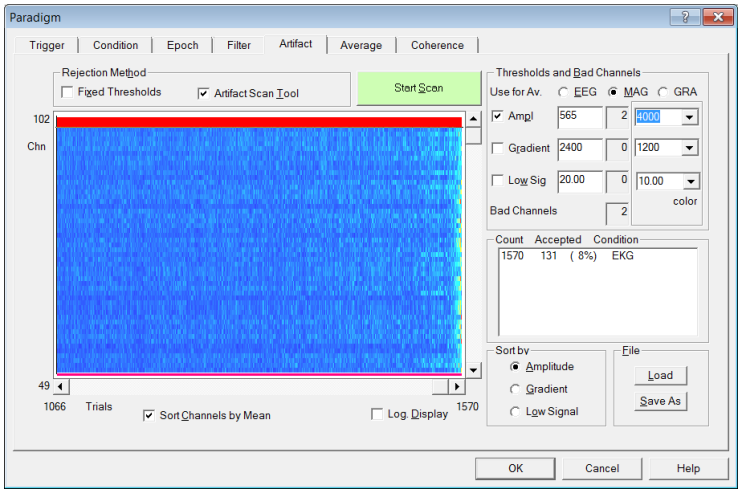
- Rename the file **Pxxx.foc** in **C-BESA-Data** using the convention LOC-Pxxxx with an appropriate subject number, anonymize the file if it contains patient information (not in Neuromag!), and move the file to a specific patient folder. You can delete the intermediate, exported BESA files at this stage in **C-BESA-Data**.

## 3. Register the concatenated original MEEG file with the individual MRI

- In **BR**, open the concatenated, renamed EEG/MEG file **%basename%.foc**.
- Type **V** to view the surface point / electrode cloud. Digitized surface points, i.e. fiducials, electrodes, reference coils etc. are typically contained in original MEEG files (e.g. Neuromag).
- Press **Edit/Coreg** to start registration. In **BM** follow the work steps as described in manual.
- **Important note:** With digitized electrodes, un-tick **Scaling…** in **Advanced Settings** before Fit. In manual corrections, you may only do rotations and shifts but no scaling to avoid distortions of the MEG sensor space.

## 4. Average EKG for correction and rejection of artifact channels

- Press **F3** to set **Av33** montage, **F4** to set narrow filters. **Add** EKG channel at bottom. If an EKG channel is not available or bad, you may use pattern search to find and average EKG/MKG artifacts by marking the magnetometer channels with pronounced MKG artifact. Make sure there are no triggers 41-45 in the file. Otherwise, delete using ERP menu.
- **Drag to set a block** of about +-100 ms around the R-wave in EKG (or the selected MAG channels with artifact) and press **SAV**. Use **current** filter and epoch settings.
- The selected view appears. Inspection is not needed. Press **R** to run the batch function: **4_Average-EKG-or-MKG-artifact_to-Reject-Bad-Channels.bbat**.
- In upcoming box for artifact check, tick **GRA** (only with Neuromag). Check for bad channels at the top and drag horizontal cursor down to exclude. Then, tick **MAG**. Check again for bad channels at the top and drag horizontal cursor down to exclude.




*Two MAG channels with high amplitudes were excluded.*

*Then, then 1st number in the Ampl. row was reduced to 565. When changing this number, click into the next field on the right (sets color level) to activate.*

*Modify 1st number in the Ampl. row until the number of accepted EKG epochs is about 120, or drag the scroll button at the bottom and the vertical cursor to the left.*

- **Optional:** Repeat the check for artifact channels by ticking **Low signal** at the bottom in the 'Sort by' box (to check for channel drop out!). Tick again **Amplitude** in the 'Sort by' box.
- Finally, reduce the number of accepted epochs to about 120 by either by modifying the amplitude level (first number in **Ampl.** row) or by dragging the horizontal scroll button and vertical cursor to the left (cf. figure legend above).Thus, we will use only the cleanest epochs to get a sufficient EKG average without too many triggers, since these will be averaged as an extra segment together with every spike average for later correction. Using all triggers would be too time-consuming.
- This work step creates the EKG average and trigger file (**%basename%_EKG.fsg /.evt**).

## 5. Create artifact corrected MEG source montage for easy spike scan

While the averaged EKG file is open, we will use the topography of the averaged MKG artifact in the sensor space to create an artifact-free source montage covering 29 brain regions.

- Type **R** to run the batch **5_MAG_Create_MEG-SourceMtg-M29K_MKG-corrected.bbat**. An alternative batch is available for the gradiometer channels of the Neuromag system in folder **\Gradiometers**. However, the resulting montage **G29K** is usually noisier than **M29K**.
- This batch first loads the MKG and performs a PCA. Adjust the epoch as advised and decide whether to keep 2 components (often, the 2$^{nd}$ MEG component has less than 5% of variance and you can switch it off by clicking **On**).
- **Right click** onto the R-wave of the 1$^{st}$ source waveform to invert if peak is not upward.
- **Optional:** Label the source waveforms as MKG (and MKG2), if you want to create an additional, virtual MKG channel (e.g. if EKG is not available). When you are in the montage editor in the next step, first delete all channels except for the first channel (MKG). Press **Save** button to save as additional montage with name **MKG.sel**. Then, reload the source montage M29K and continue as explained in the next step.
- Follow the instructions in the batch box and press **Continue without single step**. When the instruction comes up to press EdM, press the **EdM** button and delete the MKG channels. Then, press the **Exit** button on the left, save and overwrite the montage **M29K.mtg**.
- As suggested in the last box, press **–F** to reopen the original MEEG data file.

**Note:** the EKG triggers have been deleted automatically and the selected EKG triggers (71) will be reloaded by the averaging batches.

## 6. Scan MEG source and virtual EEG channels - create templates

- In the original MEEG file, press **F3** to set **Av33** montage. For MEG press **F4** to set narrower filters, since spikes are usually sharper in MEG.
- Press **Add** to view the EKG channel or (virtual MKG) at the bottom of the screen.
- Press **Usr** to select montage **M29K** (or G29K).
- Press **Pos1** key to start visual spike scan at the beginning of the file. Use **<space>** key to page forward.
- If you find a spike, **Click** onto the peak and use the **Scroll wheel** of the mouse to adjust to the maximum in the MEG map. You may have to press the **EEG** button (at the right of the button row) to switch to MEG mapping (type **M** to remap at the cursor and adjust to peak).

- Type **T** and keys **1…5** to tag as pattern 1…5. Try to use the same # for each spike type.
- After completing the MEG source channel scan, type **R** to run the averaging batch:

  **6_MEG_Average-Visually-Detected-Spikes.bbat**
- For the visual EEG scan, press **–F** to reopen the original MEEG file.
- Press **F3** to set **Av33** montage, standard EEG spike filters and the standard epoch.
- Press **Pos1** key to start visual spike scan at the beginning of the file.
- **Click** onto a detected spike and adjust to peak maximum observing the EEG map.
- Type **T** and keys **1…5** to tag as pattern 1…5. Try to use the same # for each spike type.
- After completing the EEG virtual channel scan, type **R** to run the averaging batch:

  **6_EEG_Average-Visually-Detected-Spikes.bbat**

**Note:** The averaged template files %basename%.VS-MEG and …VS-EEG could be used for preliminary spike localization. However, it is recommended to use them as templates for pattern search (see section 8), because more and only similar spikes will be found and alignment will be more precise using pattern search.

# 7. Optimized source channels for spike pattern search

The averaged spike template files can be used to create an optimized source channel for each spike type Sp1...Sp5. This procedure is described in detail in chapters 6 and 7 of the tutorial:

**BESA - Spike Detection and Localization in MEG - Tutorial.docx**.

Here, only a brief outline is given.

- Open a spike template file %basename%.VS-MEG and …VS-EEG. This contains at least segments SP1 (and Sp2…) and EKG.
- According to the spike type you want to use for creating an optimized source channel, select the batch function and type **R** to run:

  **7_MAG_Create_MEG-SourceMtg-M1K_from-Sp1-PCA2_MKG-corr.bbat** (for Sp1) or

  **\ MAG_Sp2-5\7_MAG_Create_MEG-SourceMtg-M1K_from-Sp2**… (for Sp2….5).
- Type **R** to run the batch function, and, after pressing **EdM** as requested, delete all channels except for the initial specific source channels (and MKG, if wanted – drag to move MKG to the end). Make sure to save the montage as Additional channels montage when exiting.

# 8. Use MEG and/or EEG spike templates for pattern search

Details on pattern search can be found in the following tutorials:

**BESA - Guideline for Mapping and Localization - VIREPA Tutorial.pdf** and

**BESA - Spike Detection and Localization in MEG - Tutorial.pdf**.

Here, only a brief outline is given.

- Open a spike template file %basename%.VS-MEG and …VS-EEG. This contains at least segments SP1 (and Sp2…) and EKG.
- Press **F3** for EEG filters and, then, **F4** for sharper MEG spikes. **Note:** The same filter settings must be used later in the original file before starting pattern search!
- **Drag** to mark the whole (or nearly the whole) spike segment you want to use as template.

- Type **Ctrl+C** to copy the marked segment into buffer 5 (recommended in order to use tag buffers 1-4 for the averaged results of pattern searches).
- Open the original MEEG file. Press **F3** to set **Av33** montage and EEG filters
- If useful, you may select another montage for EEG, e.g. **TR** – temporal region.
- For MEG, press **Usr** to select source montage **M29K** (or G29K).
- For sharper MEG spikes, press **F4** (i.e. same filter as you had when copying the template!).
- Press **Add** to add special source channels at the bottom, e.g. **M1K**, **E1** etc.
- Select **View → Average Buffers** to view the averaged template.
- **Click** onto the template and adjust to peak.
- If you wish, **mark** selected channels with large signals. Hold the **Ctrl** key when marking several channels.
- You may also **mark only the specific** additional channel, or, this channel in combination with the source channels having large signals (e.g. in **M29K**). When using the **Av33** montage for EEG pattern search, marking is not needed, since all channels can be selected in the SAV box.
- Press **SAV**, select current filters and epoch (!), and choose an appropriate tag buffer (1-4) to store the average (related buffer will be overwritten!).
- Press **OK** to start pattern search. Inspect the detected events and delete bad epochs.
- To do another search with a different combination of marked channels, use a different tag buffer in the SAV box and start again by selecting **View → Average Buffers** to view the current averages including the template (in buffer 5).
- After completing the pattern searches, type **R** to run the averaging batch

  **8_MEG-Average-Pattern-Search-Spikes.bbat** (for MEG) or

  **8_EEG-Average-Pattern-Search-Spikes.bbat** (for EEG).

# 9. Localize and image spike onset automatically with individual MRI

Details on the localization procedure and interpretation can be found in the tutorials.

- Open an averaged pattern search file %basename%.PS-MEG or …PS-EEG
- According to the spike type you want to localize select the batch function and type **R** to run:

  **9_MEG_Fit-Averaged-Spike_Sp1.bbat** (for Sp1) or

  **\ MAG_Sp2-5\9_MEG_Fit-Averaged-Spike_Sp2**… (for Sp2….5).

**Important note:** Localization batches for MEG are currently slightly different from the standard EEG localization batches in …\Batch\Epilepsy. For independent EEG localization, use the batches in \Batch\Epilepsy.

# Summary of function keys and fast operations

## Function keys in BESA Research 6.0 for VIREPA

| ***F2-F5/8*** | ***Set montage to*** | ***Set filter*** | ***Set block around cursor*** |
|---|---|---|---|
| **F2** | **BiHL** - bipolar mixed | LF: 0.53 Hz fw / TC 0.3 s | +- 20 ms |
| **F3** | **AV33** – aver. ref. a10 | LF: 2 Hz zp – 35 Hz zp | -250 ms : +150 ms |
| **F4** | no change in montage | LF: 4 Hz zp – 30 Hz zp | -150 ms : +90 ms |
| **F5** | no change in montage | LF: 5 Hz fw – 40 Hz zp | -250 ms : +150 ms |
| **F8** | **TR-source** for seizure | LF: 3 Hz fw – 20 Hz zp | -500 ms : +500 ms |

| ***F6-F7*** | ***Run autom. process*** | ***Batch - modify association by pressing Shift+Fkey*** |
|---|---|---|
| **F6** | Convert tags to triggers 41-45 and average | F6_Spike_Convert-Tags_and_Average.bbat |
| **F7** | Fit sources to 1st spike onset & peak (Sp1) | F7_EEG_Sp1_Fit.bbat (also prepares CLARA image) |

| ***F9-F12*** | ***Set montage to*** | ***Optionally modify by*** |
|---|---|---|
| **F9** | **AV33** - average ref. a10 | pressing Shift+F9 to associate key with current montage |
| **F10** | **BiHL** - bipolar mixed | pressing Shift+F10 to associate key with current montage |
| **F11** | **TR** - temporal sources | pressing Shift+F11 to associate key with current montage |
| **F12** | **FR** - frontal sources | pressing Shift+F12 to associate key with current montage |

## Paging and navigation

| | | |
|---|---|---|
| **<Space>** | page forward | start & stop of automatic paging, if on. |
| **B** | back half page | |
| **N** | next half page | |
| **A** | automatic paging | toggle on/ off |
| **Scroll wheel** | page for- / backward | easy paging by using the mouse wheel |
| **<Tab>** | Go to next event | type as defined in Tab menu |
| **Shift+<Tab>** | Go to previous event | type as defined in Tab menu |
| **S** | Selected view | select trigger or tag to view epochs |

## Mapping

| | | |
|---|---|---|
| **Click onto EEG** | 3D map | center view shown automatically |
| **Scroll wheel** | shift cursor | easy to find peak and remap at cursor |
| **Arrows ← →** | shift cursor | 3D map rotates automatically |
| **<Esc>** | remove cursor and | close map & top view windows |