Guidelines to MEG Data Analysis Software

TRIUX™ and TRIUX™ neo Customer training

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MEGIN

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1 Symbols on the equipment

The following symbols may be used on the labels and in the manuals. Familiarize yourself with each symbol and its meaning before operating the MEG system.

Table 1: List of symbols on the equipment.

Label	Meaning
	Caution. Parts of the system are marked with this label when it is necessary to draw the attention of the user to avoid a potential hazard or to ensure safe, correct or improved operation or to avoid damage.
	Refer to the instruction manual. Parts of the system are marked with this symbol when it is *mandatory* for the user to refer to instructions given in the manuals accompanying the system to ensure safe operation. In the manuals, it also calls attention to these instructions.
	Consult instructions for use. Parts of the system are marked with this symbol when it is necessary for the user to refer to instructions given in the manuals accompanying the system. In the manuals, it also calls attention to these instructions. They are intended to ensure correct or improved operation and/or increased safety or to avoid damage.
	Type BF (body floating) equipment symbol. The applied parts (parts in direct contact with the person being investigated with the system) and the type plate are marked with this symbol to indicate that they fulfill the leakage current requirements of the safety standard IEC 60601-1.
	Alternating current (power line) symbol.
	Protective ground (earth) terminal symbol. Used to identify terminals which are intended for connection to an external protective conductor for protection against electrical shock in case of a fault, or to the terminal of a protective ground (earth) electrode.
	Static electricity symbol. The parts of the system marked with this symbol indicate the presence of components susceptible to static electricity and require the use of special static-electricity preventing techniques.
	Non-ionizing radiation, RF transmitter. Marking on equipment or equipment parts that include RF transmitters or that intentionally apply RF electromagnetic energy.
	Disposal instruction symbol. Separate collection of waste electrical and electronics equipment (WEEE) necessary (European Union directive 2012/19/EU on WEEE).
	Name and registered address of the manufacturer, optionally combined with date of manufacture (year followed by month and day, if applicable).

	Date of manufacture: year (four digits) followed by month and day (if applicable).
#	Model or type number.
SN	Serial number.
MD	Medical device.
UDI	Unique device identifier.

2 Introduction

2.1 Scope

This document presents the basic pre-processing and analysis steps for functional mapping and epilepsy source localization for MEG data collected with TRIUX™ or TRIUX™ neo systems.

The content is divided into sections which allows the user to first learn the basic steps and then build on that knowledge with additional topics. This document is intended to provide step-by-step guidance using the *Data Analysis Software Release 3.4.* Throughout this document, the software will be referred to as Data Analysis Software or DANA.

The data analysis steps described in this document aim to follow the conventions and recommendations presented in American Clinical Magnetoencephalography Society Clinical Practice Guidelines (https://www.acmegs.org/clinical-resources/practice-guidelines) and it is recommended that you get familiarized with the following guidelines before starting to use the DANA software:

- *American Clinical Magnetoencephalography Society Clinical Practice Guideline 1: Recording and Analysis of Spontaneous Cerebral Activity.*
- *American Clinical Magnetoencephalography Society Clinical Practice Guideline 2: Presurgical Functional Brain Mapping Using Magnetic Evoked Fields.*
- *American Clinical Magnetoencephalography Society Clinical Practice Guideline 3: MEG-EEG reporting.*
- *American Clinical Magnetoencephalography Society Clinical Practice Guideline 4: Qualifications of MEG–EEG Personnel.*

Learning to use the DANA software for analyzing patient data requires that the user already has sufficient clinical background, or that the learning is supervised by a trained clinician. Guideline 4 states that "Specific MEG training should also include supervised learning of and practice in clinical MEG recording, reviewing, and source analysis of clinical MEG for at least 6 months and the independent interpretation and reporting of at least 50 MEG studies of epilepsy and 25 MEG studies of evoked fields (auditory, visual, somatosensory, motor, and language). The majority of epilepsy studies should be abnormal and include a mixture of clinical findings."

Warning: MEG and EEG data can be inherently explained by many different source distributions, and measurements often contain various kinds of artefacts. Data used for clinical purposes must be interpreted by a trained clinician who is capable of judging the relevance and quality of the data.

2.2 User roles

The following types of end-user profiles can be defined in MEG data acquisition and analysis:

MEG technologist	A person who performs the MEG acquisition.
MEG analyst	A person who performs the MEG data analysis.
MEG key user	A person who performs routine and emergency administrative (IT, electrical) operations on the MEG system.
Neurosurgeon	A person who operates patients to treat epilepsy or other neurological disorders. Uses MEG results to guide the operation.

The instructions in this guideline manual are targeted mainly for customer training of MEG technologists, MEG analysts and MEG key users.

Note that the roles of MEG technologist and MEG analyst vary according to the site. In some clinics, MEG technologist does only the MEG measurement, in some clinics MEG technologist does preparatory steps of the analysis, and in some, the MEG technologist does the entire analysis and a MEG doctor (MEG analyst in this terminology) approves the results.

2.3 Data Analysis Software

The Data Analysis Software (DANA), once installed on a workstation, is a group of software applications designed to perform the necessary tasks for MEG data analysis. They can all be started from the Neuromag menu under Applications in the toolbar. You can also drag each icon from the Neuromag menu to your Desktop if you wish to start the application from a Desktop icon.

Some applications can be referenced two ways, for example, SourceModelling application starts the *Xfit* software, and may be used interchangeably.

The software applications and their naming conventions are:

- *DicomAccess* – Import MRI
- *Graph* – Review raw data, perform spectral analysis, mark events (e.g. spikes)
- GraphicsClipboard (*Cliplab*) – Capture and print results for reporting
- *MaxFilter* – Suppress interference, compensate for head movement and average pre-processed data
- MEG-MRI-Integration (*Mrilab*) – Co-register MRI images with MEG head coordinate frame, overlay and export fitted dipoles
- MRI-segmentation (*Seglab*) – Segment brain surfaces
- Plotting (*Xplotter*) – Explore responses at the sensor level
- SourceModelling (*Xfit*) – Apply spherical or BEM head models and compute single- or multidipole source models
- *ViewBrain* – View segmented surfaces (not covered in this manual)

Figure 1: DANA software modules.

Detailed technical documentation of the Data Analysis Software modules is included in the manuals:

NM20568A-* Source Modelling Software User's Guide
NM10238A-* Data Plotting User's Guide
SW21301A-* DICOM Access User's Guide
NM20419A-* *Mrilab* User's Guide
NM20420A-* *Seglab* User's Guide
NM20421A-* *Cliplab* User's Guide
NM10239A-* Signal Processor User's Guide
NM10240A-* Signal Processor Reference Manual
NM24057A-* *MaxFilter* 2.2 User's Guide (not USA)
NM24124A-* *MaxFilter* 2.2 User's Guide (USA only)
NM25410U-* Addendum to MaxFilter™ 2.2 User's Guide: Individual MEG Channel Artifacts
NM21902A-* *ViewBrain* User's Guide

Printed manuals can be found in the manual binders. The manuals in pdf form documents are accessible in the directory `/neuro/manuals` after the Data Analysis Software has been installed in the analysis workstation.

The manuals contain important hazard information which must be read, understood and observed by all users. General limitations of the programs are included in the following Chapters. For your convenience all warnings that appear in the manuals are presented in the appropriate sections of this manual.

2.4 FIFF file naming

The primary file format in DANA software modules is FIFF (Functional Image File Format), a proprietary file format of MEGIN. The MEG data files have typically the following extensions:

_raw.fif	unprocessed raw continuous data file
_raw_sss.fif	*MaxFilter* -processed files (spatial SSS)
_raw_tsss.fif	*MaxFilter* -processed files (spatiotemporal SSS, tSSS)
_raw_mc.fif	*MaxFilter* -processed files (movement compensation and SSS)
_raw_tsss_mc.fif	*MaxFilter* -processed files (tSSS and movement compensation)
_ave.fif	averaged data files

2.5 Training data

The instructions in this document refer to a specific training demo data set which is described in *NM26084D-* MEG Training Dataset Specification*. The demo data set represents:

1. Spontaneous and evoked field recordings from a healthy case subject.
   Spontaneous recordings were performed with eyes open and eyes closed conditions. The evoked field stimuli were designed to probe mainly the primary sensory areas so that the data are relatively straightforward to analyze. Continuous raw data includes continuous head position indicator (cHPI) signals. *Maxfilter* can be applied for pre-processing continuous data for interference suppression (tSSS and SSS), as well as movement compensation.
2. Simulated interictal epileptic activity.
   The spontaneous data recording from the healthy case was used as basis for adding simulated interictal spike activity. The simulated data can be used for training of the various software modules in analyzing interictal epileptiform activity.

Please note the paths stated in the document (i.e. /neuro/data/…) are for example only. Actual data location may be different for each site.

3 MEG analysis workflows

3.1 Workflow for functional mapping

Modelling averaged evoked-response field (ERF) data with current dipoles is one way to perform functional mapping. According to the *American Clinical Magnetoencephalography Society Clinical Practice Guideline 2: Presurgical Functional Brain Mapping Using Magnetic Evoked Fields*, the following fields can be evaluated with spherical head models.

- **Somatosensory Evoked Field (SEF):** average 100-300 trials per stim location, high-pass filter [1,20] Hz, low-pass filter [40,100] Hz, localize N20m and/or P35m.
- **Motor Related Field (MEF) finger tapping:** average 50-100 trials, band-pass filter [1,25] Hz, localize movement related field [30,40] ms before movement onset.
- **Auditory Evoked Field (AEF):** average ~100 trials, band-pass filter [1,30] Hz, localize N100m.
- **Visual Evoked Field (VEF):** average 100-200 trials per stim location, high-pass filter [1,9] Hz, low-pass filter [50,100] Hz, localize P100m.

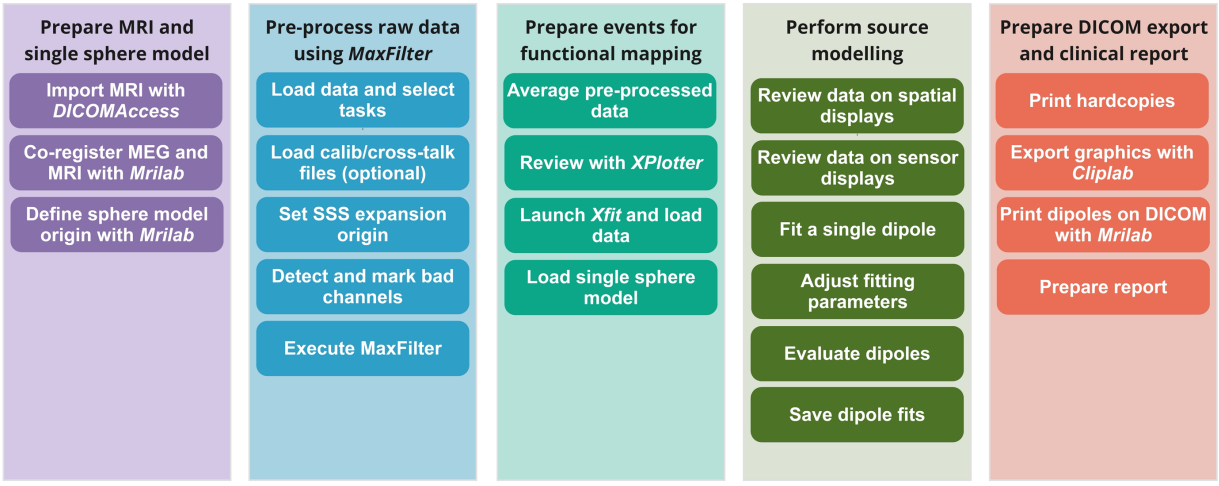


Figure 2: Recommended workflow for functional mapping.

The following workflow is recommended for basic functional mapping using the DANA software:

1. Prepare MRI and single sphere head model, Section 4.
2. Pre-process raw recordings of SEF, MRF, AEF and/or VEF using *MaxFilter*, Section 5.
3. Prepare events for functional mapping, Section 6.
4. Perform source modelling and display the best fitting dipoles on the MRI, Section 8.
5. Prepare DICOM export and clinical report, Section 9.

3.2 Workflow for epilepsy source localization

According to *American Clinical Magnetoencephalography Society Clinical Practice Guideline 1: Recording and Analysis of Spontaneous Cerebral Activity*: "Evaluation of a magnetic isofield map at selected time points is necessary for estimating the number of generator sources and their spatial distributions. These maps will vary with the type of sensor coils in a particular MEG system. When the magnetic isofield map at a selected time point contains a single, distinctive, dipolar pattern, a single ECD can be used to estimate the generator source. Multiple ECD analysis may have to be implemented if more complex fields are evident. It is useful to view maps sequentially over the time course of the spike. If during a single phase of the spike, its magnetic field increases and decreases but does not rotate or change the shape, then one can assume a stable MEG source. If the field rotates during a single spike phase, the MEG source may be propagating".

Warning: MEG and EEG data can be inherently explained by many different source distributions, and measurements often contain various kinds of artefacts. Data used for clinical purposes must be interpreted by a trained clinician who is capable of judging the relevance and quality of the data.

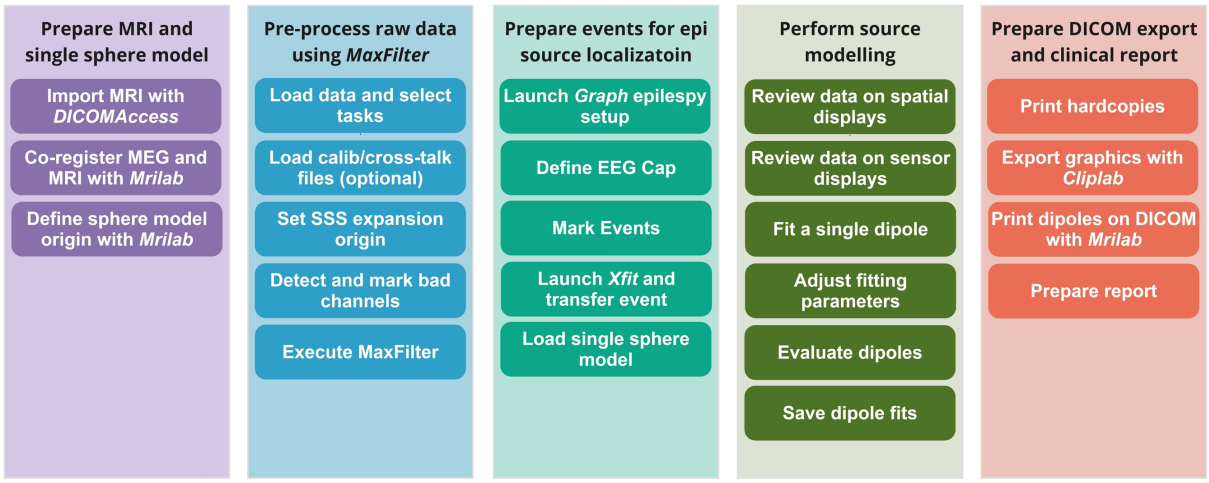


Figure 3: Recommended workflow for epilepsy source localization using the DANA software.

The following workflow is recommended for spike localization using the DANA software:

1. Prepare MRI and single sphere head model, Section 4.
2. Pre-process raw recordings of SEF, MRF, AEF and/or VEF using *MaxFilter*, Section 5.
3. Prepare events for source localization of epileptiform activity, Section 7.
4. Perform source modelling and display the best fitting dipoles on the MRI, Section 8.
5. Prepare DICOM export and clinical report, Section 9.

4 Prepare MRI and sphere model

This section presents the steps needed to import MRI data to the MEG data analysis workstation or file server, co-registering the MRI images with the MEG head coordinate frame and define a sphere model origin with *Mrilab*.

In general,

- The MRI should have T1-weighted contrast.
- It should have close to isotropic voxel size (preferably around 1x1x1 mm).
- The image should contain as little spatial distortion as possible.
- The patient should have been as fixed as possible to reduce movement artifacts.

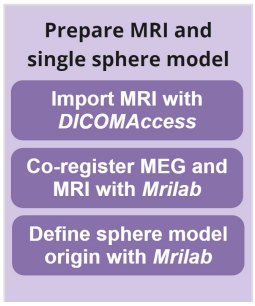


Figure 4: Workflow steps for preparing MRI and sphere head model.

4.1 Import MRI with *DicomAccess*

4.1.1 Start the program

Launch Applications -> Neuromag toolbox -> *DicomAccess* (Figure 5).

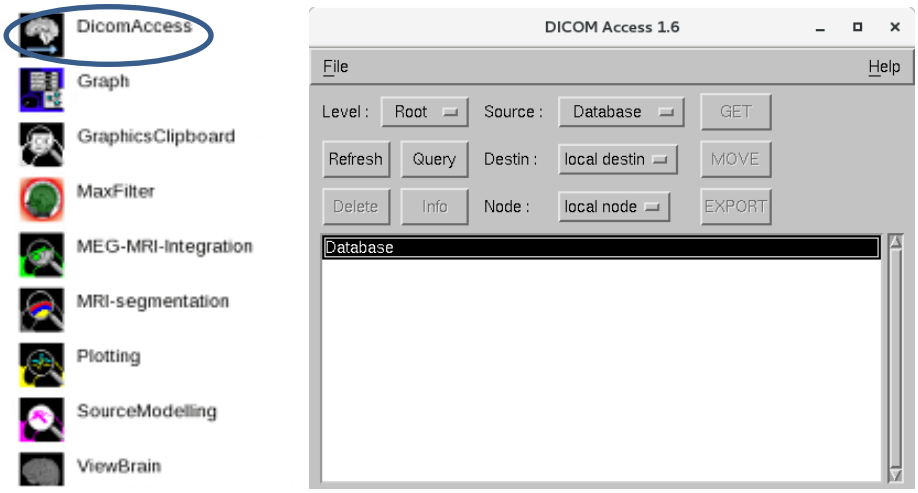


Figure 5: *DicomAccess* user interface.

4.1.2 Get the DICOM slices

- Change **Source: Directory** and navigate to the DICOM slices: `/neuro/data/demo/mri/slices`.
- Double-click the series which contains the 3D-volume T1 images of the whole head. If the slices are read without errors, you can see information of the slices (Figure 6).

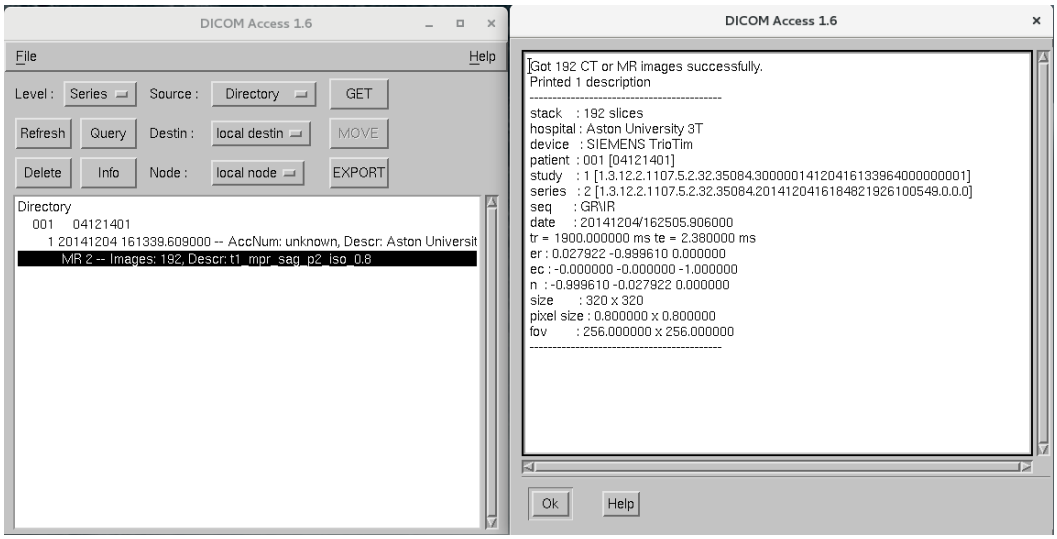


Figure 6: Importing DICOM data from the source directory.

Warning: When connecting to a new 3rd party system, the DICOM transfer shall be validated, to make sure that the 3rd party system is compliant with this software and that the images can be transferred without problems.

- If the DICOM slices are not read correctly and you see error messages, you can try to change the settings to 'DICOM Part 10', 'Ignore VR mismatches', 'Ignore missing values', and try again (Figure 7).

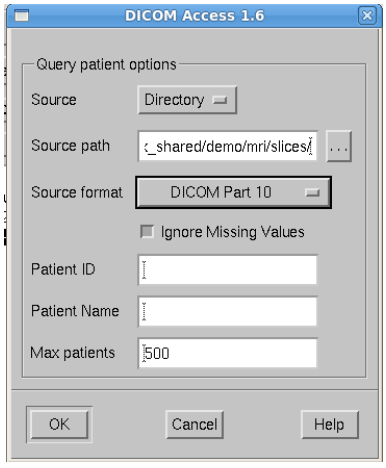


Figure 7: *DicomAccess* parameters.

Warning: The user makes use of the Add missing values feature (see section 3.3.8) at his/her own risk. The program only checks that something is entered into each field. It does not check the validity of input in any way. Furthermore, the user is assumed to be familiar with the semantics of the attributes. E.g. in case of Patient Name delimiters are used to separate components and component groups.

4.1.3 Transfer the slices and sets to the storage volume

- Note that the demo data set images are used both for research and simulated epilepsy cases.
- Select **GET**, set the **Destination directory** to `/neuro/mri/example_case/`.
- Select **Create** (Figure 8).
- DICOM slices are saved in `/neuro/mri/example_case/slices`.
- A FIFF file which has the links to individual slices is saved in `/neuro/mri/example_case/sets`. **Note**: this FIFF file contains only the link to the MRI data, it does not contain head position information from the digitized landmark and head surface points obtained during the MEG preparation. That information is stored with the MEG recordings for now.

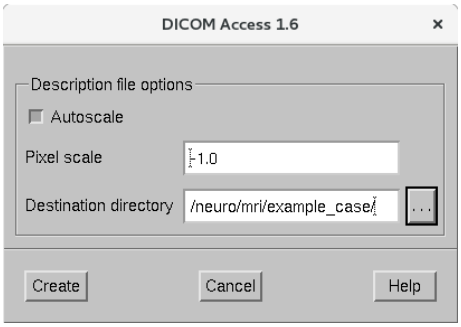


Figure 8: Set destination directory.

4.2 Co-register MEG and MRI with *Mrilab*

4.2.1 Start the application MEG-MRI-Integration (*Mrilab*)

- Launch Applications -> Neuromag toolbox -> MEG-MRI Integration.
- Select **File -> Preferences->General** to adjust slice setup 'Right on right' or 'Right on left'.

Warning: The user should note that the program has no deeper "understanding" about the patient orientations and when calculating the orientations it purely relies on the coordinate systems specified in the file loaded into use. Although very unlikely to happen in practice, it is quite possible to create data sets where the labels point to completely wrong directions. Files based on original images coming straight from the imaging devices should be safe but those that have experienced one or several file format conversions might be in risk. In any case, it is totally the user's responsibility to check that the labels can be trusted.

4.2.2 Load the MRI image (.fif) of the subject

- Select **File -> Open (Alt-f + o)** and select the FIFF MRI-file `/neuro/mri/example_case/sets/001_1_01.fif`.
- Click **Apply** on the pop-up window (Figure 9).

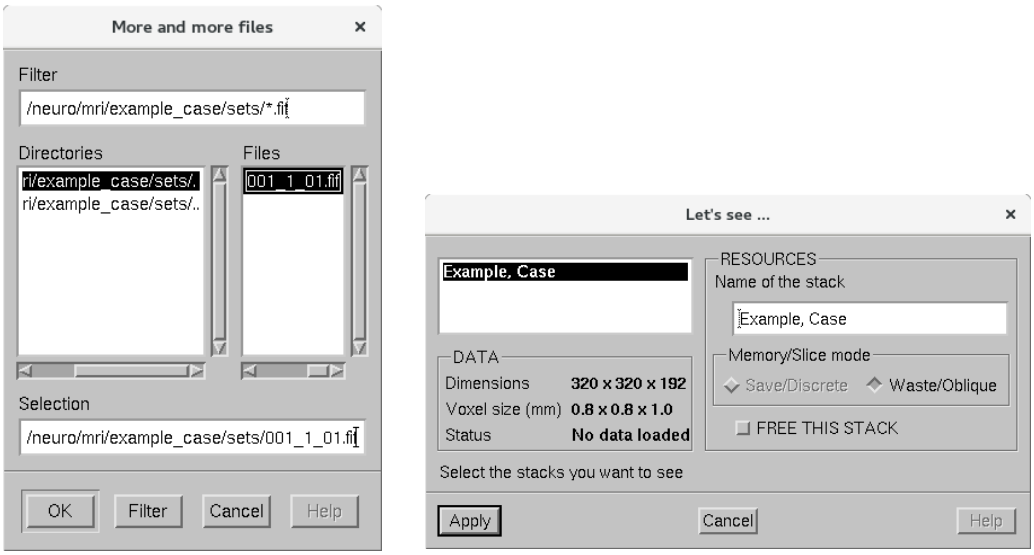


Figure 9: MEG-MRI Integration file loading.

4.2.3 Review the images

- Adjust the contrast and brightness sliders at the lower right corner of the window (Figure 10).
- Select the **Move Slice** tool and scroll through the slices to review the subject's anatomy.
- The crosshair position is adjusted by keeping the left mouse button pressed and moving the cursor up and down in each window. Move the mouse pointer on
  - Left lower window for head-feet slicing.
  - Upper right window for left-right slicing.
  - Upper left window for anterior-posterior slicing.

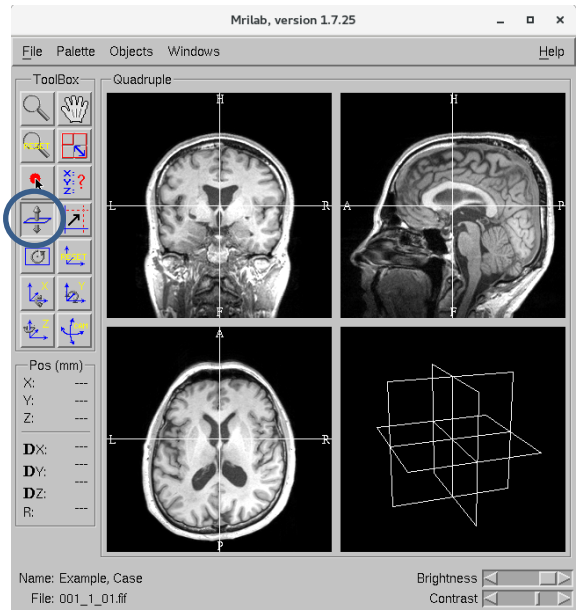


Figure 10: *Mrilab* user interface. The **Move Slice** tool is circled.

4.2.4 Set the anatomical landmarks

- Open **Windows -> Landmarks** (Figure 11).
- Select the landmark to set by clicking in the X coordinate box, click **Goto**, adjust the crosshair to the proper location and click **Get**.
- Repeat for all three landmarks. Be sure the landmarks are the same as those marked during digitization; refer to the photos if they have been taken during the preparation.
- Select **OK.**

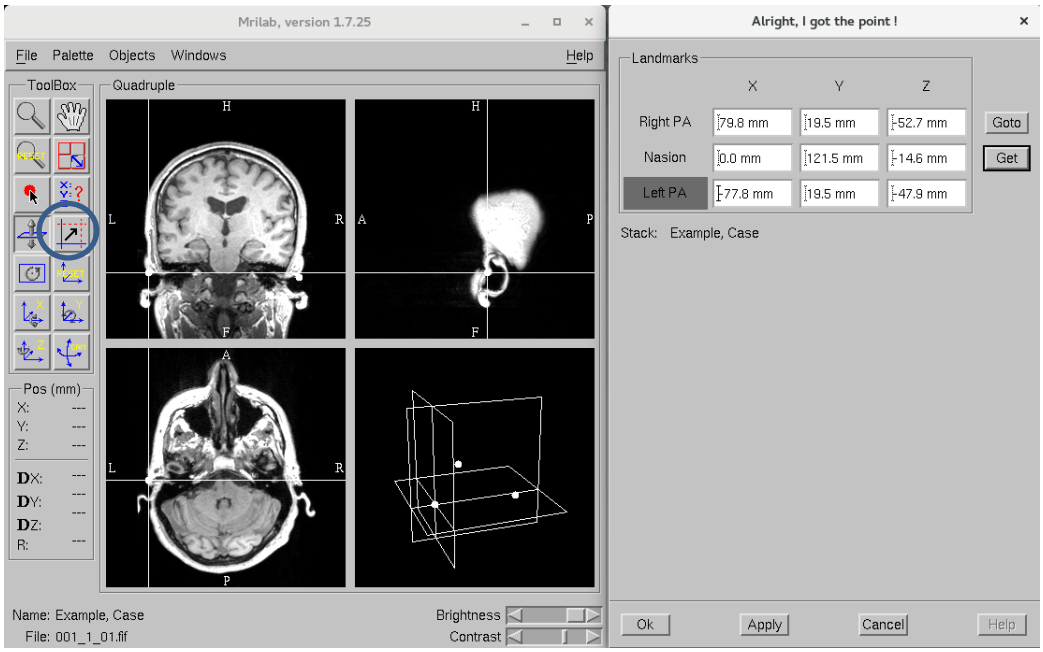


Figure 11: Setting the landmark points. Note: selecting the **Move Cross-section** tool (circled) enables to grab and move the crosshair directly to a desired location.

Warning: The transformation obtained should be verified by displaying points digitized from the surface of the head, and checking that the points lay near the surface also on the MR images. Only coils, EEG electrodes, and extra points digitized should be used for verification. The digitized cardinal points do not bear information about correct landmark positions.

4.2.5 Import digitized points from MEG file and check co-registration

- Open **File -> Import -> Isotrak data (Alt-f + i + i)** and select a FIFF file containing the recorded MEG data, e.g. `/neuro/data/demo/example_case/190122/*.fif` . Note: all the MEG data files from the same measurement session contain the same digitization info.
- Click **Make Points** (Figure 12).

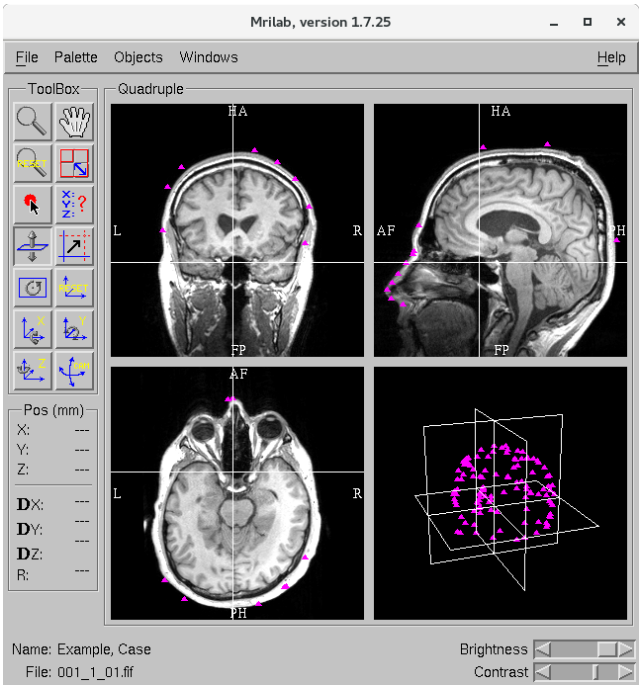


Figure 12: Import digitized points from a FIFF file.

- Check that head shape points align with the head surface. If not, fine tune the landmarks until they do. This can be done in two ways:
  - Select the **Move Slice** tool and adjust the crosshair to the desired landmark location
  - Shift the landmarks by directly changing the coordinate values. To avoid rotation, change all the coordinates that are zero by the same amount for a given direction.
- Select **Apply** to apply changes and **OK** to confirm and close the window.
  Save the co-registration for later use: Select **File -> Save** and navigate to the corresponding subject directory. The co-registration file will be named as *NN-operators_name-date.fif*, e.g. `/neuro/mri/example_case/sets/001_1_01-meg-181001.fif`.
- Remove the head shape points: **Objects -> Clear all -> Points.**
- Do not exit program yet!

Warning: As the flipping changes the way the patient is oriented in the views it may cause misinterpretation of the data.

Warning: *Slice Setup* controls the default patient orientation in the views. The user should note that a setting different from the one he or she is used to can cause misinterpretation of the data.

4.3 Define sphere model origin with *Mrilab*

4.3.1 Mark the inner surface of the skull

- Adjust the views and cursor so that the cursor is in the center of the head, see Figure 13.
- Select the **Point** tool.
- Hold the Shift key and click the images to make points around the inner skull. The points should cover the brain in several directions, leaving the bottom part without points.
- It is recommended to obtain approximately 15-20 points per orthogonal plane (sagittal, axial and coronal; Figure 13).
- Note: This is an important workflow step for defining the optimal origin both for the MaxFilter processing (section 5.4) and for source modelling (section 6.4).

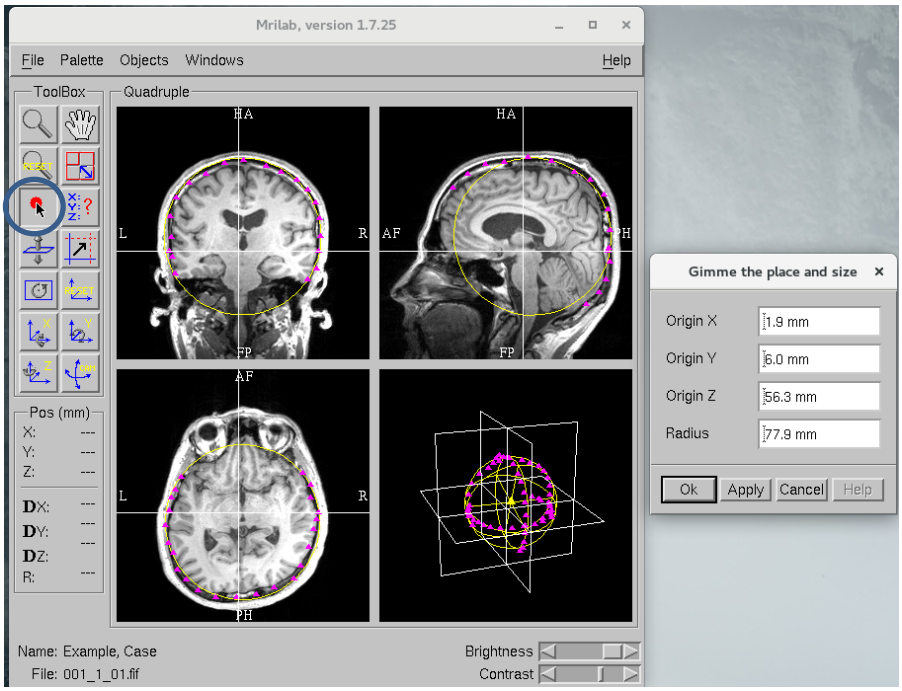


Figure 13: Fit a sphere on the point set. The **Point** tool is circled.

4.3.2 Obtain the best fitting sphere

- Select **Objects -> Fit sphere.**
- Locate and observe the center of the sphere, marked by a yellow triangle (Figure 13). Confirm the sphere is correctly placed over the brain, following the curvature of the skull.
- Save sphere origin coordinates to a text **File -> Export -> Spheres (Alt-f + e + s)** or take a screenshot and save it with the dataset.
- **Note:** If you launch SourceModelling (*Xfit*) or *MaxFilter* at this point, you can drag-and-drop (using the center mouse button at the label left to textboxes) or manually type the sphere origin coordinates directly to the origin setting dialog of the other application.

4.4 Head position inspection

Correct head position information is crucial for the source modelling, because inaccurately determined head position can lead to incorrect localization of brain activity and subsequently to wrong diagnosis and treatment decision leading to incorrect resection of cerebral cortex. Therefore, it is recommended to inspect the head position visually before the MaxFilter pre-processing and source modelling steps.

The most straightforward way to visualize the head position inside the MEG helmet is to launch the Source Modelling Software Xfit). Load the measured file in Xfit and select *Overlay: Std head* and *Overlay: Isotrak* in the bottom part of the main display (Figure 14; see also Source Modelling Software User's Guide section 5.1).

Note that you can open also a raw data file in Xfit; it can then load only HPI data, but the program shows both the digitized points and the head position. If the visual inspection shows a strange head positions, see Chapter 11 for more detailed instructions for trouble shooting and correcting the problem with a wrong head position determination.

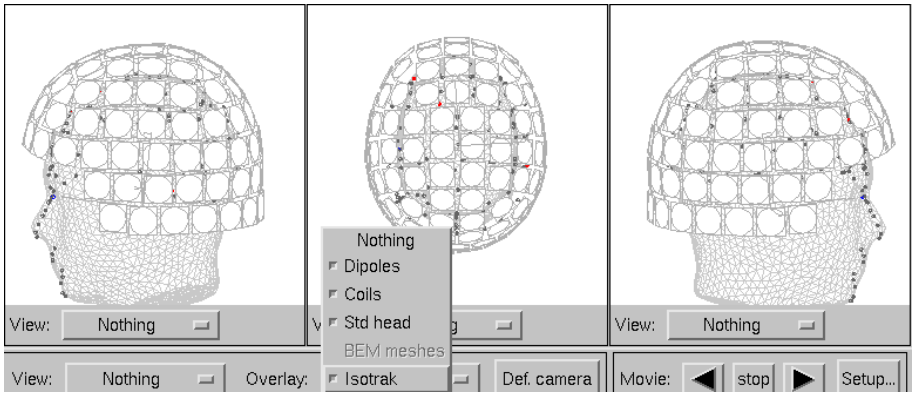


Figure 14: Visualization of the head position and digitized points in Xfit.

5 Pre-process raw data using *MaxFilter*

MaxFilter software is intended to be used with the MEGIN products for suppressing magnetic interference coming from outside of the sensor array, reducing measurement artifacts, transforming data between different head positions, and compensating disturbances due to magnetized material or other close-by artifact sources on the head and due to head movements.

The main functions of *MaxFilter* are

- Signal Space Separation (SSS) for suppressing external interference.
- Temporal SSS (tSSS) for suppressing close-by interference.
- SSS-based data transformation between head positions[1].
- SSS-based head movement compensation[2].

This section presents the default use of MaxFilter. See Section 12 and MaxFilter User's Guide for more detailed description of optimizing the MaxFilter processing.

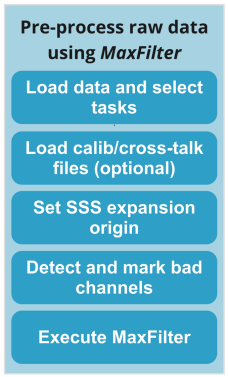


Figure 15: Workflow steps for *MaxFilter* preprocessing.

5.1 Start *MaxFilter*

- Launch Applications -> Neuromag -> *MaxFilter.*

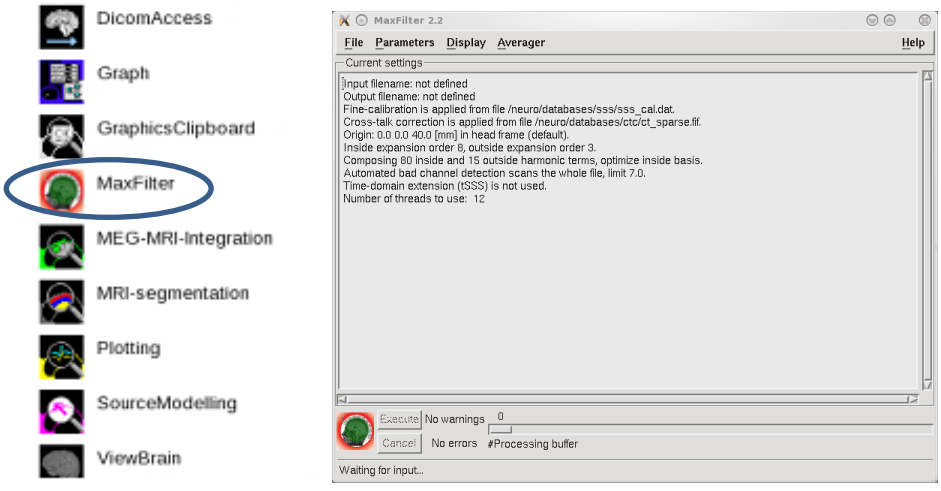


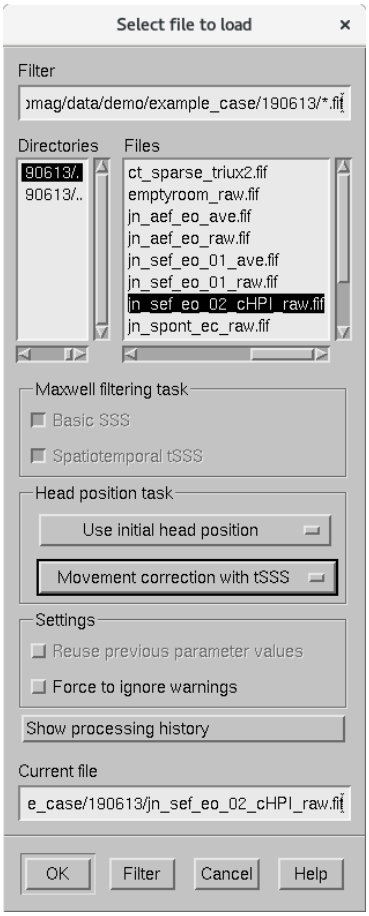
Figure 16: *MaxFilter* launching and the main GUI display.

[1] SSS data transformation between head positions is not approved for clinical use in USA.

[2] Movement compensation is not approved for clinical use in USA.

5.2 Load data and select tasks

- Select **File -> Load data... (Alt-f + l)** browse to the folder and select `/neuro/data/demo/example_case/190613/*_raw.fif`
  Note: the subject had a magnetized tooth which created movement-related artifacts. Therefore, tSSS is needed to suppress such nearby artifacts.
- File selection and the Maxwell filtering default tasks are depicted in Figure 17.
- The basic SSS is always included when tSSS and/or movement compensation are performed. If MaxFilter detects that there are no disturbance waveforms to be projected out, tSSS automatically transforms to the spatial SSS. Therefore, tSSS can always be selected even if there were no magnetized material or head movements in the recording. However, tSSS processing takes longer time than the basic SSS.
- Select **OK** to close the file selection dialog.



The following default tasks will be used for each file:

File	**Maxwell filtering task**	**Head position task**
*01_raw.fif *Continuous HPI was not used.*	Spatiotemporal tSSS	No head position estimation
*02_cHPI_raw.fif *Continuous HPI was active.*	Spatiotemporal tSSS	*USA version*: Head position estimation *Non-USA version*: Head movement compensation

Figure 17: Selecting the input file and Maxwell filtering tasks. When continuous HPI was used, the recommended task is *Movement correction with tSSS.* Otherwise, you can always select the *Spatiotemporal tSSS* task without any head position task.

5.3 Load fine-calibration and cross-talk correction files

- This step is *not* necessary if *MaxFilter* is being applied to data that was collected locally – the default files are already stored in the system: `/neuro/databases/sss/*` with a name that indicates the site and used by *MaxFilter* by default.
- When using data not recorded on the local system, it is necessary to change the fine-calibration and cross-talk correction files. These should always be supplied with external data (by the lab that supplied the data), as is with the demo data.
  - Select **Parameters** -> **Fine-calibration**… **(Alt-p + f)**, select `/neuro/data/demo/example_case/190613/sss_cal_3142.dat`
  - Select **Parameters** -> **Cross-talk correction**… **(Alt-p + c)**, select `/neuro/data/demo/example_case/190613/ct_sparse_triux2.fif`
  - This needs to be done *every time* a new dataset is loaded for pre-processing.

Warning: If the fine-calibration and cross-talk correction data are not available, the performance of MaxFilter™ may not be as good as with the fine-calibrated system.

Warning: Special care should be taken to ensure that right fine-calibration data are used for imported or old data for which the default calibration does not apply.

5.4 Set SSS expansion origin

For optimal SSS performance, it is recommended to find the sphere origin from MRI data (see Section4.3.2) and provide the coordinates before processing.

- The default origin is [0,0,40] mm.
- Select **Parameters** -> **Origin**… **(Alt-p +o)** and enter the coordinate from *Mrilab*, screenshot or notes, or drag and drop from *Mrilab* (see section 4.3).

5.5 Detect and correct bad channels as needed

Bad channels are excluded from MaxFilter processing. The data on the bad channels is reconstructed from the information on all other channels.

- Automatic detection: *MaxFilter* can detect automatically if there are MEG channels with spurious sensor artefacts that need to be excluded in SSS processing.
- Manual detection: the automated bad channel detection may fail to recognize an abrupt artifact on a single MEG channel. In such cases, *MaxFilter* processing spreads the channel artifact on multiple channels in vicinity of the affected one. Therefore, it is important to inspect the raw data to which *MaxFilter* processing was applied. If a suspected artifact activity is present only on a single MEG channel in the raw data, it is most likely a channel artifact and the channel must thus be disregarded. Known and suspected bad channels need to be manually marked as bad ones, using **Parameters -> Bad channels… (Alt-p + b)**
  - See *NM25410U-** "*Addendum to MaxFilter™ 2.2 User's Guide: Individual MEG Channel Artifacts — A Case Example*" for more details.

Warning: It is important that the user inspects both the input and the output data visually to judge the quality of the MaxFilter™ result.

Warning: If the threshold of the automated bad channel detection is too small, the program may classify good channels as bads, and if it is too high, some bad channels may remain undetected.

5.6 Execute *MaxFilter* processing

- Select **Execute** in the main window.
- *MaxFilter* now processes the loaded file and generates a new file. In the example of Figure 17, the output file is `jn_sef_eo_02_chpi_raw_tsss_mc.fif`.
- Observe the progress by viewing the output log: **File -> Show log…**
- When head positions are estimated for movement compensation, observe the head positions by selecting **Display ->Head positions… (Alt-d + h)** (Figure 18).
- Each file should be loaded and executed to result in the following output files in directory `/neuro/data/demo/example_case/190613:`
  `*_raw_sss.fif, *_cHPI_raw_tsss_mc.fif`

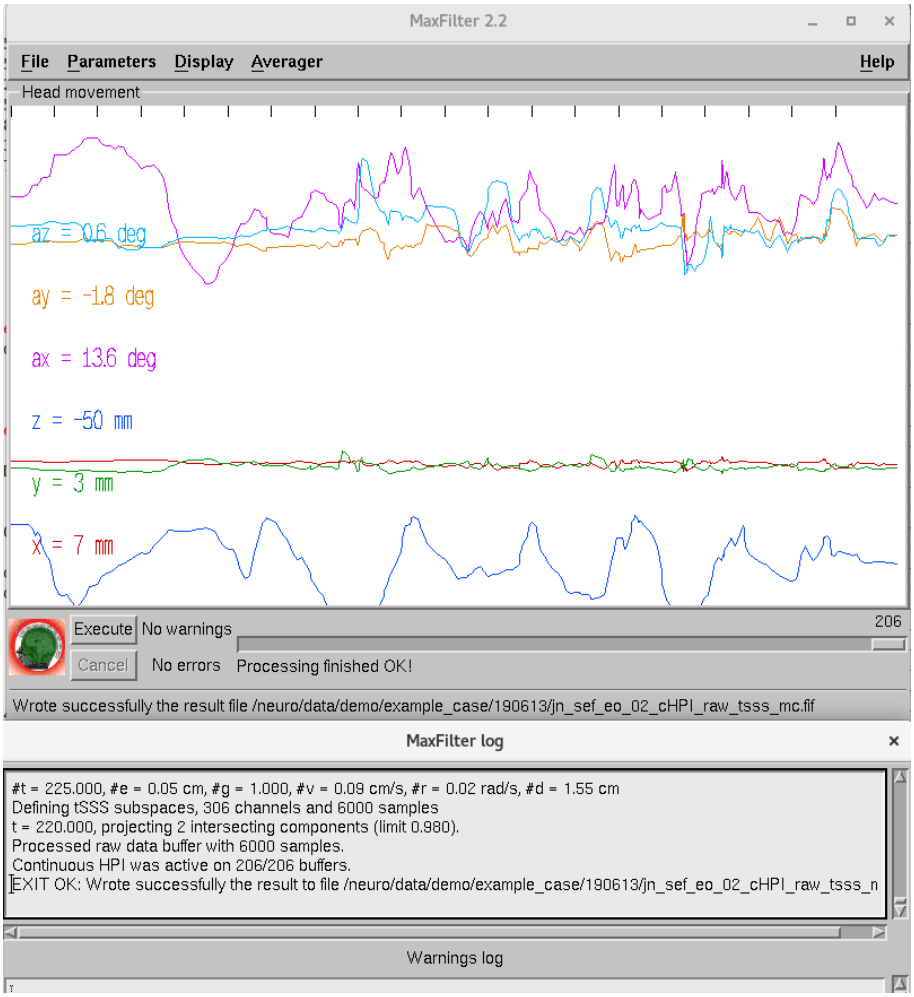


Figure 18: *MaxFilter* head position display and log window for the example case of Figure 17.

Note: If the output files are written in a different directory than input files, special care should be taken to avoid mixing files of different patients.

Warning: If *tSSS* is applied on averaged data or if there were several saturated or bad channels in raw data, the result must be inspected very carefully.

Warning: The user must judge the result carefully if the *tSSS* correlation limit is lowered from the default value.

Warning: Head position transformation operations require that the initial and reference coordinate transformations are defined correctly.

Warning: Head position calculation errors affect the data quality after movement compensation. The user must inspect the head position fitting error and goodness before data analysis.

6 Prepare events for functional mapping

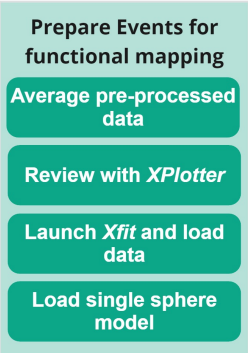


Figure 19: Workflow for preparing events for functional mapping.

6.1 Re-average pre-processed evoked response data

According to ACMEGS Clinical Practice Guideline 2, off-line averaging after data acquisition allows for noise-reduction processing (i.e. *MaxFilter*), elimination of artifact-containing traces and judicious selection of band-pass filtering.

- After processing continuous evoked data with *MaxFilter*, re-average the events to create a clean evoked file.
- In *MaxFilter*, select **Averager -> Load raw data… (Alt-a + l)**, and select the continuous *MaxFilter* -processed data `(*_raw_tsss_mc.fif or *_raw_sss.fif)`.
- Optionally, you can define the output filename using **Averager -> Output file… (Alt-a + o)** and adjust rejection limits using **Averager -> Rejection limits… (Alt-a + r)**.
- Press **Execute.**
- The result is saved alongside the original with extension `*_ave.fif`.
- Note: baseline correction is not applied to the average. It is recommended that baseline noise estimation and correction is used during source modelling in *Xfit*.

6.2 Explore evoked responses at the sensor level with *Xplotter*

Plotting (*Xplotter*) module allows you to view the readings of each sensor plotted against time, and to measure latencies and amplitudes of responses. It is possible to view several data sets simultaneously, so that the plots are superimposed on top of each other. For this section, we will use the dataset `/neuro/data/demo/example_case/190122`.

6.2.1 Launch Plotting (*Xplotter*)

Select Applications -> Neuromag toolbox -> Plotting (Figure 20).

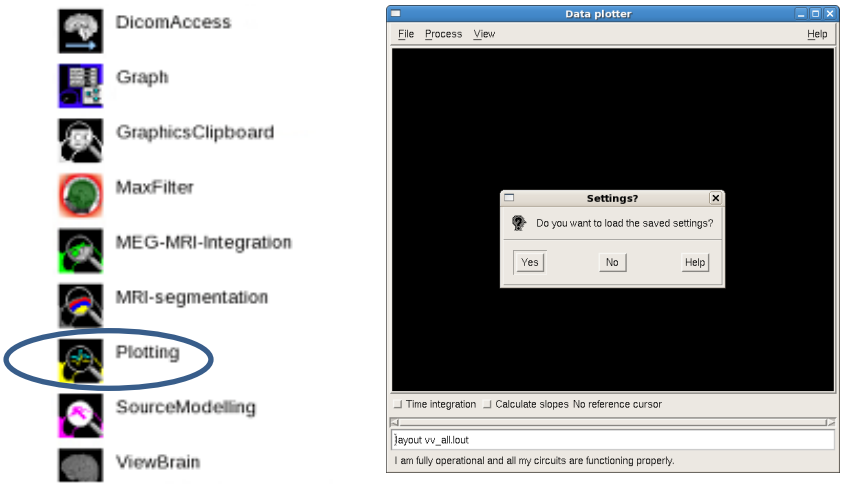


Figure 20: Launching *Xplotter*.

6.2.2 Load two datasets that will be superimposed

- Select **File -> Load data (Alt-f + l)** and select `jn_vef_ave.fif`.
  - **Available data**, select *>Vis ur>average.
  - **How to load?**, select **Replace old data.**
  - **Time scale modification**, select **No time shift.**
- Select **OK.** The selected data is now visible in a topographical plot (Figure 21).
- Select **File -> Load data (Alt-a + l)** and select `jn_vef_ave.fif`.
  - **Available data**, select *>Vis ul>average.
  - **How to load?**, select **Overlay old data from viewport.**
  - **Time scale modification**, select **No time shift.**
- Select **OK.**
- The second dataset is overlaid with the first one in the topographical plot (Figure 21).

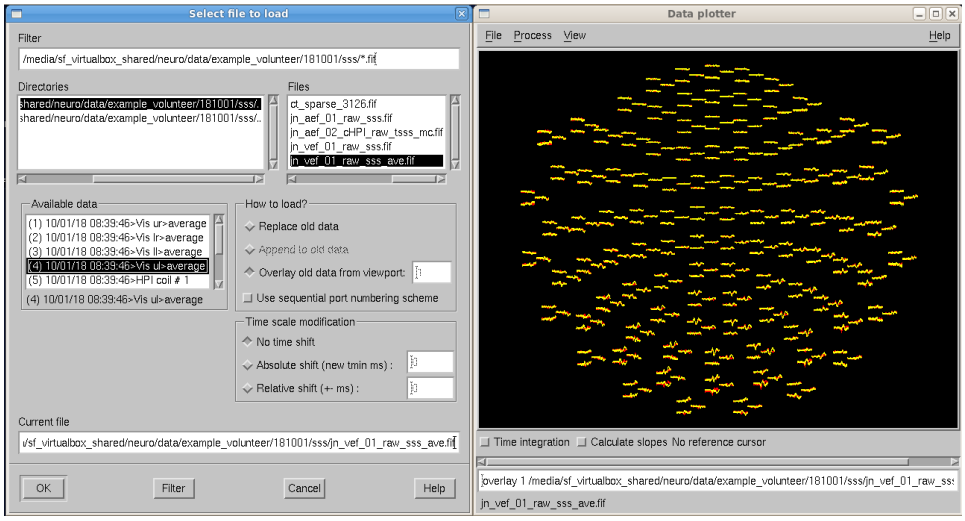


Figure 21: *Xplotter* data loading and overlaying.

6.2.3 Review the display

- The *Xplotter* display layout shows the channel-level epoch waveforms in a topographical view, nose up, right on right (Figure 21). The curves are organized in triplets, where the three channels are in the same physical location:
  - On the right-hand side of a triplet (Figure 22) you see the readings of a *magnetometer*; it measures the magnetic flux penetrating the sensor. Magnetometer channel numbers end with number one (e.g. 1741).
  - On the left-hand side of a triplet you see the plotted readings of two planar *gradiometers*. They are sensitive to two orthogonal components of the *gradient* of the magnetic field along the helmet surface. Gradiometer channel numbers end with numbers two or three (e.g. 1742 and 1743).

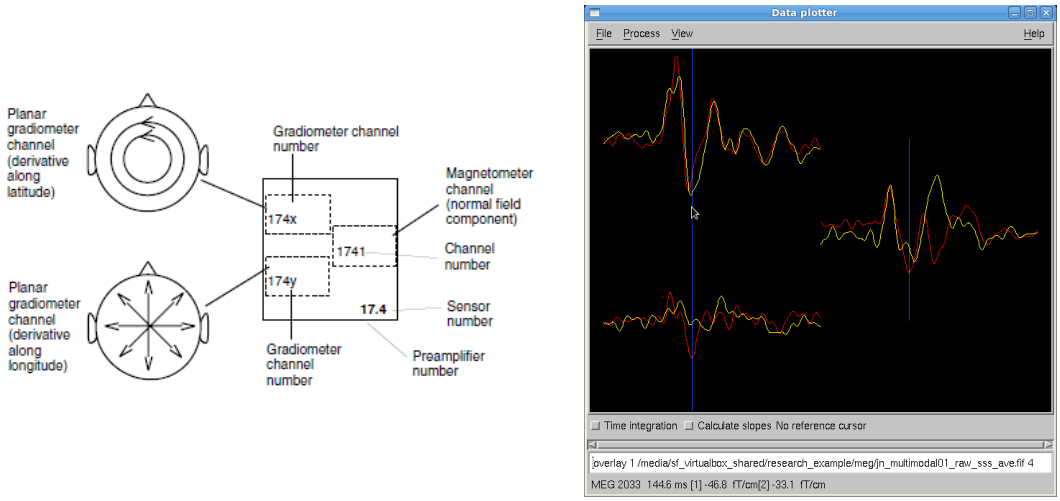


Figure 22: MEG channel naming convention and triple-sensor layout.

- Display the plot channel number: Click and hold the left mouse button over any plot. The channel number is displayed at the bottom of the window (Figure 22).
- Display the cursor position: Click and hold the left mouse button over the plot. The time corresponding to the cursor position is displayed at the bottom of the window.
- Display the amplitude: Click and hold the left mouse button over the plot. The amplitude at the time corresponding to the cursor position is displayed at the bottom of the window.
- Zoom in: Select and hold the **Shift** key, then click and hold the left mouse button and drag over the area to zoom (Figure 22).
- Zoom out: Select and hold the **Shift** key, then click left mouse button on any part of the graph.
- Autoscale the time: Select **Process -> Autoscale (Alt-p + a)**.
- Autoscale the amplitude: Select **Process -> Autoscale amplitudes (Alt-p + p)**.

6.2.4 Adjust the trigger-to-stimulus delay

- You can adjust the trigger-to-stimulus delay in *Xplotter* and *Xfit* if it was not recorded into the acquisition parameters. The result will be that the zero timepoint will represent the onset of the stimulus.
- The actual delay values are site and configuration specific and should be measured for all equipment at the time of install.

- To determine if the delays were recorded, read out the acquisition parameters from the FIFF file.
  - Open a system terminal: Applications -> System Tools -> **Terminal**. Type the command:
    ```
    cd /neuro/data/demo/example_case/190122/
    /neuro/bin/util/show_fiff -vt150 *raw_sss.fif > temp.txt
    ```
  - Open the text file and scroll down to parameters **ERFeventDelayNN** and locate the event you are analyzing (**ERFeventCommentNN** contains the names of the stimuli).
  - If the field is 0, then the delay was not recorded and can be entered when loading a file to *Xplotter* or *Xfit*.
- For the demo dataset, stimulus delay for visual is 33 ms and for auditory 6 ms.
  - Open the FIFF file again, **File** –> **Load data**, and select **Absolute shift** (see Figure 21).
  - Change the value of **tmin** manually to the required delay (e.g. 33 ms or 6 ms) and click **OK**.
  - When you have loaded the data, you can **Autoscale** the responses once again.

6.2.5 Adjust the filters

- Select **Process -> Filter… (Alt-p + f)** (Figure 23a).
- Select the **Lowpass** toggle and enter 40 Hz with a width of 5 Hz.
- Select **Rescale** to see the effect of the current filters on a sample response. The original and filtered response are shown in the bottom row of the window.
- Select **Apply.**

6.2.6 Set the baseline

- Select **Process -> Baselines… (Alt-p + b)** (Figure 23b).
- Select **Use baseline** toggle.
- Enter **Baseline start** = -200, **Baseline end** = -5 (to avoid the trigger artifact).
- Select **OK.**

a) b)

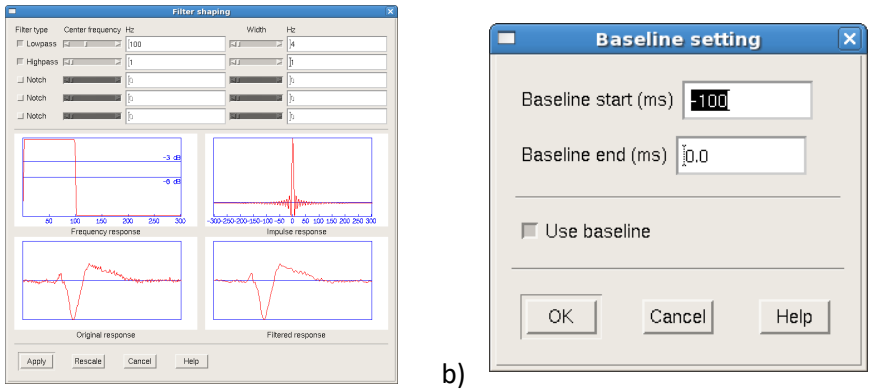


Figure 23: *Xplotter* a) filter and b) baseline settings.

6.2.7 Set operations

- To see a list of loaded data sets and controls for changing their display, filters, baseline and SSP status (Figure 24).
- Select **Process -> Set operations... (Alt-p + o)**
- Load or delete the SSP projections for individual sets: Select **Load projection…** or **Delete projection.** Note that if the data has been *MaxFilter* -processed, it does not contain the SSP vectors anymore.
- Create derivatives: In the **expr** field type arithmetic expressions for two or more sets. An expression is composed of operands and operators, separated by one or more spaces or tabs. An operator defines the operation to be performed on one or two operands. The operands are entered before the operator:
  - For computing the difference between the sets, use the expression " **#1 #2 – "** and select **Evaluate**. A third trace (blue) showing the difference of the two original ones should now appear on the main Plotter window (Figure 24).
  - For computing the average of the sets, use expression " **#1 #2 + 2 /** " (note blanks between operators and operands).

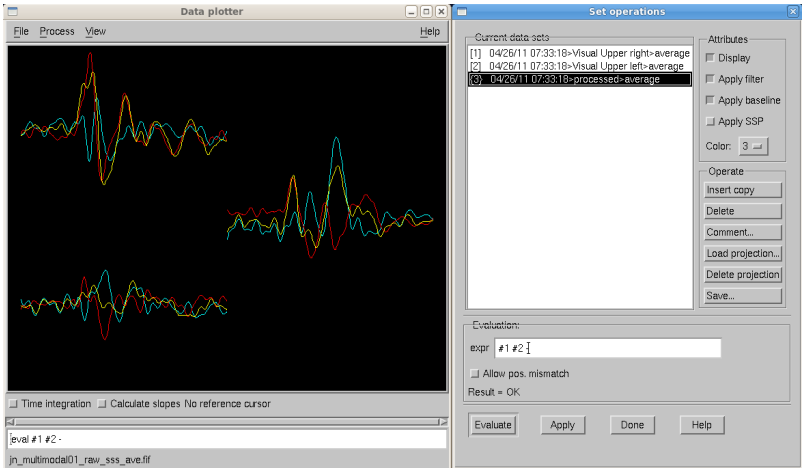


Figure 24: *Xplotter* Set operations.

Warning: If one saves a derived data set for source modelling and SSP has been applied explicitly to the data, one must ensure that the appropriate SSP operator is included with the data. Otherwise the result of modelling can be biased.

6.3 Launch SourceModelling (*Xfit*) and load data

- Select **Applications -> Neuromag toolbox -> SourceModelling** (Figure 25).
- Select **File -> Open (Alt-o)** and select `jn_sef_01_raw_sss_ave.fif`.
- From **Available data**, select *>SEF right>average.

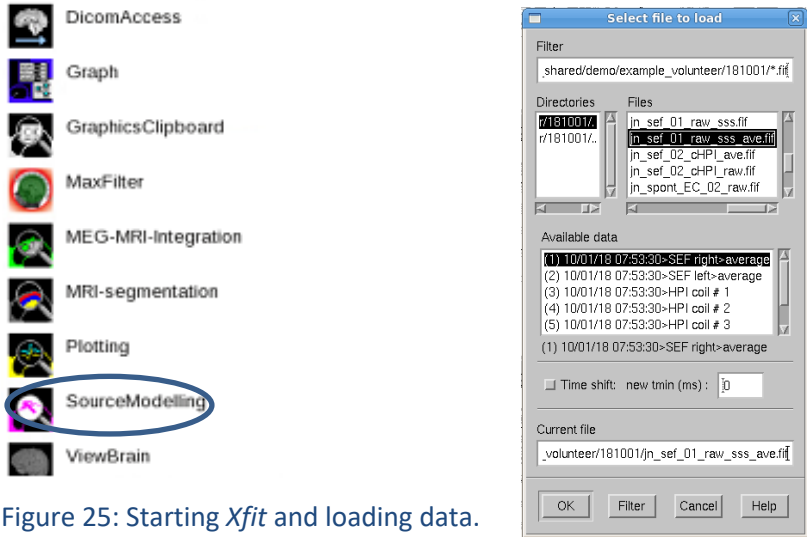


Figure 25: Starting *Xfit* and loading data.

6.4 Load single sphere head model

- The best-fitting sphere model was computed on the subject's MRI in section 4.3.
- Add the resulting origin coordinates to the Sphere model parameters in the Conductor model parameter window in *Xfit* (Figure 26) using either method:
  - Use the center mouse button to click and hold over the sphere origin dialog in *Mrilab.* Drag and release the mouse on the Sphere model parameters dialog in *Xfit* (the blue arrow in Figure 26).
  - Type the sphere origin coordinates manually into the dialog.

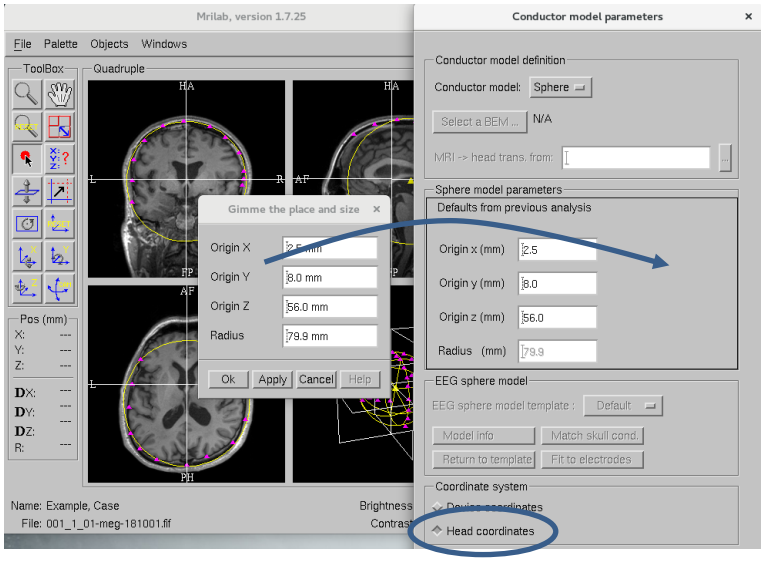


Figure 26: Drag and drop the optimal sphere origin from *Mrilab*. Make sure that you have selected the **head coordinates** in the *Xfit* conductor model parameters dialog.

7 Prepare events for epilepsy source localization

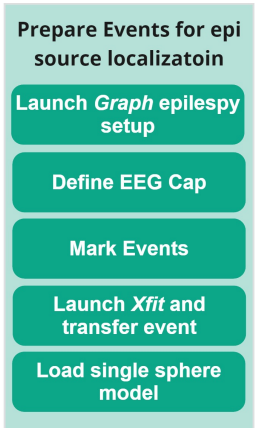


Figure 27: Steps for preparing events for epilepsy source localization.

7.1 Load *Graph* setup epilepsy-3.3

- Open Applications -> Neuromag -> *Graph* (Figure 28). The *Graph* display shows text 'Nothing connected'.

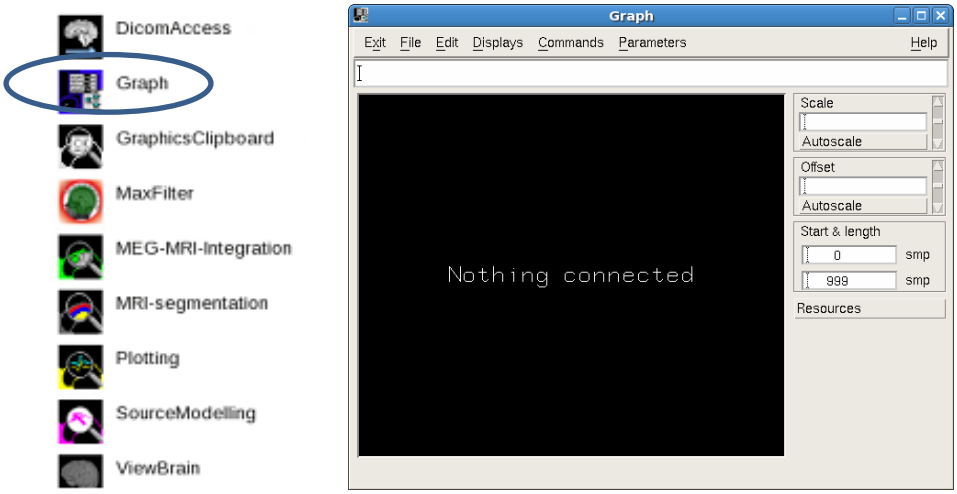
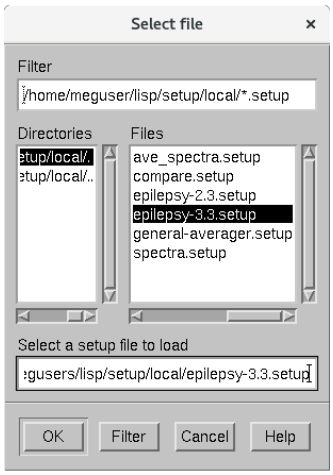


Figure 28: *Graph* launching and initial display.

- Open **File -> Load Settings and select setup file** `~HOME/lisp/setup/local/epilepsy-3.3.setup`.
- **File -> Change directory**, select `/neuro/data/demo/example_epi/190122`.
- **File -> Open Diskfile**, select file `sim_spikes_raw_tsss_mc.fif`.



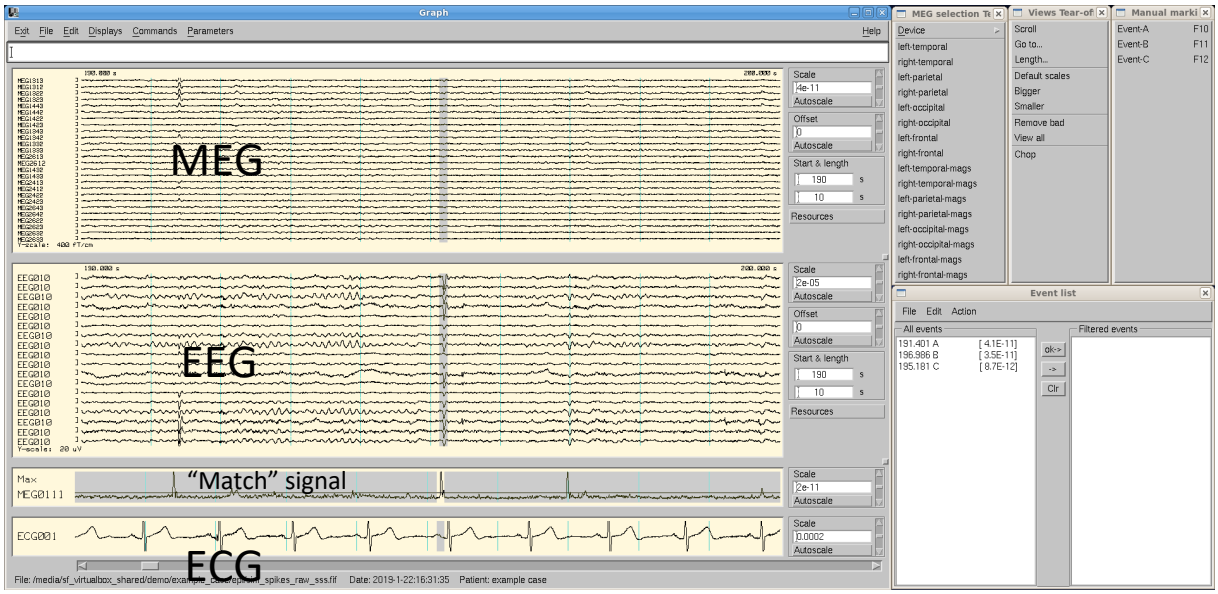
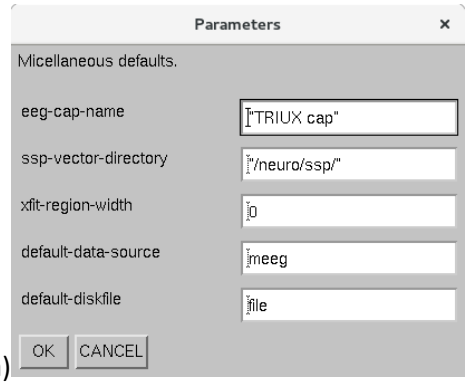


Figure 29: Graph epilepsy-3.3 setup showing one selection of MEG data, EEG and a match signal channel with threshold and ECG. Tear-off menus is also shown.

- Menu selections **Displays->Views, Parameters->Displays** and **Commands->Search** are explained in detail in Appendix B: Quick reference for *Graph* Epilepsy setups (chapter 16).
- Open **Commands -> Search -> Event lists** and detach tear-off menus **Displays->Views**, **Displays -> MEG selection**, and **Commands -> Search -> Manual marking** by clicking the dashed line in the list so that it will remain open and on top of screen (Figure 29). Note that all the menus that have the dashed line work the same way.
- To select a sensor, or group of sensors, left click and drag over display.
- To select a time point, right-click.
- To de-select, left click in the grey area to the left display.
- You can use **Views -> Scroll** to make a quick visual review of the data.
- Adjust scales as needed: Select a group of sensors, then select **Views -> Bigger** or **Smaller.**
- Adjust filters as needed: **Displays -> Control Panel -> meg-filter,** e.g. `(band-pass 3 70)`. To include a line noise notch filter, enter `(combinef (bandpass 3 70) (notch 60))`.
- You can define the length of displayed data in all windows by editing **Views -> Length…**

7.2 Define EEG cap

- If EEG was recorded with a cap (32/64/128 channels), first define the EEG cap type in **Parameters -> misc-defaults** (Figure 30a).
- Currently supported choices are: "Headbox", "TRIUX cap", "Vectorview cap", and "Easycap" (see section 16.1 for details).
- Note that in the demo file `sim_spikes_raw_tsss_mc.fif`, the proper selection is "Headbox".
- Change the EEG montage using the **Displays -> Derivations**.
- The standard choices include longitudinal, transverse and referential bipolar montages, as well as all EEG channels referenced to Cz in groups of 32 channels (Figure 30b).
- Tailored derivations and site-specific preferences can be defined in the configuration file `/neuro/lisp/local/graph-2.94/config/eeg-derivations2.lsp` (see section 16.2 for details).

a) 

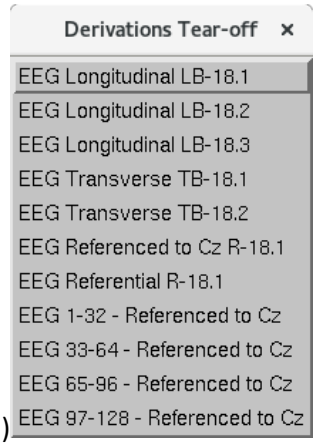
b) 

Figure 30: a) Set the EEG cap. If it is not set, Displays -> Derivations will show an error message. b) Default EEG derivation choices.

7.3 Mark events

- Review the data to find an event.
- **Right-click** the peak of the event. Note that there is no automatic alignment of the event, so you need to select the "same" time point from the events (typically peak).
- Assign the event type by selecting **Event-A/B/C** from the manual marking menu or use the shortcuts F10, F11 and F12, respectively (check that NumLock is turned off).
- Manual events are added to the Event lists left-hand panel (All events).
- Review the events in the list and adjust event type if needed: Select the event in the list then select Event-A/B/C from the manual marking menu.
  - Jump to the existing events by double clicking it in the list.
  - Event lists can be saved from Event list window: **File -> Save all events/Save filtered events.**
  - See also section 14.5 for the event lists.

7.4 Launch *Xfit* and transfer event

- Open *Xfit* from *Graph*: **Displays** -> **xfit** -> **Start xfit**.
- Double-click a filtered event from the Event lists dialog. An error dialog will appear if the conductor model parameters have not been entered.
- Click on *Xfit* to reveal Conductor model parameter window. See below.
- Alternatively, select a region and send to *Xfit*: **Display** -> **xfit** -> **transfer selection**.

7.5 Load single sphere model

- The best-fitting sphere model was computed on the subject's MRI in section 4.3.
- Add the resulting origin coordinates to the Sphere model parameters in the Conductor model parameter window in *Xfit* (Figure 26) using either method:
  - Use the center mouse button to click and hold over the sphere origin dialog in *Mrilab.* Drag and release the mouse on the Sphere model parameters dialog in *Xfit* (the blue arrow in Figure 26).
  - Type the sphere origin coordinates manually into the dialog.

8 Perform source modelling

The following sections guide the user through a typical workflow for single dipole fitting using a single sphere model. The first two sections show how to Launch SourceModelling and Load Single Sphere Model. When performing source modelling on epileptic spikes, this software should be launched directly from Graph setup (see Section 7.4).

Warning: MEG data can be inherently explained by many different source distributions, and measurements often contain various kinds of artefacts. Data used for clinical purposes must be interpreted by a trained clinician who is capable of judging the relevance and quality of the data.

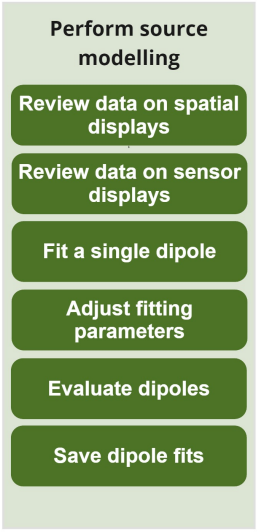


Figure 31: Workflow steps for source modelling with a single sphere model.

8.1 Review data on spatial displays

- *Xfit* user interface is shown in Figure 32; see the *Source Modelling Software User's Guide* for the details of the controls and display areas.
- In the upper left corner **Signal waveform** window, select a time point by mouse left-click.
- Enable **Show amp**. to display the blue RMS amplitude curve (encircled in Figure 32).
- Review the **Spatial distributions** displayed on the right: nine individually controllable displays of spatial distributions, such as contours, model contours, difference contours, gradient contours, EEG contours, arrows, model arrows, or MNE arrows.
- Select desired **Overlay** options (in the bottom part of the display): review the MEG sensor outlines, dipoles projected onto the isocontour surface, standard head surface, BEM meshes, and isotrak points.
- Review the spatial displays at different time points, also using the animation controls (**Movie**: forward and backward arrows) on the lower right corner of the main display.

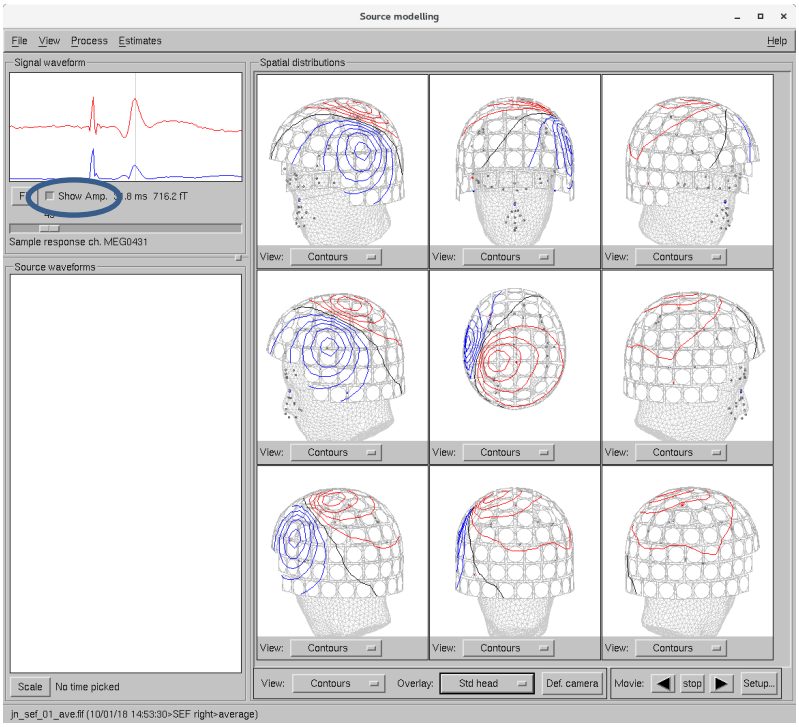


Figure 32. *Xfit* user interface main display shows nine views of MEG contours, here overlaid with the standard head surface and isotrak points.

8.2 Review data on sensor displays

Select **View -> Full view** (Figure 33).

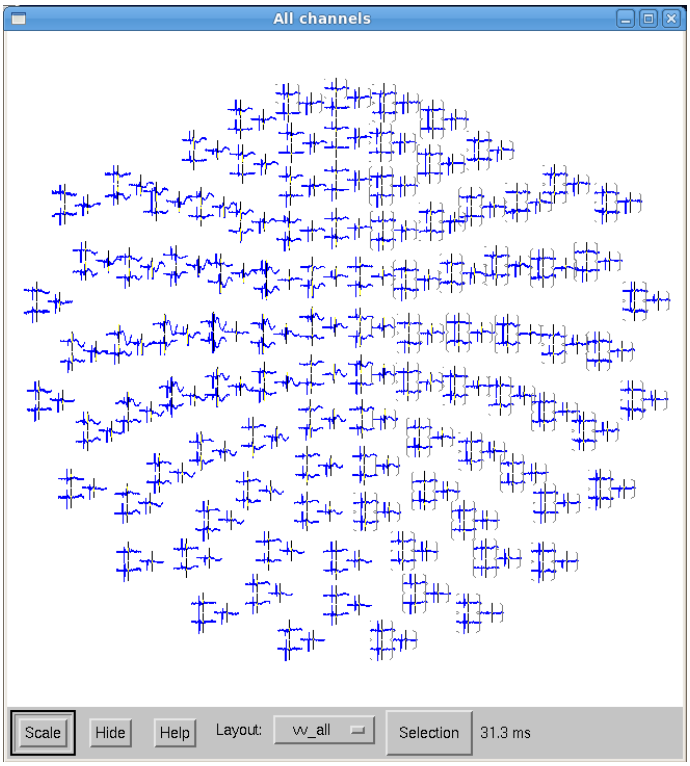


Figure 33: *Xfit* full view display. Channels on the left hemisphere have been selected, while the channels inside brackets are ignored in dipole fitting.

8.3 Fit a single dipole

- Pick a sample waveform: in the **Full view** of channels, **left click** one of the selected channels, preferably the one with the most prominent signal.
- View the **Signal waveform** in the upper-left corner of the main window (Figure 34).

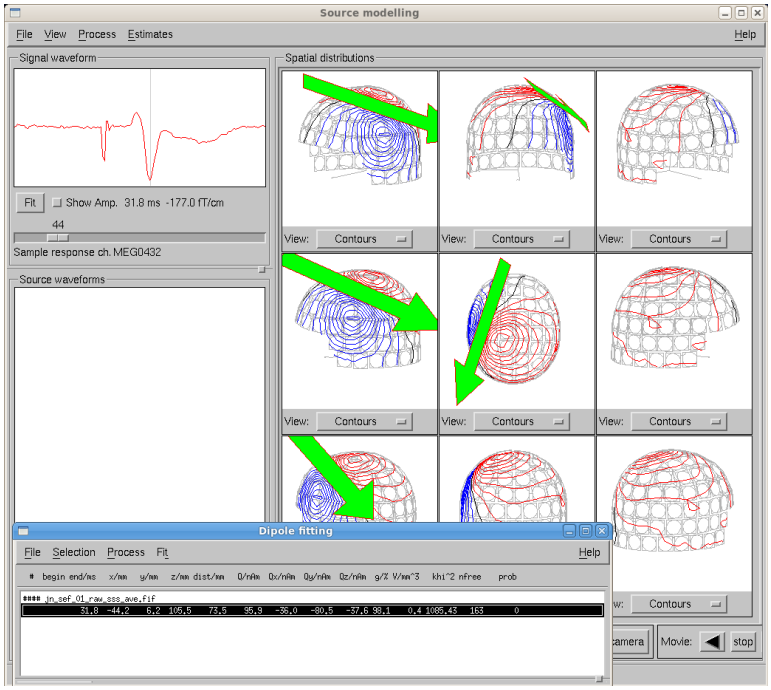


Figure 34: *Xfit* single dipole fitting at the 31 ms peak of somatosensory evoked responses, after selecting the channels on the left hemisphere.

- Select a time point: using corresponding field patterns, select a time point where the contour maps show a symmetrical dipolar field pattern containing as many contour lines as possible.
- Fit the dipole by pressing the **Fit** button.
- A Dipole fitting window will appear containing all the location and statistical parameters of your dipole (Figure 34).
- The upper part of the **Dipole fitting window** contains a list of dipoles. Each row represents one dipole. The following parameters of the dipole are given, from left to right:
  (1) Time point or time range where the dipole was fitted.
  (2) Cartesian *x*-, *y*- and *z* coordinate of the source estimate.
  (3) Distance of the dipole from the sphere model origin.
  (4) The dipole moment [nAm].
  (5) x, y and z-components of the dipole moment vector.
  (6) Goodness of fit (g-value), or how large fraction of the variance of the measured data is accounted for by the dipole.
  (7) Confidence volume within which the dipole should lie with 95% certainty (sphere model).
  (8) Khi-square (χ^2) statistics and the number of degrees of freedom of the sphere model.

8.4 Adjust fitting parameters

When fitting a dipole, it may be necessary to adjust some parameters to obtain the best fit. The example given are a good starting point. Iterative adjustments may be necessary depending on the data.

8.4.1 Channel selection

- Select channel subsets for dipole fitting – a set of channels that contain signals which appear to be generated by a single current source. In practice, this means a sub-set of one third to one half of the number of channels (~100-150).
  - Select channels with similar waveforms: **right-click and drag** a rectangle over the channels, ignored channels will appear in brackets.
  - To refine the selection, continue to press **Shift** and select individual channels on and off with the **right-click.**
  - To un-select channels, **right-click** anywhere in the white space

8.4.2 Noise level estimation

- Select **File -> Preferences -> Fitting… (F10)** in the main display, or **File -> Preferences** in the Dipole fitting dialog. For the demo dataset, select Compute from baseline.
  - *Constant value* is the default setting, corresponding to normal evoked response measurements where ~100 epochs are averaged, and signal bandwidth is 100 Hz. The default values are 5 fT/cm for gradiometers and 20 fT for magnetometers. For single, unaveraged spike events, the recommended values are 50 fT/cm for gradiometers and 200 fT for magnetometers.
  - *Compute from baseline* (recommended) means that the channel-specific noise levels are estimated from the baseline. This setting is strongly recommended if the responses have poor signal to noise ratio, such as non-averaged single epochs.

Note: The noise level values affect somewhat the accuracy of the dipole fits through weighting of magnetometer and gradiometer channels in dipole fitting (*Source Modelling Software User's Guide* section 9.1.2) and they determine the confidence limits (*Source Modelling Software User's Guide* section 9.1.6).

Care must be taken to use proper noise estimates. The default constant values have been set for normal evoked response measurements where roughly 100 epochs are averaged, and signal bandwidth is 100 Hz. If these settings are used with unaveraged epochs, the confidence limits will be grossly underestimated (the estimated confidence limits are narrower than the true standard deviation of the dipole parameters). The expected sensor noise level in the average can be obtained from the RMS noise density of the sensor by multiplying it with the square root of the ratio of bandwidth and number of averages. Even when fixed noise levels based on the known system noise are set correctly, the brain background activity can produce "noise" that is clearly higher than the estimate, causing again the confidence limits to be underestimated.

Using the baseline standard deviation as the noise estimate is independent of averaging and acquisition parameters and gives generally a bit more accurate dipole-estimate. It is the recommended setting for general cases. However, in some special situations (for example, if the

baseline is not a true baseline, but contains also the signal itself) properly set fixed values can provide better results.

The noise is also assumed to be independent on each channel, and in presence of correlated noise, the variance in the dipole estimates may be somewhat higher or lower than what the confidence limits based on the noise levels calculated from the baselines suggest. For example, with data that has been filtered with *MaxFilter*, the software has tendency to somewhat underestimate the confidence limits.

8.4.3 Baseline

- Select **Process-> Baselines… (Alt-p + b)** in the main display, check **Use baseline** and enter baseline window [-100, -5] ms. The average level of the signal during baseline is now set as the zero level of the signal (DC offset). This baseline is also used when baseline noise modelling is selected.

8.4.4 Filtering

- Select **Process -> Filter… (Alt-p + f)** in the main display, select **Lowpass** and enter 40Hz and width of 5Hz.

8.5 Evaluate dipoles

8.5.1 Compare fit statistics to acceptance criteria

- Test the residual for modeling error by inspecting the goodness of fit, confidence volume and χ^2 (khi-square) values.
- The "reduced khi-square" value is obtained by dividing the reported χ^2 with the number of degrees of freedom (nfree) which equals to the number of used channels minus the number of dipole parameters. The background noise must be estimated from the baseline or constant noise values of unaveraged epochs must be used (e.g. 50 fT/cm for gradiometers and 200 fT for magnetometers).

The following steps are used to evaluate if the result is a "good model".

- Check the statistical parameters:
  - Goodness of fit > 80 %.
  - Confidence volume < 1000 mm^3.
  - Reduced khi-square: χ^2/nfree < 2.
  - Dipole amplitude is between 100 nAm and 500 nAm.
- If the parameters are acceptable, transfer the dipole to MRI and check that
  - The fitted location is at, or close to, the cortex.
  - The orientation is roughly perpendicular to the gray-white matter boundary.

8.5.2 Review how well the dipole model explains the data

XFit contains powerful features that enable you to compare *visually* the predictions of the dipole model with measured data. This is often the best way to get an idea about the real goodness of the dipole fit.

- It is possible to review the source waveform and the residuals.
  - Select **File -> Preferences -> Fitting… (F10)** in the Dipole fitting dialog
  - Select **Show predicted waveforms**, select **Done.**
  - In the Dipole fitting window, activate a dipole display by clicking the "1" box, see Figure 35 (A)
  - **Center-click** on the dipole of interest from the list of dipoles and drag to the activated display row.
  - In the Time (amp) row, click **Full scale**, see Figure 35 (B)**.** The source waveform and residuals are displayed in the main window (Figure 35 (C)) and overlaid in the **Full View**.

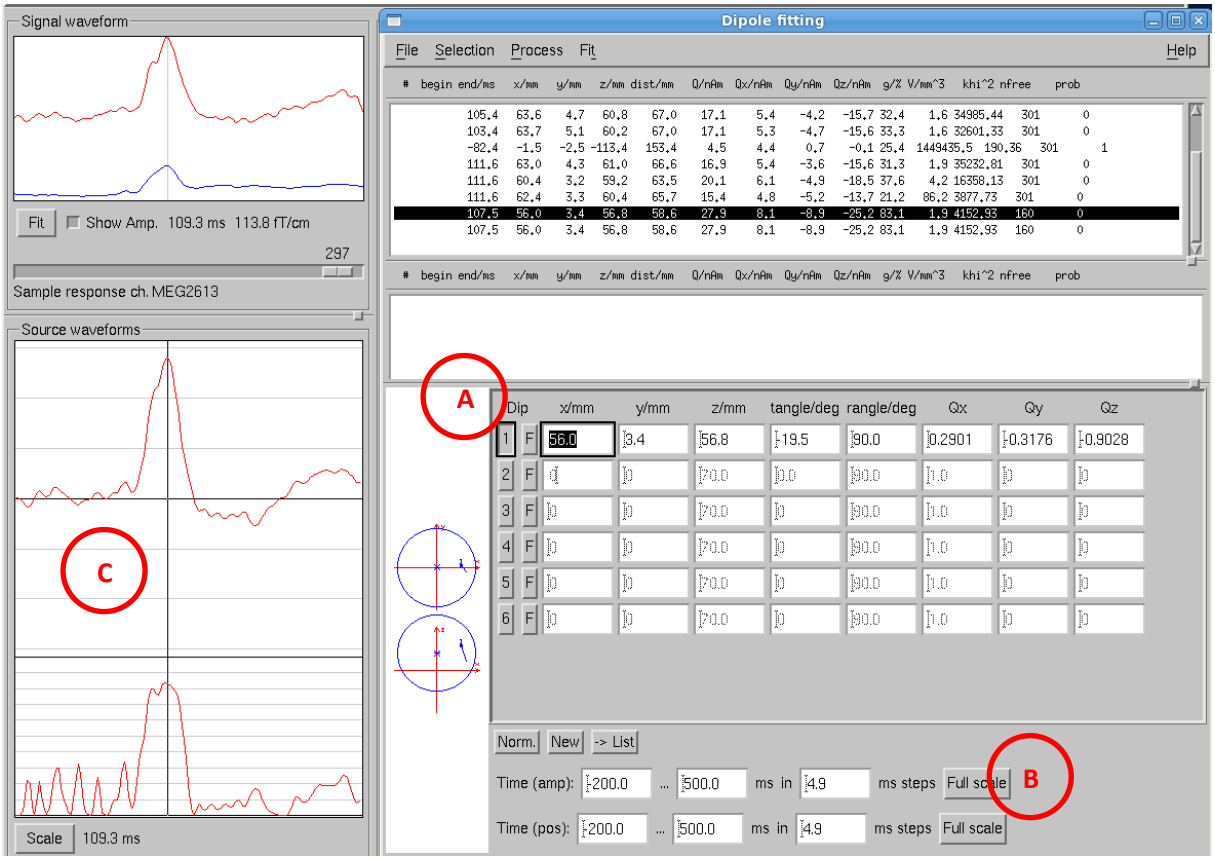


Figure 35: Plot source waveform and residuals for a dipole estimation.

- Review the **Full view** window that contains the original responses with the predicted signals superimposed (Figure 36).
- Examine how well your dipole model predicts the data: zoom in/out by using Shift + left drag/click over an area. Go to the main window. If you have selected a time point close to the signal peak, you should see your dipole as a green arrow on top of the field patterns.

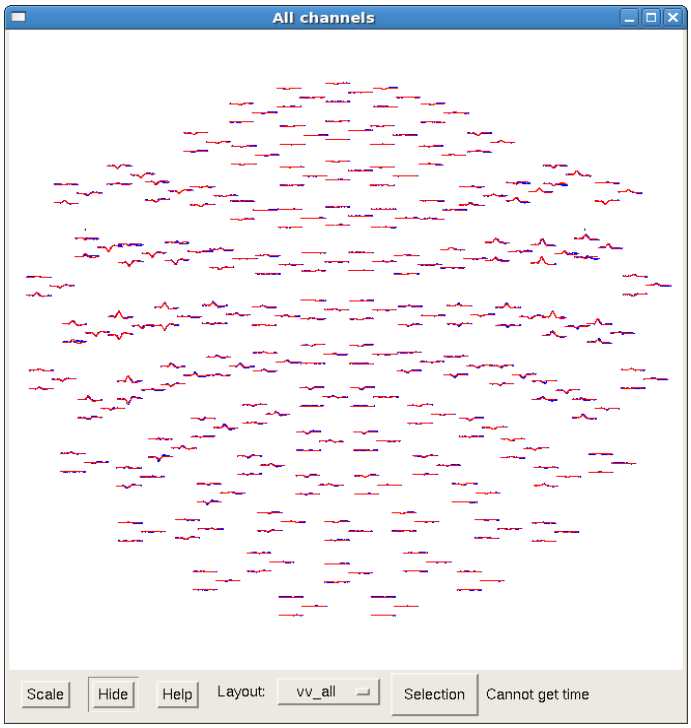


Figure 36: *Xfit* measured and predicted MEG channel waveforms.

8.5.3 Overlay fitted dipoles on co-registered MRI with *Mrilab*

Observe the location of the fitted dipole to be close to the expected location (functional mapping), close to the cortex, and the orientation is roughly perpendicular to the gray-white matter boundary

- Launch **Applications -> Neuromag -> MEG-MRI integration**
- **File -> Open (Alt+o)**, then select MRI with the correct anatomical landmarks and co-registration: `/neuro/mri/example_case/sets/*_01-<username-date>.fif`
- Click **Apply.**
- Select the dipoles from the list in the **Dipole fitting** window, **right-click -> MRI** (Figure 37).
- Set **File -> Preferences -> Interface style (Alt-f + p + i)** to 'Standard'.
- Select **Windows - > Object tree**, double-click on an object in the object tree to select a new style for the dipoles (Figure 38).
- NOTE: when you send a list of dipoles from *Xfit*, all dipoles will be treated as a single object and will have the same appearance. Send the dipoles one by one if you wish to handle them as separate objects in *Mrilab*.

Warning: The user must take specific care to apply the coordinate transformation of a correct patient or subject.

Warning: The user must take specific care to load the MRI data set or the BEM model of a correct patient or subject.

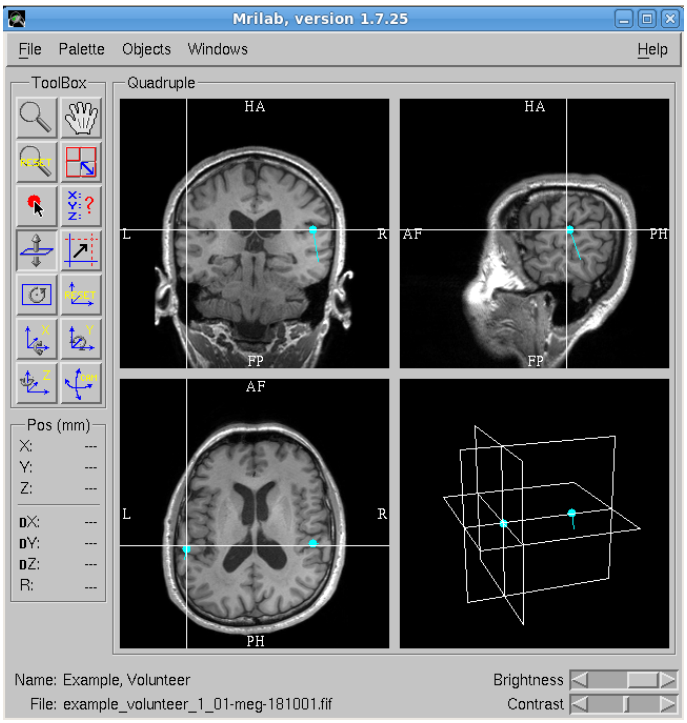


Figure 37: Importing the two-dipole fit locations to *Mrilab*.

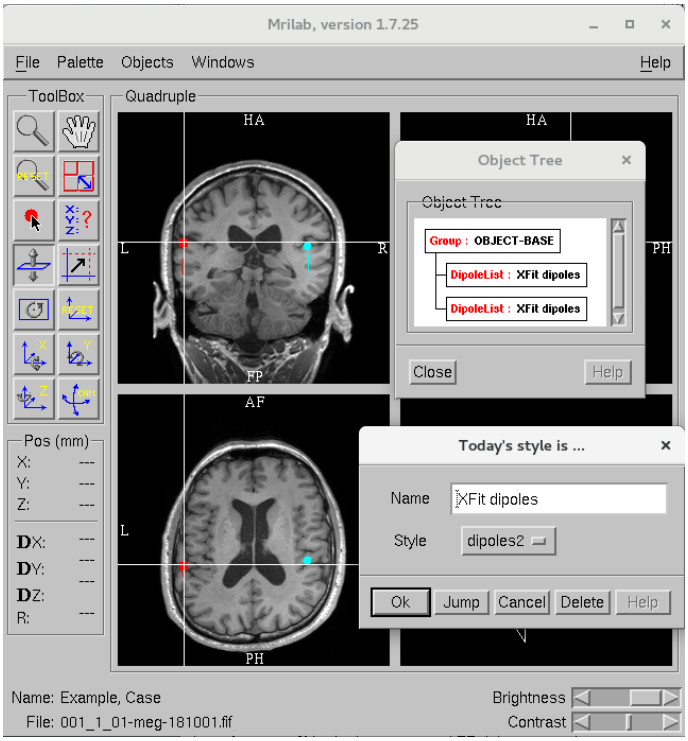


Figure 38: *Mrilab* object tree and changing the dipole appearance.

8.6 Save dipole fits

- In *Xfit* Dipole fitting window, select dipoles for saving, use **Selection -> Save** and save the dipoles in a binary *.bdip file, see Figure below.
- To save only those dipoles that were sent to the MRI, from *Mrilab* select **File -> Export -> Dipoles (Alt-f + e +d)** and save to an ASCII *.dip file.
- Saved binary (*.bdip) and ASCII (*.dip) files can be loaded back into *Mrilab* by selecting **File -> Import -> Dipoles (Alt-f + i + d)** (Figure 39).

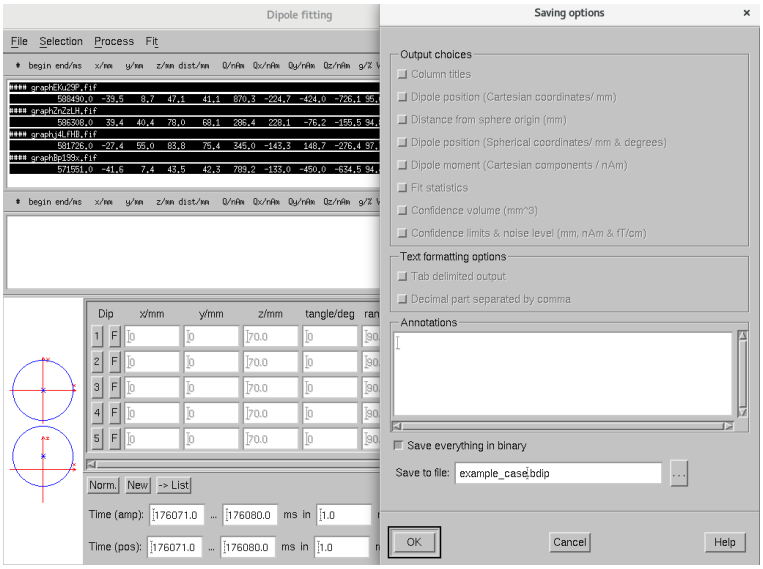


Figure 39: Selected dipoles can be saved to a binary or ASCII file.

9 Prepare DICOM export and clinical report

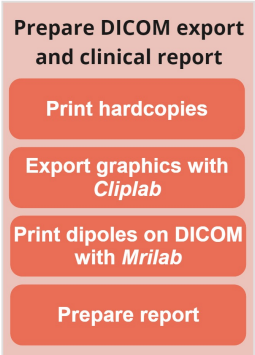


Figure 40: Workflow steps for preparing DICOM export and clinical report.

9.1 Print hardcopies

- The easiest way to create hardcopies is to press the **Print screen** button or to use a suitable Screenshot capture application in Linux. Save the output (the whole display, window under cursor, or selected region) as a png bitmap file.
- Alternatively, right-click on top of the display and choose **Print** command from the popup menu to send the captured image to printer, vector-graphic Illustrator output file, or a TIFF output file.
- Make printouts of (1) your dipole list, (2) source waveform and g-value graphs, (3) field patterns and dipoles on the helmet array on some chosen time point, and (4) Full view window or some part of it containing the original and predicted responses. Note that you can print all nine field pattern figures on one paper if you right-click on the bar below them, containing the text "View", "Contours", "Def. camera" and so on. In some cases, you may add your own notes to the printouts — in this case, an annotation window will appear before printing.
- Note: Linux operating systems generally provide feasible screenshot functionality with **Print screen** or a Screen capture application. If there is need to adjust the image resolution or other properties, you may need to search and apply a special Linux tool for modifying the picture, adjusting the borders, depth, color and a lot more while capturing screen of a particular application or a whole window.

9.2 Export graphics for reporting with *Cliplab*

- Launch **Applications -> Neuromag -> Graphics Clipboard.**
- Select the 2-by-2 layout (Figure 41). The dialog can remain open side by side with the data analysis program windows.
- Select a figure with the middle mouse button and drag-and-drop on the clipboard. Use this for any figure window from *MaxFilter*, *Graph*, *Xplotter*, *Mrilab*, and *Xfit* programs.
- Select **Layout -> Add Page** to add pages to the report.
- Export the graphics, **File->Export** or obtain a hardcopy, **File->Print.**

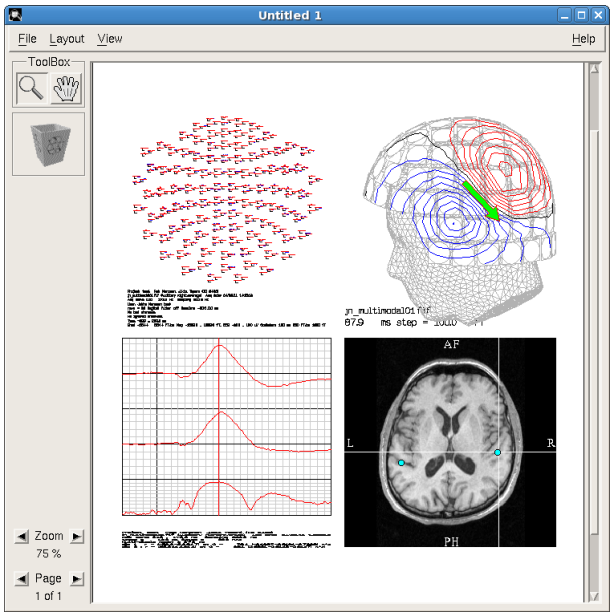
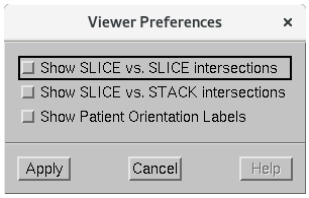


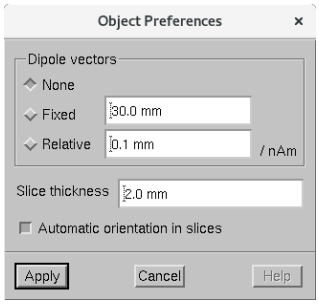
Figure 41: Graphics clipboard.

9.3 Export dipole fit results to DICOM using Mrilab

The dipole fitting results can be exported in DICOM format, and viewed in external DICOM compatible systems, such as in an intraoperative neuronavigator. The DICOM export is performed with *Mrilab*.

- Select **File** -> **Print**. A dialog pops up (Figure 42).
- Select **Destination: File**.
- Select **Target format: DICOM**, it will automatically set also **Source: Viewer, Full view(s)**; **Format: Gray-scale**.
- Select **Image & LineArt** to export also the dipoles.
- Note: In order to hide disturbing object such as the crosshair cursor, labels and dipole arrow from the exported images,
  - Right-click on the upper left viewer, check that you have **Modes -> Slice**, and select **Mode Prefs**. Uncheck all three options to hide the crosshair.
  - Select **Objects -> Object Preferences** and set **Dipole vectors: None**. Note that also the selected **Slice thickness** affects how the dipoles are shown in the exported DICOM slices.





- Create a new directory where you want to export the DICOM files, e.g. `/neuro/data/demo/mri/dicom_export`.
- Select **Destination**: **File,** browse to the freshly created export directory.
- Set output file name, e.g. `/neuro/data/demo/mri/dicom_export/example_case`.
- Press **Save**, another dialog pops up for export options (Figure 43).

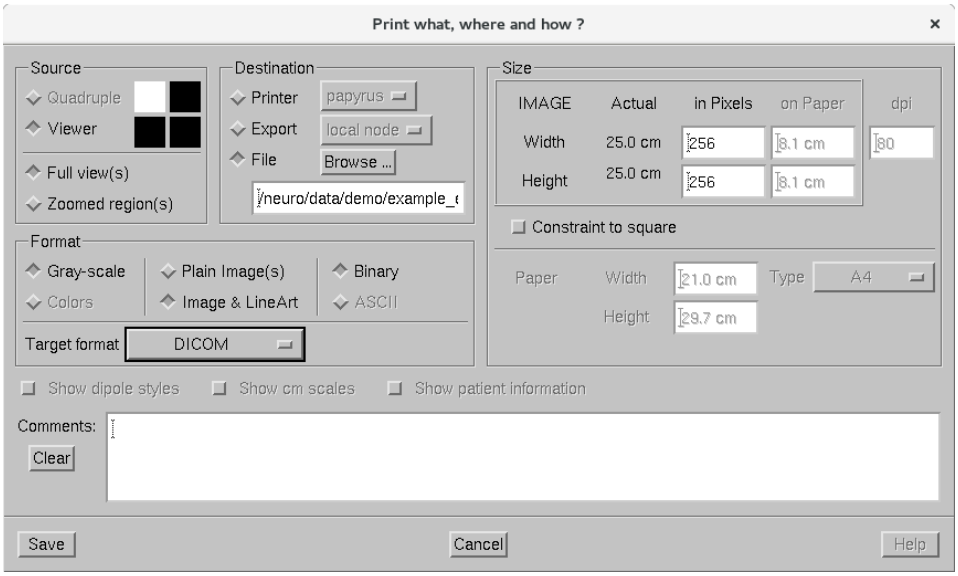


Figure 42. *Mrilab* printing dialog, DICOM export.

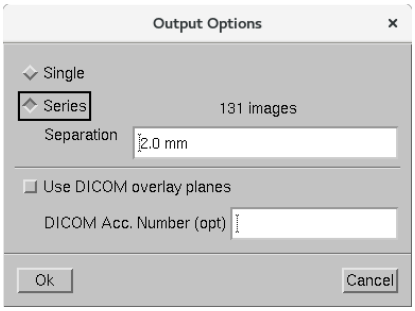


Figure 43. Options for DICOM export.

- Select **Series** to export all DICOM slices. You can also specify the separation between calculated output slices.
- By default, the dipoles will be "burned" to the MRI, i.e. high intensity pixels in the form of a cross will be added to the MR image in the dipole location. Only the location of the dipole is encoded in the output, not the orientation of the dipole.
- Optionally, you can select *Use DICOM overlay planes* to exports dipoles in DICOM overlay planes. NOTE: Please make sure that the external system viewing the DICOM exports can support overlays before using this export option.

9.4 Prepare clinical report

Guidelines for preparing clinical reports can be found in *ACMEGS Clinical Practice Guideline 3: MEG-EEG Reporting*. It is necessary that clinical staff receive specialized training from a clinical MEG expert before commencing with MEG data collection and analysis. Formalized training should include additional information about clinical reporting.

10 Next steps: Topics for advanced SourceModelling

10.1 Estimate spike onset activity – sequential single dipole fits

If the dipole model result is acceptable, the analysis can proceed to estimate the spike onset activity.

- Select **Signal waveform** window in the upper left corner of the main display, right-click above the displayed curve and choose **Sequential single dipole fit** from the popup menu.
- Press and hold Shift, then select a time range by clicking and dragging with the left mouse button. The background color in the selected area will turn gray.
- In **Sequential fitting** window, confirm appropriate values and select **Fit**.
- In **Dipole fitting window**, select the whole list by left-dragging, then right-click to make a popup menu appear.
- Select **Filter** command from the popup menu. Select the g > (%) checkbox and type in the limit value 95. Select **Ok**.
- Those dipoles whose g > 95 % should appear in the selection window below the list. If none appeared, the criteria were too strict, and you must try another value.
- Find the earliest time point at the onset that fulfills the acceptance criteria above.
- Check that the dipoles form a cluster, highlight the filtered dipoles, right-click, **Print -> MRI**.
- Estimate the distance peak fit and earliest time point fitted for assessing propagation of the source location.

10.2 Fit a two-dipole model

You can apply the preceding principles to expand the model to a set of multiple concurrent dipoles. This can be used when you suspect there are more than one simultaneous active sources.

- Load file `/neuro/data/demo/example_case/190613/jn_aef_eo_ave.fif` and select *>AEF right>average dataset.
- Enter the sphere origin coordinates defined earlier for the demo subject.
- Adjust the baseline, **Process -> Baselines… (Alt-p + b),** Use baseline [-100,-5] ms.
- Adjust the filter, **Process -> Filters… (Alt-p + f),** Lowpass 40Hz, width 5Hz.
- Open **Full view (F5)**, select a set of channels over the *right hemisphere* and fit a dipole.
- Activate **Row 1** in the multidipole dialog (Figure 44, bottom window of the Dipole fitting window).
- Select the dipole from the list with the center mouse button and drag it into Row 1.
- Select another set of enabled channels over the *left hemisphere* and fit a dipole.
- Activate **Row 2** and add the second dipole (Figure 44).
- Right click on the Full view window to activate all channels (no channel sub-sets).
- Select **Full scale** on the Time (amp) row in the bottom part of the multidipole dialog.

Review the **Source waveforms**: The dipole source waveforms appear on the left frame of the Source modelling window, presenting the amplitudes of the dipoles as a function of time (Figure 44). The time scale is the same as in the signal waveform graph on top of it. The bottom curve represents the goodness of fit and tells you how many percent of your data can be explained with your dipole model.

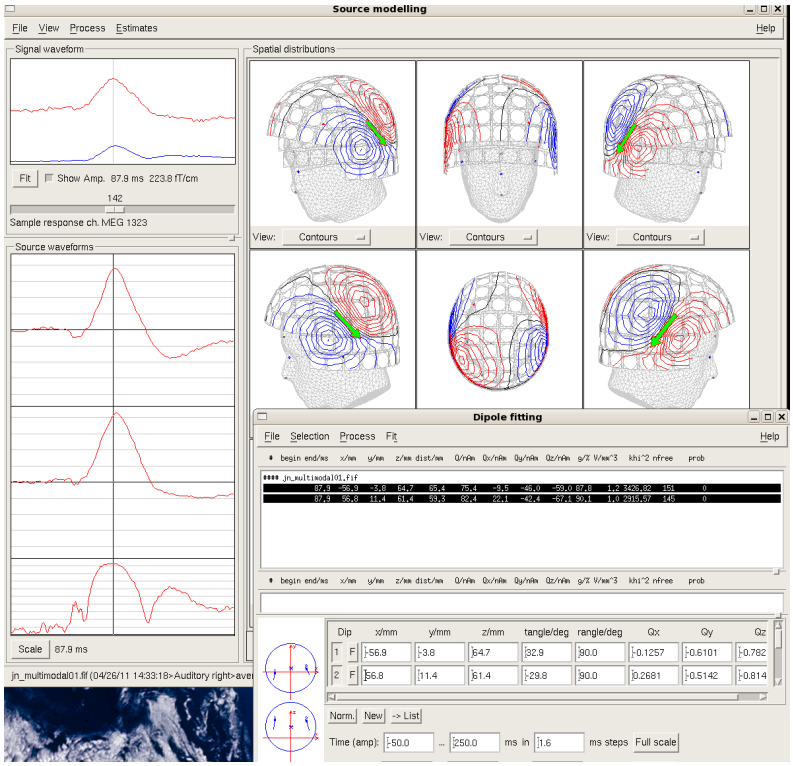


Figure 44: A two-dipole model in *Xfit*.

Note that this is a demonstrative example of a two-dipole model where the dipole locations are first determined using separate single-dipole models for selected channel groups. The locations are then fixed over the amplitude fitting period, and all channels are utilized to determine the time-courses of the dipoles. The full multidipole modelling is beyond the scope of this guideline; see the *Source Modelling Software User's Guide* Chapter 9 for the details.

In general, beware of *interactions* in multidipole modelling. If you have multiple dipoles and their temporal activation curves show similar timing but with opposite polarities, the dipoles may try to explain each other, not real brain signals. Make a multidipole model to explain as much of the data as you think is necessary. Pay special attention to the goodness-of-fit of single dipoles, to the absence of interactions, and to the similarities of the measured and predicted signals (see the next section).

10.3 Characterize a dipole using PCA projections

The dipole fit can also be characterized using a PCA projection.

- After fitting a dipole, select **Process -> Projection…**
- In the Linear projection window select **Add -> Selected dipoles (fixed)**.
- Then inspect the results, select **Use -> Projection, Compliment and Original** to determine residuals that may have different onset latency from the fitted position. See *Signal Processor User's Guide*, Chapter 10 for additional information.

11 Next steps: Inspect and correct the head position

11.1 Head position inspection

If the visual head position inspection (section 4.4) reveals a problem, the following steps provide guidance for trouble shooting and correcting the problem.

The head position in FIFF files is determined by a device->head coordinate transformation. To inspect it, apply the terminal window command `/neuro/bin/util/show_fiff –vt222 filename.fif`. For instance the transformation in Figure 14 is:

```
222 = transform         device -> head
       0.999533 0.030220 -0.004530
      -0.030521 0.994591 -0.099281
       0.001505 0.099373 0.995049
      -1.473818 -4.034752 57.537861 (inv. 1.263396 -1.660221 -57.660248)
```

The last row after the 3x3 rotation shows where is the device coordinate origin in the head coordinate frame. Here -1.47 -4.03 57.54 means that the device coordinate origin is 1.5 mm left, 4.0 mm back and 57.5 mm up from the head coordinate system origin. If the z-value is large (>70 mm), it usually points to a low head position.

MaxFilter GUI and Xfit dialogs for the origin parameters is also useful (MaxFilter User's Guide section 3.2.2 and Source Modelling Software User's Guide section 5.2). When you type the selected origin in the head coordinates, select 'Coordinate system -> device' to display the origin coordinates in the device frame. If the resulting point is >25 mm from (0, 0, 0), the trans-operation in movement correction may increase reconstruction noise.

Head positions estimated from continuous raw data can be viewed in the MaxFilter Graphical User Interface, see *MaxFilter User's Guide* section 4.5. Note: During data collection, cHPI should be selected BEFORE selecting Raw. This ensures the initial position is properly reflected in the display.

11.2 HPI order verification

You can verify the detected HPI coil order in the following manner. Open a terminal window and navigate to the directory where your datafile is located. Issue the following command:

```
/neuro/bin/util/show_fiff -vt247 <filename.fif>
```

This shows the detected coil order, for example:

```
247 = HPI coil order       5 ints (2 5 4 3 1)
```

Note: you need show_fiff version 1.4 or later to display the coil order. Next type the following command to see the digitized points:

```
/neuro/bin/util/show_fiff -vt213 <filename.fif> | more
```

Inspect the first lines which look like the following:

```
213 = dig. point  hpi       1 ( -68.2, -24.7, -50.8)
213 = dig. Point  hpi       2 (  69.8, -25.6, -58.4)
213 = dig. Point  hpi       3 (  54.6,  76.0,  28.4)
213 = dig. Point  hpi       4 (  29.6, 102.5,  24.2)
213 = dig. Point  hpi       5 ( -46.8,  87.2,  24.7)
213 = dig. Point  cardinal  1 ( -67.4,   0.0,   0.0)
213 = dig. Point  cardinal  2 (   0.0, 105.4,   0.0)
213 = dig. Point  cardinal  3 (  67.6,   0.0,   0.0)
213 = dig. Point  hpi       1 ( -46.7,  91.7,  43.8)
213 = dig. Point  hpi       2 ( -67.1, -32.2, -1.6)
```

```
213 = dig. Point  hpi        3 (  32.4, 101.1,  43.9)
213 = dig. Point  hpi        4 (  56.0,  78.0,  34.6)
213 = dig. Point  hpi        5 (  68.0, -35.1,  -1.5)
```

The first five lines give the fitted coil locations in the device coordinate frame, the next three lines show the digitized landmark points, and the following five lines give the digitized coil locations in the head coordinate frame. In this example the fitted coil locations follow the colour-coded hardware order and match the following regions: 1. Left frontal, 2. Right frontal, 3. Right posterior, 4. Middle frontal, 5. Left posterior. By comparing these with the digitized coordinate values, we can judge that the first (blue) coil matches with the second digitization, the second (white) coil with the fifth digitization, the third (red) with the fourth digitization, the fourth (black) with the third digitization, and the fifth (yellow) with the first digitization, thus confirming that the correct coil order 2 5 4 3 1 was used and saved in the file.

11.3 Correct the head position

If the comparison between the fitted and digitized coil locations results in a different order than it was written in the file, the head position can be fitted again with the corrected coil order. Log into the data acquisition workstation, open a terminal window and navigate to the directory where your datafile is located. If you have digitized the coils in the colour-coded order or defined the correct order as in the previous section (for example, 1 2 3 4 5), issue the following command:

```
/neuro/dacq/bin/hpifit -file <filename.fif> -swap 12345
```

This command writes the new head position in a new file `hpi_coils.fif`. Copy the new head position into the FIFF file using the command

```
/neuro/bin/util/copy_trans_fiff -r hpi_coils.fif <filename.fif>
```

Inspect the corrected head position as advised above. If the correction still produces an incorrect head position, you should report the problem to support@megin.fi and request for further advice.

12 Next steps: Optimize MaxFilter Processing

MaxFilter is easy to apply and the default settings provide good results in most cases. The program has a set of parameters which can be adjusted if tuning of the performance is needed. Please see *MaxFilter User's Guide* chapter 3 for detailed description of the parameters and pay special attention to possible warnings associated with changing the parameter values.

12.1 Selecting the task

1. **Determine if *MaxFilter* processing is necessary**
   - Has IAS been ON during the data recording?
     - YES -> SSS or tSSS required.
     - NO -> SSS or tSSS recommended.
   - Are there considerable interference artifacts on the data?
     - YES -> SSS or tSSS recommended.
2. **Select between SSS and tSSS processing**
   - Is there low-amplitude external interference only?
     - YES, external only -> use SSS (tSSS also possible for reducing noise and artifacts).
   - Are there also close-by artifacts or artifacts inside of the sensor helmet, or strong external interference?
     - YES, close-by artifacts -> use tSSS.
3. **Set tSSS parameters**
   - Buffer length usually 10 s; sometimes longer buffer (e.g. 30 s) may be more effective.
   - Correlation limit 0.98; sometimes reduction (e.g. to 0.9) is needed for better interference suppressions.
4. **Select the Head position task**
   - Has cHPI been ON during the data recording?
     - YES, cHPI on -> use head movement compensation.
     - NO -> Not possible to use head movement compensation.
   - When head movement compensation is used, does the initial head position represent well the overall head position in the data file?
     - YES -> head position transformation to the initial head position.
     - NO -> head position transformation to the average head position.
   - When no head movement compensation is used, will there be sensor level comparison of different data sets?
     - YES –> use head position transformation to align the data sets to same position.
     - NO –> no head position transformation needed.
5. **Select movement compensation**
   - Movement compensation usually requires combined tSSS processing.
   - When processing raw data with cHPI signals, the recommended settings are
     - Use initial head position.
     - Movement correction with tSSS.

Warning: If the threshold of the automated bad channel detection is too small, the program may classify good channels as bads, and if it is too high, some bad channels may remain undetected.

Warning: If *tSSS* is applied on averaged data or if there were several saturated or bad channels in raw data, the result must be inspected very carefully.

Warning: The user must judge the result carefully if the *tSSS* correlation limit is lowered from the default value.

Warning: Head position transformation operations require that the initial and reference coordinate transformations are defined correctly.

Warning: Head position calculation errors affect the data quality after movement compensation. The user must inspect the head position fitting error and goodness before data analysis.

Warning: If internal active shielding was applied in the input file, the user must not perform data analysis on MaxFilter™ output files obtained with the maintenance options `-nosss` or `-ctc only`.

Warning: Spatiotemporal signal space separation (*tSSS*) may diminish brain signals arising from very strong, superficial sources.

Warning: Head movements generate physiological background signals due to muscle and motor cortex activation. These disturbances are not suppressed by MaxFilter™ and may deteriorate the source localization accuracy.

Warning: MaxFilter™ cannot suppress movement artifacts in data segments with rapid head movements, such as those arising during motor seizures. Movement artifacts may deteriorate the localization accuracy of the system.

12.2 General recommendations for successful MaxFilter processing

- Generally, (t)SSS and movement compensation give robust performance for suppressing the interference and disturbances cause by head movements when the head is placed well inside the helmet. Then the choice of the origin does not play a significant role, and the recommendation to use the origin according to a sphere fitted to isotrak points or MRI data is aligned with the spherical head model definition in source modelling (see section 4.3).
- The head should be well positioned inside the helmet. This can be inspected during an HPI measurement by checking the measurement Head origin (see the Data Acquisition Guidelines Chapter 7). If the absolute value of the z-value is > 70 mm, the subject head may be too low in the helmet. See also Chapter 11.
- Transforming the head position more than 25 mm shows increased noise on some MEG channels. It you suspect the subject has move a lot during the recording, it may be helpful to take an HPI fit at the end and compare the positions. This would require that you take note of the position at the beginning of the measurement as well.
- MaxFilter checks for quality HPI fit. If poor fits are present, then movement compensation can create noise in the recording. If you suspect poor fits, it is helpful to take an HPI fit at the end of the recording for quality control. HPI can be measured and saved with a very brief recording.
- Whenever possible, the patient sphere origin should be use instead of the default position for all MaxFilter processing.

13 Next steps: Topics for using Graph standard setups

This section complements the *Graph* manuals and contains detailed instructions for using two general *Graph* setups: i) Basic setup for simple data viewing, and ii) Comparison setup for opening and viewing data from two datafiles.

The basic operations of *Graph* are described in detail in the *Signal Processor User's Guide* section 1.2. The basic setup is available when the Data Analysis software has been installed. The reader is suggested to consult the Signal Processor User's Guide (Part 2) for more detailed explanation of Graph setups and widgets.

13.1 Review data with *Graph* basic.setup

After applying pre-processing to a raw dataset, it is recommended to visually review the results to confirm proper automatic detection and correction of interference artifacts.

- Open Applications -> Neuromag -> *Graph* (Figure 45). The *Graph* display shows text 'Nothing connected'.

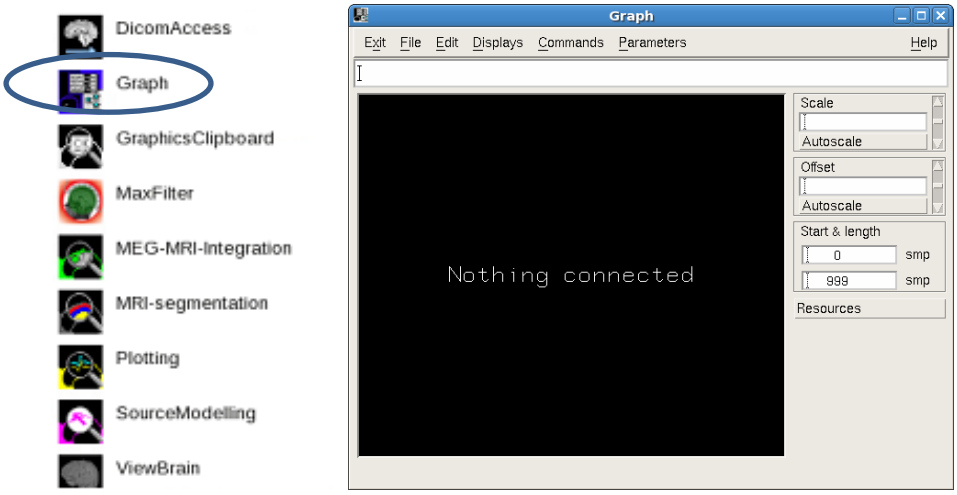


Figure 45: *Graph* launching and initial display.

- Select **File -> Load settings**, select `~HOME/lisp/setup/examples/basic.setup`.
- Select **File -> Open Diskfile** and load a *MaxFilter* -processed raw datafile, e.g. *_raw_sss.fif. (Note: this review needs to be repeated for all the pre-processed files).

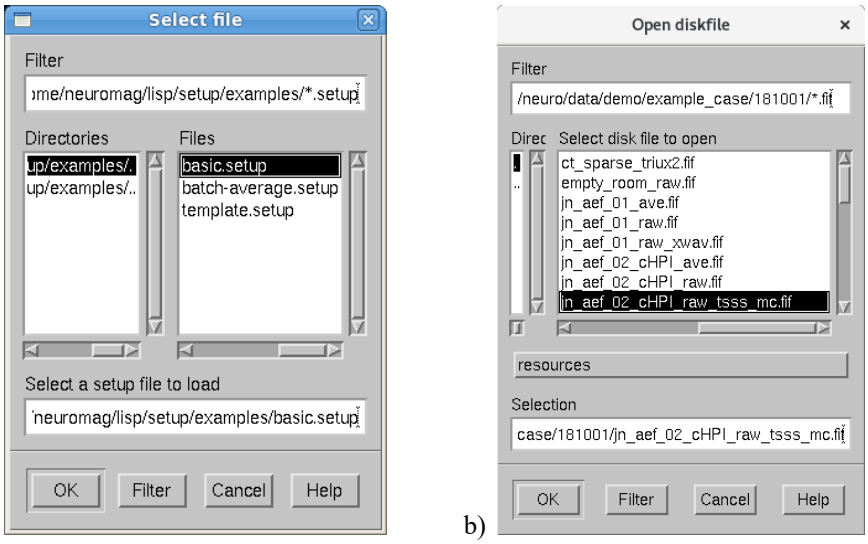


Figure 46: a) Select the basic.setup file. b) Select a FIFF datafile.

13.1.1 Review the *Graph* display

- The main display shows now a set of MEG channels (Figure 47).
- Adjust the channels: **Displays -> Selection (Alt-d + m)**, select a channel group. To keep the selection menu open, select the dashed line as the top of the menu (**Selection Tear-off**).
- Change the display time: adjust using the slider at the bottom of the display, or by typing values in the fields **Start & length.**
- Adjust the amplitude scales using the **Scale** and **Offset** controls in the upper right corner of the dialog.

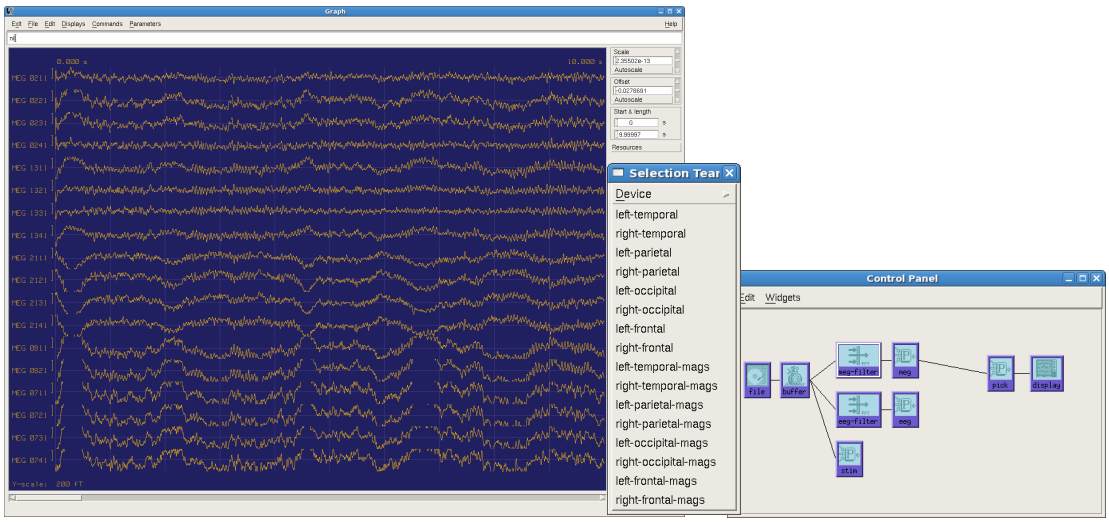


Figure 47: *Graph* display when the basic.setup and a FIFF file have been loaded. The channel selection menu is opened from Displays -> Selection. The control panel is shown on the right.

- Select **Displays -> Control panel** to view the widgets in this setup. Double-click on a widget to see the resources (see the *Signal Processor User's Guide* sections 2.2-2.4 for details).
- If the datafile has EEG channels, you can select them instead of MEG: right click on the widget **eeg** in the control panel, keep the right mouse button pressed, drag a connection from widget **eeg** to widget **display**, and adjust the amplitude scale.

13.1.2 Adjust the time scales

- Note: this section does not apply to TRIUX™ neo data. FIFF files recorded with Data Acquisition Software release 6.0.5 (or later) do not contain initial data skip tags.
- For older acquisitions, using **compress-skips** allows for all initial data skip tags between pressing the GO button in data acquistion and starting saving raw data are neglected. Thus, the raw data time scale in the display usually starts from 0.
- Select **File -> Open Diskfile**, select the button **resources** in the file selection dialog (Figure 46b). By default, **compress-skips** is active (Figure 48).
- However, the initial skips are meaningful when the data viewing time scale must be the same as in *MaxFilter* (see *MaxFilter User's Guide* section 2.6 for details of the raw data time scale). In such cases you need to deactivate the button **compress-skips**.

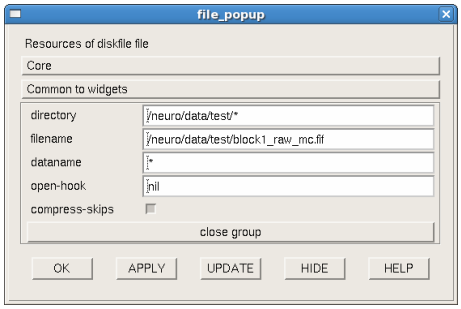


Figure 48: Compress skips.

13.1.3 Adjust the filtering

- Select **Displays -> Control panel (Alt-d + c)** and double-click on widget **meg-filter** (or **eeg-filter**) to adjust the filter settings. The details of the filtering are presented in the *Signal Processor User's Guide* section 4.2. In brief, you can set high-pass, low-pass, or band-pass by typing in the text field next to **pass-band** (Figure 49).
- Enter `(band-pass 1 100)` in the **pass-band** field.

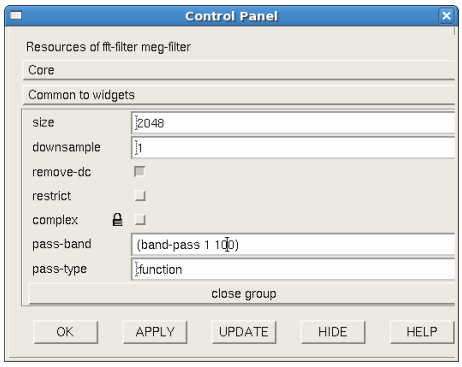


Figure 49: Adjust the filtering parameters.

- Available options are
  - `(high-pass <corner> [<transition-width>])`
  - `(low-pass <corner> [<transition-width>])`
  - `(band-pass <corner1> <corner2> [<transition1>] [<transition2>])`
  - `nil` (= no filter)
- In addition, button **remove-dc** affects like a high-pass filter which has the lowest possible corner frequency. If **pass-band** is `nil`, **remove-dc** has no effect.

13.2 Compare two files with *Graph* compare.setup

Sometimes it becomes necessary to compare MEG data in two files visually, either by looking the same data before and after *MaxFilter* -processing or by viewing two comparable data sets. Therefore, the **compare.setup** is useful because it provides the controls and connected displays to open and view two datafiles in synchronized manner.

- Select **File -> Load settings**, select `~HOME/lisp/setup/local/compare.setup`.
- The *Graph* display shows two synchronized windows (Figure 50). The control panel has separate controls for both windows (Figure 51).

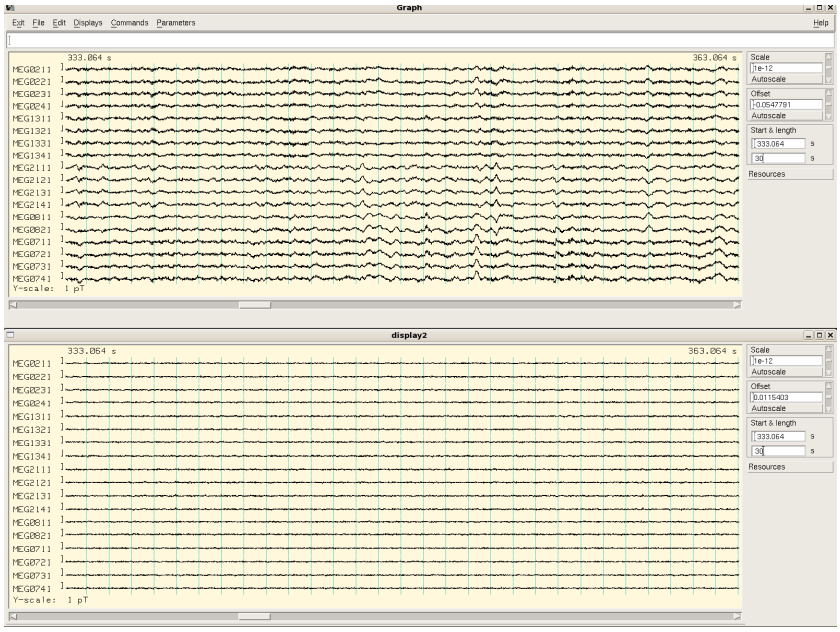


Figure 50: *Graph* displays in compare.setup. The windows are connected so that changing the channel selection or time point on one display automatically adjusts also the second one.

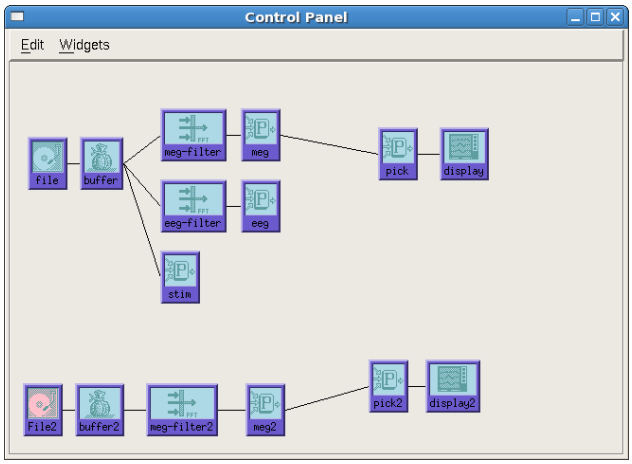


Figure 51 : The control panel for compare.setup.

- A typical comparison is between original and pre-processed data, such as the raw data before and after *MaxFilter* processing.
- The selections in the *Graph* menus, e.g. **File** and **Displays** affect the first source **file.**
- Open the first source file from **File -> Open Diskfile**, select a raw file (*_raw.fif).
- Open the second source file by double-clicking widget **file2** and select a *MaxFilter* -processed file (*_raw_tsss_mc.fif).

- Channel selections **Displays -> Selection** affects both windows.
- The time scale is the same for both files whether **compress-skips** is active or not.
- Ensure the amplitude and time scales and filter settings are similar in both windows.
- Note that when changing the channel selection from gradiometers to magnetometers (and vice versa), it is necessary to adjust the amplitude scales in both windows.
- If the source files originate from different data sources, their time scales may be different. Activate **compress-skips** in the widgets **file** and **file2** on the control panel, if needed.

13.3 Add or remove SSP vectors in a Graph display

When *MaxFilter* is not applied, the spatial SSP vectors saved in the recorded file can be used for interference suppression.

- To apply Signal Space Projection (SSP), add an SSP widget by typing on the command line below the menus in the *Graph* display (Figure 52):
  `(require "ssp")`

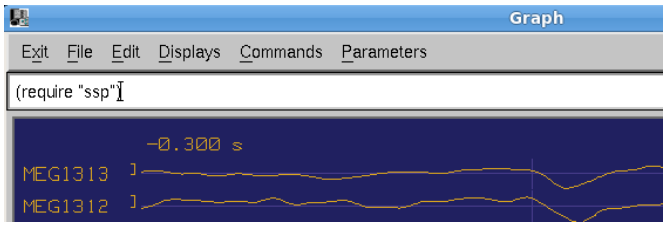


Figure 52: Add the ssp widget to a Graph setup.

- Select **Displays -> Control panel (Alt-d + c)** and link widget **ssp** (Figure 53):
  - Drag widget **ssp** between widget **meg** and widget **pick.**
  - Select widget **meg**, right-click and connect to widget **ssp.**
  - Select widget **ssp**, right-click and connect to widget **pick.**
- Select **Commands->SSP dialog**… to open controls for loading and activating SSP vectors.
- Select **File->Load** to select the raw file from which to load the SSP vectors.
- Select vectors on the left panel of the **SSP vectors** dialog and click the arrow **(->)** button to make them active (Figure 54). The vectors can be turned on and off using the buttons **On** and **Off**. The label on the right column then indicates SSP vectors ON or SSP vectors OFF.

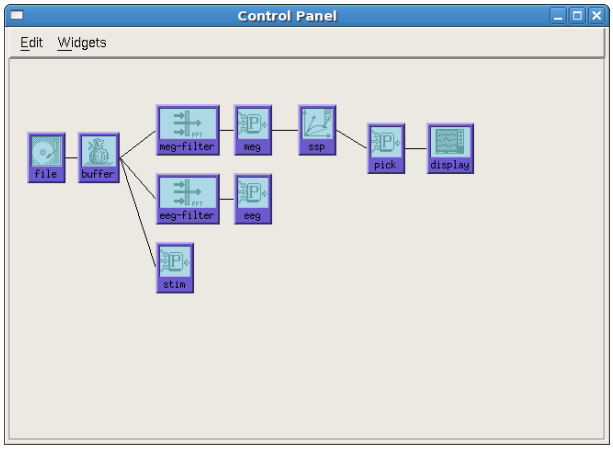


Figure 53: Link widget ssp in the control panel between 'meg' and 'pick'.

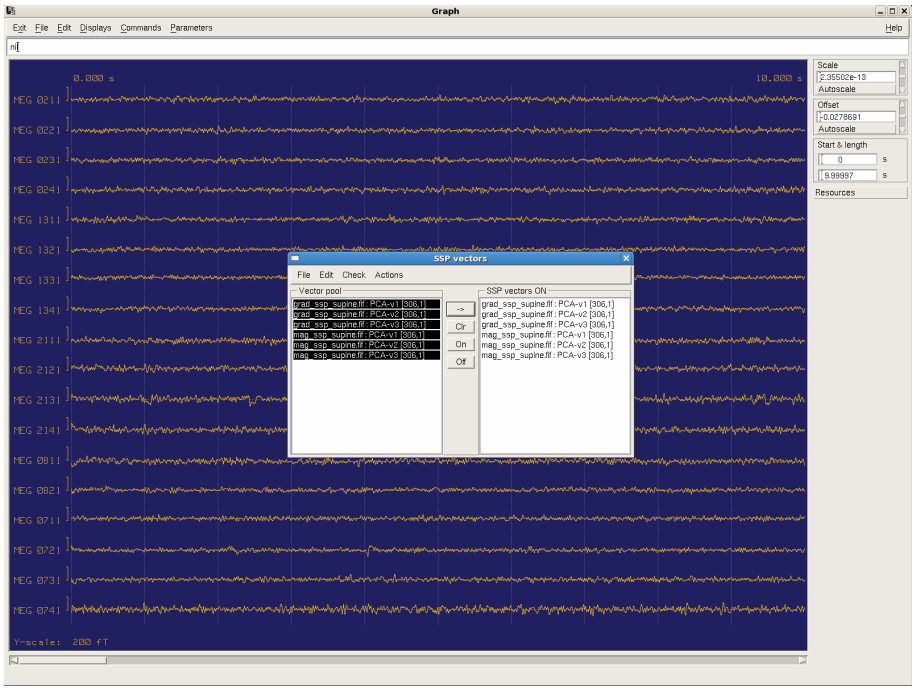


Figure 54: Select Commands ->SSP dialog to load and activate the SSP vectors.

13.4 Connect Xfit to Graph setup

Working with the plotting and source modelling programs (*Xplotter* and *Xfit*) can be done by selecting a time window of raw data and making an evoked file (**File -> Make evoked file**).

It is, however, more convenient to apply special lisp routines "*xplotter.lsp*" and "*xfit.lsp*" which makes direct data transfer from *Graph* to *Xplotter* and *Xfit*. See the *Signal Processor Reference manual* for detailed description of the *xfit* and *xplotter* items.

- If *Xfit* and *Xplotter* modules are not included in your setup (i.e. not listed in the Displays menu), type on the command line: `(require "xfit")`
  This will add item "*xfit…*" in the **Displays** menu.
- Select **Displays- > xfit -> Start xfit**.
- Select **Parameters -> misc-defaults** to change the **default-data-source** which defines the channels for the data transfer.
- Double-click the data source (e.g. widget **meg**) to edit the **names** field and specify the channel selection. For example, selection "`MEG *`" sends the data on all MEG channels.
  If the file has EEG data and you wish to see them in *Xfit*, type a second line "`EEG *`".
- Use the right mouse button on the Graph waveform display to select a short time interval.
- Select **Displays- > xfit -> Transfer selection** to send the selection from *Graph* to *Xfit* (an example is displayed in Figure 58 below).

13.5 Connect *Xplotter* to Graph setup

- Type on the command line: `(require "xplotter")`
  This will add items "*xplotter…*" in the **Displays** menu.
- Select **Displays- > xplotter -> Start xplotter**.
- Use the right mouse button on the Graph waveform display to select a short time interval.
- Select **Displays- > xplotter -> Show selection** to send the selection from *Graph* to *Xplotter.*

13.6 Adjust parameters in a Graph display

- Select the **Resources** button on the right side of the main display to access the parameters controlling the display appearance (Figure 55).

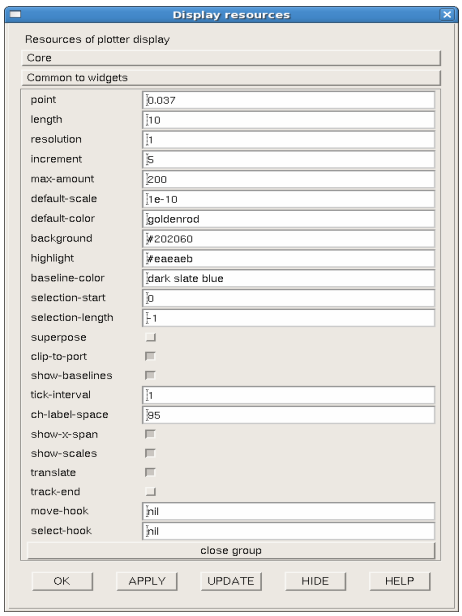


Figure 55: Graph display resources.

- Edit the values to change the appearance of the display (see the *Signal Processor User's Guide* section 2.4 on page 40 for detailed description of the display widget 'Plotter' resource parameters).
- Enter `snow` in the **baseline-color** field to change the color of the markers on the display.
- Available colors are listed in text file `/usr/share/X11/rgb.txt`.

13.7 Compute instantaneous spectra using Graph spectra.setup

Calculation of frequency spectra is described in the *Signal Processor User's Guide* section 4.4. Here we show two setups for evaluating and displaying frequency spectra from a selected piece of the raw data or by averaging the spectra over longer time intervals.

- Select **File -> Load settings**, select `~HOME/lisp/setup/local/spectra.setup`.
- Adjust the two *Graph* displays to fit on the screen (Figure 56).
- Select **File -> Open Diskfile** and select a raw FIFF file `(*_spont_EC_02_raw_sss.fif)`.
- Select **Displays -> Selection (Alt-s + m)** to pick the `left-occipital` MEG channels to show in both windows.
- Select **Displays -> Control panel (Alt-d + c)** and double click widget **meg-filter**.
  Set **pass-band** field to `(low-pass 40)`.
- Change the display time **Start & length** to change the time in the top window and the frequency spectra results in the bottom window.

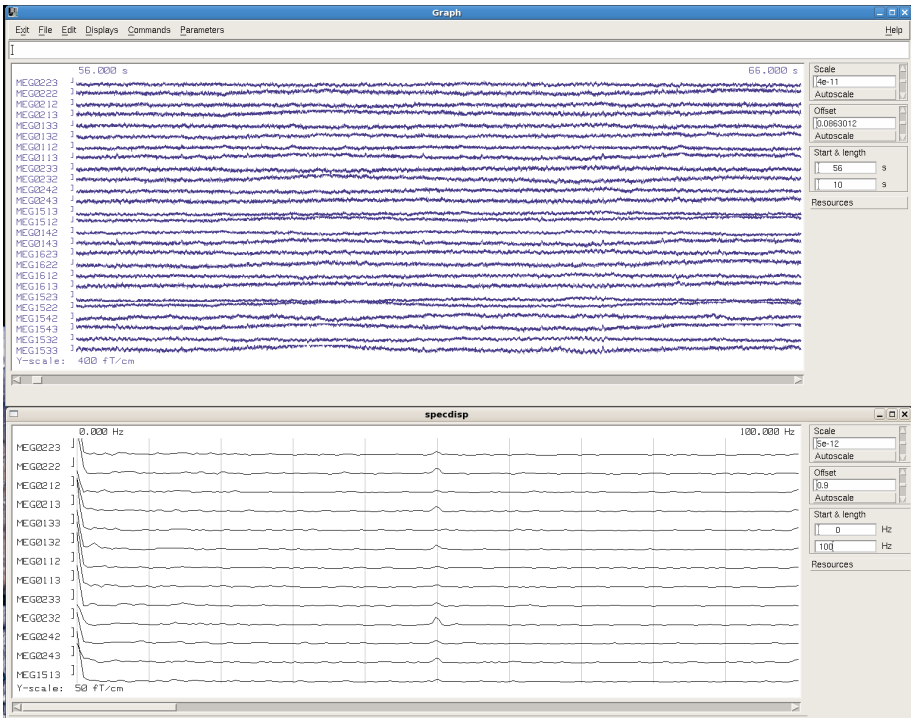
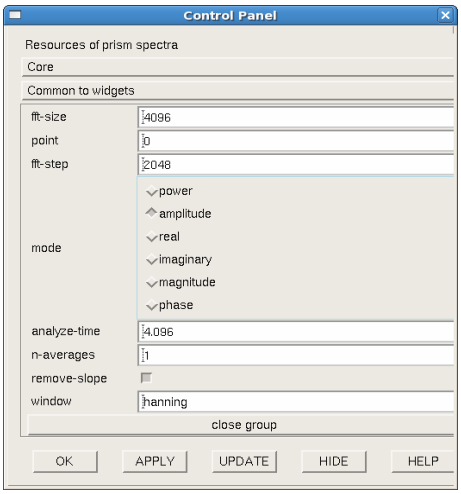


Figure 56: *Graph* displays of spectra.setup. The upper window shows the raw data signals on selected MEG channels, and the lower window displays their frequency spectra computed from the beginning of the time scale in the upper window.

- Select **Displays -> Control panel (Alt-d + c)** to change the FFT length and averaging step:
  - Double-click widget **spec** and adjust **fft-size** and **fft-step** if needed (`fft-size = 4096, fft-step = 2048` in Figure 57a).
  - Double-click widget **win** to set **Start** and **End.** Note that the window length (defined by **start** and **end**) must be longer than **analyze-time** value (`Start = 0, End = 4.1` in Figure 57b).
  - Click **Apply.**

a)



b)

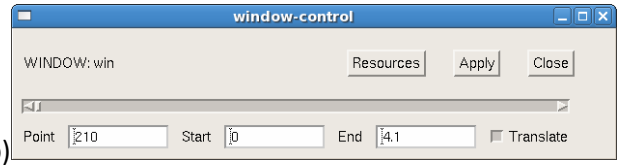


Figure 57: Changing a) the FFT and b) the window parameters for evaluating the spectra.

13.8 Practice example: alpha waves

In this example, both instantaneous spectra in *Graph* and **View -> Full view** display in *Xfit* show clear alpha oscillations. The timepoint selection at one of the peaks displays a bipolar field pattern in the left occipital region.

- Review the spectra in the lower window of Figure 56. Set `Start = 0` and `length = 40`. Notice the increase in 8-10 Hz alpha power.
- Connect to *Xfit* by typing the command `(require "xfit")` in the command window (see *View spatial distributions*, section 5.1.5).
- Scan through the data and select a time window of recording containing alpha waves.
- Select **Displays -> xfit -> Transfer selection** (Figure 58).
- *Xfit* will show the origin selection dialog. If you don't have the origin fitted to anatomy in *Mrilab*, you can always use the default origin 0,0,40.
  Note: make sure to select the **Head coordinates** (cf. Figure 26).
- Review the spatial displays. In this example, both instantaneous spectra in *Graph* and **View -> Full view** display in *Xfit* show clear alpha oscillations (Figure 59). The timepoint selection at one of the peaks displays a bipolar field pattern in the left occipital region.

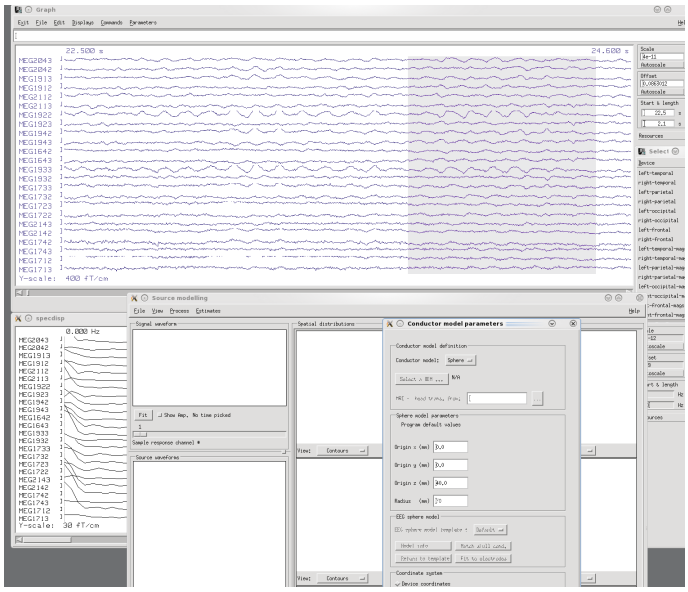


Figure 58: Sending data from *Graph* to *Xfit*.

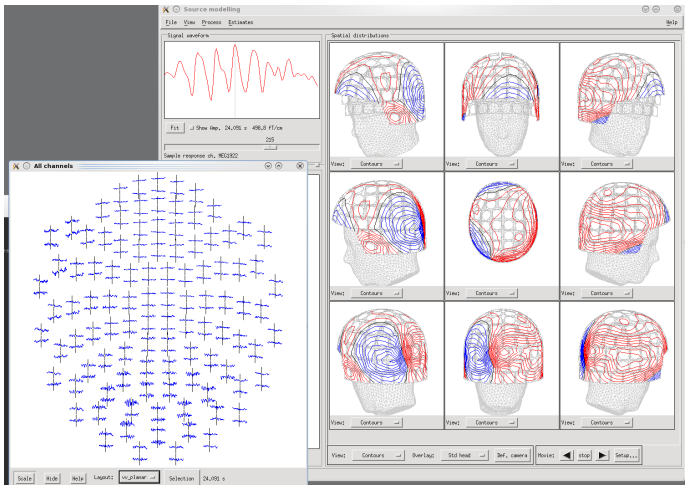


Figure 59: *Xfit* displays of alpha waves.

13.9 Compute averaged spectra using Graph ave_spectra.setup

- Select **File -> Load settings**, select `~HOME/lisp/setup/local/ave_spectra.setup`.
- Adjust the two *Graph* displays to fit on the screen (Figure 60). An *Xplotter* window is also opened for displaying a topographical view of the averaged spectra (Figure 61).
- Select **File -> Open Diskfile** and select a raw FIFF file (*_raw_tsss_mc.fif).
- Select **Displays -> Selection** to pick the left-occipital MEG channels to show in both windows.
- Change the display time **Start & length** to change the time in the top window and the frequency spectra results in the bottom window.
- To display average spectra, type the following lisp-command on the command line below the menus and press enter:

```
(average <start> <end>)
```

- The start and end times are given in seconds and must be consistent with the earliest and latest time in the file.
- You can use the *Xplotter* controls in the **Process** and **View** menus to change the amplitude and time scales and channel layouts, e.g.
  - Time (ms): `0.0 … 100000` to set the frequency from 0 to 100 Hz.
  - MEG (fT/cm): `0 … 20.0` to set the amplitude range (the spectra have only positive values).
  - Axial mult.: `4.0` to set the relative vertical scale between magnetometer and gradiometer channels.

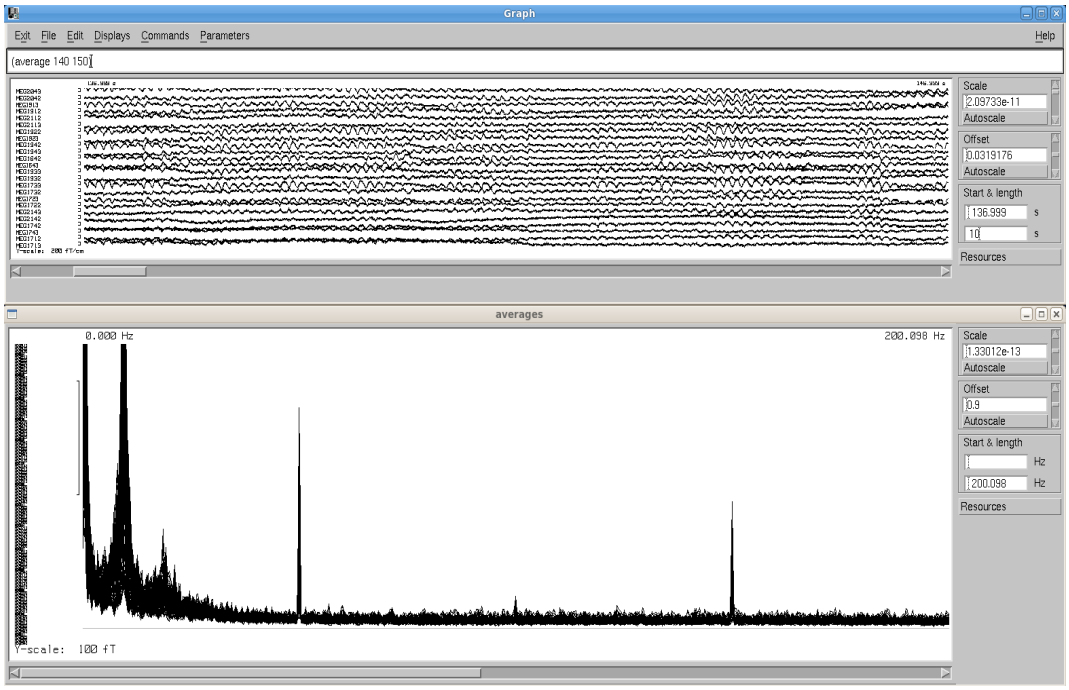


Figure 60: *Graph* displays in ave_spectra.setup. The upper window shows the raw data signals on selected MEG channels. The lower window displays superposed frequency spectra from all left occipital channels averaged between 140 and 150 seconds.

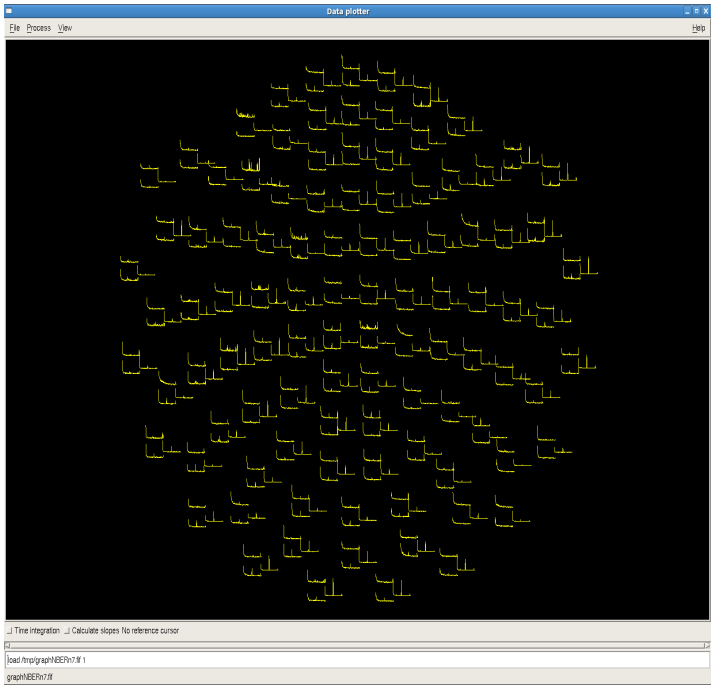


Figure 61: *Xplotter* display shows the updated frequency spectra during and after averaging.

- Select **Displays -> Control panel (Alt-d + c)** to adjust the parameters and views (Figure 62).
- To display averaged gradiometer spectra instead of magnetometers, connect the selector widget **grads** to the display widget **averages**, and adjust the amplitude scale in the display.

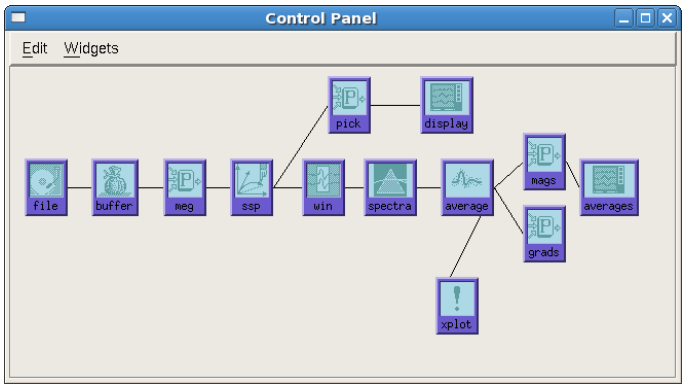


Figure 62: Control panel in ave_spectra.setup.

- Double-click on the prism widget **spectra** for adjusting the FFT parameters. The details are explained in the *Signal Processor User's Guide* section 4.4.
- To save the averaged spectra, type the following lisp-command on the command line below the menus:

  ```
  (save-average)
  ```
- It opens a file selection dialog for setting the output directory and filename.
- Optionally, enter the output file directly by typing the path and filename after *save-average*. For example, the following command will save the averaged spectra in an evoked-format file *amp_spectra.fif* under */neuro/data/demo/example_case/180613*:

  ```
  (save-average "/neuro/data/demo/example_case/190613/amp_spectra.fif")
  ```
- Saved spectra can be opened and overlaid in *Xplotter*, like in Figure 61.

14 Next steps: Topics for using Graph epilepsy setups

14.1 Overview of *Graph* setup epilepsy-2.3

Both *Graph* setups presented in this guideline (epilepsy-2.3 and epilepsy-3.3) provide the same functionality, but with difference interfaces. The spike search in epilepsy-2.3 displays only the gradiometers, while epilepsy-3.3 (see Section 7.1) shows both gradiometers and magnetometers. Both setups use all channels for source modelling.

- Open **File -> Load Settings** and select setup file `~HOME/lisp/setup/local/epilepsy-2.3.setup`.
- **File -> Open Diskfile**, select file `sim_spikes_raw_sss.fif`.
- The epilepsy spike search setup is shown in Figure 63.

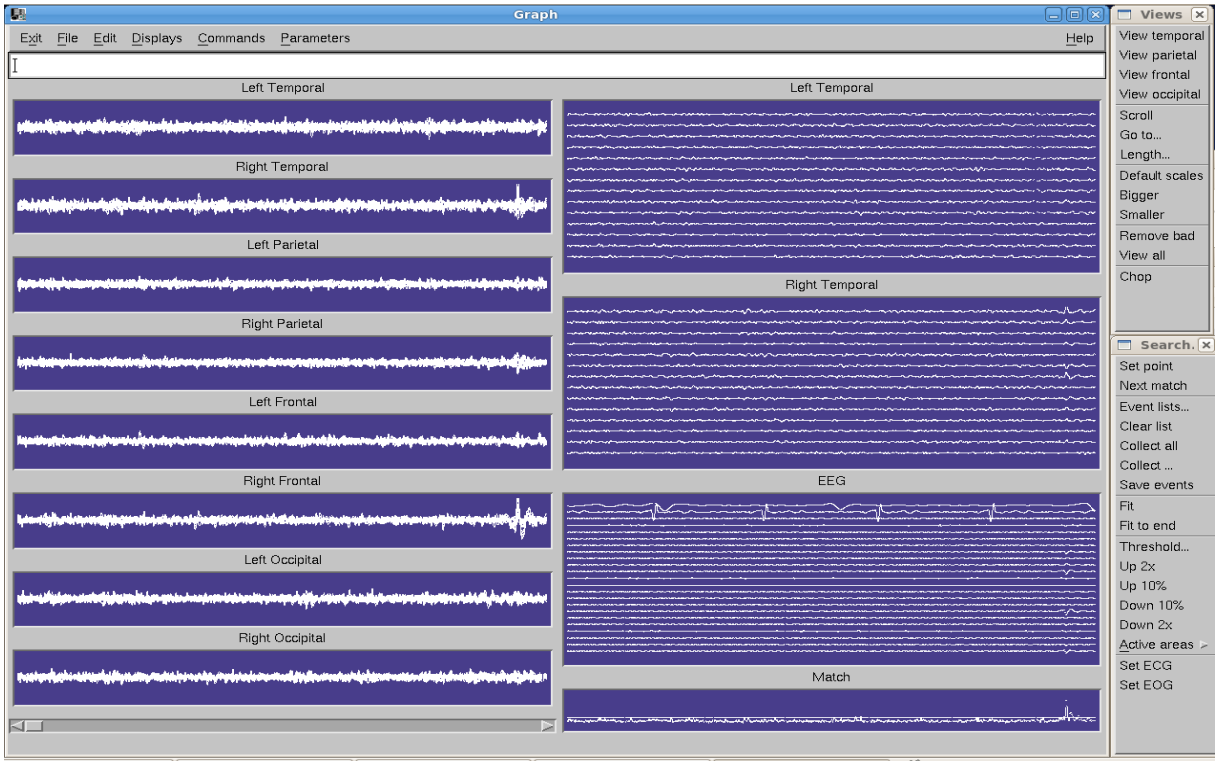


Figure 63: *Graph* epilepsy 2.3 setup and tear-off menus.

- MEG gradiometer channels are superimposed and grouped into eight groups shown on the left.
- Selected groups of channels trace by trace are shown in the top two displays on the right.
- EOG, ECG, and EEG signals are show in the third panel down on the right.
- A processed "match" signal used in the spike search (see Appendix B: Quick reference for *Graph* Epilepsy setups, 16.6) is shown in the bottom right display. In addition, a threshold is displayed that is used for automatized spike event search.
- The scroll bar on the bottom of the left side is used to move the view to different time ranges.
- Menu selections **Displays->Views, Parameters->Displays** and **Commands->Search** are explained in detail in Appendix B: Quick reference for *Graph* Epilepsy setups (chapter 16).

- Detach tear-off menus **Displays->Views** and **Commands->Search** by clicking the dashed line in the list so that it will remain open and on top of screen (Figure 63). Note that all the menus that have the dashed line work the same way.
- Select **Displays-> Views -> View temporal, parietal, frontal,** or **occipital** to change the right column views of Figure 63.

14.2 Define bad channels and threshold for artifact rejection

- Examine the MEG and EEG channels on the displays to find if there are very noisy or jumping channels.
- Select the bad channel(s). Select **Displays -> Views -> Remove bad**. Repeat with all groups until all bad channels are removed.
- Note: files processed properly with *MaxFilter* (such as `sim_spikes_raw_sss.fif`) should not have bad channels. If there are notable artefacts like spikes or step-like jumps, you may need to inspect the original data for determining the bad channels and reprocess the data with *MaxFilter* (see section 13.1).
  Adjust the threshold levels for EOG and ECG artifact rejection. Note that this works only when EOG and ECG are included in the datafile, see section 16.5 to ensure ECG-blanking is set. Select a time span which contains a beat or two, then select **Commands -> Search… -> Set ECG**. The threshold level for detecting ECG peaks is set to 70% of the maximum signal value in the ECG channel within the selected interval.
- The value is not saved and is updated if a new selection is made and used to set ECG. This should be repeated for EOG.
- After performing the spike search, it may be necessary to evaluate how well the ECG/EOG detection worked and adjust as needed. Events categorized with "`corrupted-ecg`" or "`corrupted-eog`" are rejected because they overlap with ECG and/or EOG events.

14.3 Create SSP projector for suppression of cardiac signals

- Observe the **ECG signal** (bottom panel).
- If cardiac artifact exists in the data and you wish to suppress it, PCA is provided for this.
- An SSP projector can be created to suppress the artifact.
  - Select a time selection that clearly represents the artifact (right-click and drag).
  - Select **Commands -> PCA on selection.**
  - The program produces three PCA choices for 1/3/5 SSP vectors in the **SSP Vectors window.**
  - Select e.g. **PCA [306,3]** (Figure 64a), apply (**->**) and inspect the data in the signal displays to assess the efficacy of the cardiac signal suppression.
  - Note: The same SSP projection must be applied also in source modelling. However, *Graph* does not transfer the projection together with MEG-EEG data when an epoch is transferred to *Xfit*. Therefore, save the SSP projection to a FIF-file (**File -> Save**).
  - The SSP saving directory is defined in **Parameters -> Misc defaults -> ssp-vector-directory** (default /neuro/ssp).
  - Load the saved SSP vectors in *Xfit* (**Process -> Projection -> File -> Open,** Figure 64b).
  - *Xfit* will keep the vectors for new epochs from the same file if you paint the SSP vectors and select **Edit -> Set permanent** on the *Xfit* Linear projection dialog.

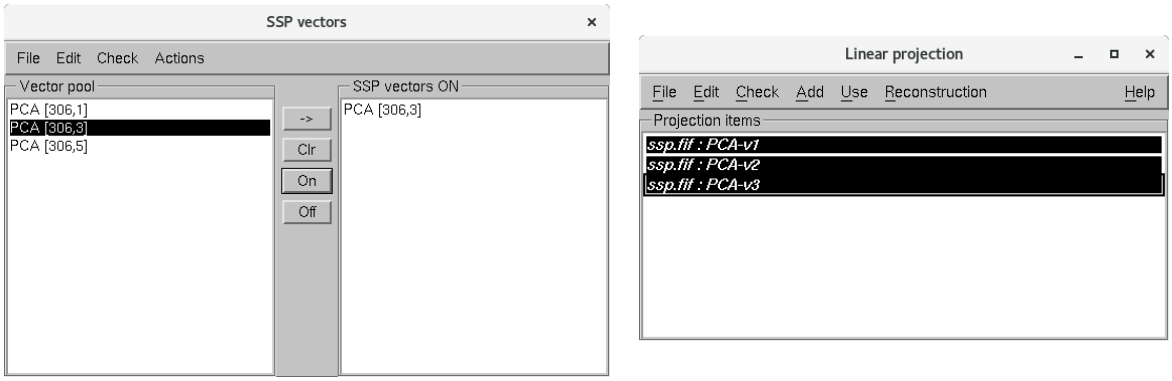


Figure 64: a) Select 3 PCA components for the SSP. b) Load SSP in Xfit.

14.4 Automated event search

14.4.1 Review the "match" signal

The "match" signal is used for detection of high amplitude events, typically spike-like activity (see Appendix B: Quick reference for *Graph* Epilepsy setups, 16.6 for details).

- The spike search setup is configured to calculate the gradient signal power in 14 different brain areas.
- The "match" signal shown in the display is composed of the maximum local absolute average values of these signals and is used for triggering in the search.
- The "match" signal is effective for detection of high amplitude signals in any of the channel groups, even those not displayed on the current MEG channel selection.
- Adjust the trigger level shown in the lower right corner to suitable level using **Search... -> Threshold... -> up/down 10 %, up/down x2** menu. If there is nothing interesting in the current view, scroll through the data, or adjust the level to the maximum of the background activity.

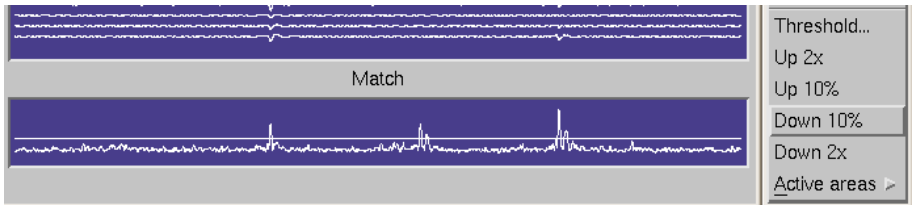


Figure 65: The signal and threshold level shown in the "Match" display. The threshold adjustment menu is shown on the right.

14.4.2 Search for events with spike search

Spike search is controlled from the tear-off menu **Commands -> Search…** (see Appendix B: Quick reference for *Graph* Epilepsy setups, 16.4). It contains buttons that are used to define the search procedure.

- Use the right mouse button to select a time point where scanning should begin, select **Search… -> Set point**.
- Select **Search… -> Next match** to search for the next event where the "match" signal exceeds the current trigger level. Check that this is reasonable.
- If needed, change the threshold **Search… -> Threshold... -> up/down 10 %, up/down x2.**

Figure 66: "Match" signal with event highlighted after detection. Selecting the "Next match" button will select the next trigger event.

- By default, all channels are included in the search. To select a subset of channels for using in the spike search, use **Commands -> Search… -> Active areas.** Select only the regions of interest and de-activate other regions.
- Use **Displays -> xfit…** menu to transfer the current data to *XFit* for spatial viewing and setting of the fitting parameters. For description of this menu see "*Graph Reference Manual*" chapter *XFit*.
- To list the events that are larger than the threshold, use **Commands -> Search -> Collect all** for the whole file.
- For specified time windows, use **Commands -> Search -> Collect** and give specified time window for events.
- The scan can be interrupted using the **Cancel** button in the working dialog only if the routine can find some events. If the trigger level is very high, the whole file would be scanned even if **Cancel** is pressed.
- When a spike event is found, a classification routine is run. By default the event is labeled with symbol `:ok` , but several other classifications may also appear (Appendix B: Quick reference for *Graph* Epilepsy setups, 16.6).
- The events are listed in the **Search -> Event lists…** utility (tagged with `:ok`). The time point recorded is the maximum of the first peak in the data interval that exceeds the limit.
- Review the events by double clicking them, one at a time, or using the arrow keys and Enter to select.

14.5 Filter and sort events using the event list

The event list utility provides an editor which allows sorting and filtering the event list (Figure 67).

- All events detected during the spike search are listed in the primary event list (left column). After the spike search, this list can be saved to disk for later study, or a subset of the events can be transferred to a filtered event list (right column).
- In addition, previously saved events can be loaded into the event list by selecting **File -> Load** and selecting a `*.evl` file.
- Each line in a list corresponds to one event. It shows the time and amplitude of the trigger point and the classification of the event.
- Selecting the **ok->** button sends all events labeled `:ok` to the Filtered events list.

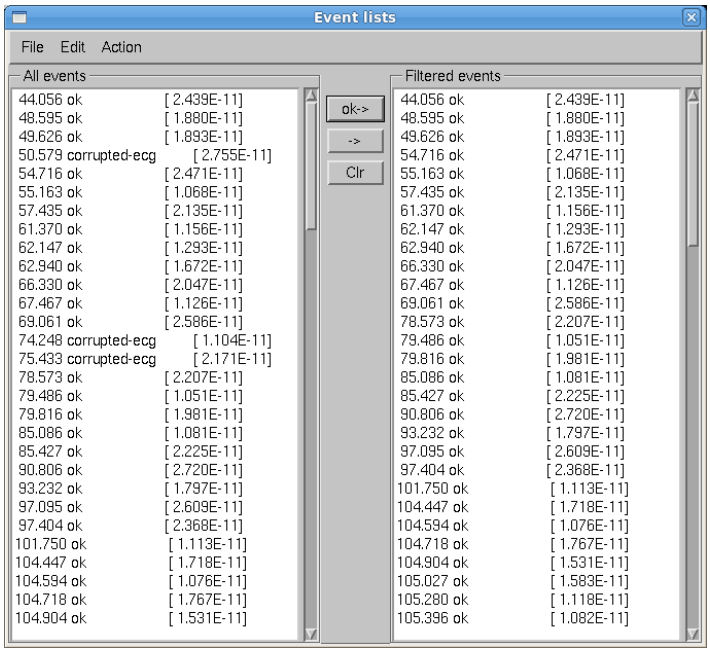


Figure 67. Event lists.

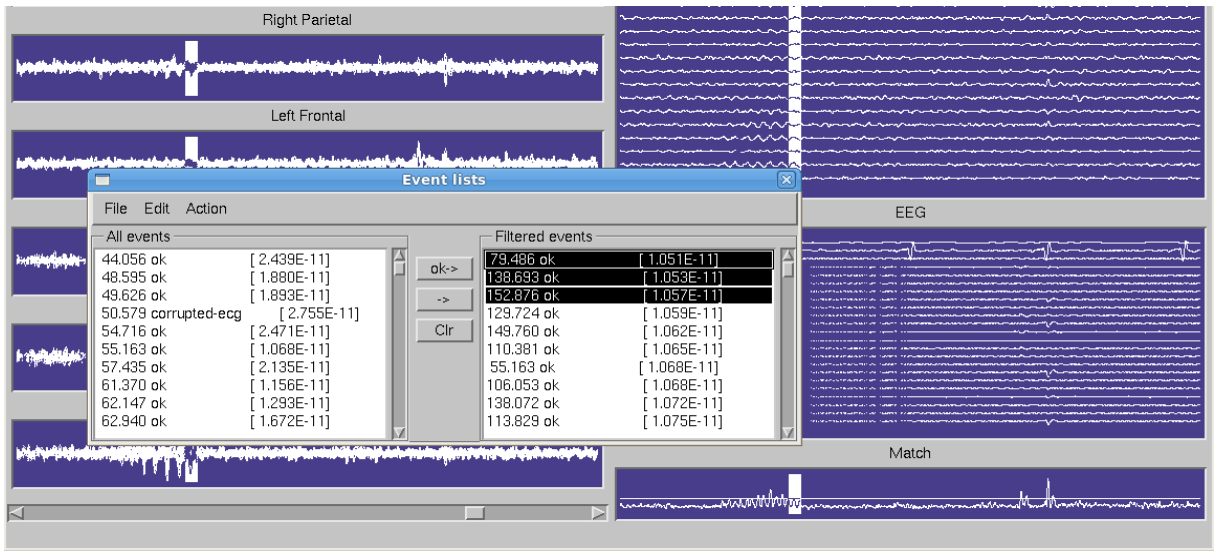


Figure 68: The Filtered events have been sorted by amplitude and the first three in the are selected for deletion because they are not suitable events, as seen in the lower right “Match” window.

- Confirm that the event is a spike or other epileptic activity by viewing the MEG signals. Select the events by double clicking them one at a time or using the arrow keys and **Enter**.
- The highlighted selection can be transferred to *Xfit* for review of the field maps or open the **xfit -> View -> Full view** and see the topographical view of the selection.
- Select **Edit -> Sort by amplitude.**
  - Examine small and large amplitude events to identify suitable amplitude range for fitting.
  - If the trigger level was slightly too low (many “false positives”), throw away the smallest amplitude events by selecting them and pressing **Clr** button.
  - Examine also the largest amplitudes for possible artifacts.

When a suitable range of amplitudes is selected, save the event list for documentation, **File -> Save filtered events**, and proceed to dipole fitting.

14.6 Classify events

It may be necessary to classify the events into different categories (with an event tag) if they arise from different areas, have differing field patterns or waveforms. This is particularly important if the events will be averaged later.

- Assigning an event tag can be done while marking events manually: **Commands -> Search -> Manual marking -> Event-A/B/C**
- To change an event tag after spike search to event type A/B/C, double click the event tagged with **:ok**, then select **Commands -> Search -> Manual marking -> Event-A/B/C.** The event type is changed in the All events panel on the left.

14.7 Average, save and load events

The event lists allow averaging of filtered events. Note that only events that can be assumed to arise from a same source should be averaged, and you should perform event classification before averaging.

- Review the events and move the good events into the filtered events in Event lists one by one or by selecting a list them, then press **->** (Figure 69).
- If more than one event type is listed in the filtered events they will be grouped and averaged according to their tag.
- By default, the averaging window is -100...100 ms with respect to the selected time point.
- To change this window: **Display -> Control panel** and double click average-A (and/or B, C) widget and change the start/end time.
- Average the event(s): **Event list -> Action -> Average filtered.**
- Review the averaging information window (i.e. number of events).
- Review the average-A in the *Xplotter* window (may be behind the *Graph* window).
- Save the averages from Event list: **File -> Save event averages.**
- Transfer to xfit: **Action -> Show average A** (or B/C).

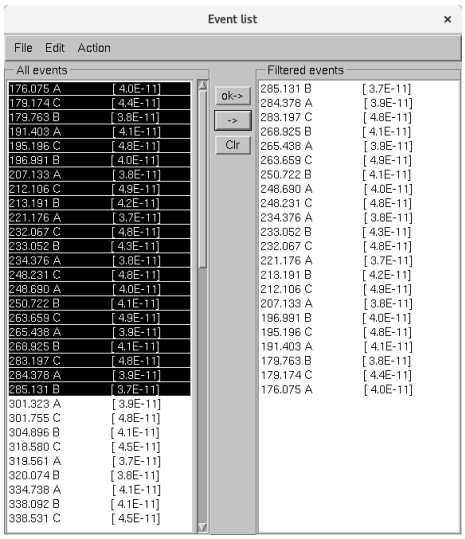


Figure 69: Transfer classified events to Filtered events list.

- To load existing marked events , open the event list: **Commands -> Search -> Event lists**.
- In the Event lists window: **File -> Load events**, select an existing event file (`*.evl`).

14.8 Source modelling on averaged events

- Use the *Xfit* connected to *Graph* or start *Xfit*: **Displays -> xfit -> Start xfit.**
- Create average waveforms from Event lists (see section 14.7) and send to *Xfit*: **Action -> show Average-A (or B/C)**
- Alternatively, open a saved averaged file in *Xfit*: **File -> Open** and select the data file (`*_average-A.fif`).
- Select **View -> Autoscale.**
- Select the baseline (as explained previously) for reliable confidence volume estimates.
- Proceed as for fitting a dipole to a single event (Section 8).

14.9 Fit dipoles to a large list of events

If you have large number of events in the list, you can do automated dipole fitting on the listed events.

- Clear the *Xfit* Dipole Fitting window, **right-click** and select **clear.**
- Press **File -> Preferences -> Fitting -> Send fitted dipole automatically to *Mrilab.***
- Double-click the first filtered event from the Event lists dialog.
- Execute **Action -> Fit events.**
- Look at the list of fitted dipoles in **Dipole fitting window** in *Xfit*. By default, the dipoles are fitted every 10 ms from the beginning of event, visible as gray window in *Graph* or the event transferred in *Xfit.*
- Change the fitting parameters (as needed) in *Graph***: Parameters -> Spike-search**. Parameters `search-fit-start` and `search-fit-end` define the window length with respect to the defined event, and `search-fit-interval` defines the interval with which the dipoles are fitted.
- Select **Event lists -> Action -> Fit events** to fit dipoles for each event in the event list using these parameters.
- The result is a long list of dipoles fitted on the Dipole Fitting window. Select all the dipoles, **right-click and select Filter** in the menu that appears. Use goodness of fit threshold (`e.g., g > 80%`) to filter only the best of the dipole fits. Select the filtered dipoles, **right-click and select -> MRI** to see the dipoles overlaid the MR image.
- If needed, adjust the event window and dipole fitting parameters, for example, if the spike is 70 ms long, define a window [-20 0] ms, with respect to the event marker, and fit a dipole every 2 ms to fit the beginning of a spike and the peak value, but nothing after the defined event marker.
- Note that here the baseline is not automatically defined, and thus the confidence volume estimates are not reliable.

15 Appendix A: Installing and tailoring *Graph* setups

15.1 Installation of the setups

The Graph setups require a standard Linux analysis workstation where Data Analysis software release 3.4 has been installed. The setups described in this manual are automatically installed with the Data Analysis Software release 3.4.6 and later. You can inspect the release version from the contents of the text file /neuro/setup/Release. If it is older than 3.4.6, you can install the setup files in the following way.

To install the general setups,

- Open a system terminal: Applications -> System Tools -> **Terminal**.
- Login with administrative priviledges and type the following commands
- `cd /neuro`
- `tar -xvzf dana-graph-apps-general_setups-1.0.0-bin-1811301450.tar.gz`

Continue with the spike search setups,

- `tar -xzvf dana-graph-apps-epilepsy-2.3.6-bin-1912202127.tar.z`
- `tar -xzvf dana-graph-apps-epilepsy-3.3.6-bin-1901141622.tar.z`
- `tar -xzvf dana-graph-modules-eeg_caps-1.0.2-bin-1910251541-so.tar.z`
- `tar -xzvf dana-graph-modules-montages-1.0.0-bin-1910251630-so.tar.z`
- `tar -xzvf dana-graph-modules-spike_search-2.0.0-bin-1901071213-so.tar.z`

- Open file `/neuro/app-defaults/Graph-2.94` in a text editor
- Add the following line (e.g. at the end) and save:
- `#include "Graph_custom"`

After installation, the setup and lisp code files are located in `/neuro/lisp/local/graph-2.94/` subfolders `setup` and `code`.

15.2 Tailoring the setups

Any user can tailor the *Graph* setups and save own versions in directory `$HOME/lisp/setup` where `$HOME` refers to the user's home directory. For example, you can save your own version of the epilepsy-3.3 setup after setting the EEG cap definition (see section 7.2) and adjusting filters (see section 13.1.3) into file `$HOME/lisp/setup/my-epilepsy-3.3.setup`.

You may need to edit the configuration file "`.graph`" in your home directory for setting the file path for the setup and lisp code files (see the *Signal Processor User's Guide* section 3.2). An example of the contents of file `$HOME/.graph`:

```
(setq *setup-file-path* (str-append (getenv "HOME") "/lisp/setup"))
(add-path (str-append (getenv "HOME") "/lisp/code/") :first t)
(setq graph::max-evoked-data-size 100000000)
```

16 Appendix B: Quick reference for *Graph* Epilepsy setups

16.1 EEG configuration

- Define the EEG cap as described in section 7.2. Available selections are:
  - "`Headbox`": 32-channel EEG headbox (part no. NM24116N, Figure 70a).
  - "`TRIUX cap`": 32/64/128 channel TRIUX EEG cap (Figure 70b); see *NM24405A-* EEG Cap User's Manual.*
  - "`Easycap`": see the Easycap electrode layouts at www.easycap.de.
  - "`Vectorview cap`": older MEGIN caps (part no. NM20884N, NM20885N, NM20886N).

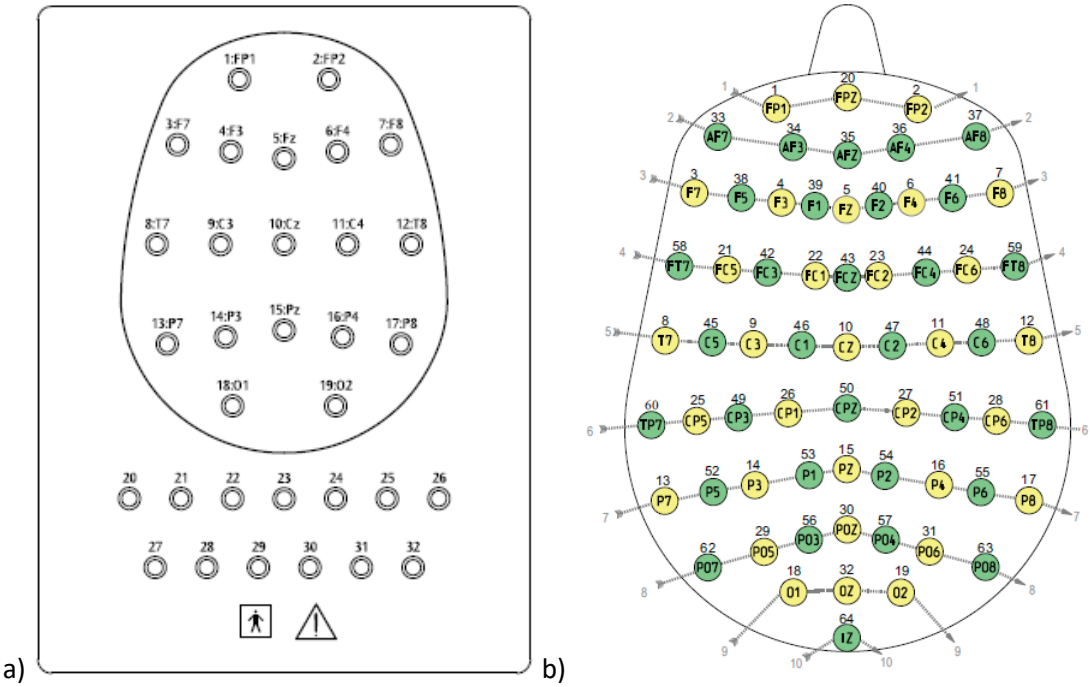


Figure 70. a) 32-channel unipolar head box. Separate electrodes are connected to the pins; mapping of channels 1–19 are the same than in the TRIUX EEG cap. Channels 20-32 can be connected to other desired electrode locations. b) Layout for the 64-channel TRIUX EEG cap. Yellow circles indicate the electrodes in the 32-channel cap. The first 19 channels are the same in the head box and in all TRIUX EEG caps.

16.2 EEG derivations

- The EEG montages follow *American Clinical Neurophysiology Society Guideline 3: A Proposal for Standard Montages to Be Used in Clinical EEG* [ACNS].
- EEG montages are either bipolar montage or referential (Figure 71). Bipolar montages mean computing and displaying waveforms of difference between the signals of two channels. The referential montage means that the differences are taken between each channel and a common reference electrode signal.
- Bipolar EEG derivations listed in Tables 2-4 are defined in the configuration file `/neuro/lisp/local/graph-2.94/config/eeg-derivations2.lsp`.

- This file can be edited to select and modify the preferred EEG montages by a user with administrative priviledges:
  - Make a backup copy e.g. to `eeg-derivations2.lsp.orig`.
  - Copy `eeg-derivations2.lsp` e.g. to your home directory and modify with a text editor.
  - Copy the edited file back to `/neuro/lisp/local/graph-2.94/config/eeg-derivations2.lsp`, and verify that the derivations appear correctly.
- Note that some of these derivations require ear-reference electrodes A1 and A2 which are not included in the EEG caps. They can be connected e.g. via the headbox (Figure 70a).
- If a channel required by a derivative is missing, *Graph* EEG window does not show anything.

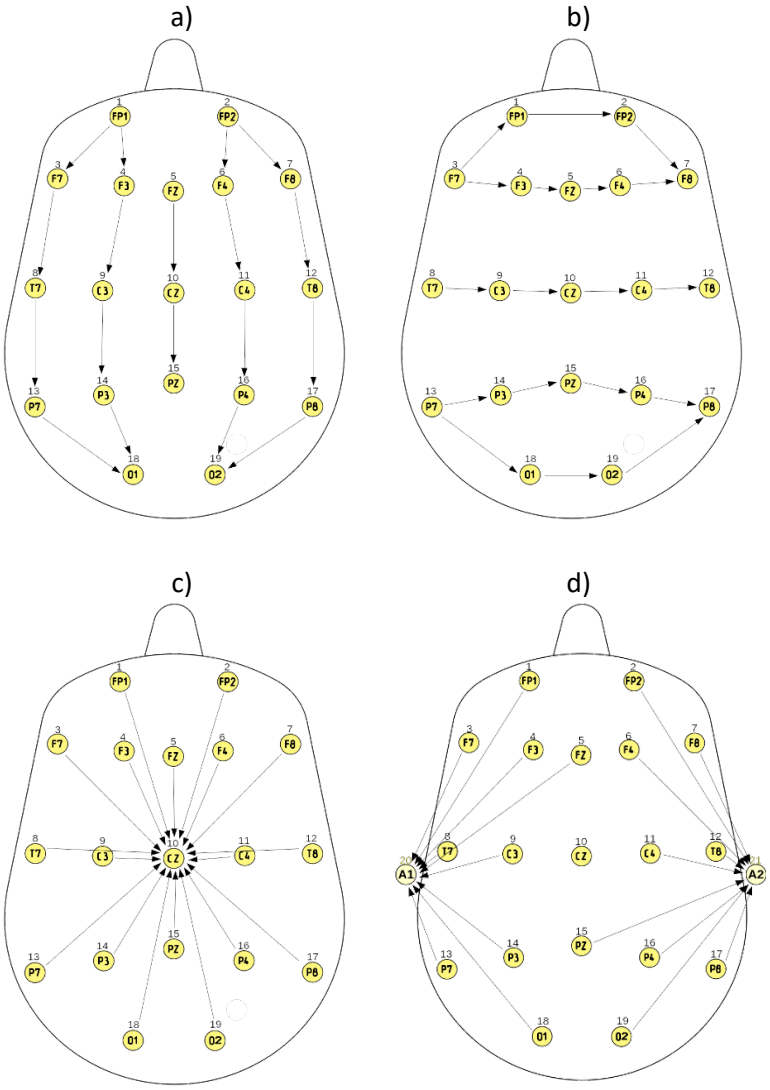


Figure 71: Standard bipolar EEG montages according to [ACNS]. a) Longitudinal (double-banana) LB-18.1, b): transverse TB-18.1, c) Cz-referential, d) Ear-referential R-18.1.

Table 2: Longitudinal bipolar EEG montages according to [ACNS].

Channel	LB-18.1		LB-18.2		LB-18.3	
1	Fp1	F7	Fz	Cz	Fp1	F7
2	F7	T7	Cz	Pz	F7	T7
3	T7	P7	Fp1	F3	T7	P7
4	P7	O1	F3	C3	P7	O1
5	Fp1	F3	C3	P3	Fp2	F8
6	F3	C3	P3	O1	F8	T8
7	C3	P3	Fp2	F4	T8	P8
8	P3	O1	F4	C4	P8	O2
9	Fz	Cz	C4	P4	Fp1	F3
10	Cz	Pz	P4	O2	F3	C3
11	Fp2	F4	Fp1	F7	C3	P3
12	F4	C4	F7	T7	P3	O1
13	C4	P4	T7	P7	Fp2	F4
14	P4	O2	P7	O1	F4	C4
15	Fp2	F8	Fp2	F8	C4	P4
16	F8	T8	F8	T8	P4	O2
17	T8	P8	T8	P8	Fz	Cz
18	P8	O2	P8	O2	Cz	Pz
19	ECG		ECG		ECG	

Table 3: Transverse bipolar EEG montages according to [ACNS3].

Channel	TB-18.1		TB-18.2*	
1	F7	Fp1	Fp1	Fp2
2	Fp1	Fp2	F7	F3
3	Fp2	F8	F3	Fz
4	F7	F3	Fz	F4
5	F3	Fz	F4	F8
6	Fz	F4	A1	T7
7	F4	F8	T7	C3
8	T7	C3	C3	Cz
9	C3	Cz	Cz	C4
10	Cz	C4	C4	T8
11	C4	T8	T8	A2
12	P7	P3	P7	P3
13	P3	Pz	P3	Pz
14	Pz	P4	Pz	P4
15	P4	P8	P4	P8
16	P7	O1	O1	O2
17	O1	O2	Fz	Cz
18	O2	P8	Cz	Pz
19	ECG		ECG	

*If A1 and A2 are included

Table 4: Referential EEG montages according to [ACNS3].

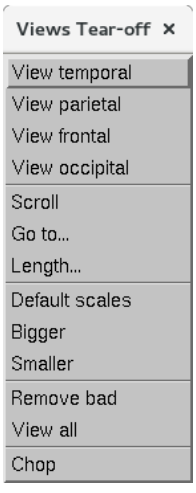
Channel	R-18.1		R-18.1*	
1	F7	Cz	F7	A1
2	T7	Cz	T7	A1
3	P7	Cz	P7	A1
4	Fp1	Cz	Fp1	A1
5	F3	Cz	F3	A1
6	C3	Cz	C3	A1
7	P3	Cz	P3	A1
8	O1	Cz	O1	A1
9	Fz	Cz	Fz	A1
10	Pz	Cz	Pz	A2
11	Fp2	Cz	Fp2	A2
12	F4	Cz	F4	A2
13	C4	Cz	C4	A2
14	P4	Cz	P4	A2
15	O2	Cz	O2	A2
16	F8	Cz	F8	A2
17	T8	Cz	T8	A2
18	P8	Cz	P8	A2
19	ECG		ECG	

*If A1 and A2 are included

- If you prefer to use the nomenclature terms T3/T4/T5/T6 instead of the modified 10-10 terminology T7/T8/P7/P8, make the following substitutions in `eeg-derivations2.lsp`:
  T7 -> T3
  T8 -> T4
  P7 -> T5
  P8 -> T6

16.3 Displays menu

- Select **Displays->Views**, left-click on the dashed line at the top of the sub-menu, and place the tear-off menu position at a convenient location. The menu in epilepsy-2.3 setup has first channel selections:



View temporal

Pressing this button selects channels from the temporal areas to be displayed on the right-hand side displays.

View parietal

Pressing this button selects channels from the parietal areas to be displayed on the right-hand side displays.

View frontal

Pressing this button selects channels from the frontal areas to be display on the right-hand side displays.

View occipital

Pressing this button selects channels from the occipital areas to be display on the right-hand side displays.

- The remaining choices in the menu are common to both epilepsy setups:

  Scroll

  Scroll data forward automatically until the data ends or user stops the scrolling by pressing the Stop button on the working dialog that is shown during the operation.

  Go to...

  Move the view to start from given time. Pressing this button will pop up a small dialog that asks the starting time. Pressing the OK will move the view to given time point.

  Length...

  Change length of the displays. The default length is 5 seconds. This button pops up a dialog that allows the change of the length of all the displays.

  Default scales

  Change the scales of all displays to default settings. Default values for different kinds of channels are defined in the parameter set displays. See “Parameters” below.

  Bigger

  Change the scale of the displays so that the signals look bigger. To select some channels use the right mouse button and click a curve or drag over a range of curves. To deselect channels, click on the narrow dark border of the display outside the curve viewing area.

  Smaller

  Change the scale of all selected displays so that signals look smaller.

  Remove bad

  Remove selected MEG signals from being viewed or used in analysis. Click first the signal that looks bad on the right-hand side window to select it (check that there are no other curves selected) and press this button. The selected curve should disappear from the displays and a flat signal with no name should appear on the bottom of the channel by channel display.

  View all

  View all channels, that is, no channel is marked as bad channel any more.

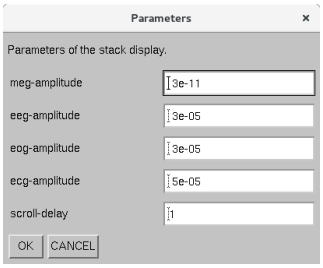
  Chop

  Make an evoked format data file from the data in the current time selection on the display.

- Select **Parameters->Displays** to adjust parameters that affect the displays:

  meg-amplitude

  This defines the default amplitude for MEG displays. When the **Default scales** button is selected from the **Views** menu, this value will be used in MEG displays.



  eeg-amplitude

  Default value to be used in scales for EEG displays.

  eog-amplitude

  Default value to be used in EOG displays.

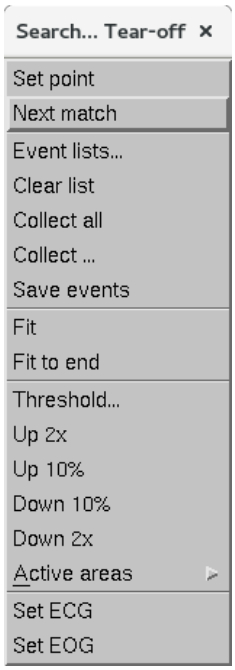
  ecg-amplitude

  Default value to be used in ECG displays.

  scroll-delay

  Scroll delay. When the **scroll** command is activated from the **views** menu, there will be a delay of this many seconds before next search is activated.

16.4 Search menu



- The **Commands -> Search** menu has the following buttons:

Set point
Set search start point. Before first search, you should define the starting point for the search. Select first one time point (using the right mouse button) and then press this button to select this time point as the start point for the searches. After a search for the next event, the next starts from the previous event found plus some minimum step that can be defined. See "Parameters of the search" below.

Next match
Scan trigger channel until a new peak exceeding the trigger level appears. The view on the display is moved so that the trigger point is visible, and the time selection is set so that it shows the time interval that would be transferred to fitting program. The scan returns only events that are classified as "ok".

Clear event list
Clear all entries from the event lists. See "Event lists" below.

Collect all events
Scan the whole file for all events and collect the found events into the event list.

Collect events within
Search some interval of data, and add the events found in it to the event list. Pressing this button pops up a dialog that asks for the start and stop time for the scan.

Save event list
Save current event list into a file. Pressing this button pops up a file selection dialog where you should enter the name of the file where to save the list. The data is saved as textual LISP object.

Event lists...
Pop up the display list editor dialog.

Fit
Fit the last found event. This is used in interactive mode, where one manually asks program to proceed to next event, and it this looks good, one can fit dipoles to the data around the spike by pressing this button. Before applying this operation, the source modeling program (*Xfit*) should be started from the **xfit** menu.

Fit to end
Fit all the rest of the events. When one has examined some candidate events using the **Next match** and **Fit** buttons, and the trigger level is set to correct value, one can proceed to fit all the rest of the events by pressing this button. This will fit all events automatically labeled with `:ok`. Collecting all events first to an event list and then performing the fitting is preferred over usage of this button, since the event lists provide more flexibility and better documentation on what was selected into the fitting.

Up 2x
Increase the trigger search threshold level by factor of 2.

Up 10%

Increase the trigger search threshold level by 10%.

Show threshold

Show current threshold, e.g. for documenting the trigger level used in the search.

Down 10%

Decrease the trigger search threshold by 10%.

Down 2x

Decrease the trigger search threshold by factor of 2.

Set ECG

Set the threshold level for ECG artifact rejection. Select first a time span which contain a beat or two, and then press this button. The threshold level for detecting ECG peaks is set to 70% of the top signal value in the ECG channel within the selected interval.

Set EOG

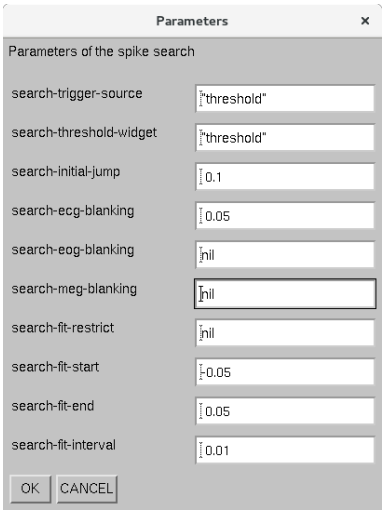
Set the threshold level for EOG artifact detection level. Works in similar fashion as the Set ECG button, except that it uses the EOG channel instead of ECG channel.

16.5 Parameters of the search

Parameters affecting the searching operations are defined in the parameter set **spike-search** in the **Parameters** menu. The parameters are as follows:

search-trigger-source

Name of the widget from which the trigger signal is taken for the search. This must be a widget that supplies a proper trigger signal in its first channel. If you are using this with the setup provided with this utility, you should not change this value.



search-threshold-widget

Name of the widget performing the thresholding of the trigger signal. Do not change this parameter unless you have a custom setup.

search-initial-jump

Initial time leap in the beginning of each search to prevent double fitting of events very near each other. Suitable value for this is the length of the fitting interval (see below).

search-ecg-blanking

Minimum time distance from a trigger point to nearest ECG signal. If this value is e.g. 0.2, this means that if there is large signal in the ECG channel (over the ECG threshold) nearer than 200 ms from the trigger point, this trigger point will be labeled as `:corrupted-ecg` instead of `:ok`. If you do not want to use the ECG blanking you can set this parameter to `nil`. If your data does not have a proper ECG channel, you must set this parameter to `nil` in order to use the search.

search-eog-blanking

Minimum distance to nearest EOG event. Similar to `search-ecg-blanking`. Use `nil` if no EOG blanking is required. If there is a strong EOG signal near to the trigger point, the event will be labeled as `:corrupted-eog`.

search-meg-blanking

Minimum distance to nearest MEG artifact. The MEG artifacts are detected from the trigger signal by using a threshold level higher than the threshold level used for the spike detection. If this higher threshold level is exceeded near the trigger point, then the event is classified as `:corrupted-meg.`

search-fit-restrict

This parameter is currently not used.

search-fit-start

Define the staring time for fitting dipoles. Time is in seconds and relative to the trigger point.

search-fit-end

Define the end time for dipole fitting. Time is in seconds and relative to the trigger point.

search-fit-interval

Dipole fitting density. Dipoles will be fitted starting from the beginning of the fitting region in steps defined by this parameter. Steps are in seconds.

16.6 "Match" signal spike searching

The gradiometer properties can be utilized efficiently for searching spike-like activity. Denoting the signals of a single triple-sensor unit by *Bz* (magnetometer), $\partial Bz/\partial x$ (latitude gradient) and $\partial Bz/\partial y$ (longitude gradient), the gradient magnitude (or power) is obtained from the gradiometer pairs as $(\partial Bz/\partial x)^2 + (\partial Bz/\partial y)^2$. Information compression is obtained by dividing the 204 gradiometers into 14 groups according to anatomical locations, each having 8 – 12 gradiometer pairs. The gradient powers of the associated sensor pairs are summed and the "Match" waveform shows at each timepoint the maximum value among the 14 channel groups.

MEG gradiometer data is scanned until the match signal power exceeds a predefined threshold level, after which it continues to the first peak top in the data. This time point is returned as the time point of the current event. This time point is then labeled using the following considerations: If the time distance from the point to the nearest ECG signal (exceeding the ECG threshold level) is less than `ecg-blanking` time, this event is labeled as `:corrupted-ecg`. Similarly if there is large EOG signal within `eog-blanking` time, event is labeled as `:corrupted-eog-1` or `:corrupted-eog-2`, depending on which EOG channel did cause the condition. If the event is so near beginning or end of the data that either of the blanking time would go beyond the existing data, event is labeled as `:too-near-edge`.

16.7 Adjusting the setups

The part which is most likely to vary from site to site is the usage of the EEG channels. It is unlikely that the default settings would match your needs. The following things should be taken into consideration.

Adjusting EOG channels

If EOG channels are not used, set the `eog-blanking` to `nil` in the search parameters. Otherwise open the control panel and double click the "eog" widget icon. Modify the channel definitions in the editor box so that the electric channels used to measure EOG are selected. Only the first two channels are used, if more than two channels are selected.

Adjusting ECG channels

If ECG is not measured, set the `ecg-blanking` to `nil` in search parameters. Otherwise set the channel name in the "ecg" widget to pick the electric channel used to measure the ECG signal.

Adjusting EEG channels

The setup shows 20 EEG channels on the display and uses the derivation-menu module to enable forming of various easily selectable derivations. You need to define the derivations that are needed in your EEG cap. For instructions see reference pages for the derivation-menu module.

16.8 Event-list dialog

- **File** menu in the event-list dialog (Figure 67) contains following buttons:

Save all	Save events in the left hand side list.
Save filtered	Save events in filtered event list.
Load	Load events from a file into the left hand side list.
Close	Close the dialog.

- **Edit** menu contains the following buttons:

Sort by time	Sort events in the filtered list by event time.
Sort by amplitude	Sort events in the filtered list by the event amplitude.
Clear all	Clear all events from both event lists.

- **Action** menu contains the following buttons:

Collect all events	Scan all data and add found events into the complete event list.
Collect events within...	Popup a dialog to define the time limits between which the events are scanned. When the dialog is closed by pressing OK, given time interval is scanned and events found are added into the complete event list.

17 Revision history

Revision A

- Company name change (Megin Oy).
- Scope TRIUX™ and TRIUX™ neo customer training.
- Improved flowchart figures.
- Reordered the contents to basic MEG analysis workflow and separate advanced steps.
- Added more information on Graph setup installation and tailoring, and EEG montages.

Revision B

- Inspection and correction of the head position, section 4.4 and Chapter 10.
- Graph setups are included in DANA software release 3.4.6, section 14.1.
- Note about avoiding mixing files of different patients, section 4.6.

Revision B1

- Company address change.
- Added symbols on the equipment as Ch 1.