Tutorial – draft 1

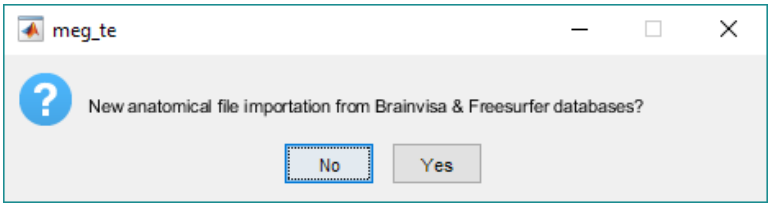
The connectivity pipeline under development aims to facilitate the analysis of MEG data with Fieldtrip, with source reconstruction based on anatomical data from the MarsAtlas pipeline (using BrainVisa and Freesurfer).

Parameters in cp_main

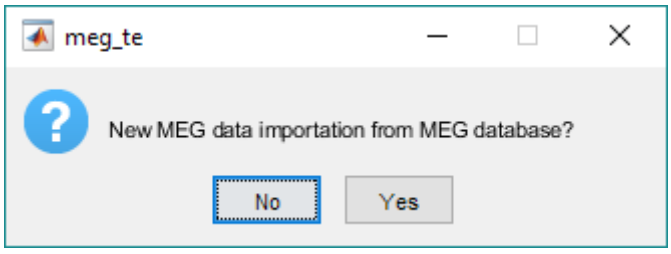
The first step is to manually define the parameters in the cp_main script, which include database paths, preprocessing options and frequency analysis parameters for DICS beamforming.

Data importation

At the launch of the cp_main script, a first dialog window asks if an import of anatomical data is to be done. Click on “Yes” if you run it for the first time or if new subjects in Brainvisa and Freesurfer databases have been added. The anatomical files necessary for the construction of the head model will be copied in the Fieldtrip database in the “anat” directory (MRI, surface, MarsAtlas volume files and transformation matrices files).



A second window asks if MEG data importation is to be done. By clicking on “Yes”, pointers to the data in the MEG database will be defined (MEG data being too large to be copied in the Fieldtrip database).



It is possible to import only anatomy or MEG data paths if only one of the data types is available for now. This allows to progress on the pre-processing of the data. For anatomical files, it consists in identifying the fiducial points and for MEG data in data cleaning. The source analysis will be performed by running cp_main only when both the anatomical and MEG data files will be available.

Fiducial identification

The fiducial identification is based on the interactive method from Fieldtrip. During this selection, you should keep the figure active (do not click on the Command Window for instance). When the yellow cursor is on one of the fiducial points that you wish to validate, stay on the figure and simply press the key code for this point on the keyboard (you will see the associated coordinates change on the command window).

1. Find the white pastille that indicates the right side
2. Find the Right Pre-Auricular point – the INS MEG laboratory uses the tip of the tragus convention – press on the "`r`" key to select the point (without leaving the figure)
3. Find the Left Pre-Auricular point – press "`l`" to validate
4. Find the Nasion – press "`n`" to validate
5. Indicate a z-point (anywhere at the top of the head) – press "`z`"
6. Press "`q`" to validate (before, you can change your fiducial selection as many time as required)

Link: [RPA/LPA conventions]

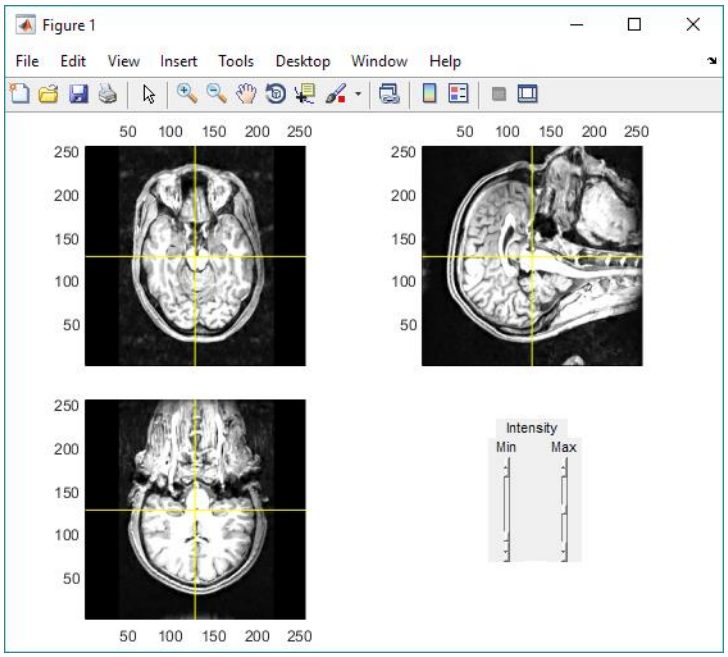


Figure 1: Fieldtrip's interactive interface for fiducial selection

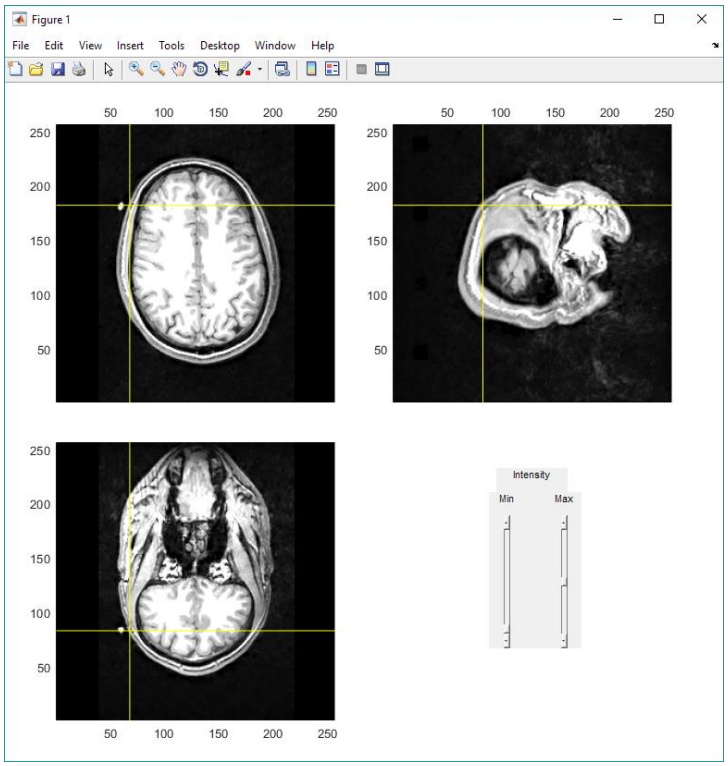


Figure 2: white pastille that indicates the right side of the head

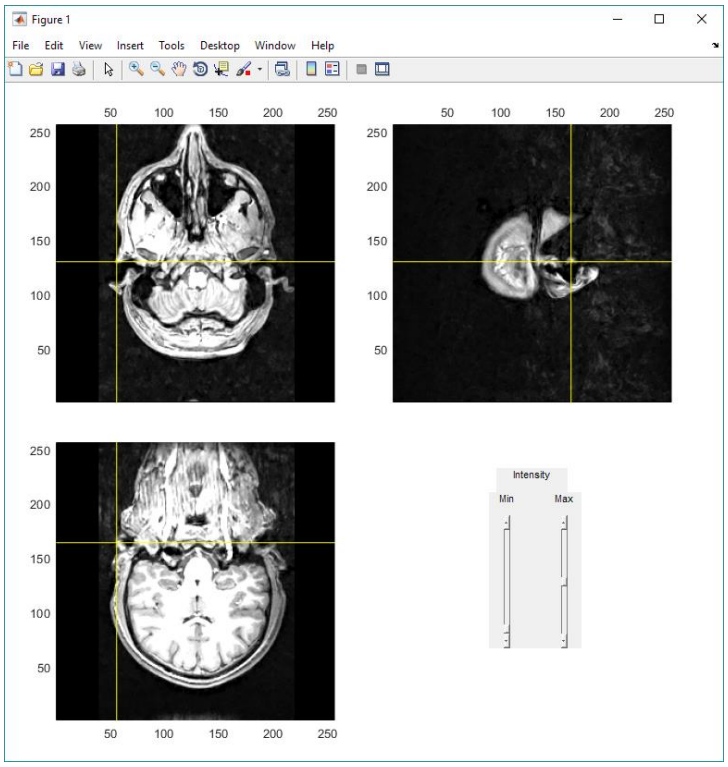


Figure 3: Cursor position indicating the Right Pre-Auricular point (RPA) - a click on 'r' letter has then been done with the keyboard to confirm selection.

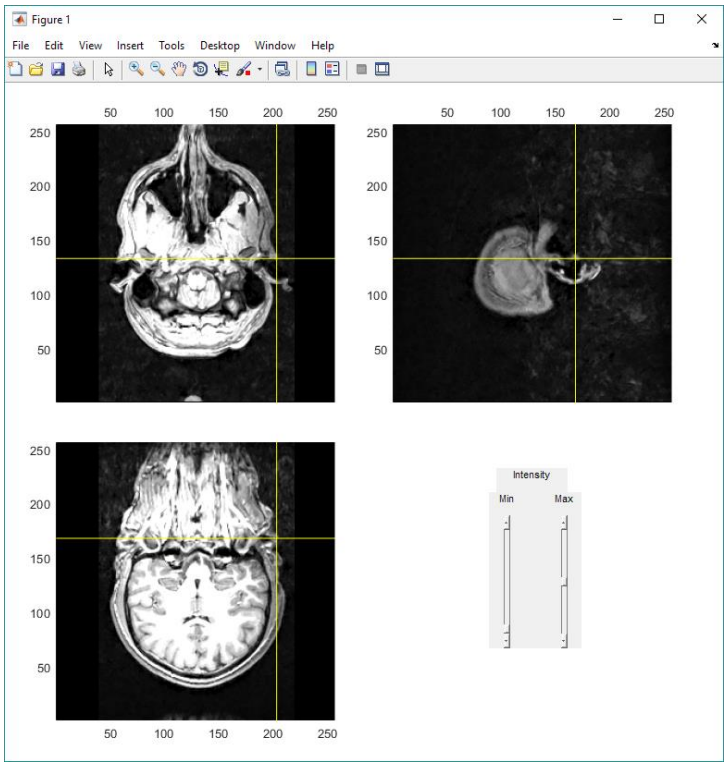


Figure 4: Left Pre-Auricular point (LPA)

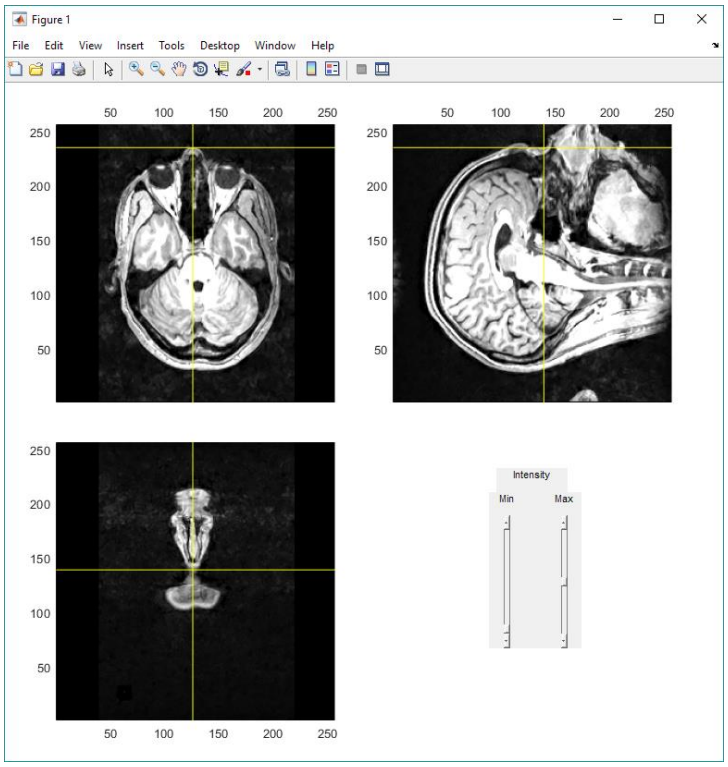


Figure 5: Nasion

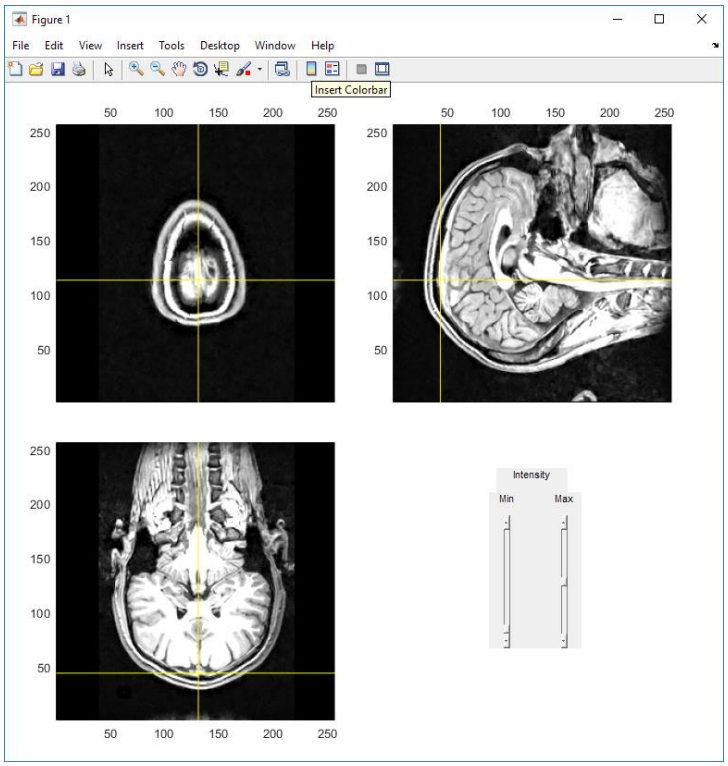


Figure 6: a z-point indicating the top of the head

Bad channel selection

This selection is made by two steps. An interactive figure showing the spectra of the continuous data per channel appears first. The channel with recording issues can be identify by an abnormal spectrum shape. To add a channel to the bad channel list, select the spectrum with an anomalous waveform and click on “Declare as bad”.

After the selection has been confirmed, a second window is showing, which allows you to select other artifact channels (that were not identifiable from the spectrum). Continuous data can be inspected from the figures in the Fieldtrip dataset. The associated folder can be opened by clicking on “Open the figures folder” (*to be tested for other OS than Windows!*). To add a channel in the list of the bad one, select it in the “Good” panel and then click on “>”. Ctrl + Click to select several channels at a time in the Good panel before transferring them to the Bad panel by clicking on the “>” symbol.

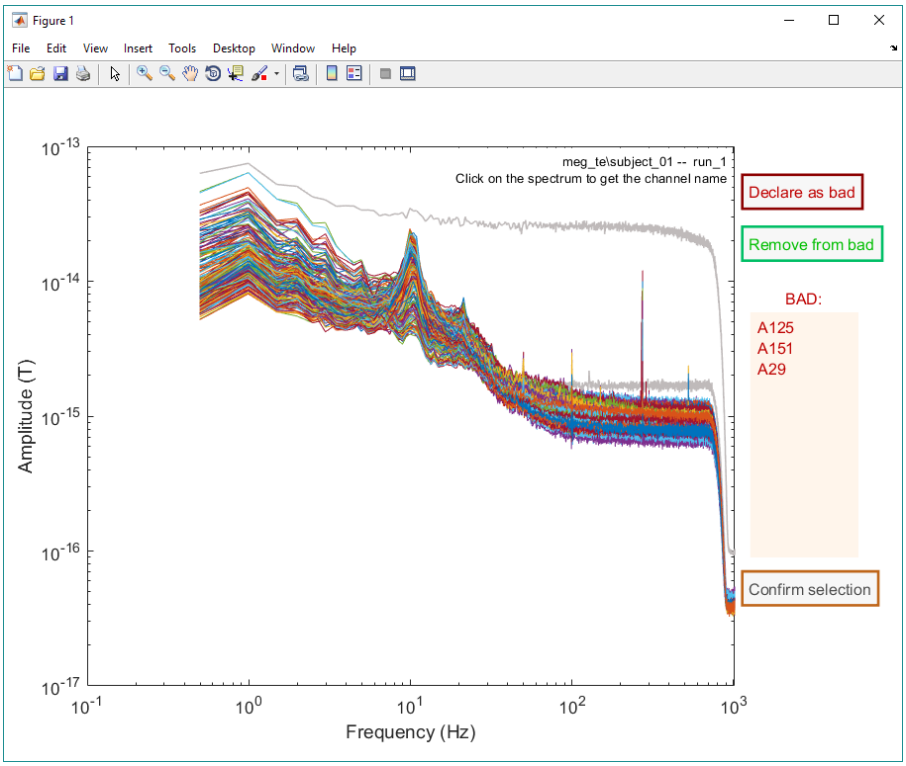


Figure 7: two spectra with a waveform far from the others were reported as bad. One of the channels (A125) was already in the list of bad channels as its amplitude was zero.

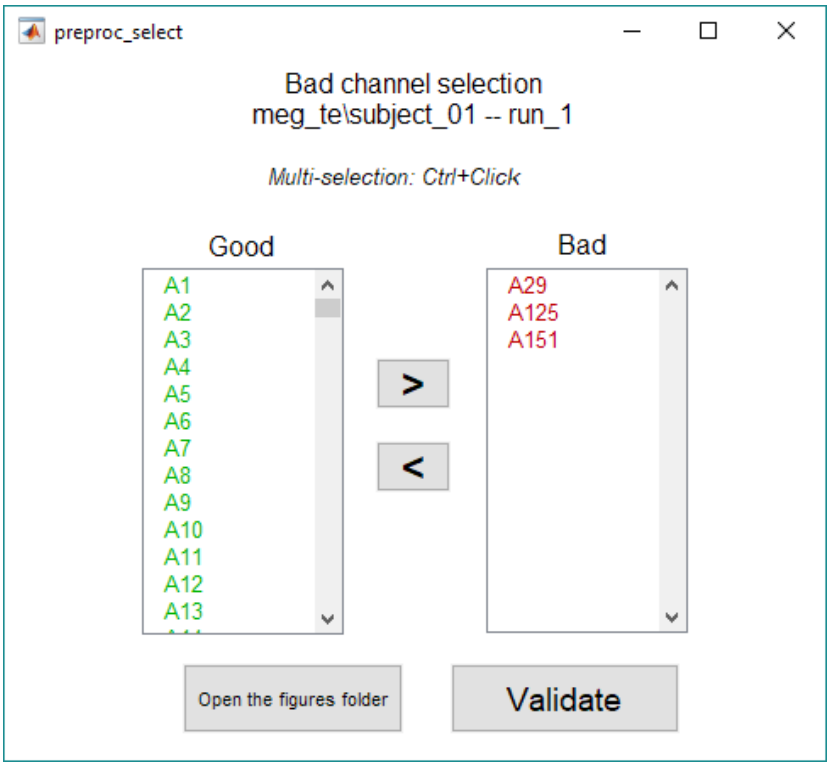


Figure 8: the window to add bad sensors that was not identifiable in the frequency domain

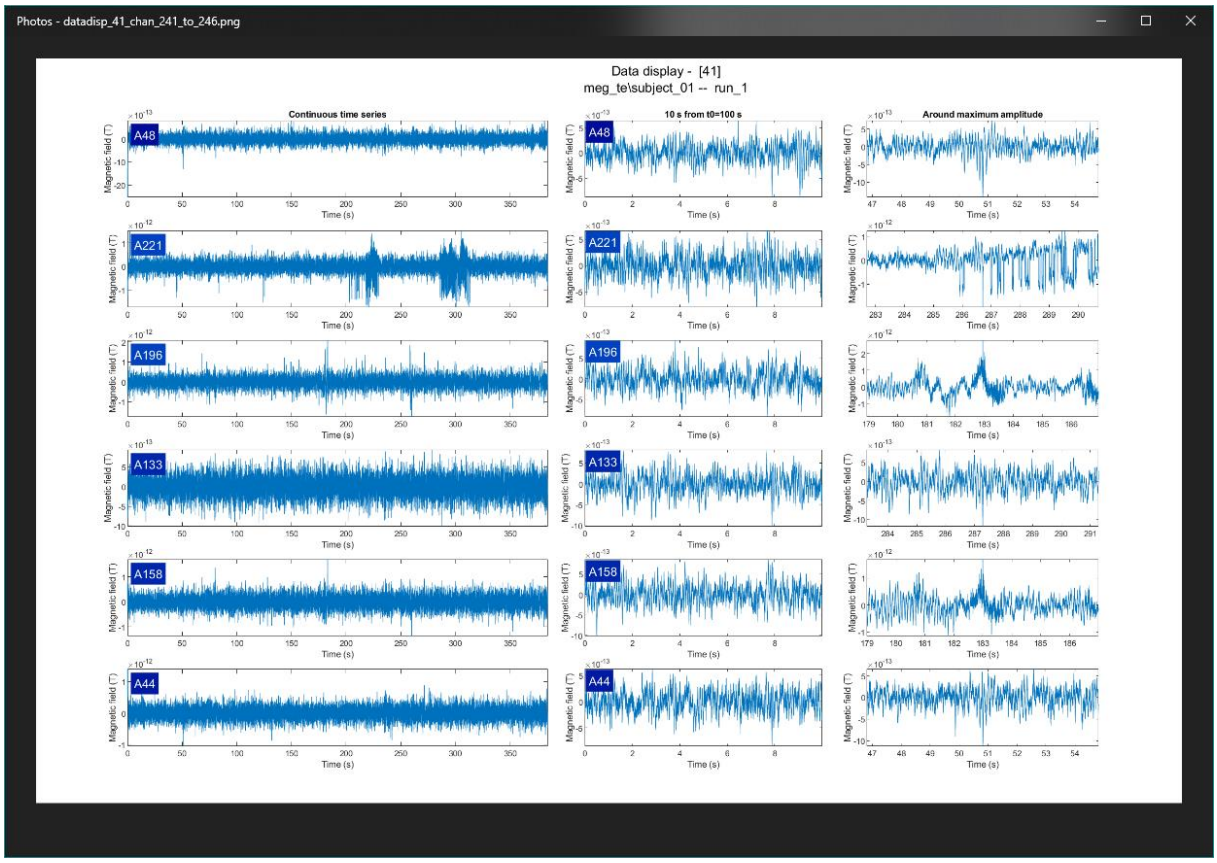


Figure 9: one of the figures showing continuous dataset. The data at channel A221 shows noisy periods, so will be excluded from further analyses.

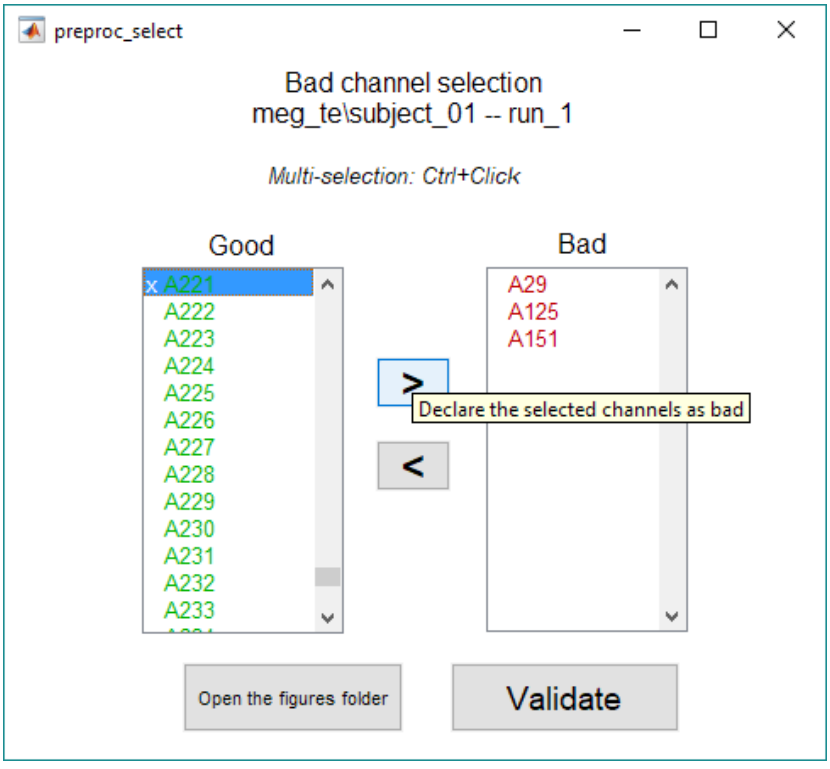


Figure 10: adding the A221 to the bad channels list

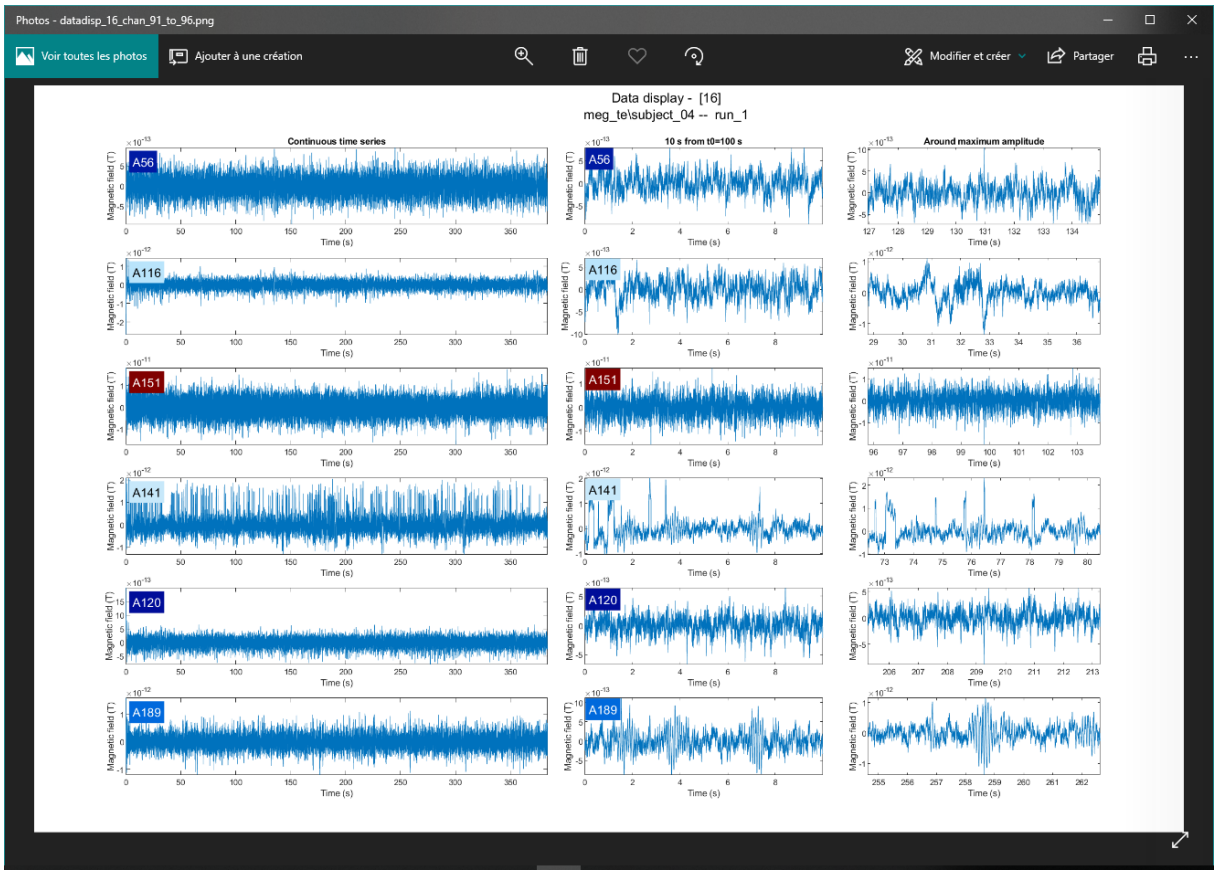


Figure 11: another example of noisy data (A141) for another subject than in previous figures. The spikes are neither cardiac nor eye movement signals.

ICA components selection

If the ICA cleaning option has been selected, the ICA is performed on continuous data after the bad channels were removed from dataset. Figures showing topographic representation of each component and the associated time signal are saved in the meg/run_*/_preproc/ica/ica_fig folder of the Fieldtrip database.

A window appears allowing the selection of the components corresponding to artefact signal to be rejected to the dataset (eye movements, cardiac pulses, electronical signal…).

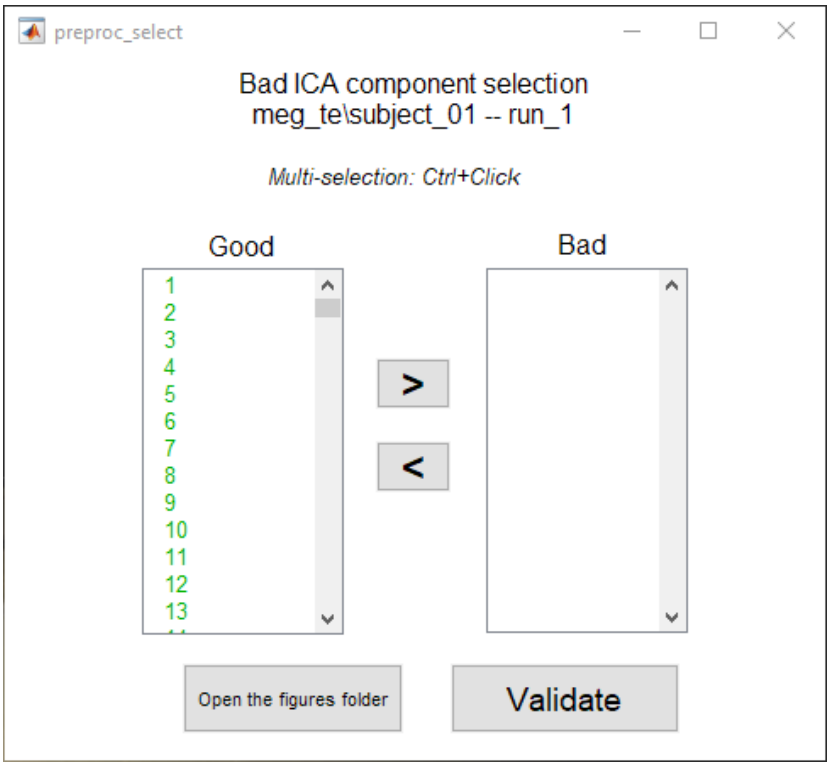


Figure 12: the window for ICA component selection

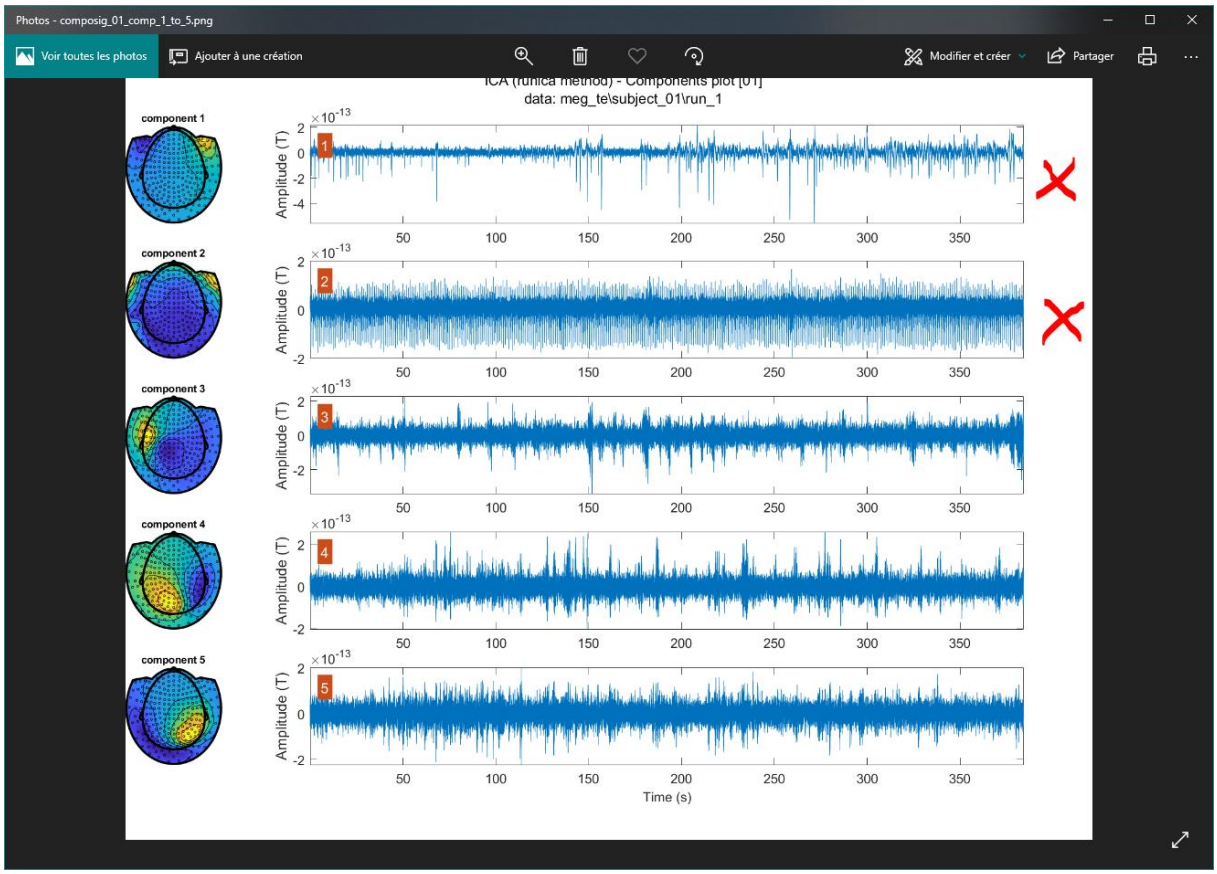


Figure 13: component 1 is associated with eye movements whereas component 2 presents characteristic of cardiac signal.

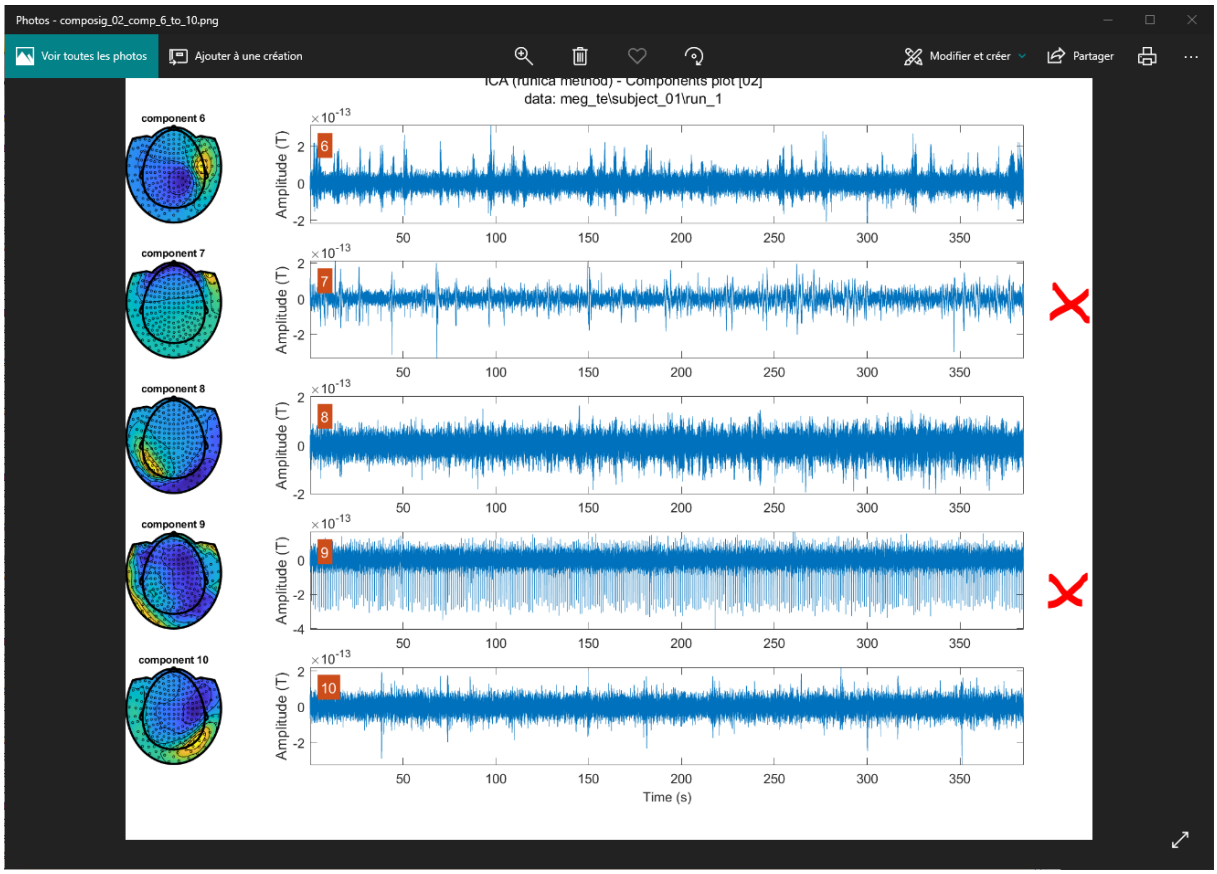


Figure 14: the component 7 is also linked to eye artefact and the component 9 to cardiac artefact

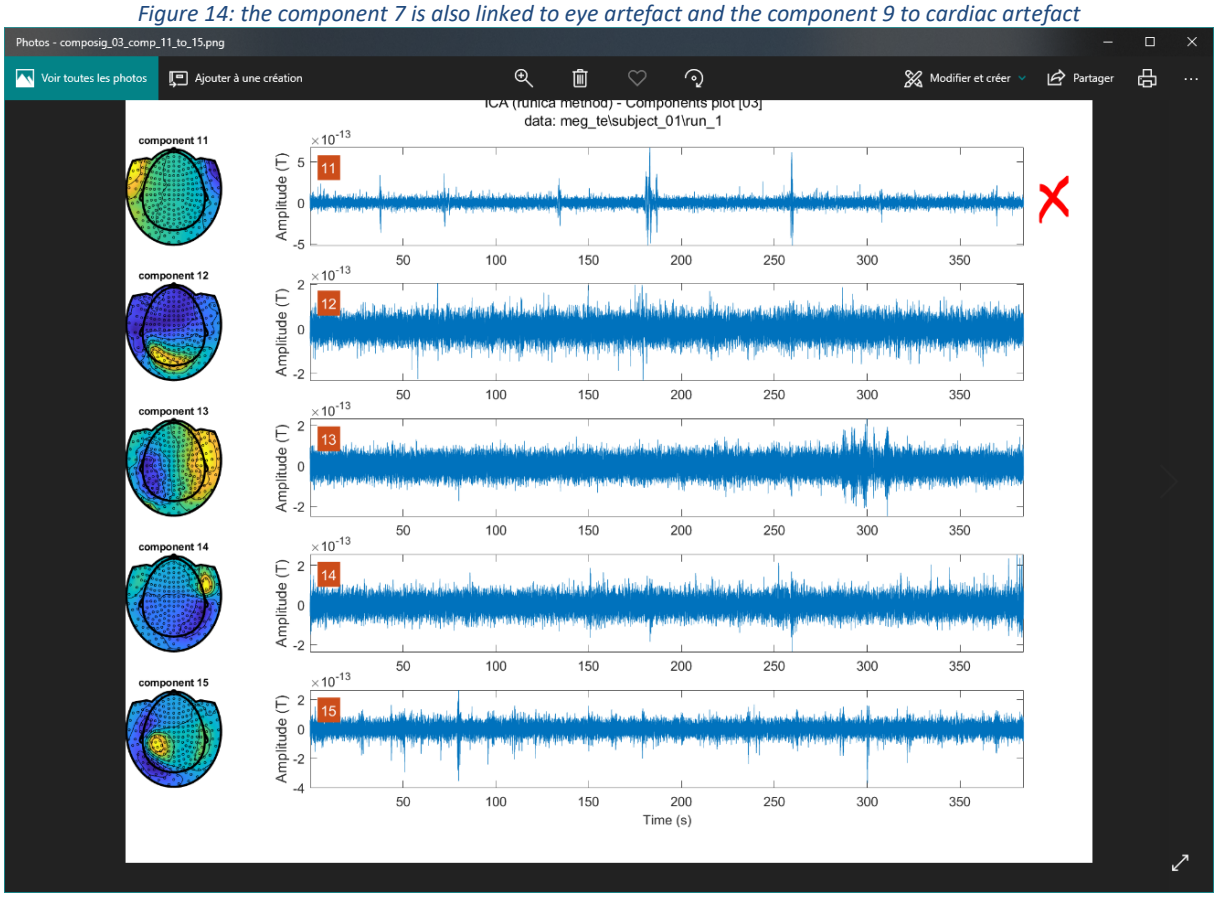


Figure 15 : the component 11 is linked to eye movements

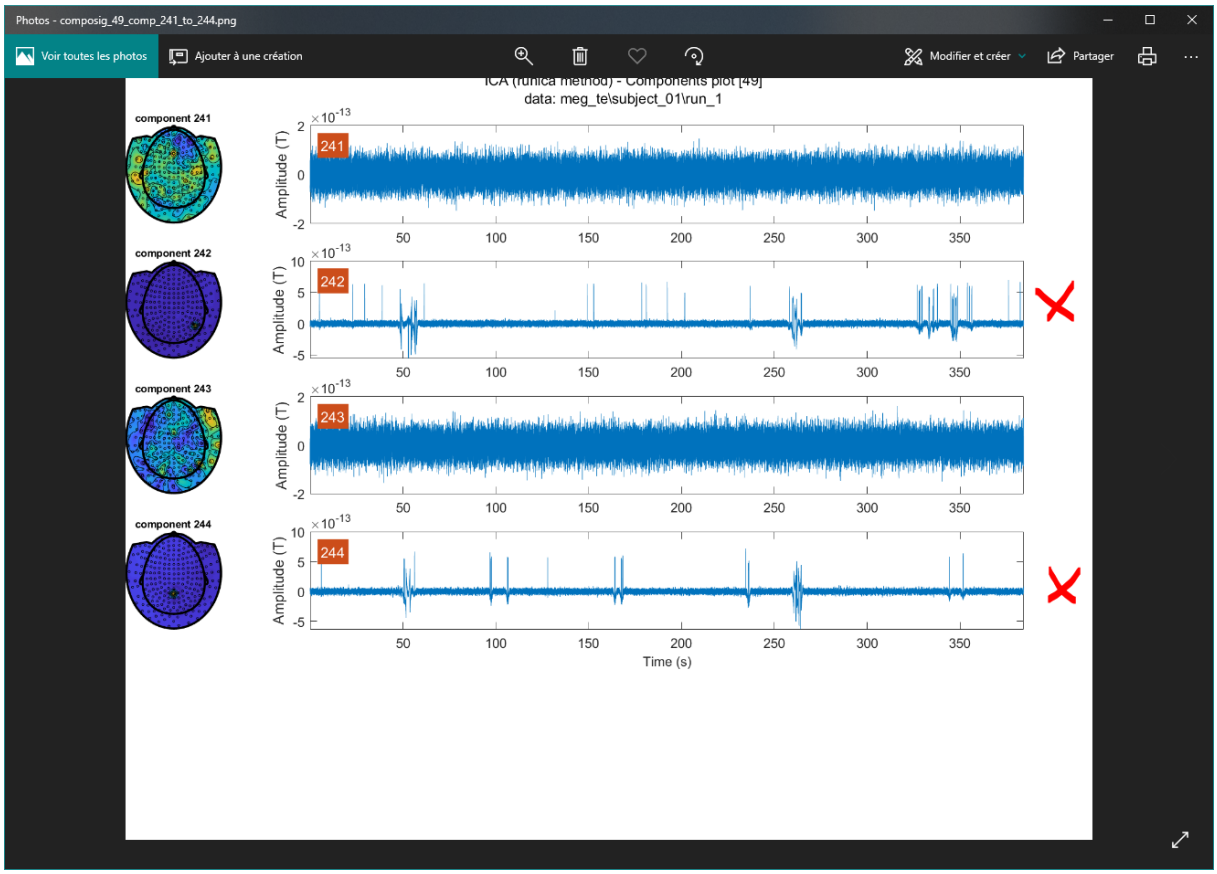


Figure 16 : the last components (which are the less energetic ones – that is, that explain the less the data variance) are showing peaks that could be related to specific problem on specific sensors (as each topographic plot is very focal to one sensor).

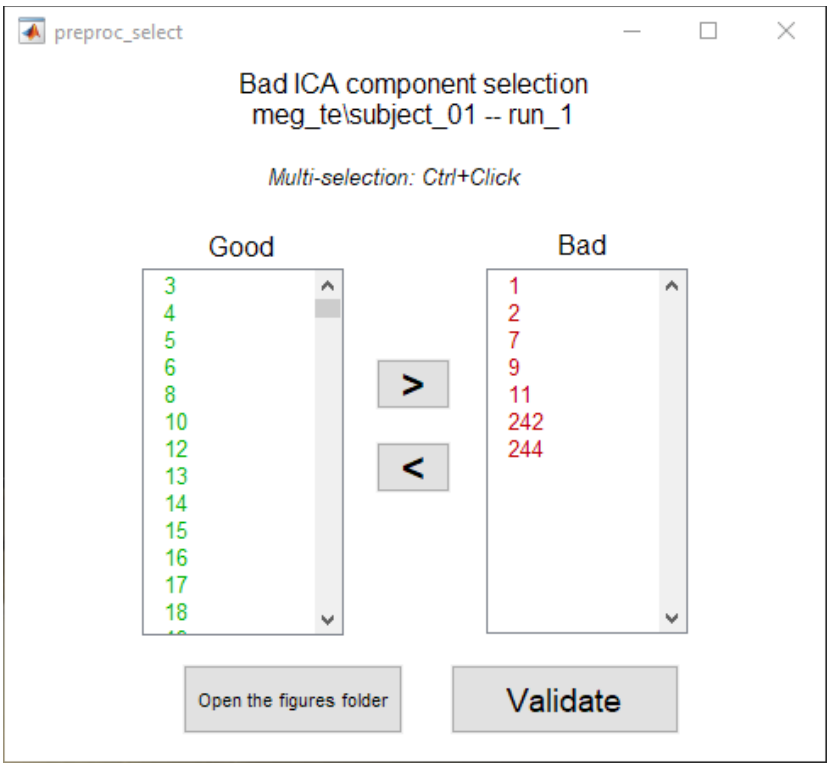


Figure 17: final component selection

Because of the way ICA decomposition is performed (blind source separation with a maximization method), the output and the bad component list will not be the same as mine.

Some links: [ICA for dummies], [variability of ICA decomposition]

Bad trials selection

This step uses the Fieldtrip interactive method. To have only one selection to do by dataset, all conditions are concatenated. This allows to gain time and a more uniform selection across the dataset. All trials metrics are indeed on the same plot with a common scale, that allows a same empirical/visual threshold to be manually chosen (by mouse).

If the main option mopt.epoched.rm_trials_cond is set to 'same', the same bad trial numbers will be removed for all conditions (case when a trial = a succession of conditions like Stimulus / Action / Response). Keep bad trials independent across condition by setting mopt.epoched.rm_trials_cond = 'each'.

At this step, you can also select new bad channels in the top-right plot.

After the bad trials and/or channels manual selection was done, or if no one is to remove, you can press the "quit" button.

A confirm dialog box is then shown – in case of doubt, you can start again the manual selection by clicking "No (redo)".

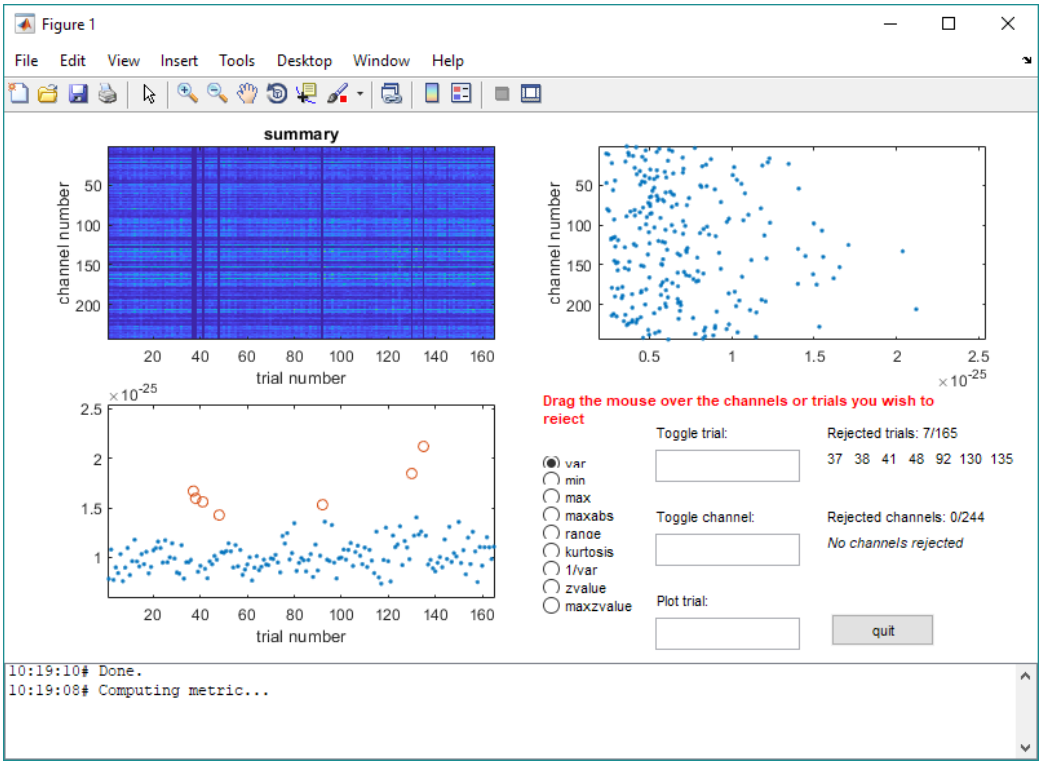


Figure 18: example of bad trial selection (the red circle on the bottom-left plot)

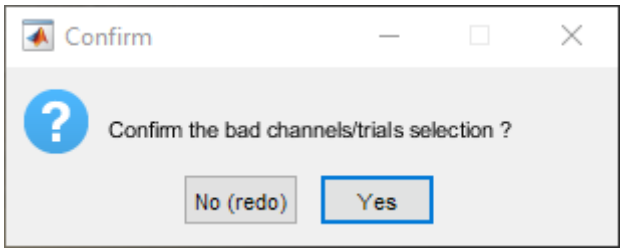


Figure 19: confirmation

Final review

You can check each dataset preprocessing parameters. This is your last chance to change the bad channels, ICA components and/or trials selection. For now, the strong artefact windows identification is not working.

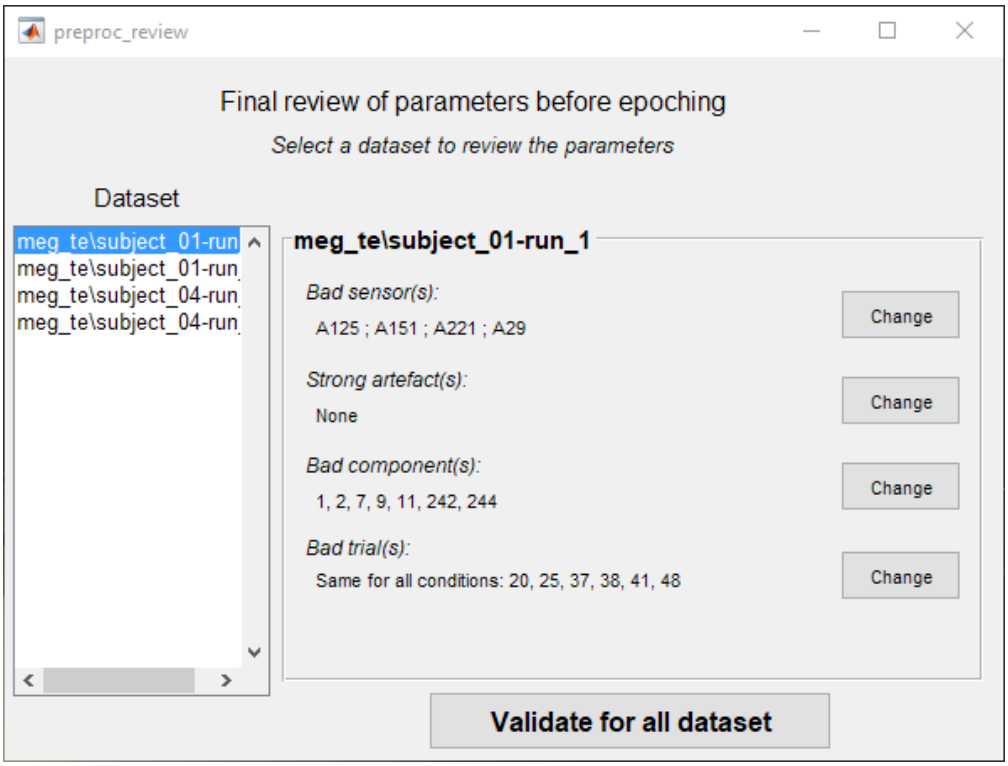


Figure 20: final review window

By clicking on "Validate for all data sets", all other automatic steps leading to source analysis are performed if anatomical and MEG data files are present.

Appendix

Structure in DB_FT