

TAPEEG

Toolbox for **A**utomated **P**rocessing of **EEG** files

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v2.9

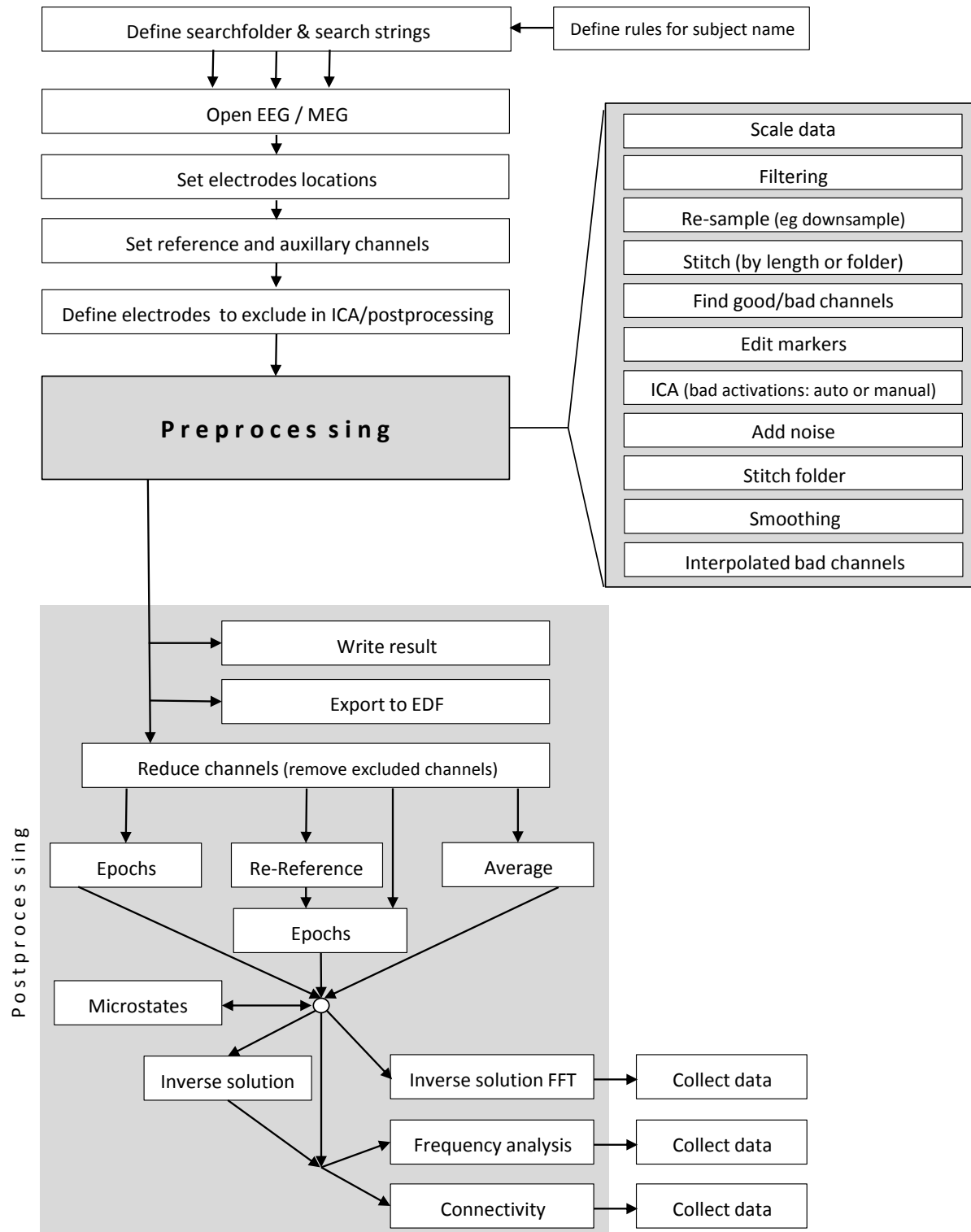
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Flow Chart of processing files



Purpose

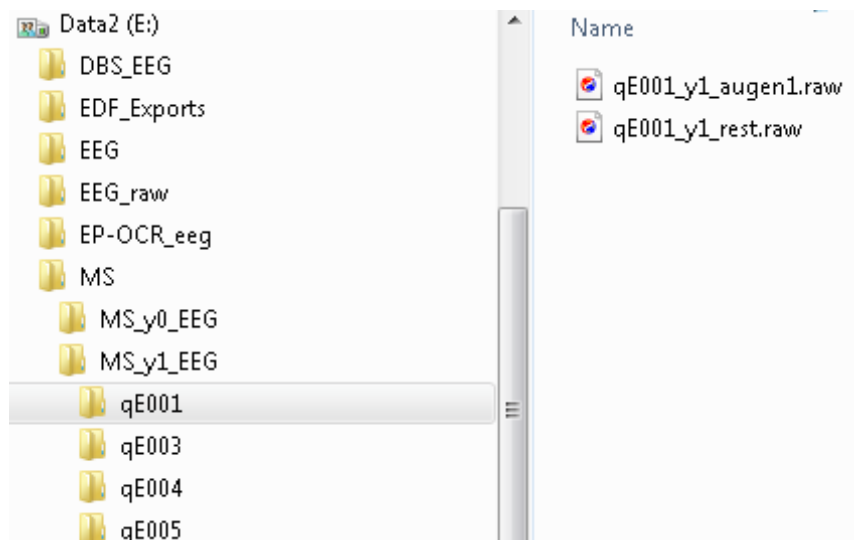
TAPEEG is a Matlab® software for processing EEG/MEG-files. TAPEEG is able to process EEG or MEG files at all needed steps of analysis. The manual allows conducting a standard EEG/MEG-processing with the TAPEEG application. For displaying results the software Cartool is recommended.

I. Data Structure

To start processing files, files should be stored in a folder structure as follows:

- Study folder
 - Patient folder (name of folder = patient-name)
 - EEG/MEG file(s) (if '.mff': EEG-file = mff-folder)

In the subsequent example, the study folder *MS_y1_EEG* contains the patient folders *qE001* and *qE002*, etc. There are two EEG-files in the patient folder *qE001*, *qE001_y1_augen1.raw* and *qE001_y1_rest.raw*.



Notes:

- Supported file formats in TAPEEG are: EGI (.raw .mff), EDF (.edf), Elekta (.fif), ASCII (.txt), Cartool (.sef .ep .eph .iris), CTF (.meg4,.res4,.ds), Brainvision (.eeg), Neuroscan (.cnt, .eeg), NXE (.nxe)

(For EGI .mff reading, delays of markers due to the anti-aliasing filter are corrected after selection of the amplifier-type)

- Files with electrodes information (.els,.sfp,.xyz) should be stored in the 'Study folder' as 'electrodes.els/.sfp/.xyz' or in same folder as EEG's ('Name_of_EEG.els').
- Marker: Marker file must be stored in same folder as eeg/meg-file with name *Name_of_EEG.** (* = .mrk,.xls,.edf)
 - .mrk: Cartool marker format
 - .xls: Excel-files: header {'Onset' 'Duration' 'Event'} or {'Onset' 'Event'}
 - .edf: Standard edf-file with equal length in TF as eeg/meg-input file (only markers of edf-file are used)

- **Bad channels:**
When bad-channels of eeg/meg are already known, a separate xls-file ('Name_of_eeg/meg.xls') can be stored in same folder as eeg/meg. First line of the xls-file must be 'Bad channels'. In following lines (always first column) bad channels can be noted (separated by spaces), whereas first line is for first segment, second line for second segment...

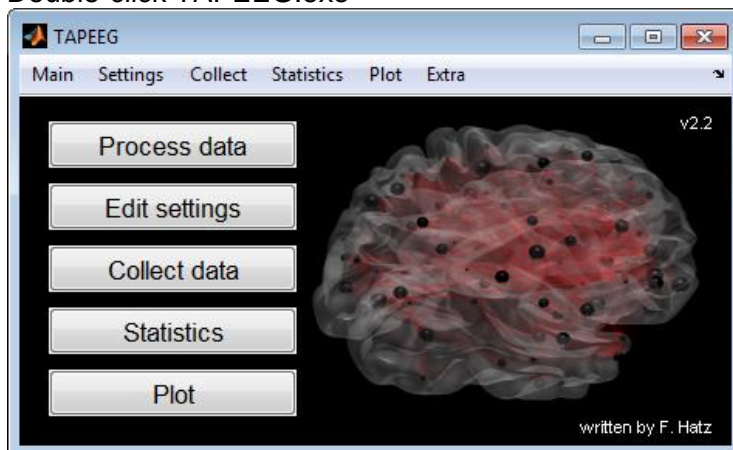
The following example shows an xls-file for excluding bad channels during the TAPEEG-processing. The eeg/meg-file contains five segments (therefore there are five lines). For the first segment, the channels 45 and 12 are defined as bad; respectively channel 11 for segment three. Segments two, four and five have no bad channels, therefore there is a zero.

	A	B
1	bad channels	
2	45 12	
3		0
4		11
5		0
6		0
7		
8		

II. Start analysis

1. Start analysis

Double-click TAPEEG.exe



Select '**Process data**'

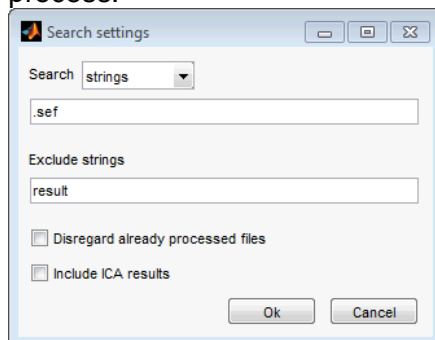
2. Select 'File' or 'Folder'

Depending on the number of files to process, select *Folder (more than one file)* or *File (one EEG/MEG-File to process)*

Folder: all EEG/MEG-files in a Folder will be processed (= 'Study folder'). You can also select a folder containing different 'Study folders'. They will be processed independently.

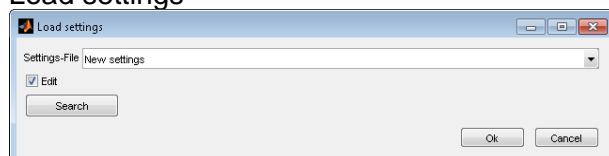
File: only a single EEG/MEG-file will be processed

If Folder: Select search- and exclude-strings, e.g. file-extension of eeg/meg-files to process.



- If desired either 'ICA', 'Filtered', 'Results' or 'Matrix' can be selected in the menu. This will replace strings entered in the first line:
 - ICA: Search results of ICA and do ICA-backtransform
 - Filtered: Search for *filt.sef, stored before starting ICA
 - Results: Search for files stored as *results.sef
 - Matrix: Search for *matrix.txt (-> perform graph analysis on multiple matrices)
- Disregard already processed files
(TAPEEG creates log-files for already processed files and segments)
- Include ICA results: Search includes ICA-results with selected bad activations
(Search is looking for *.exclude.txt)

3. Load settings



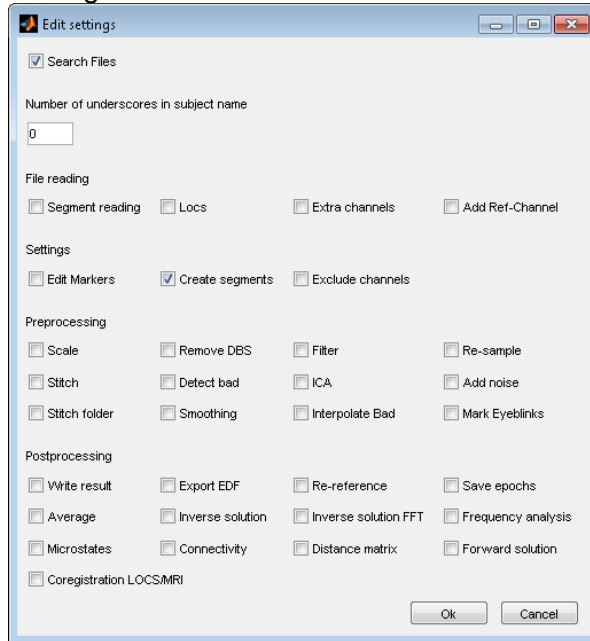
Select one of the previous 'settings.mat' in the list and select 'Edit', if you want to edit the settings before starting the processing.

Search: File-dialog to load a specific settings.mat

4. Select files

A list is shown with detected files, where you can select / deselect files

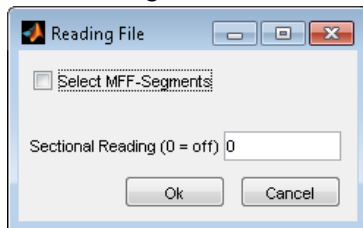
5. Settings



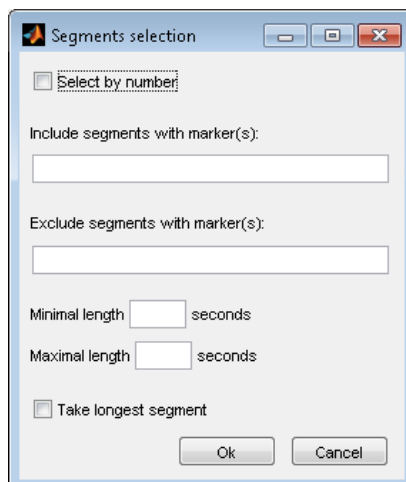
5.1. Subject name

TAPEEG uses patient-names to store results. These names can be extracted from the file- or folder-name. Select in this dialog the appropriate number to define the patient-name (-1 for folder / 0... for parts of filename)

5.2. File reading



• Select MFF-Segments:

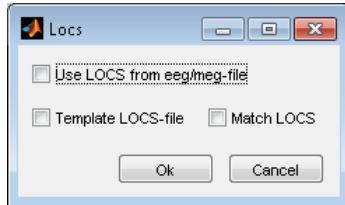


MFF-Files are recorded in segments (pause = new segment)

- Select by number
- Include segments with marker(s)
- Exclude segments with marker(s)
- Segments with minimal or maximal length
- Take longest segment

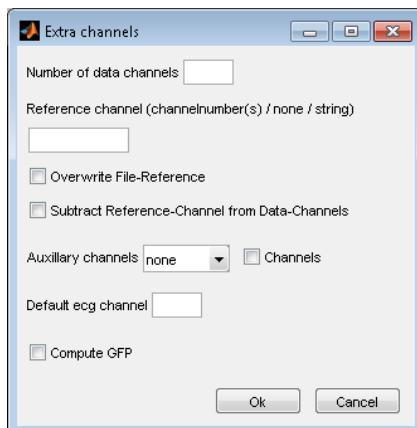
- Sectional Reading: For very large files (e.g. sleep recordings) file reading can be splitted in segments (length in timeframes, 0 = disabled)

5.3. Locs (position of electrodes / sensors)



- Use LOCS from eeg/meg file: LOCS information of input files (if available) is used
- Template LOCS-file: Load a template LOCS-file, used for all processed EEG/MEG-files.
- Match-LOCS: In case of a template LOCS-file, only channels existing in the input EEG/MEG-files and the Template-LOCS-file are used for processing

5.4. Set extra channels

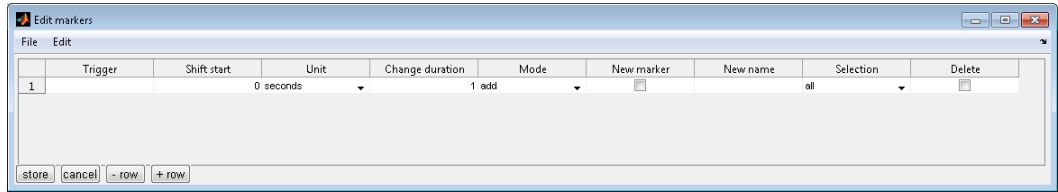


- Number of data channels (usually set automatically)
- Reference channel: As reference channel information is not stored in most input files, you have to enter that information manually. Channel-numbers or 'strings' (e.g. mean / none) are allowed. (Standard value is last channel for EEG, 'none' for MEG).
- Overwrite File-Reference: Reference-Channel, stored in EEG-info is overwritten by given value. Reference channel is always set to zero-values.
- Subtract Reference-Channel from Data-Channels: If reference channel is not zero, data of reference channel can be subtracted from all other data channels (e.g. back-conversion of file with mean reference to original reference)
- Auxiliary channels: Default = automatic
(If some EEG channels are used as auxiliary channels, there numbers have to be entered. The data of those channels will be added as additional channels without deleting them at the original position)
- Ecg channel: channel number of ecg channel
- Compute GFP: add GFP (global field power) as auxiliary channel

5.5. Add reference channel

- Add and define name of reference channel

5.6. Edit Markers



Marker: Select one of the markers in file
(‘New Marker’ = new marker at timeframe 0)

Shift start: Move marker by ... seconds / timeframes

Duration: timeframes (add or fixed)

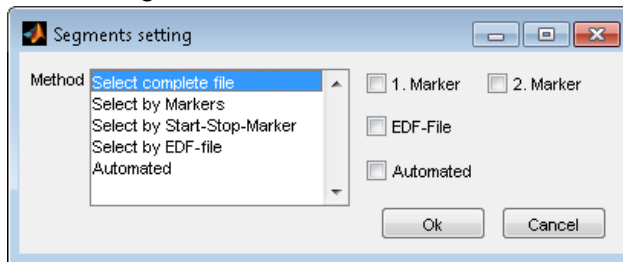
New marker: If set, a new marker is created, otherwise original marker is replaced

New name: Name for new marker

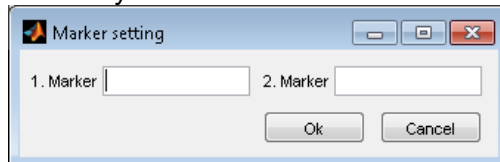
Selection: Select if only first, only last or all markers are altered

Delete: Delete marker(s)

5.7. Create Segments

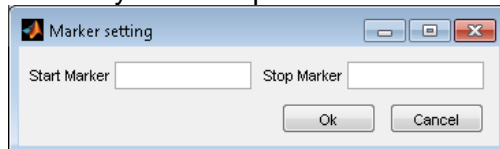


- Select complete file: complete file
- Select by Markers:



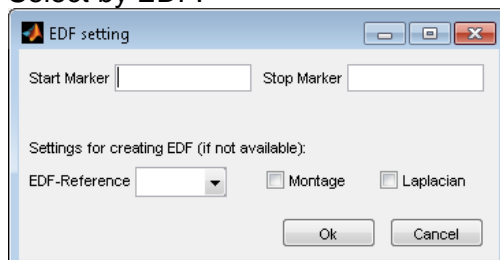
Define Markers to be included in segments (duration of markers must be > 1)

- Select by Start-Stop-Marker:



Define start and stop marker for segments

- Select by EDF:

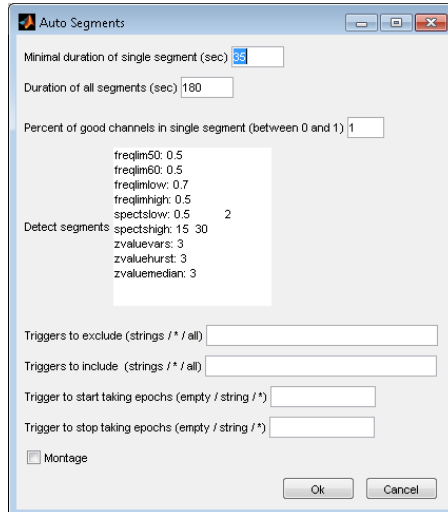


- Start & Stop marker for segments

(Program looks for edf-files ('name_of_EEG.edf'), if not found creates one and stops processing. If edf-file is found, TAPEEG reads markers and cuts EEG in segments)

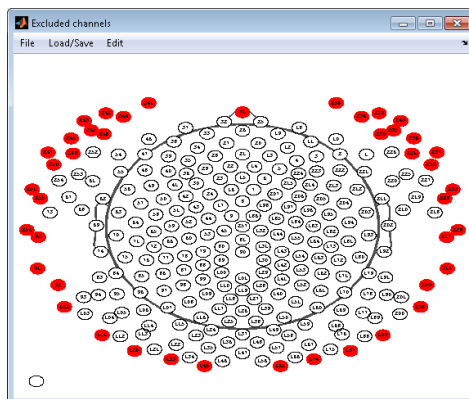
- If no EDF-File is found, a EDF-File is created (EDF Reference: mean / median / laplacian / montage / channels)

- Automated



- Minimal duration of single segment in seconds
- Duration of all segments together in seconds
- Percent of good channels in single segment: *see appendix 'Bad settings'*
- Detect segments: *see appendix 'Bad settings'*
- Markers to exclude / include: select markers to in- or exclude in segments
- Marker to start / stop: empty = begin / end of data
- Montage: is a montage-file (*see appendix*) is loaded, a edf-file with segments-selection is written

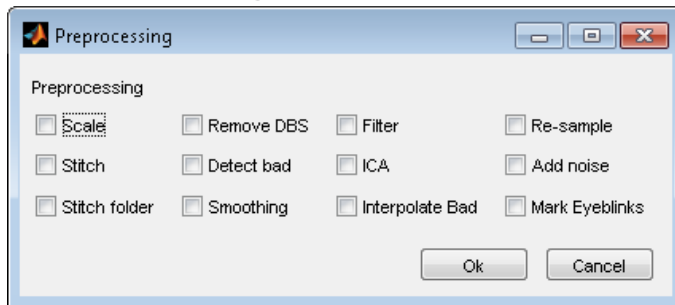
5.8. Select excluded channels



Channels to exclude in final results

(If EEG with 257 channels: uhbs standard of 43 channels is preselected, standards for different number of data-channels are set in file 'Exclude.xls' in application folder)

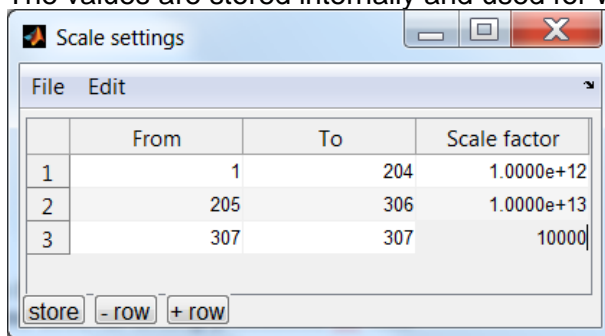
III. Preprocessing



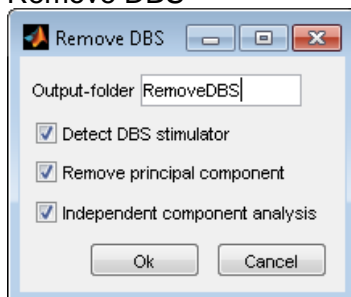
(If **filt.sef*-file is selected as input, preprocessing is reduced to ICA)

1. Scale data

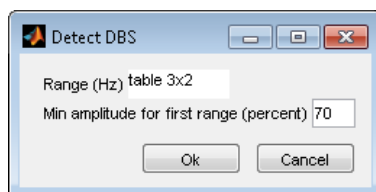
For processing MEG, data has to be up-scaled. Normally, just use standard values. The values are stored internally and used for writing processed fiff-files



2. Remove DBS

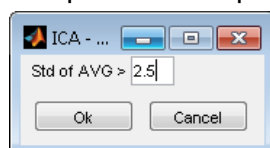


- Output-folder: Folder to store results
- Detect DBS stimulator:



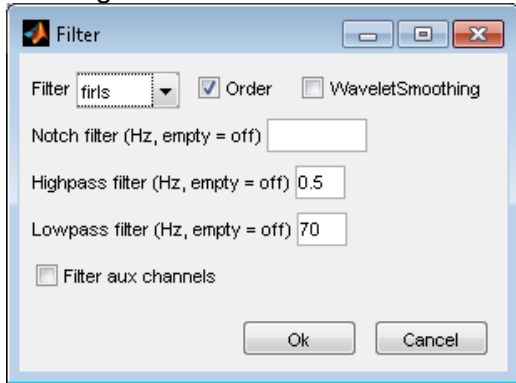
Search for stimulator artifact using predefined frequency ranges and create a marker for every stimulus

- Remove principal component: Remove the first principal component
- Independent component analysis (ICA):



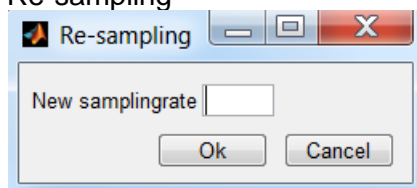
Use ICA, followed by averaging on the stimuli and removing the components with averaged activity larger than given 'Std'

3. Filtering



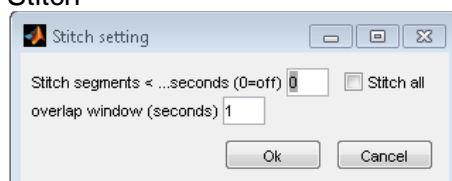
- | | | |
|----------------------------|--------------|--|
| Filter: | butter | Matlab butterworth filter |
| | firls | Matlab least square |
| | freq | -> FFT -> deletion of frequency-bins -> inverseFFT
(warning: no windowing of data!) |
| | wavelet | Filtering by wavelet transformation (Matlab wavelet toolbox needed!) |
| | cheby | Matlab Chebyshev Typ2 filter |
| Order: | Filter order | butter: default = 2
firls: 0 = automatic (4.8*samplingrate)
cheby: 0 = automatic (min order) |
| Wavelet Smoothing: | | For wavelet filtering, the smoothing factor determines scales of wavelet transformation. 4 is standard value, higher values will increase pseudofrequency steps and therefore result in a more smoothed output |
| Notch filter: | | multiple values allowed |
| Higpass / lowpass filter: | | single value in hertz |
| Filter auxiliary channels: | | off = filtering of auxiliary channels disabled |

4. Re-sampling



Enter new samplingrate, down- and up-sampling is allowed

5. Stitch

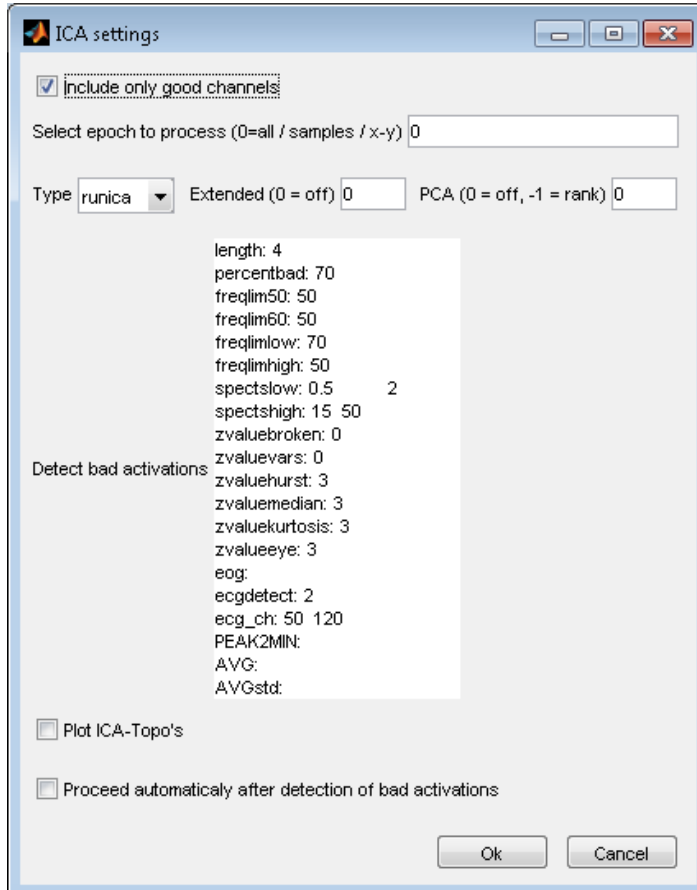


- Stitch segments: segments are stitched together for minimal segment length of ... seconds (Stitch all = One segment per patient folder)
- Overlap window (inverse hanning window of ... seconds)

6. Detect bad

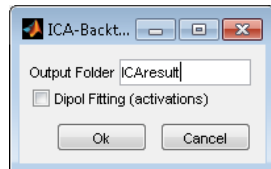
see Appendix 4

7. ICA



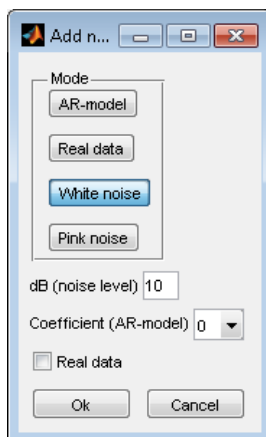
- Include only good channels: without good reason, leave 'on'
- Select epoch to process:
 - 0 = complete EEG/MEG (default)
 - samples = length in timeframes (start is at 5 sec)
 - x-y = start and end in timeframes
- Type: runica = eeglab runica implementation
 - Extended: Perform tanh() "extended-ICA" with sign estimation N training blocks. If N > 0, automatically estimate the number of sub-Gaussian sources. If N < 0, fix number of sub-Gaussian comps to -N [faster than N>0]
 - PCA: Number of principal components, -1 = rank of input data defines number of principal components
- binica = binary version of eeglab, only linux!
 - Extended: *see runica*
 - PCA: *see runica*
- fastICA = Fast-ICA algorithm (<http://www.cis.hut.fi/projects/ica/fastica>)
 - Extended: *disabled*
 - PCA: Number of principal components, -1 = rank of input data defines number of principal components
- jader = JADE (v1.5, Dec. 1997)
 - Extended: *disabled*
 - PCA: *disabled*

- Detect bad activations: see *Appendix 4*
- Plot ICA-Topo's: Plot topographies of activations (2D signal space plot)
- Process automatically after detection of bad activations:
 - Disabled: Activations to exclude must be selected manually and stored in file ('exclude.txt'). After that restart TAPEEG for same 'Study folder', search for ('_ICA.mat') and postprocessing will start
 - Enabled: Activations to exclude are selected automatically and postprocessing is run



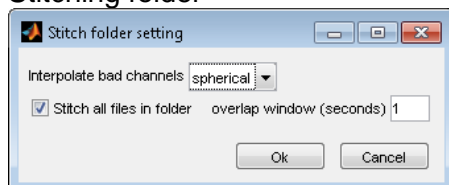
Note: Runica = Independent Component Analysis (ICA) decomposition using the logistic infomax ICA algorithm of Bell & Sejnowski (1995) with the natural gradient feature of Amari, Cichocki & Yang, or optionally the extended-ICA algorithm of Lee, Girolami & Sejnowski, with optional PCA dimension reduction. Annealing based on weight changes is used to automate the separation process. Initial ICA learning rate is $0.00065 / \log(\text{number of channels})$

8. Add noise



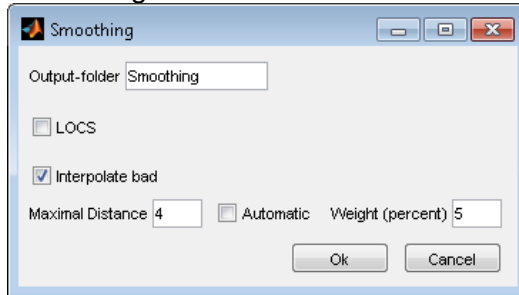
- Mode: AR-model (Green et al. 2012) with selected coefficient
- Real data: real eeg/meg input data
- White noise
- Pink noise
- dB: Amount of noise to be added to data

9. Stitching folder



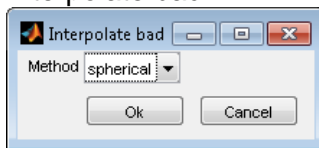
- Interpolate bad channels: spherical or 3D interpolation of bad channels before stitching
- Stitch segments: segments are stitched together for minimal segment length of ... seconds
(Stitch all = One segment per patient folder)
Overlap window (hanning window of ... seconds)

10. Smoothing



- Output-folder: Folder to store verbose-file...
- LOCS: Electrodes-file
- Interpolate bad: Spherical spline interpolation of bad channels
- Maximal Distance/Weight: For smoothing a Gaussian kernel is used. Size of Gaussian kernel is defined by Distance, weight of most peripheral channel in distribution by Weight (percent of central channel)
- Auto: Optimal value for 'Distance' is calculated based on input data

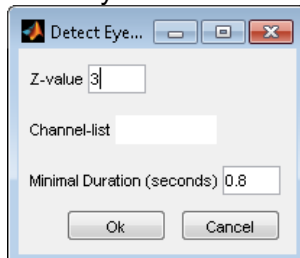
11. Interpolate bad



Select method for interpolation:

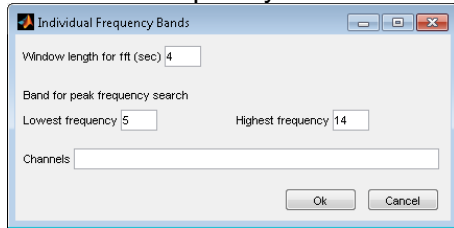
- spherical = spherical spline method
- 3D = 3D interpolation

12. Mark Eyeblinks



- Z-value: Z-value for detection of eyeblinks
- Channellist: Table to define channels for eyeblinks detection
- Minimal duration: minimal duration in seconds for single eyeblink marker

13. Individual Frequency Bands

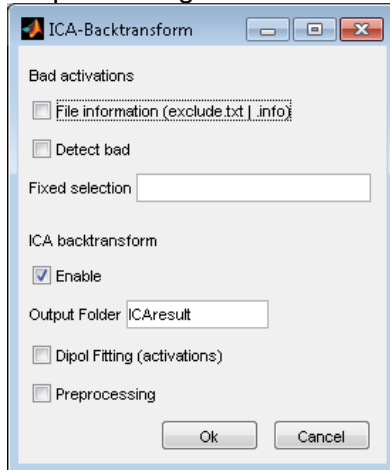


- Window length for fft: Seconds, default = 4 (if < 12'000 timeframes 'multitaper', otherwise 'welch' method is used)
- Band for peak frequency search: Lowest and highest frequency in Hz
- Channels: Channel numbers to include for definition of individual frequency bands

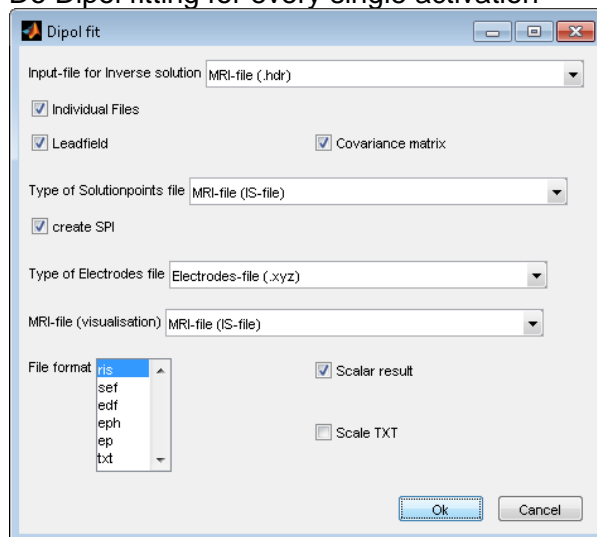
Individual frequency bands are calculated according to Moretti et al 2004:

- *Peak frequency (PF) is found by first detection median frequency in given frequency range, follow by detection of the peak at Median frequency +/- 1 Hz*
- *Theta/alpha transition frequency (TF) is found by detection of the lowest amplitude left to PF, higher as lowest frequency in detection range - 1 Hz*

14. Preprocessing ICA-result



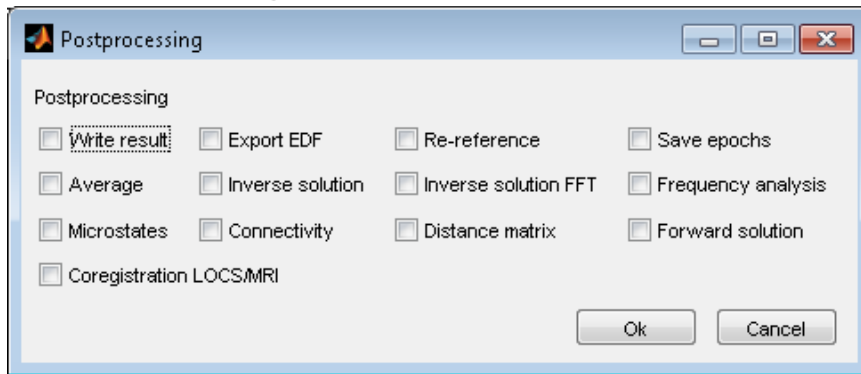
- File information: Bad activations are defined in *ICA_exclude.txt (if available) or *ICA.info
- Detect bad: Do automatic detection of good/bad activations
- Fixed selection: Manual selection of activations
- ICA backtransform: Exclude selected/defined bad activations and convert ICA back to EEG/MEG
- Output-Folder: If empty standard folder is used ('ICAresult')
- Dipol Fitting: Do Dipol fitting for every single activation



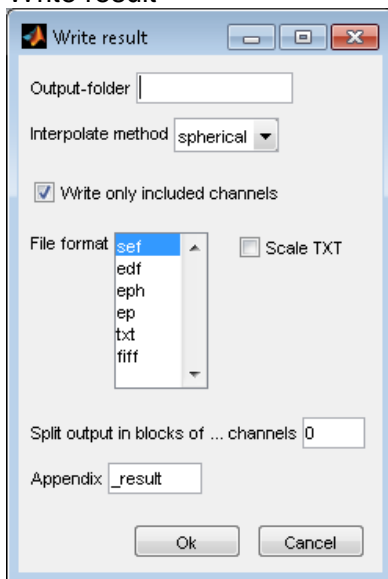
see 'Inverse solution' for settings

- Preprocessing: After backtransform, do selected preprocessings

IV. Postprocessing

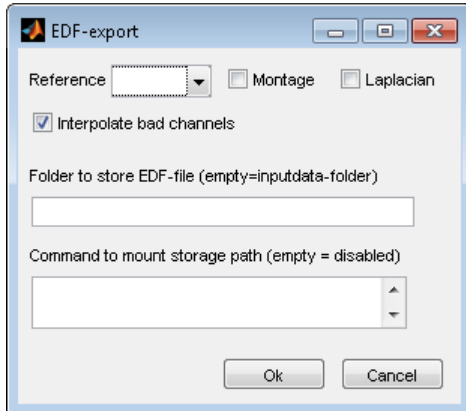


1. Write result



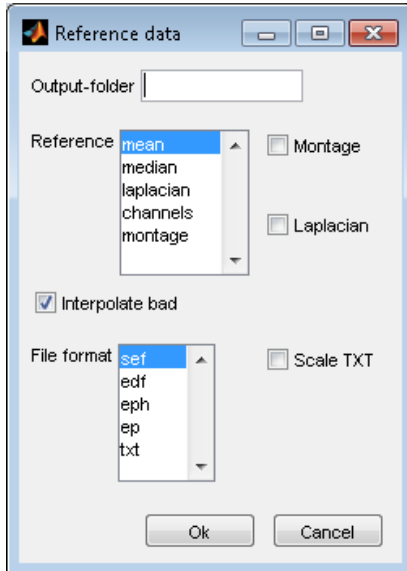
- Output-folder: Folder to store results
- Interpolation of bad channels can be enabled / disabled. Two methods are available for interpolation: spherical spline (routine from eeglab) and 3D-interpolation (TriScatteredInterp, 'nearest')
- Write only included channels: write with or without excluded channels
- Supported file formats are .sef / .ep / .eph (Cartool), .edf (= edf+), .txt (ASCII-export) and .fif (Elekta-fiff). For fif-export the data is scaled before writing with scale-factors from data-preprocessing.
- Split output in blocks of ... channels: number of channels per block (e.g. if 100 is selected for file with 300 channels, 3 blocks are written)
- Appendix: Filename-appendix for output-file

2. EDF export



- Select reference: mean
median
laplacian: *see appendix*
channels: single or multiple channels (e.g. [94 190])
montage: *see appendix*
- Interpolation of bad channels (spherical spline method)
- Path to store edf files: Folder-Path: e.g. network drive folder)
Empty: same folder as input-file
- Command to mount storage path: command to execute before storing the edf file
(e.g. mount a network drive)

3. Re-reference data



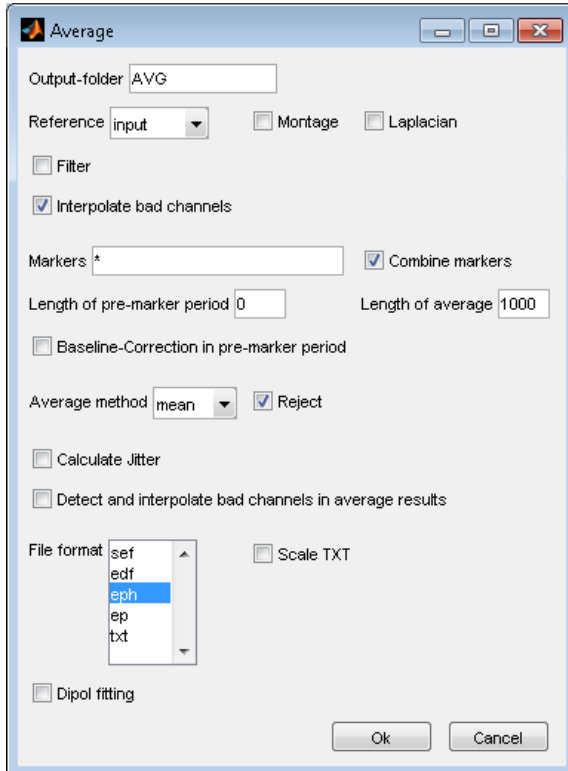
- Output-folder: Folder to store results
- New references to calculate: mean (only good channels included)
median (only good channels included)
laplacian: *see appendix*
montage: *see appendix*
channels (single or multiple channel numbers)
- Interpolation of bad channels (spherical spline method) after setting new reference (in case of montage, interpolation is done in advance)
- file formats to store files (multiple file formats possible)
 - If 'txt' selected, factor for scaling txt-export has to be defined (default = 1)

4. Save epochs

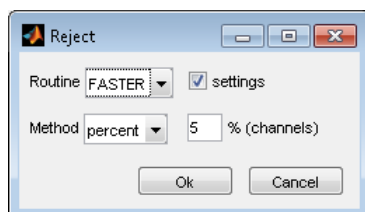
The function allows splitting eeg/meg data in epochs of predefined lengths. For selection of epochs channels data is labeled good or bad every $\frac{1}{2}$ second and in respect to value 'Percent of good channels in single epoch' final epochs are selected. If the sum of selected epochs is lower than 'Minimal part of summed epochs on eeg length' the first value is lowered stepwise by 1% until enough epochs are found.

- Output-folder: Folder to store results
- Interpolate bad channels: Spherical spline interpolation of bad channels at the beginning
- Length of resulting epochs in timeframes
- Minimal part of summed epochs on eeg length: value between 0 and 1. Values > 1 = fixed number of epochs
('Percent of good channels per epoch' is lowered until this value is reached)
- Settings bad detection: *see appendix*
- Markers to exclude: epochs containing listed markers are excluded
- Markers to include: only epochs with listed markers are included
- Marker to start/end taking epochs: Search for valid epochs will be limited accordingly
- File formats to store epochs (multiple file formats possible)
- Replace bad channels: replace bad channels with new results of bad channels detection for epoch's selection
- Plot quality control: Head-plots with alpha power to control quality

5. Average

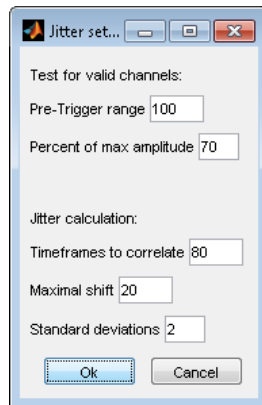


- Output-folder: Folder to store results
- Reference for average:
 - mean (only good channels included)
 - (multiple selections possible) median (only good channels included)
 - laplacian *see appendix*
 - montage *see appendix*
 - channels (single or multiple channel numbers)
- Filter settings: 'see Preprocessing'
- Interpolation of bad channels (spherical spline method) after re-referencing (in case of montage, interpolation is done in advance)
- Markers: Marker to average
 - * = a window with all found markers is shown for first processed EEG/MEG and one or more markers can be selected
 - If multiple markers are selected, separate outputs for every marker are generated
- Length of pre-marker period: Pre-marker period in time frames to include in result
- Length of average: Length of result in time frames
- Baseline-corr. in pre-marker period: correct baseline in pre-marker-period only
- Average method: 'mean' or 'median' (empty or other string = mean)
- Reject



- Routine: FASTER or TAPEEG (FASTER: SD; to lower threshold for rejection decrease the value)
- Method: 'single' (sweeps to reject are calculated for every channel separately)
- 'percent' (max number of rejected channels per sweep)

- Calculate Jitter:



Pre-Trigger range: Range (timeframes) at beginning of epoch to measure baseline mean & std

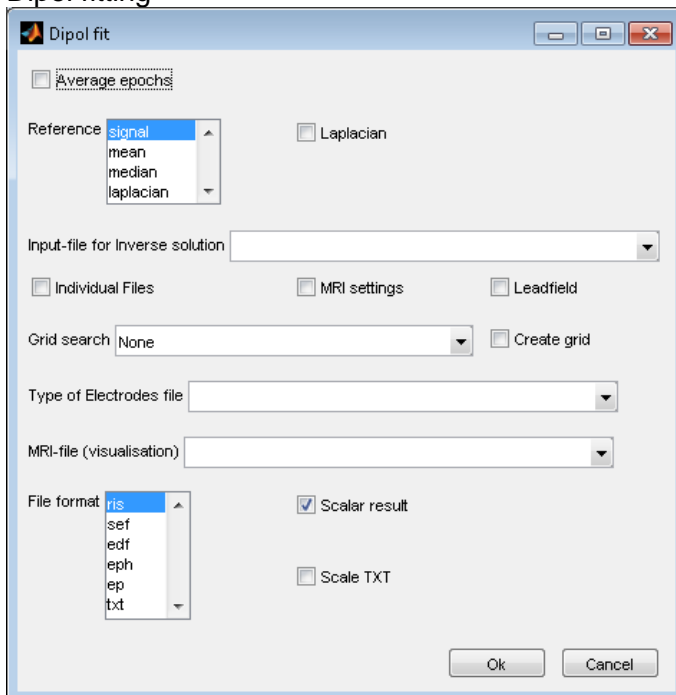
Percent of max amplitude: Amplitude of maximum absolute peak in all channels is selected, other channels are valid if their max-amplitude is > percent of maximal amplitude

Timeframes to correlate: number of timeframes around peak to correlate

Maximal shift: maximal allowed shift

Standard deviations: Std for including/excluding sweeps

- Detect and interpolate bad channels in average result
see Appendix 4
- File format: format to store files (multiple file formats possible)
- Dipol fitting



Average epochs: Enabled = average result is used for dipol fitting
 Disabled = single epochs are used for multiple dipol fitting

Other settings: *see Inverse solution*

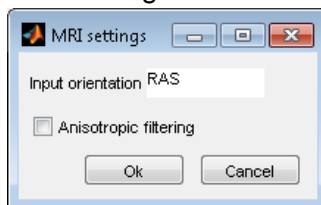
6. Inverse solution *(not included in first release)*

Calculation of inverse solution (IS) is either based on Template-Files or individual files. For processing with Template-files select the files for inverse solution, solution points and electrodes in the dialog. For individual files select only the file-types. While processing files are found by their types in the patient-folder and used for calculation of inverse solutions.

- Output-folder: Folder to store results
- Reference of signal file:
 - Signal: Only for Leadfield or MRI-file!!
(Leadfield is corrected for reference channel before calculation of IS)
 - Mean: Average reference is calculated before calculation of IS (only good channels included)
 - Median: Median reference is calculated before calculation of IS (only good channels included)
 - Laplacian: Laplacian reference is calculated before calculation of IS
- Interpolate bad channels: spherical spline interpolation of bad channels before calculation
- Exclude bad channels: Exclude bad channels for calculation of inverse solution (only for 'signal'-reference; disabled for Input-file *.is or *.spinv)

- Input-file for inverse solution:
 - Select file: One input-file for all files to process
 - Separate input files:
 - Cartool inverse solution-file (*.is)
 - sLoreta inverse solution-file (*.spinv)
 - Leadfield (*.LF.bin; Cartool-format or created by TAPEEG)
 - Fieldtrip to calculate sLoreta or LCMV-beamformer
 - MRI-file (*.hdr / *.nii / *.mri.fif / *.iso.fif / dicom)
 - Segmentation
 - Calculation of BEM-meshes
 - Leadfield-calculation
 - Fieldtrip to calculate sLoreta or LCMV-beamformer
- Individual Files: Enabled, if individual files for every subject are used
The files have to be stored in the subject-folders. Files are found by their file-endings (e.g. '.hdr').

- MRI-settings:

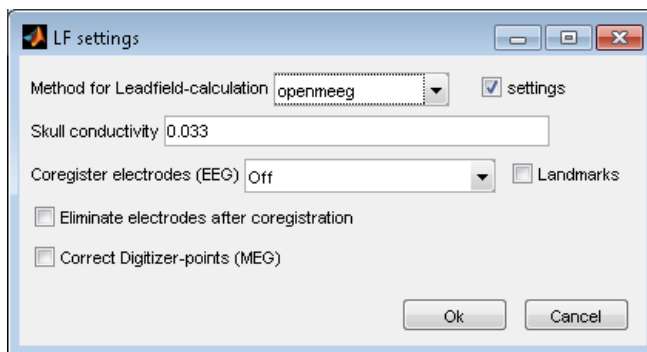


(only for MRI-file)

Input orientation: Set original orientation of MRI (with visual control)

Anisotropic filter: Settings for sampling rate, iterations and diffusion parameter

- Leadfield:

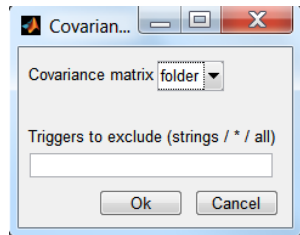


(only for MRI-file)

Method for Leadfield-calculation: EEG: openmeeg, FEM-simbio, dipoli (only linux), concentricspheres, singlesphere
 MEG: localspheres, singlesphere

Method-settings:	<p>Number of vertices for meshes</p> <p>OpenMeeg: Minimal thickness for skull and other compartements</p> <p>FEM-simbio: Shift and Resolution</p>
Skull conductivity:	<p>Standard value 0.033</p> <p>(FEM-simbio : 0.33 0.14 1.79 0.01 0.431)</p>
Co-register:	<p>Automatic translation/rotation</p> <ul style="list-style-type: none"> - Shape of electrode configuration is not altered and electrodes coregistered to the head shape using an iterative closest point algorithm (icp) <p>Interactive coregistration</p> <ul style="list-style-type: none"> - Interactive coregistration using code from the fieldtrip-toolbox <p>Use landmarks</p> <ul style="list-style-type: none"> - Electrodes have to be selected as landmarks - A window is shown to place selected electrodes/landmarks on the mri-scan <i>(if individual scans are used, you can select a MRI-template with predefined landmarks. This template will be warped to the individual scan to get the landmarks)</i> - Coregistration is performed using a new algorithm with translation / rotation / resize and morph of the electrode configuration
Eliminate electrodes	<p>Selected electrodes are deleted after the coregistration (the resulting number of electrodes must be equal to the number of data channels used for calculation of inverse solution)</p>
Correct digitizer-points:	<p>Manually delete digitizer-outliers before co-registration (only for MEG)</p>

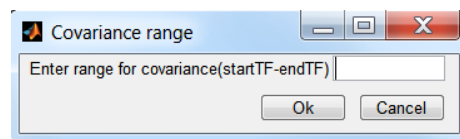
- Covariance matrix



(for scalar output & calculation of LCMV beamformer)

Method:

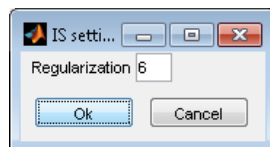
- Folder: All EEG/MEG files in same folder as input file are used to calculate covariance matrix
- File: Covariance matrix is calculated using whole input file
- Range: User is asked to input range in timeframes for calculation of covariance matrix



Markers to exclude: Indicate Markers (markers need to have a duration) marking bad segments in input-file. Selected marker-episodes will be excluded for calculation of covariance matrix

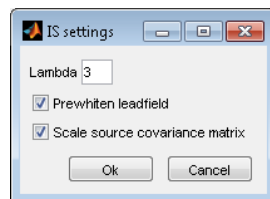
- Type of inverse solution: Cartool, sLoreta, eLoreta, LCMV beamformer, Minimum Norm Estimate, Dipol Fit

- Cartool:

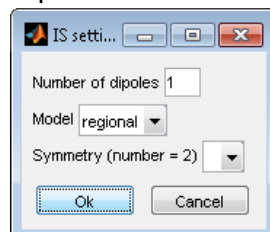


Cartool stores inverse-solution matrices for 13 different numbers of regularization, one has to be selected (default: 6; 0 = no regularization)

- Minimum Norm Estimate:



- Dipol Fit:



Number of dipoles: Default = 1

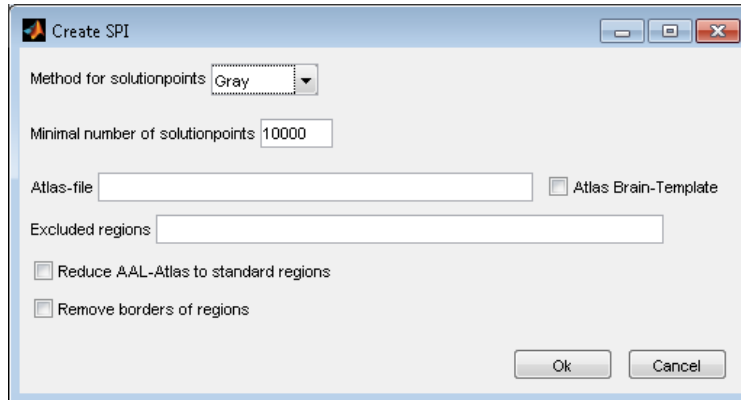
Model: Regional = One dipol for all timeframes
Moving = different dipols for every timeframe

Symmetry: Symmetry restrictions for 2 dipols

Note: If Solutionpoints-file is selected, grid-search is performed (faster)

- Solutionpoints-file:
 - Cartool-format (*.spi)
 - MRI-file (IS-file) = same file as for Leadfield-calculation
 - MRI-file (spi.hdr) = MRI with ending 'spi.hdr'
 - MRI-file (spi.nii) = MRI with ending 'spi.nii'

- Create SPI:

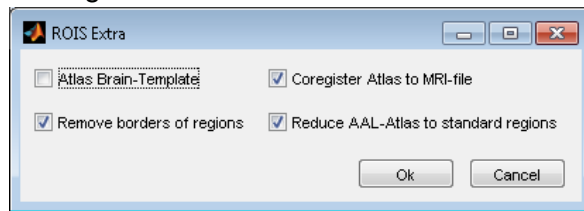


MRI is segmented to brain-surface, gray and white matter

- Method for solutionpoints: Gray / Gray&White / Surface
- Number of solutionpoints: default = 10'000
- Atlas-file: Atlas.nii-file (will by coregistered to MRI)
 - Normalize Template: Normalize Atlas before Coregistration
 - Excluded regions: Exclude regions of Atlas-file for solutionpoints
 - Reduce AAL-Atlas: Reduce to standard regions (= 76)
 - Remove borders of regions: Solutionpoints close to borders of regions are removed
- Electrodes-file:
 - Locations in input data (only .fif or .mff)
 - Electrodes-file (*.xyz or *.els file format)
- MRI-file (visualisation): MRI-file for visualisation of results in Cartool (.hdr)

- ROIS-file:
 - For Cartool, sLoreta or Leadfield has to be a *.rois-file (Cartool-format)
 - For MRI-file has to be an MRI-Atlas-file (*.nii, *.hdr)

- Settings:



(only for ROIS-file = MRI-file)

- Normalize using Template: Provide a Brain-MRI-file corresponding to the anatomy of the Atlas-file. The atlas-file will be normalized to the brain-segment before co-registration
- Co-register Atlas to MRI-file: Co-register Atlas to MRI-file (input-file for solution-points) using spm8
- Remove borders of regions: Solutionpoints close to borders of regions are removed
- Reduce AAL-Atlas: If Atlas is AAL, reduction to standard regions (Standard = 76 regions)
- ROIS-method:
 - mean (only for inverse solution FFT)
 - maxpower (voxel with maximal power in different frequency bands is found for every region, resulting in as many inverse-solution-results as spectral-bands are defined)
 - center: center voxel for every region is found
 - off: results without reduction to regions are written

- Spectral bands:

	lowfreq	highfreq
1	1	4
2	4	8
3	8	10
4	10	13
5	13	30
6	30	48

Spectral bands are defined , one spectral band per row

- File format: File-format for results
- Scalar result: Optimal orientation of inverse solution results is found by method of Sekihara (Sekihara et al 2004)
- Scale Text: For *.txt, output can be scaled, e.g. for import in BrainWave

7. Inverse solution FFT *(not included in first release)*

Settings are explained in

- Inverse solution
- Frequency analysis
- Save epochs

Inverse solution FFT is calculated using cross-spectras (method: sLoreta Pasqal Marqui, www.uzh.ch/keyinst/NewLORETA/LorHelpFiles/LorHlp.htm#AppendixMisuse)

8. Frequency analysis

Spectral Analysis

Output-folder: Spect

Reference: mean ☐ Montage ☐ Laplacian

Interpolate bad channels (method): spherical

freqlim50: 50
freqlim60: 50
freqlimlow: 70
freqlimhigh: 50
spectslow: 0.5 2
spectshigh: 15 50
Detect bad periods: zvaluebroken: 0
zvaluevars: 3
zvaluehurst: 3
zvaluemedian: 3
zvaluecorr: 0
LAPL:
triggerexclude:

Minimum percent good channels in single window: 90

Method: multitaper

FFT window (seconds): 4 Hanning-window (percent): 0

Lowest frequency: 1 Highest frequency: 50

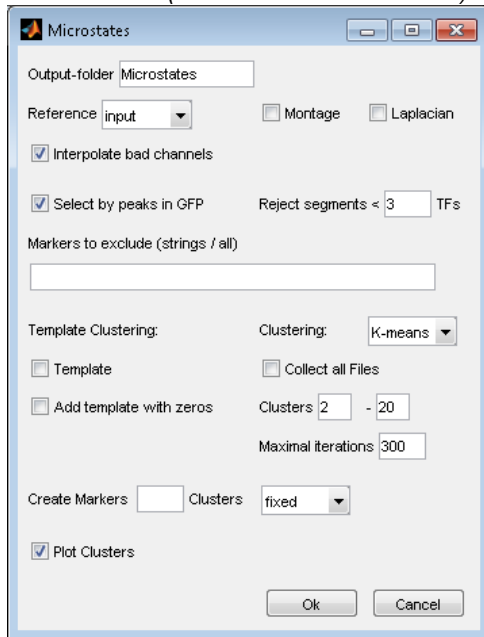
Spectral Bands: table 5x2

☐ Reduce results to Mappings
☐ Calculate power per channel
☐ Plot spectras
☒ Delete results from previous run

Ok Cancel

- Output-folder: Folder to store results
- Reference for average: for description see re-referencing
- Interpolate bad channels: Interpolate bad channels with selected method
- Detect bad periods: see appendix
(data is splitted into epochs with FFT-window length and after bad channels detection, only good epochs are included in result)
- Minimum percent good channels in single window: default = 0.9
If > half of windows is labeled bad, this value will be automatically lowered (log-file)
- Method for FFT: 'welch' or 'multitaper'
- FFT-window: Length of window for FFT in seconds
- Hanning window (percent): percent of hanning window used for frequency analysis
- Lowest frequency: lowest frequency bin to store
- Highest frequency: highest frequency bin to store
- Spectral bands: Band-power(s) to calculate for every patient
- Reduce results to Mappings: Select 'Mappings.xls'.file
- Delete results from previous run: When processing files, a Matlab-file is created for every single patient, holding results of frequency analysis of all EEG/MEG's of that patient. If the frequency analysis is run again, normally the file must be replaced and therefore 'Yes' should be selected.

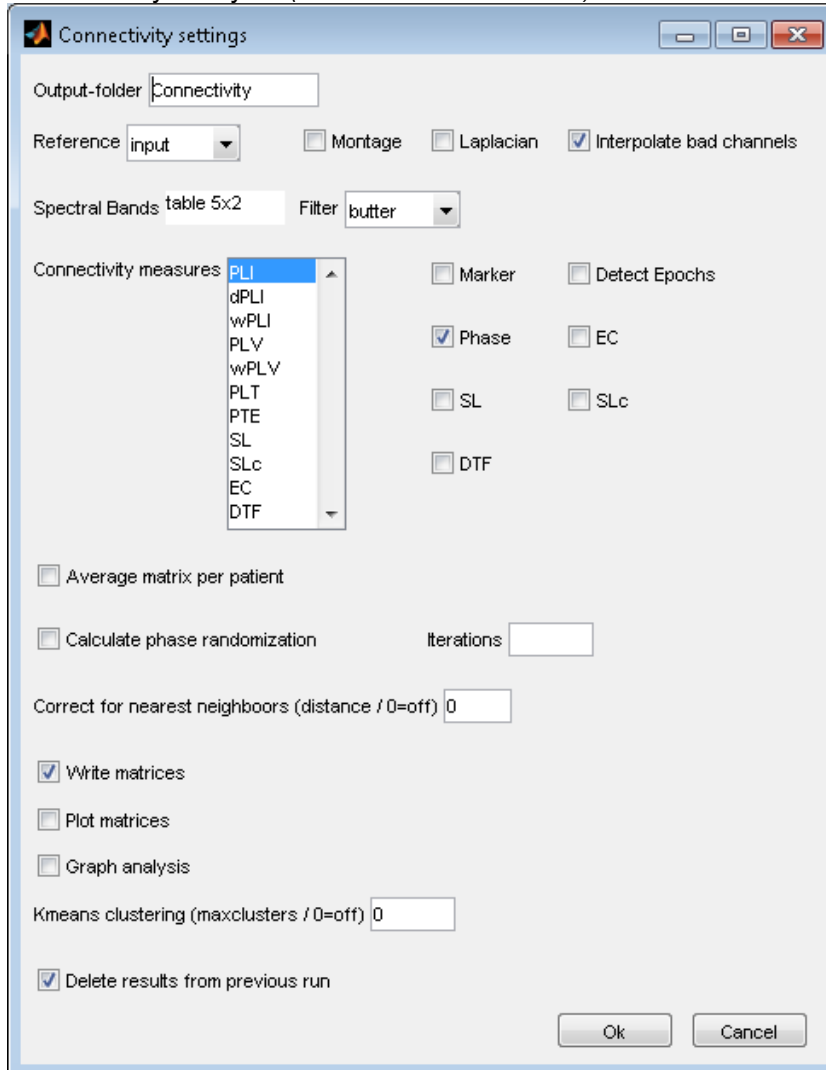
9. Microstates *(not included in first release)*



Calculation of Microstates with Global-Explained-Variance as measure for distribution

- Output-folder: Folder to store results
- Reference for average:
 - mean (only good channels included)
 - median (only good channels included)
 - laplacian *see appendix*
 - montage *see appendix*
 - channels (single or multiple channel numbers)
- Interpolation of bad channels Spherical spline interpolation after re-referencing
- Select by peaks in GFP GFP is calculated and only TF's with maximal GFP (value > values at TF's ± 1) are clustered
- Reject segments Segments with maximal GFP and length < value are added to next segment
- Markers to exclude Selected markers with duration > 1 timeframe are excluded
- Template Clustering: Load Microstates-file as template for clustering
 - Add zeros: add template with zeros for clustering (*Microstates-file are generated by Clustering in TAPEEG "*_Clusters*.sef"*)
- Clustering: K-means or T-AAHC (*see Cartool*)
 - Collect all Files: Clustering is done for all processed files together
 - Clusters: Indicate minimal and maximal number of Clusters
 - Maximal iter.: Maximal number of iterations
- Create Markers Create markers for indicated number of clusters
 - Fixed: Number ≥ 2
 - Auto first: Optimal number of clusters is found for 1. File and used for all following files
 - Auto: For all files optimal number of clusters is found separately
- Plot Clusters Plot topography of clusters

10. Connectivity analysis *(not included in first release)*



The image shows a 'Connectivity settings' dialog box with the following fields and options:

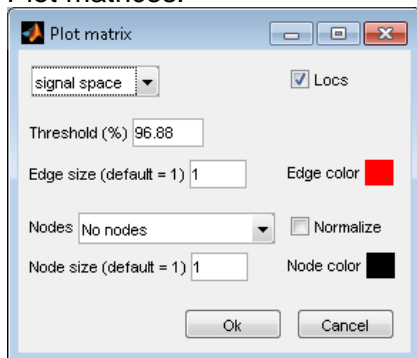
- Output-folder:** Connectivity
- Reference:** input (dropdown), Montage (checkbox), Laplacian (checkbox), Interpolate bad channels (checked checkbox)
- Spectral Bands:** table 5x2 (text), Filter: butter (dropdown)
- Connectivity measures:**
 - PLI (selected in dropdown)
 - dPLI
 - wPLI
 - PLV
 - wPLV
 - PLT
 - PTE
 - SL
 - SLc
 - EC
 - DTF
- Marker (checkbox), Detect Epochs (checkbox)
- Phase (checked checkbox), EC (checkbox)
- SL (checkbox), SLc (checkbox)
- DTF (checkbox)
- Average matrix per patient (checkbox)
- Calculate phase randomization (checkbox), Iterations: (text field)
- Correct for nearest neighbors (distance / 0=off) 0 (text field)
- Write matrices (checked checkbox)
- Plot matrices (checkbox)
- Graph analysis (checkbox)
- Kmeans clustering (maxclusters / 0=off) 0 (text field)
- Delete results from previous run (checked checkbox)
- Buttons: Ok, Cancel

- **Output-folder:** Folder to store results
- **Reference:**

mean	(only good channels included)
median	(only good channels included)
laplacian	see <i>appendix</i>
montage	see <i>appendix</i>
channels	(single or multiple channel numbers)
- **Spectral bands:** spectral bands to calculate connectivity
- **Filter: filter mode**

freq	frequency filter
butter	butterworth filter
cheby	Chebyshev filter
firls	high order least square filter
wavelet	wavelet filter
freq-shift	frequency filter with opposite shift by one frequency bin of the two frequency windows in fft

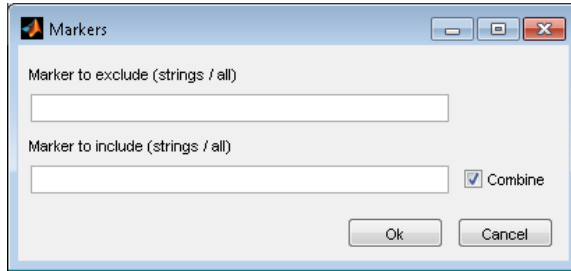
- Connectivity measure: PLI (phase lag index)¹
 - $PLI = | \langle \text{sign}[\sin(\Delta\Phi(t_k))] \rangle |$
($\Delta\Phi$ = phase difference at time point t_k)
- dPLI (directed phase lag index)²
 - $dPLI = \langle \text{sign}[\sin(\Delta\Phi(t_k))] \rangle / 2 + 0.5$
- wPLI (weighted PLI)³
- PLV (phase locking value)⁴
- PLT (phase locking time, Stam et al. 2013)
- PTE (phase transfer entropy, Lobier 2014)
- SL (synchronization likelihood)⁵
- SLc (synchronization likelihood correct for volume conduction using linear regression)
- EC (average envelope correlation & envelope average correlation)⁶
- DTF (direct transfer function)^{7,8}
- Average matrix per patient: Proceed only with average matrix per patient
- Calculate phase randomization:
Input data with randomized phases is generated and connectivity matrices calculated (Iterations = number of connectivity matrices with randomized phases).
- Correct for nearest neighbors: If >0 connections of nodes with distance < value are replaced by maximum connectivity value of resulting matrix
- Write matrices: if selected all calculated matrices are stored as txt-files
- Plot matrices:



Plot matrices in signal or source space

- Graph analysis: see *Graph analysis*
- Kmeans clustering: Kmeans clustering. If multiple matrices are calculated, entered number defines the maximal number of clusters. Calculation is done for 2 to maximal clusters
- Delete results: When processing files, a Matlab-file is created for every single patient, holding results of connectivity analysis of all EEG/MEG's of that patient. If the connectivity analysis is run again, normally the file must be replaced and therefore 'Yes' should be selected.

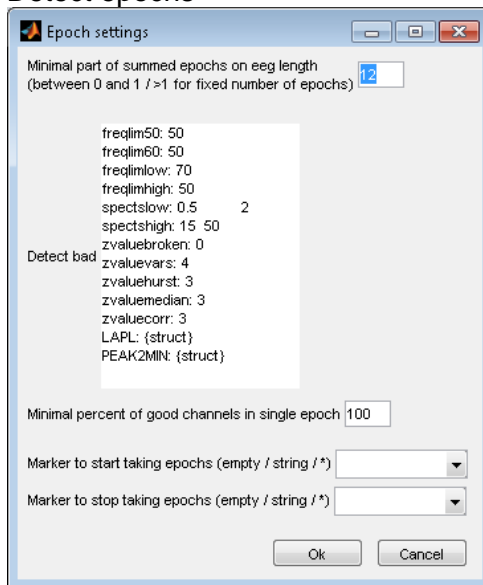
- Marker



Select Marker-Periods to exclude / include for connectivity analysis

Combine: If multiple markers to include are selected, connectivity is either calculated for all together or separately

- Detect epochs

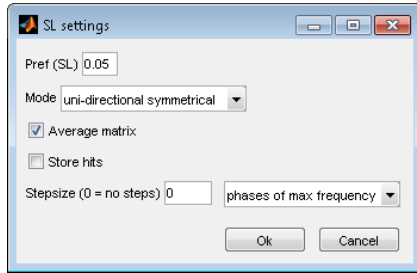


see 'Save epochs'

- Phase

Phase estimate:	Hilbert (default), Wavelet, Rihaczek, Zerocross
Use Hanning window:	If enabled, a 50%-Hanning window is used for phase-estimate (<i>disabled for wavelet and Rihaczek</i>)
Window length:	Estimation of phase is done with a sliding window of specified size (in seconds)
Markers to exclude:	Parts with selected markers are excluded, rest of data stitched.
Store phase:	Phase-Information per channel is stored in Matlab-Container-file
Stepsize:	if >0, data will be divided in segments including ... 'phases of maximal frequency' / 'timeframes' and for every segment a connectivity-matrix is calculated
Stepunit:	Timeframes (TFs) or phases of maximal frequency
wPLI: Debiased (only wPLI)	wPLI is calculated with debiased-correction
wPLV: Max Phase Lag Vol...	Maximal number of TF-shifts, explained by volume conduction. For the number of TF's an angle is calculated (in relation to maximal frequency in signal) and phase lags below this angle are disregarded
Store phase shift	Store phase shift's as separate matrix
PTE: Factor for delta	$\text{delta} = \text{mean frequency} / \text{factor}$
PTE: Make directional	convert pte to directional matrix (values / upper + lower triangle)

- SL / SLc



Pref:

For SL-calculation p-ref has to be defined manually (default = 0.01). All other values (lag,m,w1,w2) are defined automatically

(Montez et al- T., Neuroimage.2006)

Mode (only SLc):

Linear regression to correct for volume conduction

- unidirectional asymmetrical: residuals are only calculated for lagging channel, final matrix is asymmetrical
- unidirectional symmetrical: residuals are only calculated for lagging channel, final value is mean of two values (from upper and lower triangle of matrix)
- bidirectional: residual of linear regression are calculated for both channels

Average matrix:

Only averaged SL-matrix is stored

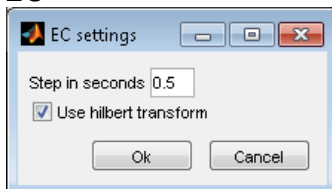
Store hits:

Hit-matrices are stored in Matlab-Container-file

Stepsize:

if >0, data will be divided in segments including ... 'phases of maximal frequency' / 'timeframes' and for every segment a connectivity-matrix is calculated

- EC



Step in seconds: default 0.5

Use Hilbert transform: standard = enabled (publications of Brookes et al.!))

- DTF

DTF

Markers (strings / all)
Start

Lag 0 Length 2000

Order 3 Optimal order

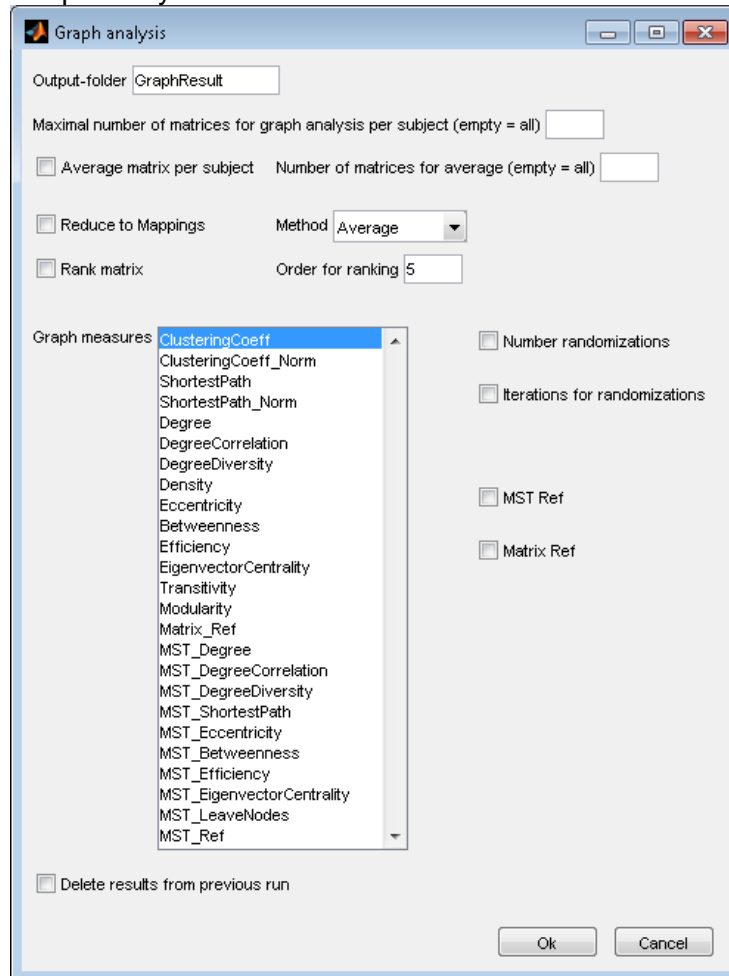
☐ Input significance test

Shuffling Times 1000 Significance Level 0.05

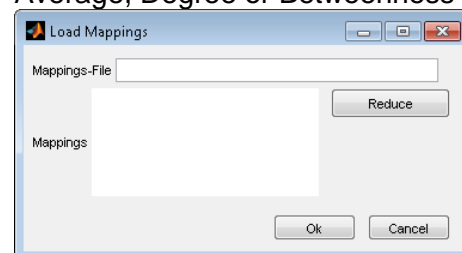
Ok Cancel

- | | |
|--------------------------|---|
| Markers: | Periods for analysis of DTF are selected by Markers (Start = 1. Timeframes of data) |
| Lag: | Start point of periods is shifted by lag-value |
| Length: | Length of period(s) for analysis |
| Order: | Order for DTF-analysis (Button 'Optimal order' calculates data driven best value) |
| Input significance test: | Set shuffling Times and Significance level |

- Graph analysis



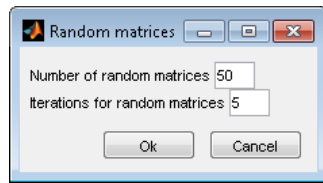
- Output-folder: Folder to store results
- Maximal number of matrices for graph analysis per subject: Empty = graph analysis for all matrices
- Average matrix per subject: Graph analysis on average matrix
- Number of matrix for average matrix: Integer value or empty
- Reduce to Mappings: Average, Degree or Betweenness



Select Mappings-file (*.xls/*.xlsx)
Reduce: Exclude channels in Mappings

- Rank matrix: If selected, values of matrix are ranked = $(\text{rank}/\text{number of connections})^{\text{order}}$
- Graph measures: see Appendix 5.
- Delete results from previous run: Results from a previous analysis are deleted

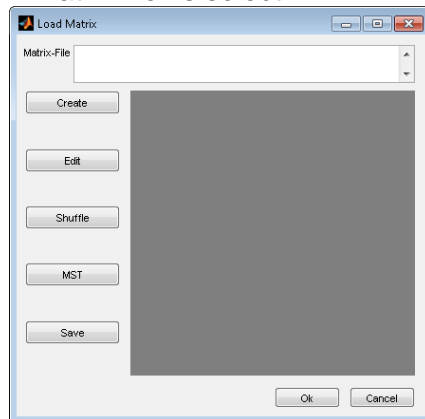
- If 'ClusteringCoeff_Norm' or 'ShortestPath_Norm' are selected, average clustering coefficient and characteristic path length are calculated for multiple random matrices with preserved degree-distribution. Results are 'original value / mean(random values)'



Number of random matrices: Default 50

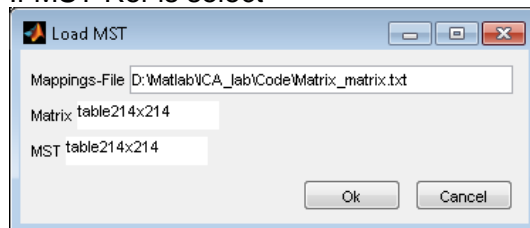
Number of iterations: Number of iterations for creating random matrix

- If Matrix Ref is select



Select matrix for calculation of Matrix_Ref.

- If MST Ref is select



Select matrix for calculation of MST-Ref-matrix.

Note: Graph measures are calculated with the toolbox 'Brain Connectivity Toolbox' (<http://www.brain-connectivity-toolbox.net>)

For calculation of MST 'kruskal_mst' is used (Mathworks File-Exchange)

For calculation of eccentricity 'Graph Theory Toolbox' is used (Mathworks File-Exchange)

Degree Correlation: Pearson correlation of node degrees (Stam et al. 2012)

DegreeDiversity: $\text{mean}(\text{degree}^2) / \text{mean}(\text{degree})$ (Stam et al. 2012)

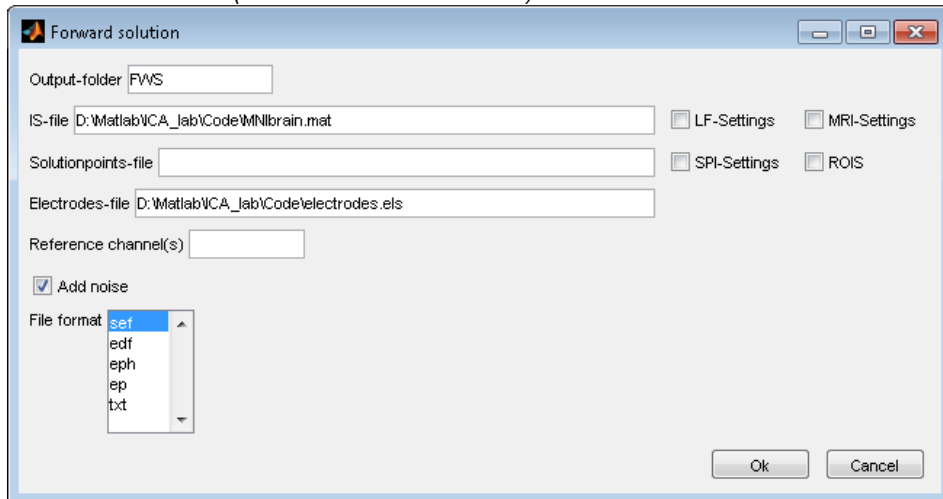
MST_Ref: mean difference of MST to MST-Ref-matrix

Matrix_Ref: Kendall-Correlation of Matrix to Matrix_Ref

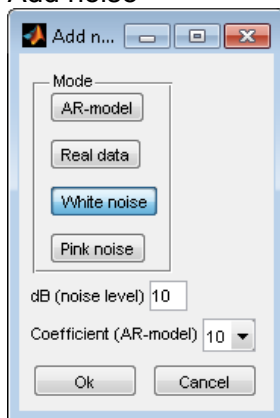
11. Distance matrix

Distance matrices of results of inverse solutions are calculated
(only interesting for results of inverse solution, especially with maxpower method)

12. Forward solution *(not included in first release)*

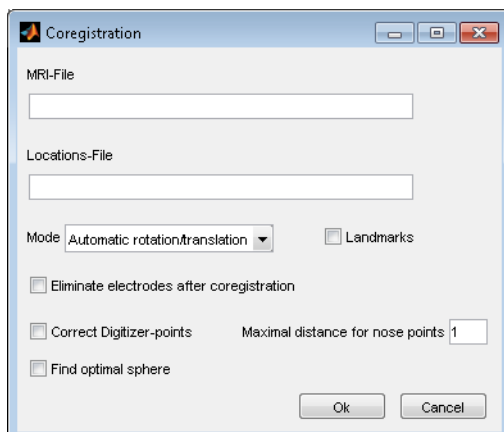


- For settings see 'Inverse solution'
- Reference channel Forward solution will be corrected for the reference channel (multiple channels possible, empty = disabled))
- Add noise



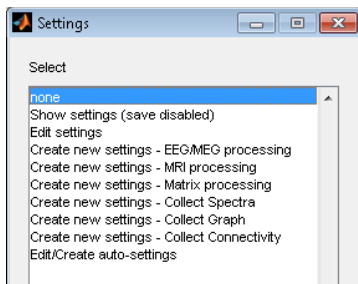
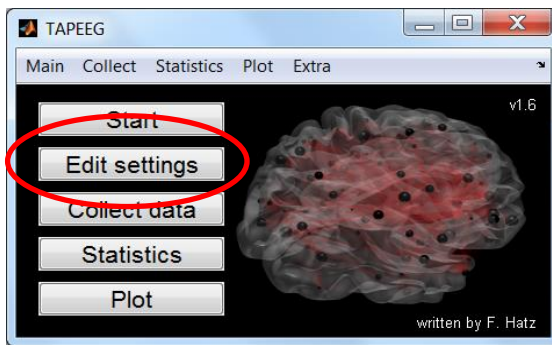
- Mode: AR-model (Green et al. 2012) with selected coefficient
Real data: real eeg/meg input data
White noise
Pink noise
- dB: Amount of noise to be added to data

13. Co-registration LOCS/MRI *(not included in first release)*



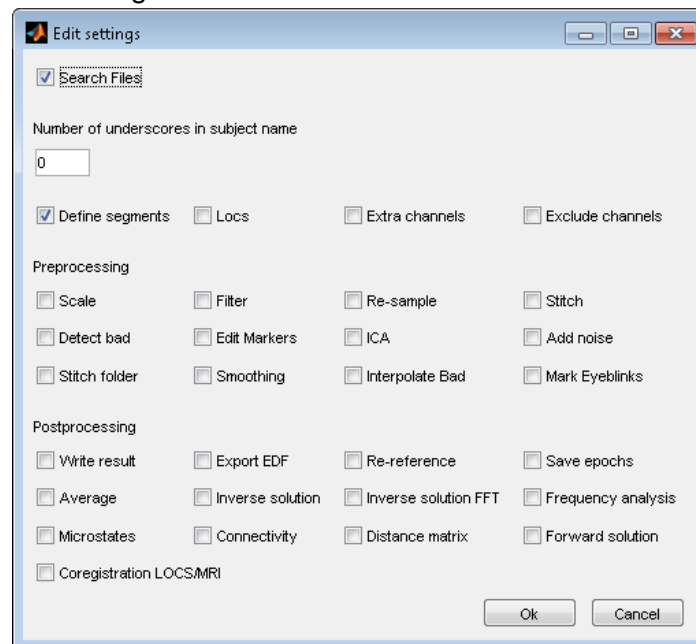
Perform co-registration of electrodes (meg: digitizer-points) with headshape (input: MRI-file)

V. Edit settings



Show: only reading, no changes are stored

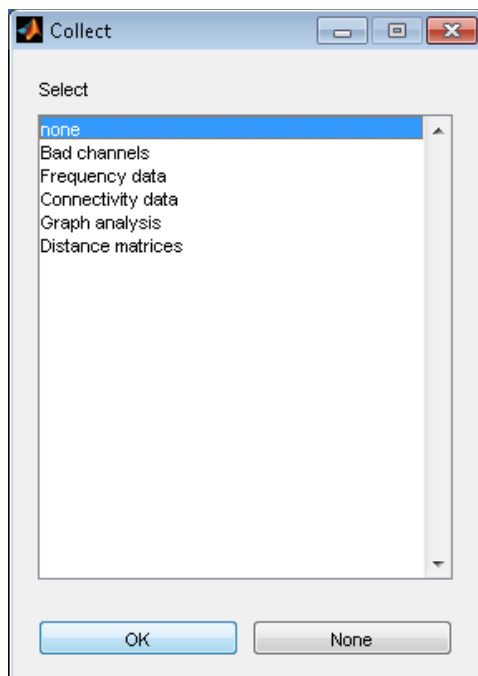
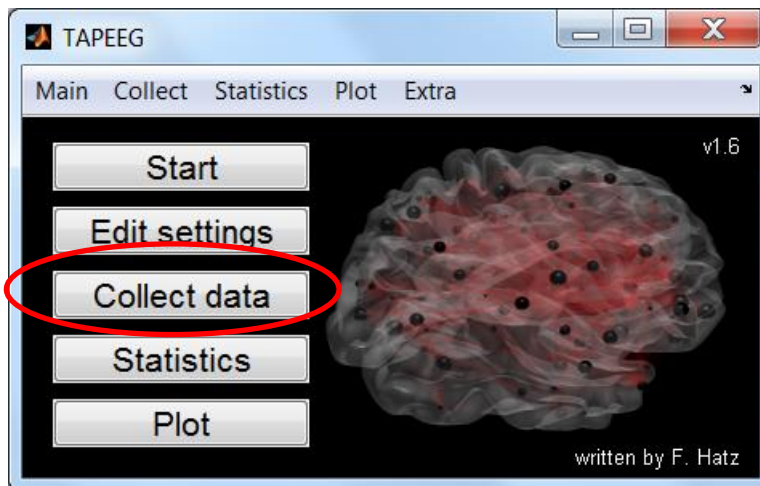
Edit: edit settings



Create: Create new settings after selection of folder to store new settings

Auto-settings: A settings-file is created in the application-folder ('settingsauto.mat'). While this settings.file is in the folder, TAPEEG starts up loading this settings-file and starting processing automatically.

VI. Collect data



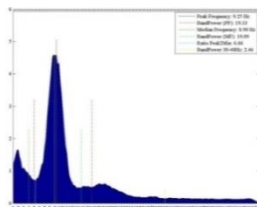
1. Collect bad channels

After selection of folder to process, *.bad.vrb-files are collected and results written to excel-files

2. Collect frequency data

- Search folder: Folder to search for results of frequency analysis (*Spectra.mat)
- Include strings: Only '*Spectra.mat'-files with specified string(s) are included
- Exclude strings: '*Spectra.mat'-files with specified string(s) are excluded
- Search Files: Search files to collect and preload first file
- Number of underscores in...: Define patient's name by filename
- Channels for background activity: Select channels for background activity
(Standard pre-selection of channels is set in file 'BackgroundActivity.xls' in application folder)
- Output-folder: folder to store results
- Mappings: Select mappings-file (see appendix)
- Source for peak and median frequency: mean or median
(Frequency-epochs are averaged by taking the mean or the median)
- Spectral Bands: Frequency ranges for band-power
For calculation of band power the absolute power of every frequency range (area under the curve) is calculated and divided by the absolute power from minimal to maximal frequency of all defined frequency ranges. To calculate the area under the curve the frequency spectrum is first interpolated to a resolution of 0.1 Hz.
- Range peak frequency low and high: Lowest and highest values for peak frequency

- Range median frequency low and high: Range to calculate median frequency
- Minimal Peak2Min: Window for detection of peak frequency is shifted towards higher frequencies until 'peak2min' (ratio amplitude of peak frequency to trough amplitude below peak frequency) reaches predefined value.
- Calculate single channel peaks: If enabled peak frequency and quality measures are calculated for every channel and for results of background-activity and mappings single-channel values are averaged (mean or median – see *source for peak*). If disabled for results of background activity and mappings, spectra are first averaged (mean or median) and then values are calculated.
- Manually correct peak frequency: A window is shown to manually correct the peak frequency. You can click on the plot and the new peak frequency is searched in the 'clicked' region (clicked frequency +/- 2 x quality-range)
- Quality: Spectral density plots will contain peak & median frequency, there ranges and band power (last entry).



- Range in Hz for quality check: For quality check the band power of the peak-frequency range and the band power of the peak-frequency (+/- range in Hz) is stored in result files. Additionally, the 'Peak2Min' and 'Peak Ratio' are calculated. The first is power of peak-frequency over power in smallest frequency bin left to peak frequency; the second is band power of peak frequency over band power in peak-frequency-range.
- Evaluate quality:

Plots are evaluated by selected criteria. An empty criterion is disabled. The 'number of positive criteria' determines the number of fulfilled criteria for selecting 'good'

- Plot spectra for channels: channel-data is averaged over all subjects and plotted (relative power)
- Plot spectra for mappings: Spectra for mappings (every subject) are plotted

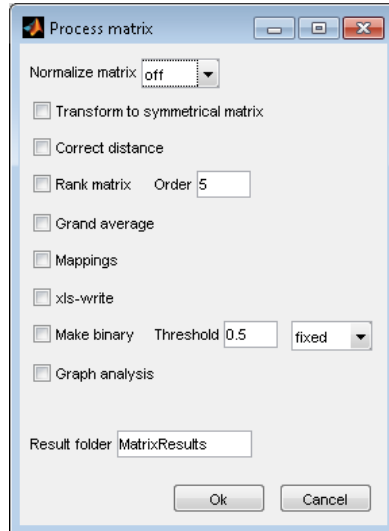
1. Collect connectivity data *(not included in first release)*

The screenshot shows a Windows-style dialog box titled "Collect Connectivity". It has several input fields and checkboxes. The "Search folder" field is at the top. Below it are "Include strings" and "Exclude strings" fields. There is a checkbox for "Search Files" and a "Preload File-Info" button. Further down, there's a field for "Number of underscores in subject name". The "Output-folder" is set to "ConnectivityAnalysis". There are checkboxes for "Select connectivity measures", "Correct by phase randomization", "Make binary", and "Number of matrices per subject (empty = all)". The "Correct by phase randomization" checkbox has a value of "0.5" and a "fixed" dropdown. The "Make binary" checkbox has a value of "0.5" and a "fixed" dropdown. The "Number of matrices per subject" field is empty. There are checkboxes for "Average connectivity matrices per subject", "Process matrices", "Write matrices", "Graph analysis", "Plot matrices", and "Kmeans clustering". The "Write matrices" checkbox is checked. At the bottom are "Ok" and "Cancel" buttons.

Search folder:	Search folder for connectivity results
Include strings	Strings to include in search for files
Exclude strings:	Strings to exclude in search for files
Search Files:	Search files to collect and preload first file
Output-folder:	Folder to store results
Correct by phase randomization:	Matrices can be corrected by phase randomization in case phase randomization was calculated
	Value: 'percent' (default = 80%) - $Threshold = value\%$ 'std' (default = 1.28) - $Threshold = mean + std * value$
	Method: $Diff = Matrix - Threshold$ Threshold = Values < Threshold set to 0 P-Value = p-value of permutation
Make binary:	Convert matrix to binary matrix with selected threshold
	- fixed: Threshold = value - std: Threshold = mean + std * value - percent: Threshold = value%
Average connectivity matrices:	Single connectivity-matrices or average matrices per subject are collected

Process matrix:

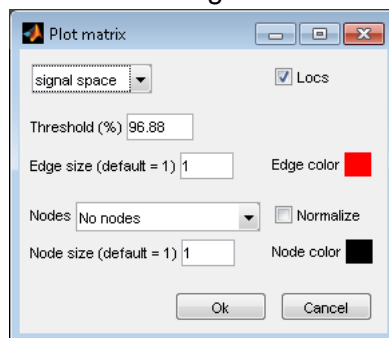
Select steps for processing matrices:



see X. 5.2 Matrix-Files

Plot Matrix

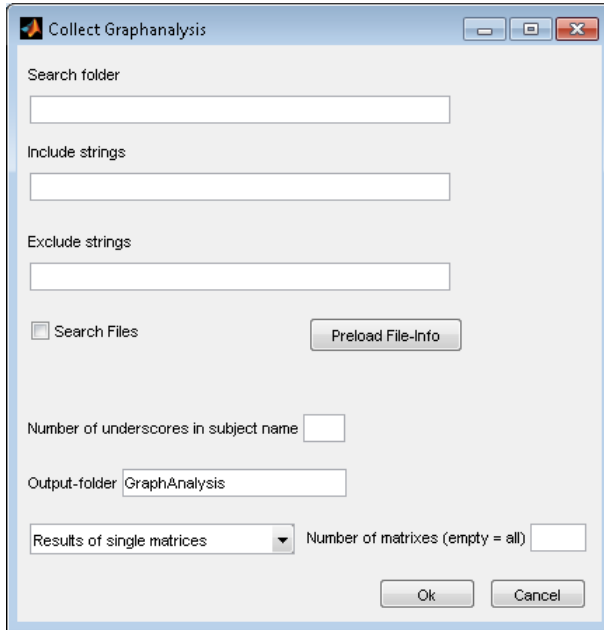
Plot matrix in signal or source space



Graph analysis:

Perform graph analysis (see IV. 4. Graph analysis)

2. Collect graph analysis *(not included in first release)*



Collect Graphanalysis

Search folder

Include strings

Exclude strings

☐ Search Files Preload File-Info

Number of underscores in subject name

Output-folder

Results of single matrices Number of matrices (empty = all)

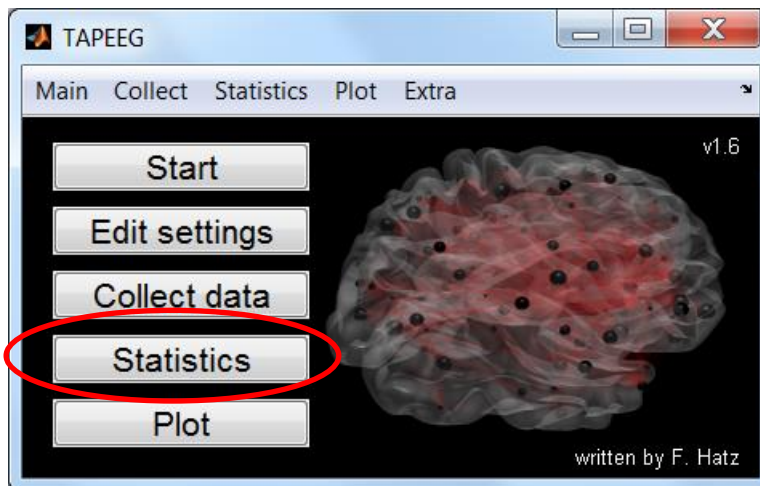
Ok Cancel

Search folder:	Search folder for graph analysis results
Include strings	Strings to include in search for files
Exclude strings:	Strings to exclude in search for files
Search Files:	Search files to collect and preload first file
Number of underscores in...	Define patient's name by filename
Output-folder:	Folder to store results
Mode:	Select if results of single matrices or average will be collected. For average two possibilities are possible: average of results of single matrices or results of average matrix per subject. Results are written to excel-files; results of a Grand-Average-matrix are included (including Grand-Average-matrix and Grand-Average-MST)
Number of matrices:	Number of matrices per patient to include

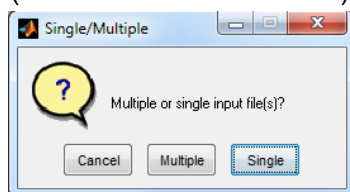
3. Collect distance matrix

For calculations of inverse solutions a distance-matrix of all resulting solution points is generated and stored. These matrices can be collected.

VII. Statistics



1. Data input
(for all statistics the same)



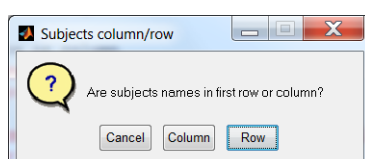
single: Results are all stored in one file

multiple: Results are stored in multiple files, files are collected until the dialog is first time closed without selecting an additional file

Data structure:

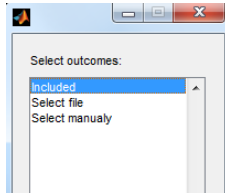
	A	B	C	D	E	F	G	H	I	J
1 C3 R1 V3	P001	P002	P003	P004	P005	P006	P007	P008	P009	
2 Measure1_C1_V1	0.898	1.115	1.115	1.072	1.630	1.701	0.236	1.373	1.601	
3 Measure1_C1_V2	1.663	1.039	1.266	1.766	2.008	1.291	0.896	1.244	1.604	
4 Measure1_C1_V3	1.809	1.312	0.793	1.938	2.145	1.361	0.815	1.464	1.654	
5 Measure1_C2_V1	1.135	1.143	1.203	1.152	2.057	1.292	0.318	0.968	1.716	
6 Measure1_C2_V2	1.456	1.301	1.277	1.790	2.220	1.289	0.651	1.414	1.869	
7 Measure1_C2_V3	1.797	1.329	1.244	1.773	2.315	1.404	0.496	1.393	2.534	
8 Measure1_C3_V1	0.323	0.564	0.635	0.088	1.048	0.182	-0.014	0.691	1.553	
9 Measure1_C3_V2	0.822	0.630	0.887	0.684	1.158	0.548	-0.253	0.432	0.914	
10 Measure1_C3_V3	1.456	1.301	1.277	1.790	2.220	1.289	0.651	1.414	1.869	
11 Measure2_C1_V1	0.595	0.345	0.642	0.658	1.965	1.017	-0.084	0.452	1.388	
12 Measure2_C1_V2	1.360	0.359	0.979	1.639	2.359	0.913	0.503	0.276	1.295	
13 Measure2_C1_V3	1.320	0.591	0.701	1.927	2.364	0.998	1.065	0.350	1.412	
14 Measure2_C2_V1	0.700	0.436	0.911	0.649	2.325	0.807	0.012	0.271	1.561	
15 Measure2_C2_V2	1.407	0.410	0.959	1.593	2.613	0.997	0.348	0.222	1.687	
16 Measure2_C2_V3	1.333	0.613	0.874	1.722	2.516	1.093	0.398	0.214	2.441	
17 Measure2_C3_V1	-0.069	-0.030	0.470	-0.056	1.706	0.072	-1.115	0.038	1.577	
18 Measure2_C3_V2	0.873	0.090	0.775	0.923	1.940	0.136	-0.469	-0.184	1.091	
19 Measure2_C3_V3	0.840	0.154	0.301	1.763	1.342	0.285	-0.169	-0.055	0.533	

Example: Subjects are listed in first row; measures are listed in first column. Here every measure as several variables (C1...C3) and these variables again have several variables (V1...V3).



Select orientation of input file (example = row)

Select mode for outcomes (e.g. Group, cognitive measures)



- If outcome is included , result-file(s) must contain outcome(s) in last row(s)
- File:

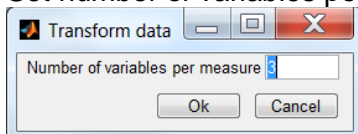
	A	B	C	D	E
1	subject	group	sex	education	MMS
2	P001	1	1	4	27
3	P002	2	1	7	23
4	P003	1	1	6	26
5	P004	2	0	5	29
6	P005	1	1	7	18
7	P006	2	0	4	26
8	P007	1	0	5	29
9	P008	2	0	5	30
10	P009	1	1	6	24
11	P010	2	0	6	23
12	P011	1	0	7	30
13	P012	2	1	4	30
14	P013	1	1	7	29

Subject-names must be equal to subject-names in result-file(s). They can be either in first row or column

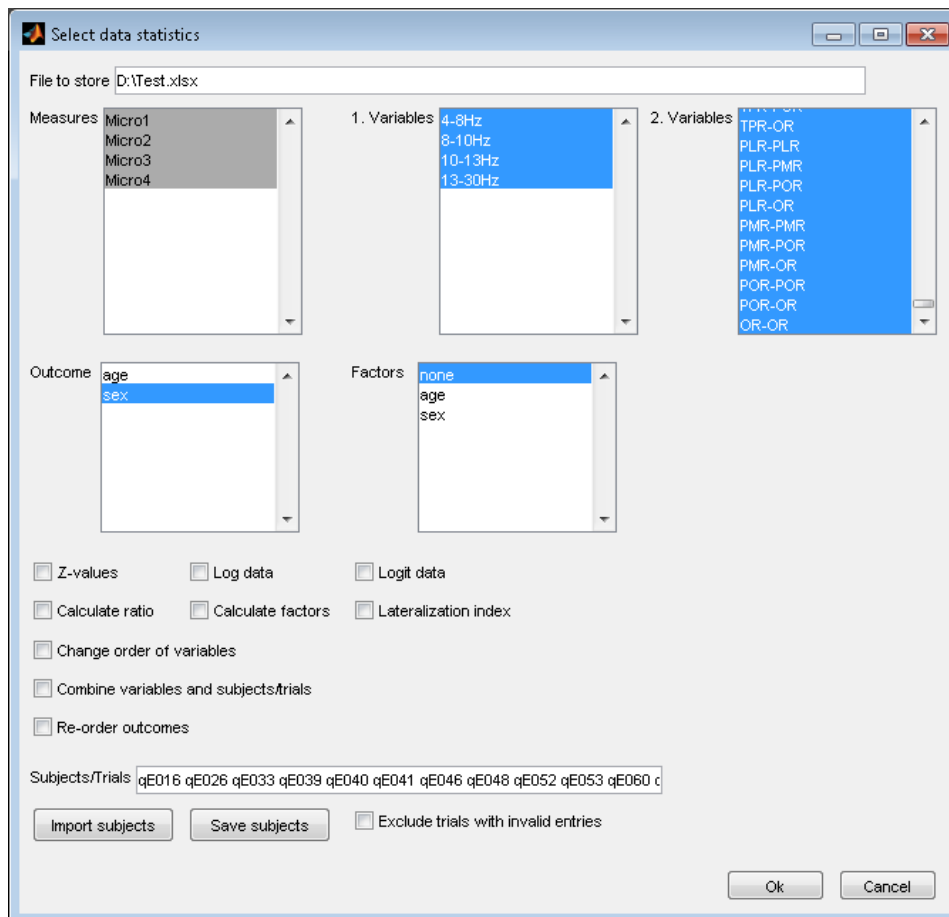
Subjects in result-file(s) and outcome-file are matched and only matched subjects are included in statistics

- Manually: First manually select subjects of group1, second subjects of group2 ...

Set number of variables per measure



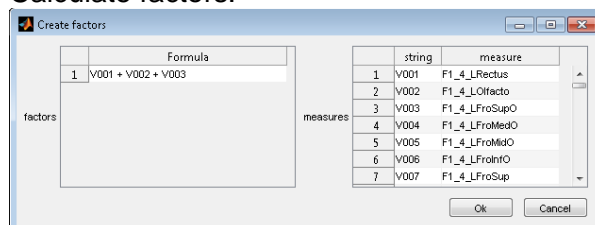
Certain input files contain multiple variables for a single measure (e.g. multiple eeg channels for the same measure) and you must indicate the number of variables per measure (default: 1 variable per measure).



- Select measures, variables, outcomes and factors for permutation

Factors (only for permutation): If selected, factors are used to calculate residuals of a generalized linear model with measures as outcome. Residuals will be used for calculation of permutation-statistics

- Z-values /Log data / Logit data: corresponding transformation of single/multiple measures
- Calculate ratio: A ratio is calculated between two measures (after selecting first and second measure)
- Calculate factors:

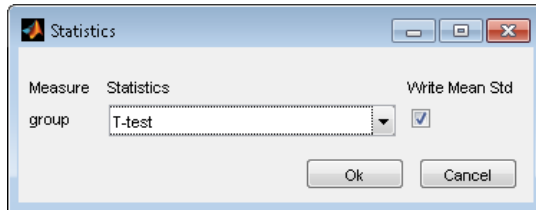


Factors are defined in left table by indicating there calculation, variables for calculation are entered by 'string' from right table

- Lateralization index: $(\text{Left} - \text{Right}) / (\text{Left} + \text{Right})$. Input data must have structure of either LRLRLR.... or LLL...RRR...
- Change order of variables: order of measures/variables/variables2 and subjects can be exchanged

- Combine variables und subjects/trials: selected variable is transposed and you get for all subjects as many columns as entries for the variable are available
- Re-order outcomes: Order of the selected outcomes is re-arranged (separate dialog is shown before storing result to select order)
- Subjects/Trials: By default all subjects/trials are selected, by clicking you can exclude/deselected.
- Exclude trials with invalid entries: Select if you have empty values in your input data

2. Basic Statistics



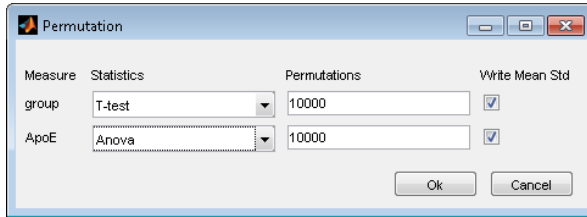
- Statistics:
 - T-test
 - Paired-T-test
 - Anova
 - Mann-Whitney-U
 - Wilcoxon
 - Spearman
 - Kendall
 - Pearson
- Write Mean Std: For every measure/variable mean, median and standard deviations are calculated

Paired-T-test & Wilcoxon are only possible if an outcome file is used with following structure:

Patient1, Control1, Patient2, Control2, Patient3, Control3

After calculation of statistics, results are written to xls-files and plotted either in signal or source space

3. Permutation

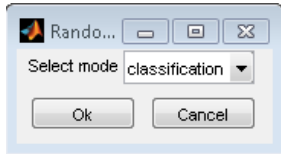


- Statistics:
 - T-test
 - Paired-T-test
 - Anova
 - Mann-Whitney-U
 - Wilcoxon
 - Spearman
 - Kendall
 - Pearson
- Permutations: default 10'000 (= stable results)
- Write Mean Std: For every measure/variable mean, median and standard deviations are calculated

4. Repeated Measures Anova

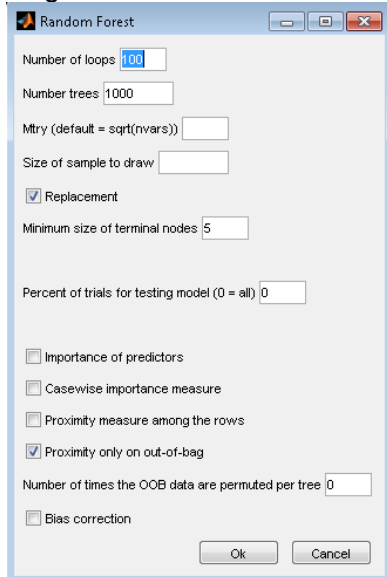
Anova for repeated measures, select with or without outcomes to include groups-information. Open for every time point a separated input xls-file.

5. Random Forest

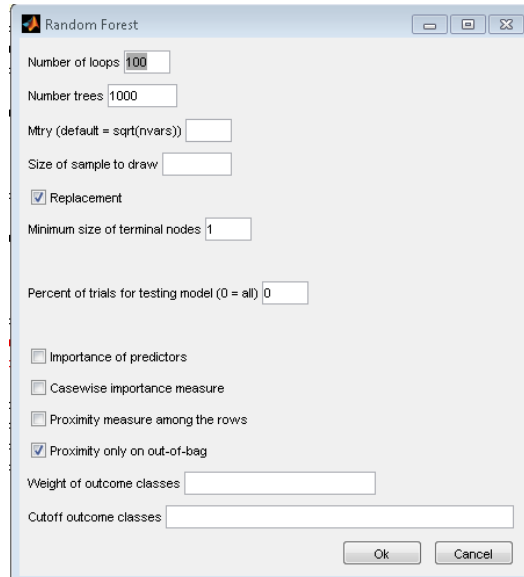


Select regression or classification

Regression:



Classification:

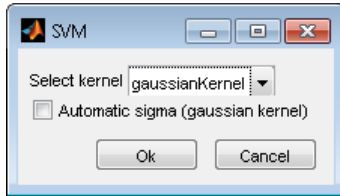


Number of loops:	Number of full random-forest calculations. Results of Gini-coefficient, Importance and SD are collected and shown as boxplot at the end
Number of trees:	Number of different trees in every calculation
Mtry:	Number of variables included in single tree
Size of sample:	Size of sample, randomly selected for calculation of single tree
Replacement:	Turn replacement on/off for random-selection of samples
Percent of trials for testing model:	<p>If >0, selected percent of trials is excluded for creating the model and finally used for testing the model</p> <p>If = 0, all trials are used for creating and testing the model (testing with a leave-one-out approach)</p>

For other selections see documentation for random forest calculation

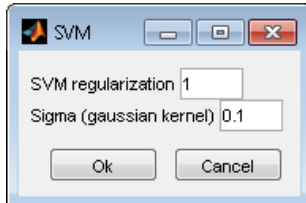
Outputs are Excel-tables & Plots of importance / mse / ROC.

6. Support vector machine (SVM) *(not included in first release)*

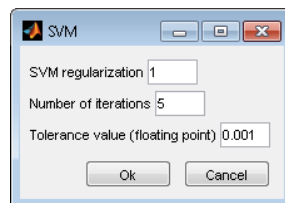


Select Gaussian or linear kernel

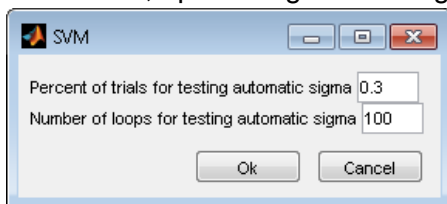
Gaussian kernel



Linear kernel



If automatic sigma is selected (only Gaussian kernel) sigma and regularization are optimized by splitting the input trials in training and testing dataset. The percent for testing and the number of loops are chosen (loops-times a random subset for testing is selected, optimal sigma and regularization over all sets is selected)

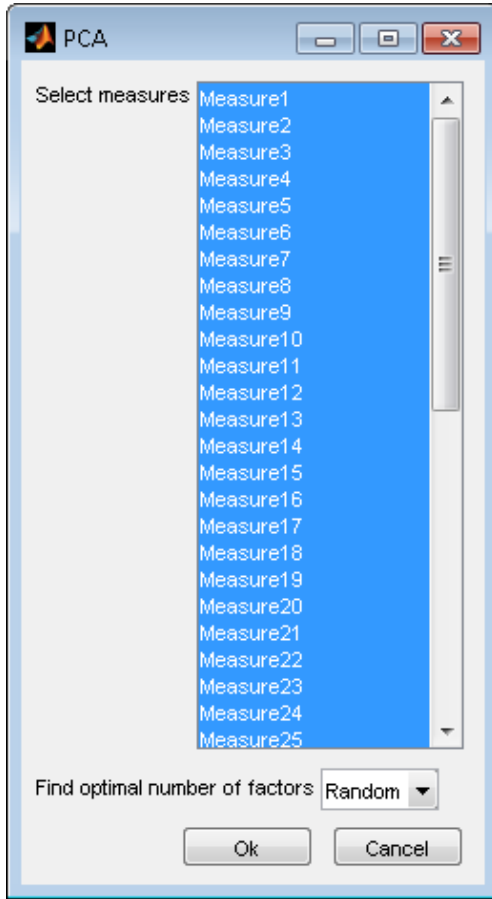


For calculation of sensitivity and specificity of the model a leave-one-out cross-validation is used (loop over all trials)

Outputs are plots of weights / ROC and Excel-tables:

- Sensitivity_Full & Specificity_Full: Results from full model
- Sensitivity_Test & Specificity_Test: Results from leave-one-out cross validation

7. Principal component analysis (PCA) *(not included in first release)*



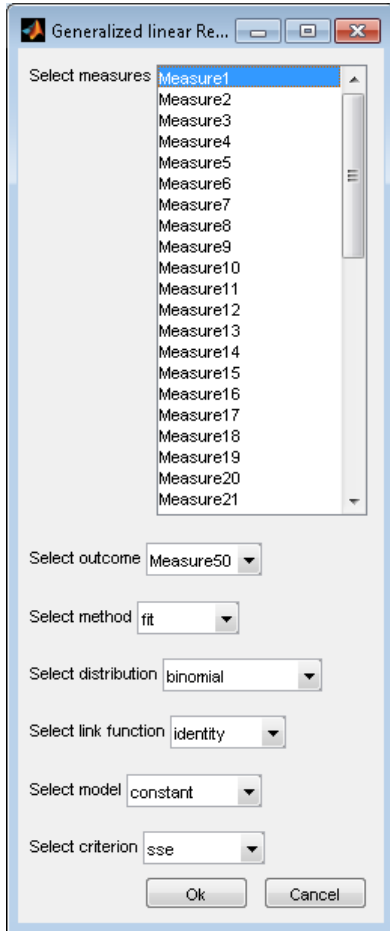
First a principal component analysis (pca) of selected measures is performed
(Matlab standard implementation, 'VariableWeights' set to ' $w = 1./var(measures)$ ')

To find the optimal number of factors select:

- | | |
|------------------|---|
| Random: | Resulting weights of pca are compared to results from randomized input data (random reordering of trials per measure). Ranked weights of initial and randomized results are plotted and level of crossing indicates optimal number of factors |
| 80% / 90% / 95%: | Ranked weights are plotted and number of components explaining 80/90/95% of variance is selected |

For calculation of resulting factors the Matlab function 'factoran' ('rotate' = 'promax') with 'optimal number of factors' is used.

8. Generalized linear model (GLM)



Selected measures and outcome

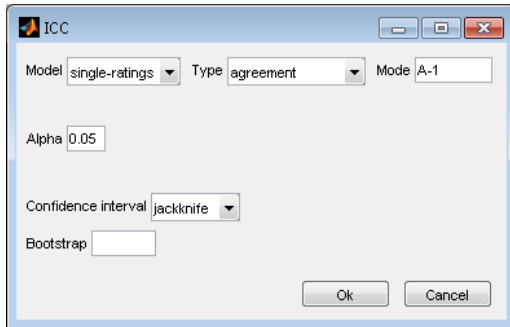
Method:	'fit' 'stepwise' (backward and forward reduction)
Distribution of outcome:	binominal / gamma / inverse gaussian / normal poisson
Link function for outcome:	identity / log / logit / probit / comploglog / reciprocal / loglog
Model:	constant / linear / interactions / purequadratic / quadratic / polyijk
Criterion for add/remove measure:	sse (p-value for F-test) deviance (p-value for chi-square test) aic (AIC) bic (BIC) rsquared (R^2) adjrsquared (adjusted R^2)

9. Intra-class Correlation

ICCs according to shrout & fleiss' schema

(Shrout PE, Fleiss JL. Intra-class correlations: Psychol Bull. 1979;86:420-428)

Input is Excel-Files whose rows represent different ratings or raters & whose columns represent different cases or targets being measured. Each target is assumed to be a random sample from a population of targets

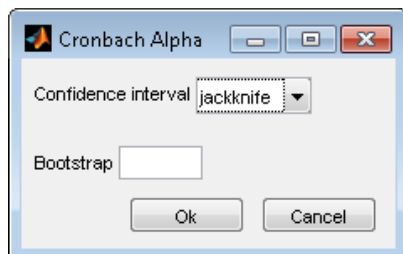


- single or average: Denotes whether the ICC is based on a single measurement or on an average of k measurements, where k = the number of ratings/raters
- method rating:
 - 1: if each target is measured by a different set of raters from a population of raters
 - 2: if each target is measured by the same raters, but that these raters are sampled from a population of raters
 - 3: if each target is measured by the same raters and these raters are the only raters of interest.
- Confidence interval: Bootstrap (number of runs see 'Bootstrap') or jackknife

Output is a excel files with result of ICC and a plot of input values

10. Cronbach Alpha

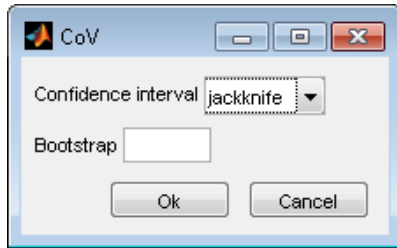
Input is Excel-Files whose rows represent different ratings or raters & whose columns represent different cases or targets being measured. Each target is assumed to be a random sample from a population of targets



Confidence interval: bootstrap (number of runs see 'Bootstrap') or jackknife

11. Coefficient of Variation

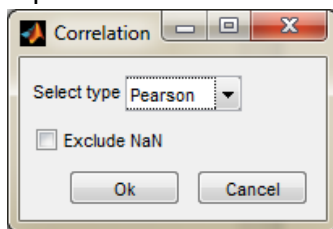
Input is Excel-Files whose rows represent different measures and columns represent different subjects / trials.



Confidence interval: bootstrap (number of runs see 'Bootstrap') or jackknife

12. Correlation

Input is Excel-Files whose rows represent different measures and columns represent different subjects / trials. Results of every file are correlated to equal results in other files per measure and subject. For correlation analysis 'Pearson', 'Kendall' and 'Spearman' can be selected.

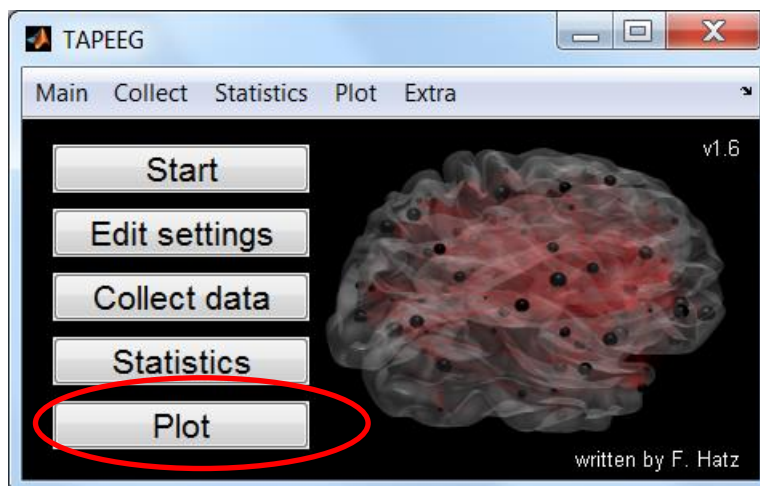


13. Kappa

Input is Excel-File whose rows represent different raters and columns represent different subjects / trials.

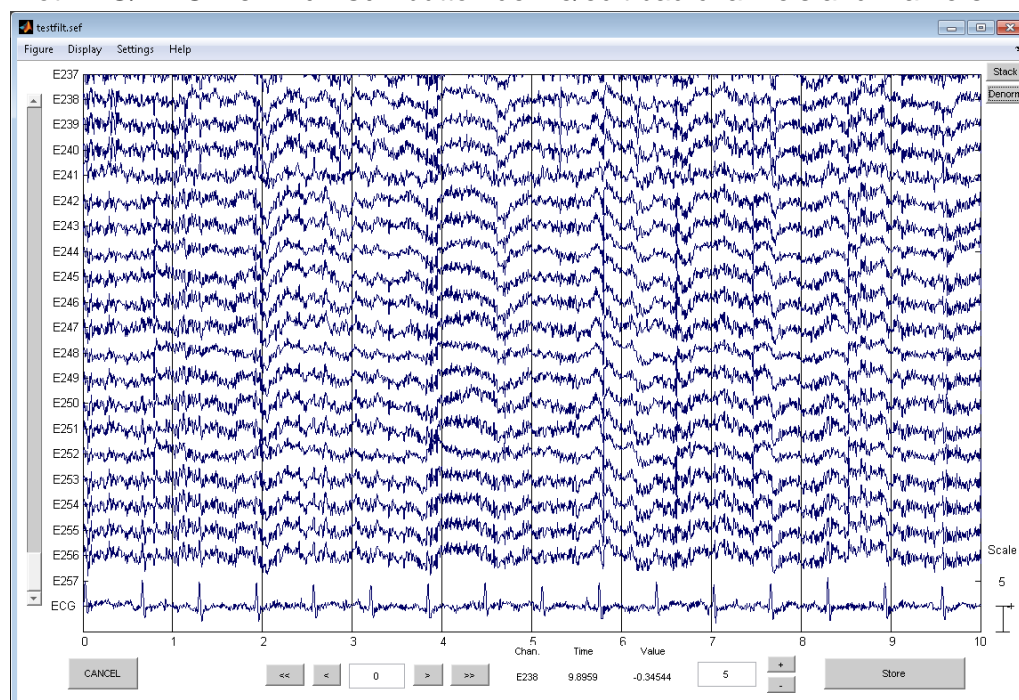
For two raters: Cohen's Kappa is calculated
For >2 raters: Fleiss'es Kappa is calculated

VIII. Plot results



1. EEG

Plot EEG/MEG-file. With 'Ctrl'-button define/edit bad channels and markers.



(for plotting the function 'eegplot' of the toolbox EEGLAB is used)

2. Signal-Space

2.1. Results

Select Method

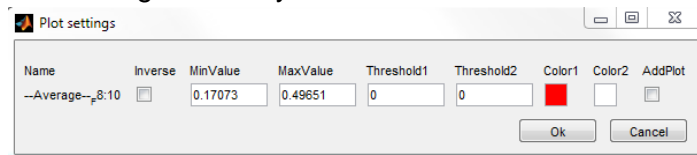


2.1.1. File

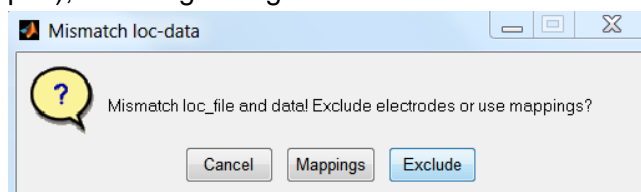
	A	B	C	D	E	F	G	
1	MapFreq	AD-001	AD-002	AD-003	AD-004	AD-005	AD-007	AD-008
2	F1:4_1	0.44154323	0.25464288	0.49203466	0.36530934	0.56581868	0.2127016	0.25
3	F1:4_F8	0.39677693	0.24829901	0.59422562	0.34251378	0.67514228	0.20923168	0.27
4	F1:4_3	0.29152442	0.19971665	0.35264131	0.33143061	0.59732671	0.21096669	0.11
5	F1:4_4	0.23009269	0.15115781	0.26395871	0.30078928	0.52889999	0.07417954	0.12
6	F1:4_5	0.18734576	0.08006724	0.2318594	0.2834834	0.48086099	0.05446155	0.12
7	F1:4_6	0.1216653	0.08051705	0.22952555	0.28597698	0.46944846	0.04923508	0.13
8	F1:4_7	0.12152896	0.07978035	0.20633077	0.27489983	0.40893754	0.04835985	0.14
9	F1:4_8	0.1546176	0.15972558	0.19308699	0.29825513	0.36993222	0.04941434	0.14
10	F1:4_9	0.18920348	0.14448171	0.16907518	0.2469221	0.50024444	0.07664558	0.18
11	F1:4_10	0.47052691	0.32460496	0.58883513	0.51565688	0.75662582	0.25667973	0.3
12	F1:4_11	0.31994179	0.27810515	0.36963575	0.43719287	0.74495349	0.12822139	0.16
13	F1:4_12	0.2574499	0.31233319	0.27942041	0.37560747	0.61493739	0.12984167	0.15
14	F1:4_13	0.1932604	0.16262887	0.24099794	0.3406732	0.51415479	0.05338066	0.14
15	F1:4_14	0.1464565	0.08114002	0.22007115	0.36509034	0.4765253	0.05424282	0.14
16	F1:4_Fz	0.1226387	0.08223558	0.21321459	0.36255392	0.45462287	0.05351362	0.14
17	F1:4_16	0.13462436	0.10815934	0.22513684	0.33435658	0.43947645	0.05237349	0.15

In case of multiple variables per measure, first rows contains all variables of first measure, followed by a block of second, third... measures

- First select measures to plot (press control for selecting multiple measures)
- Second select trials/subjects/measures in columns of input data
- Plot settings for every measure:

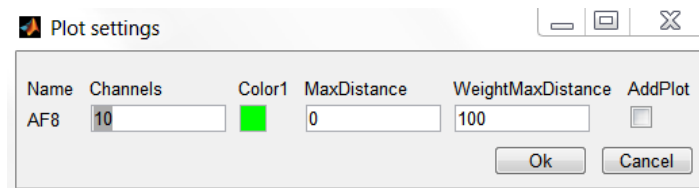


- Inverse: inverse data (eg. for p-values)
- Max and Min value: maximal and minimal values to plot (default is maximal and minimal value in data)
- Threshold 1 and 2: for inversed data 2 thresholds can be selected
- Add Plot: if selected measure is added to the plot of previous measure (inactive for first measure)
- If number of channels in input data is not equal to loc-file (only signal space plot), following dialog is shown:



Select 'Mappings' to reduce channels by mappings file (Mappings.xls) or 'Exclude' to manually exclude single/multiple channels. The dialog is shown until numbers are matching.

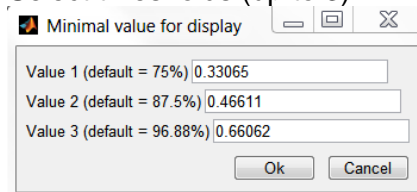
2.1.2. Selection



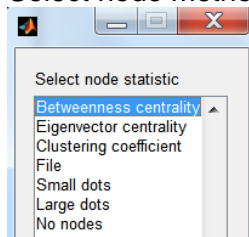
Single/multiple channels/regions can be selected. If MaxDistance > 0, a Gaussian distribution around the channel is plotted, with WeightMaxDistance for most peripheral channel in distribution

2.1.3. Matrix

- Select a matrix (xls-file).
- Select thresholds (up to 3)

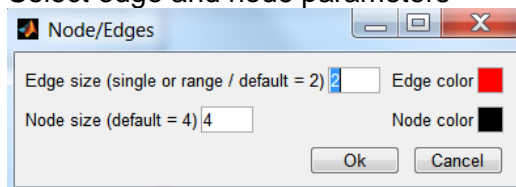


- Select node method



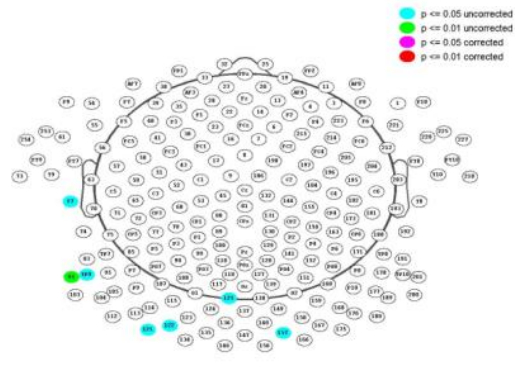
- 'Betweenness centrality', 'Eigenvector centrality' and 'Clustering coefficient' are calculated with toolbox of O. Sporns
- File: As input files select BrainWave or xls-file, if multiple input-values are selected, you can define one value for nodes and second value for surface or volume-plot (e.g. to depict a single region in final plot)
- 'Small dots', 'Large dots', 'No nodes'

- Select edge and node parameters

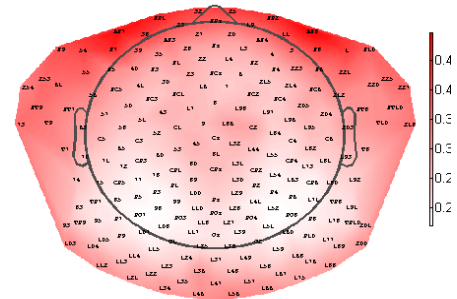


2.1.4.Examples

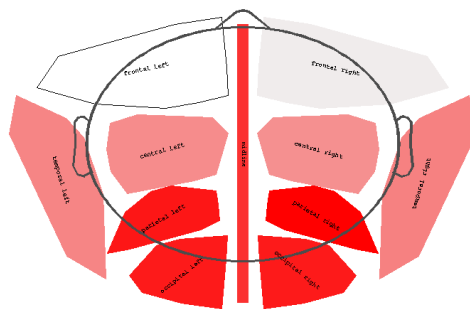
P-values



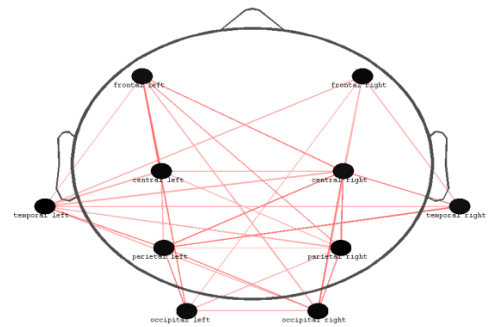
T-values



Mappings

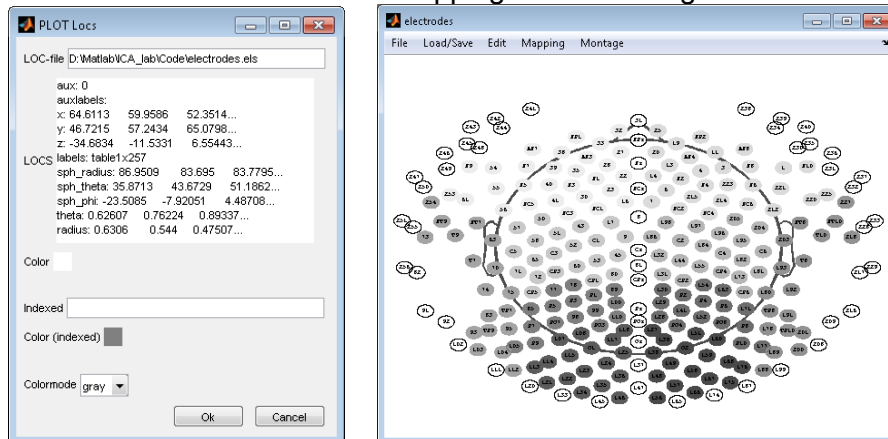


Matrix



2.2. 2D-Electrodes

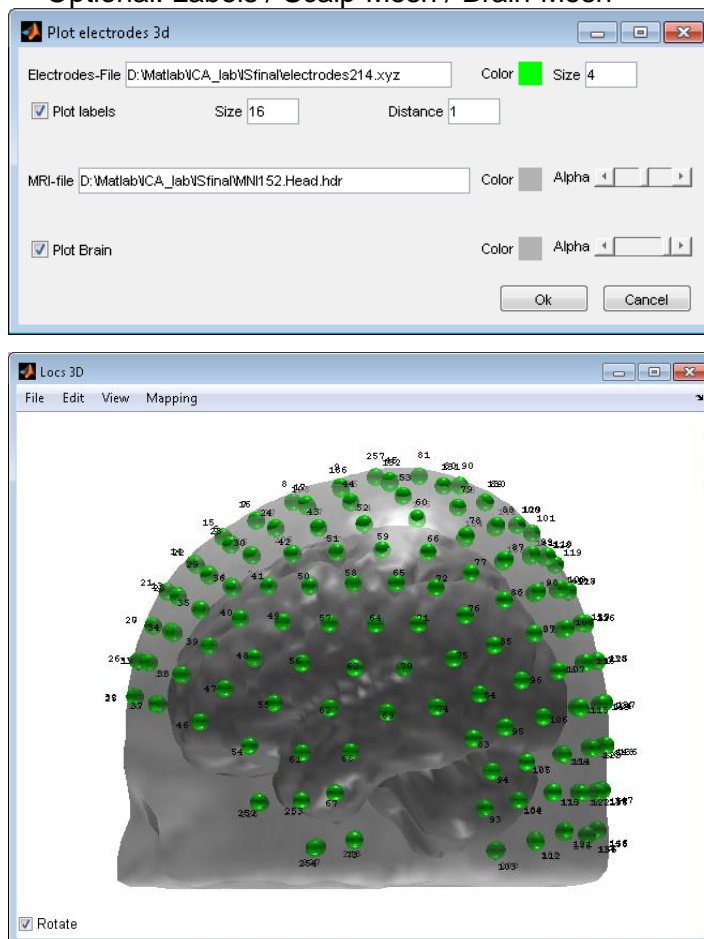
Plot electrodes and load/edit 'Mappings' and 'Montages'



2.3. 3D-Electrodes (not included in first release)

Plot electrodes-locations in 3D

- Optional: Labels / Scalp-Mesh / Brain-Mesh



3. Source-Space (not included in first release)

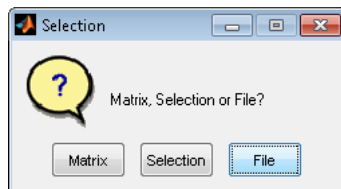
3.1. Results

Plot results in source space (atlas file: MNIbrain.mat), the included atlas-file is preconfigured to plot 76 AAL regions

If you want plot a set of different AAL regions, just process a input file with a different number of regions and answer to the question-dialog -Reset brain template- with yes. Consecutively, a reseted MNIbrain.mat is written, together with an xls-file. Edit the xls-file to only include regions to plot and restart the plotting. When asked for selecting the regions, import the xls-file

If you want to create a new MNIbrain-template, just cancel the selection of the MNIbrain.mat-file, a new dialog is asking for a mri-file. This mri-file is segmented and used to calculate the brain-mesh. For definition of regions an additional mri-atlas-file is needed.

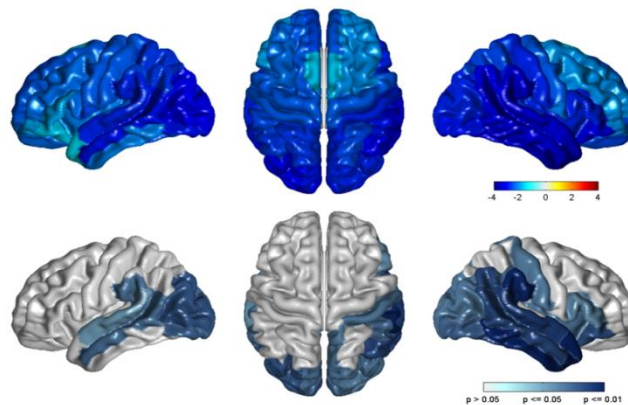
Select Method



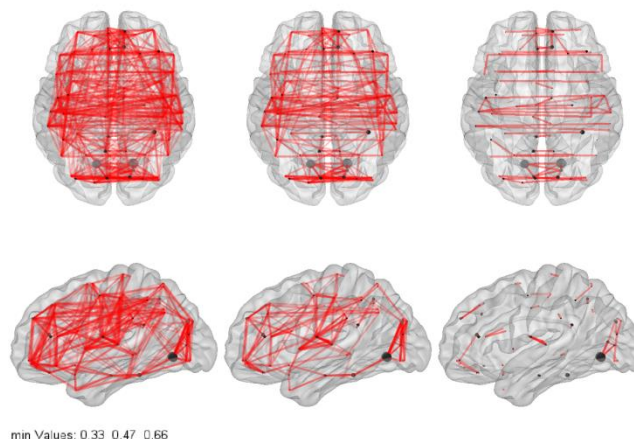
for settings see 'Plot Signal-Space'

Examples:

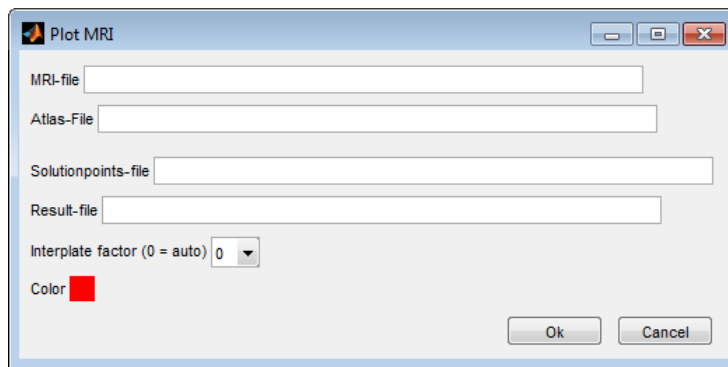
- Surface/Results:



- Matrix:



3.2. Ortho-Slides



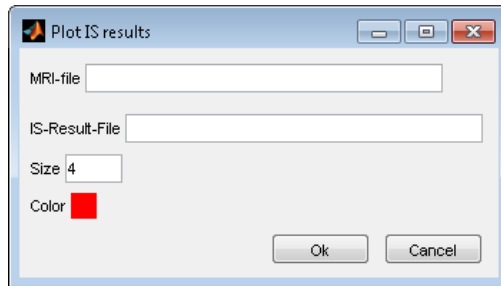
MRI-file	MRI-file (*.hdr) for plotting slices in X- / Y- / Z-axis
Atlas-file	Atlas-file (.nii;*.hdr) for labelling of voxels (<i>atlas-file will be coregistered to MRI-file</i>)
*Solutionpoints-file	*.spi-file with coordinates of results (inverse solution)
*Result-file	*.ris-file with result of inverse solution
Interpolate-factor	factor for interpolation of results (0 = auto)
Color	Color for plotting results
* = optional	

Example:



3.3. Dipol Fitting

Plots results of dipol fitting into a mesh



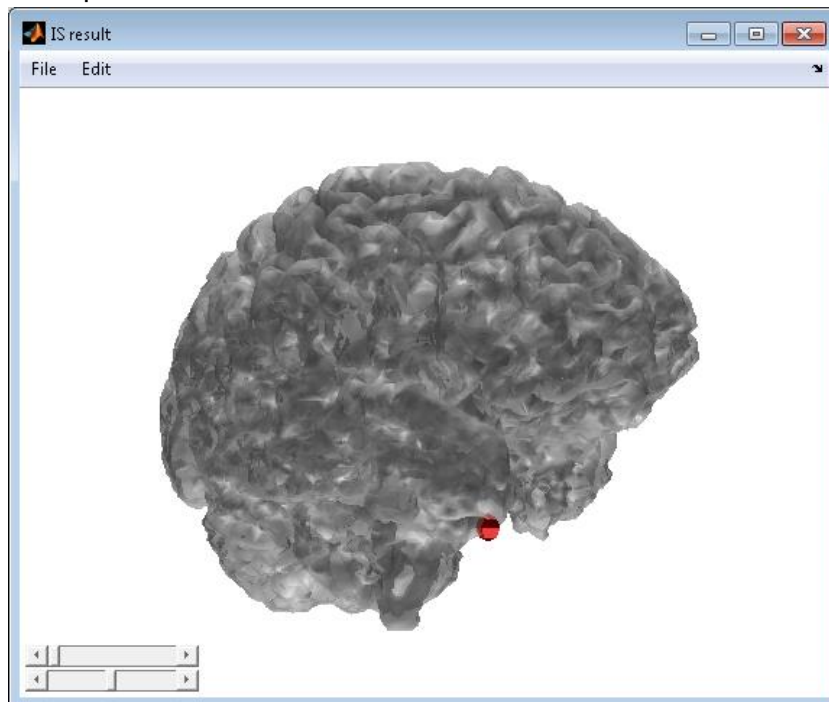
MRI-file: MRI-file (MRI-file will be converted to brain-mesh)

IS-Result-file: *.ris-file (standard result-format of TAPEEG inverse solution)

Size: Scale for displayed size of result (default = 4)

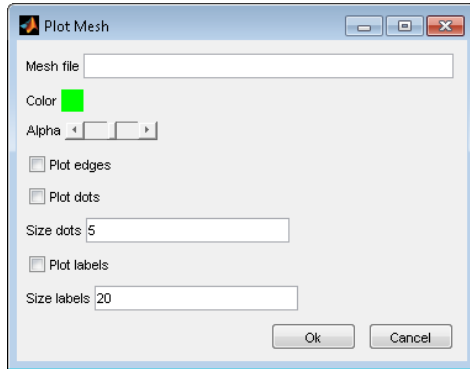
Color: Color for result

Example:



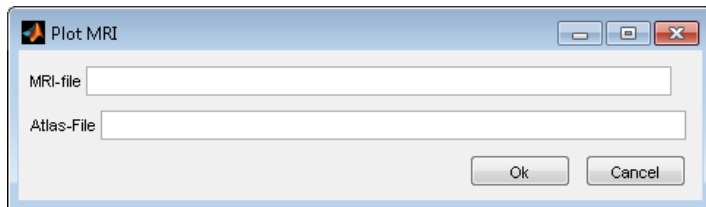
- Upper slider: intensity/size of the result
- Lower slider: time point for visualization

4. Mesh *(not included in first release)*



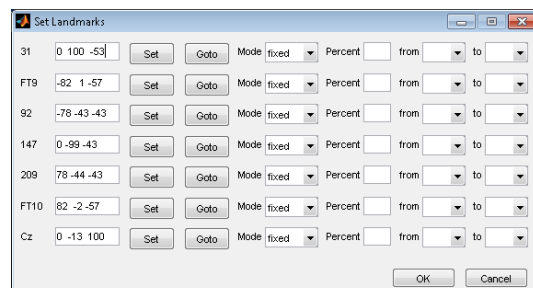
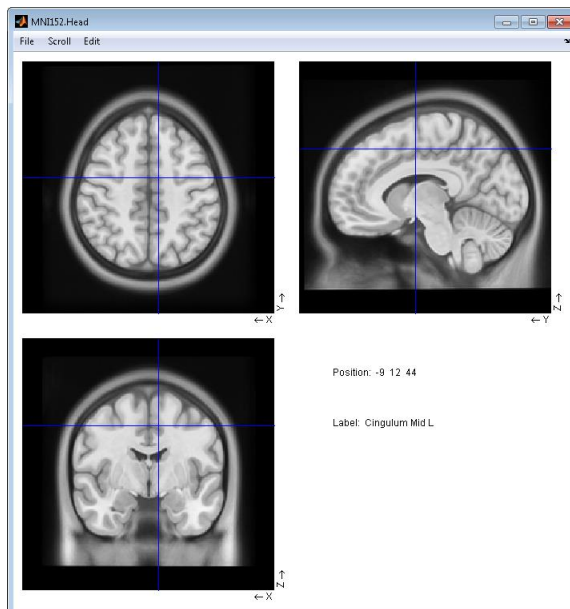
- If multiple meshes should be combined just plot one after the other, they will be combined in the same window (don't close window after plotting the first one)
- Mesh file: *.els / *.xyz / *.spi or MRI-file

5. MRI *(not included in first release)*



MRI-file MRI-file (*.hdr) for plotting slices in X- / Y- / Z-axis

Atlas-file Atlas-file (*.nii;*.hdr) for labelling of voxels
(atlas-file will be coregistered to MRI-file)

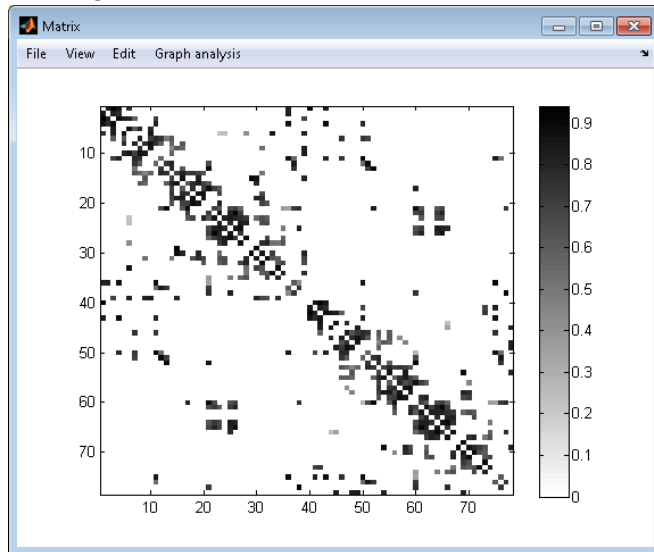


Menu File: - Save MRI

Menu Edit: - Goto position (in x y z in mm)
 - Anisotropic Filtering
 - Set orientation to RAS
 - Set landmarks

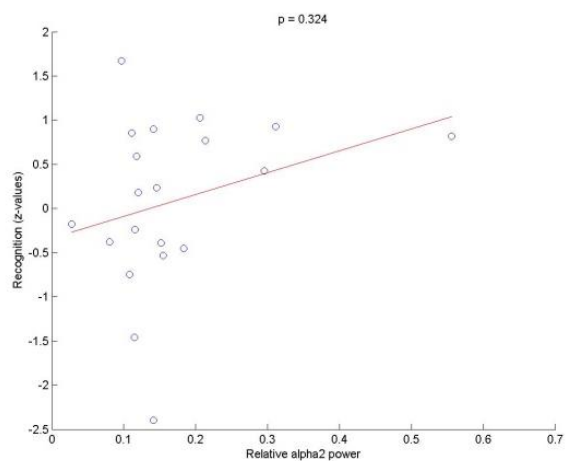
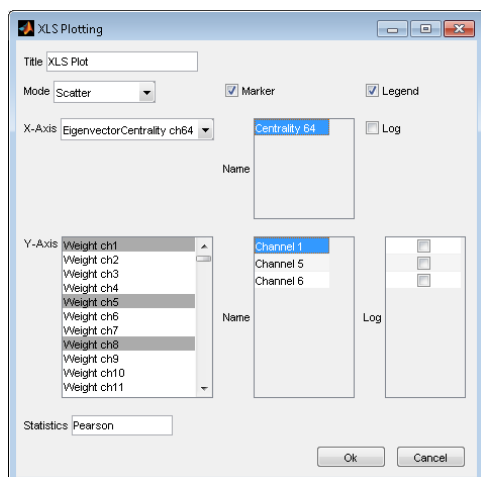
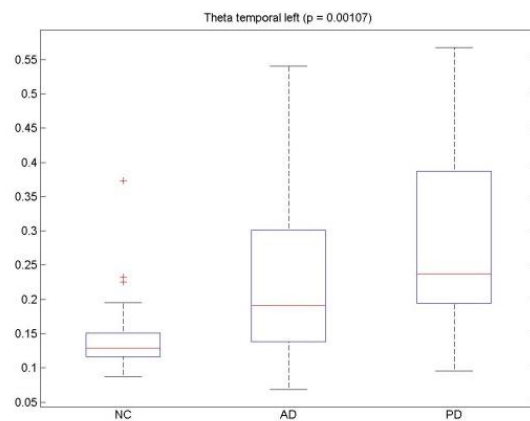
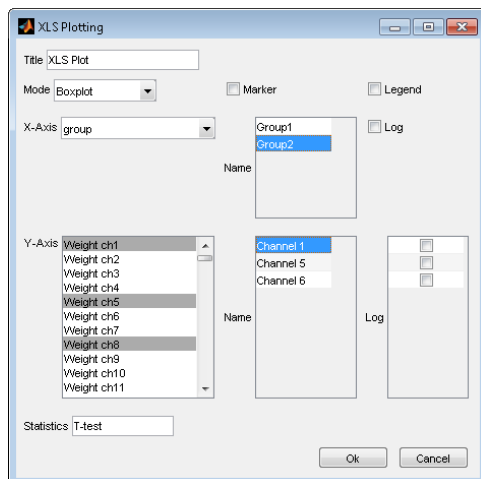
6. Matrix *(not included in first release)*

Plotting of '*_matrix.txt' or BrainWave-Matrix-file



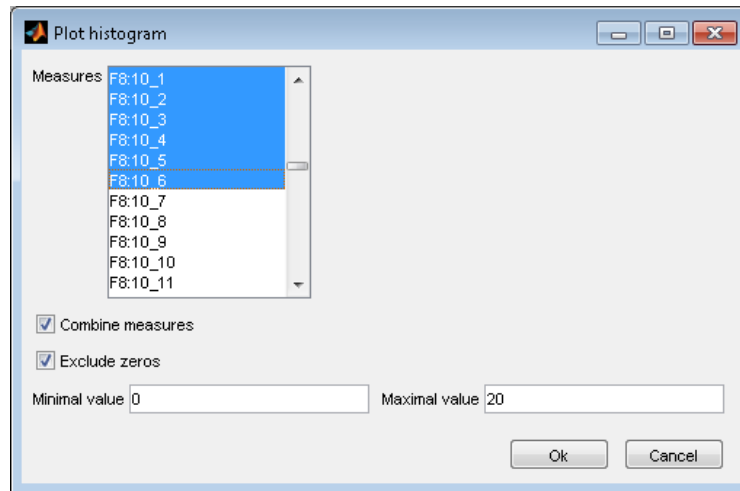
7. Boxplot/Scatter

Plot boxplots and Scatter-plots with appropriate statistics. Input-file: xls-file



8. Histogram / Distribution

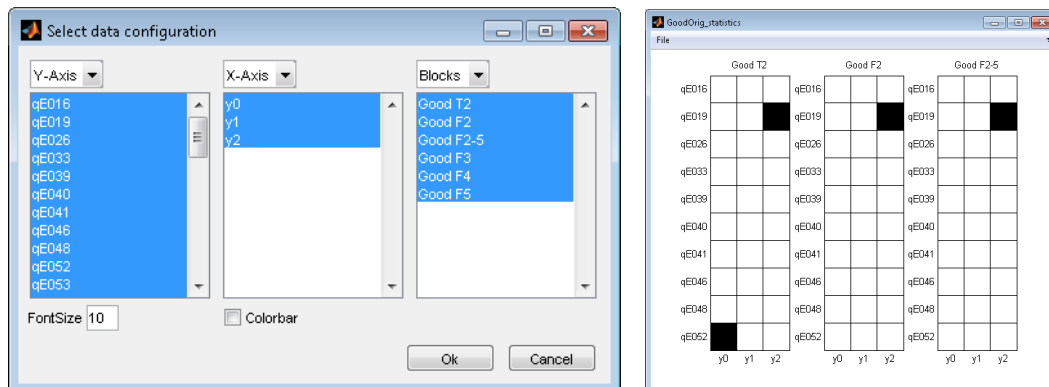
Select xls-result-file as input



- Measures: Single or multiple measures
- Combine measures: Combine measure for single histogram or plot multiple histograms (if multiple measures selected)
- Exclude zeros: Exclude zero values for plotting histogram
- Minimal/Maximal value: Set minimal and maximal value of Y-axis

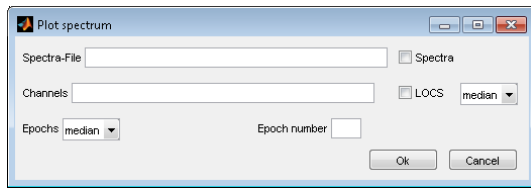
9. Data-matrix

Plot xls-files with results as matrices



10. Spectrum

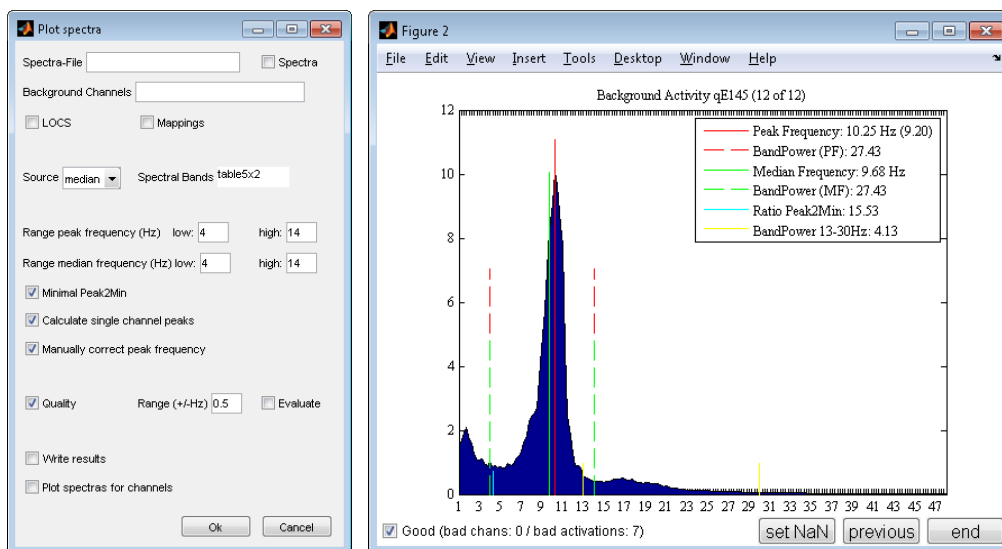
Plot simple spectrum (input is result from spectral analysis = *_Spectra.mat)



Channels: single channel or combination of multiple channels for plotting
Select 'mean' or 'median' for method of combining channels

Epochs: Select 'mean' or 'median' to plot an average of all included epochs
 or 'single' for single epochs

11. Spectrum & Evaluation



Spectrum is plotted and evaluated as described in 'Collect frequency data'

IX. Extras

1. Create random data *(not included in first release)*

Number of channels: default = 1

Sampling rate: default = 500

Number of timeframes: multiple values are allowed
(If minimal value < 20, values are replaced by 2^{values})

Model to use: 1. Autoregressiv model (Green et al. 2012), different coefficients
2. Freeman model

Connections: Introduce connectivities between channels according to this matrix. Every column of the matrix represents a channel. The diagonal holds the values (between 0 and 1) for the amount of the original signal to keep. In the columns, for every channel the weights of all other channels are defined. The final signal of every channel is defined as the sum of the amount of the original signal to keep and the weighted other channels with lag ... timeframes.

Included: lower triangle: unidirectional connectivities

Upper triangle: unidirectional connectivities

Full matrix: bidirectional connectivities

Lag: >0 = Number of timeframes for lag

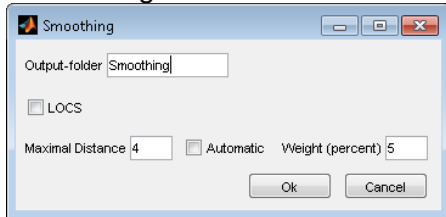
0 = Lag is defined by values in the matrix
(channels are completely replaced by lagged channel)

Calculate connectivity: Perform connectivity analysis on new created model data

Graph analysis: Perform graph analysis after calculation of connectivities

Number of repetitions: Number of datasets created for every number-of-timeframes

2. Smooth signal results



- Output-folder: Folder to store verbose-file...
- LOCS Select Loc-File with electrodes-informations (*.els,*.sfp)
- Maximal Distance/Weight: For smoothing a Gaussian kernel is used. Size of Gaussian kernel is defined by Distance, weight of most peripheral channel in distribution by Weight (percent of central channel)
- Auto: Optimal value for 'Distance' is calculated based on input data

3. Find pairs in two groups

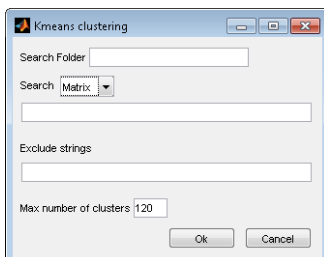
Input must be an outcome-file (xls-file) with group-variable (patients/controls). Routine finds pairs of patients/controls by matching for several other variables

4. Matrix *(not included in first release)*

Reduce to Mappings:

- Input: matrix-file (xls-file) & mappings-file (xls-file)
- Output: matrix-file with size of mappings, values are accordingly averaged

5. Kmeans Clustering



Define search folder and search/exclude-strings, maximal number of clusters

Output: Excel (mean variance of matrices by cluster)
Plot (mean variance of matrices by cluster & cluster allocations of matrices)

6. Excel

- Edit/combine files: Edit/combine xls-files with results
- Combine results and outcomes: Combine files with results and outcomes to one single xls-file. Files are matched by subject-names
- Split results by outcome: Select xls-file with results and outcomes and create new files for every outcome
- Combine power results: Take power results for different frequency bands from different result-files and write new combined file

- Reduce to Mappings: Reduce xls-result-file with multiple variables (=electrodes) per measure to a file with multiple mappings per measure using a mappings-file (Mappings.xls)
- Combine trials and variables: For a result-xls-file with multiple variables per measures create a file with only one row per measure and trials * variables columns
- XLS to Matrix: XLS files with complete link information of a matrix in rows or columns are back-transformed to matrices
(number of rows/columns are = $Nchans*(Nchans-1)/2$ for matrixes with empty diagonals or $Nchans*(Nchans+1)/2$ for matrixes with non-empty diagonals)

7. BrainWave

- Convert BrainWave to Excel: Convert BrainWave result-file to Excel, includes of averaging of multi-epoch-results for every patient
- Combine BrainWave power results: Take power results for different frequency bands from different BrainWave-result-files and write new combined file
- Convert BrainWave matrices: Open BrainWave matrix file (from batch processing) and save averaged matrix for every patient

8. MRI *(not included in first release)*

- Convert MRI to .hdr Convert different MRI-file-formats to hdr-format
- Convert MRI to RAS Convert MRI to RAS orientation (with visual control)
- Coregister MRI/Locations: Coregister locations (electrodes or digitizer) to headshape (MRI-file)
- Coregister Atlas to MRI: Coregister Atlas-file to MRI-file
- Correct digitizer: Delete outliers in digitizer-points (input: fif-file)
- Calculate Leadfiled: Calculate forward solution (input: MRI-file)

9. Files

- Collect

Search/Copy/Move EEG-files

Collect file data

Search Folder: D:\Matlab\CA_Jab\Code

Searchstrings Filename:

Searchstrings Filepath:

Excludestrings Filename:

Excludestrings Filepath:

Output folder: D:\Matlab\CA_Jab\Code\CollectFiles

☒ Copy eeg/meg files

☐ Interpolate bad channels

☐ Average eeg/meg files

Searchstrings for average:

String for average files:

☐ Collect GFP

Number of underscores in subject name:

Ok Cancel

Define:

Search strings for filename and filepath

Exclude strings for filename and filepath

Output-folder: New Path

Copy: if enabled found files are copied to output folder

Average: only for ERP

- Searchstrings: Strings in filenames that are different in files to average
- String for Avg: String for average-file

Collect GFP (global field power)

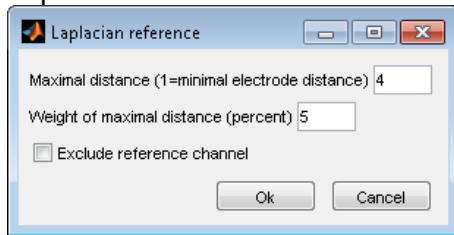
- Number of underscore in subject name: results are stored for every patient separately in xls-file

- Create subfolders:

Move EEG-files in subfolders (patient's names)

X. Appendix

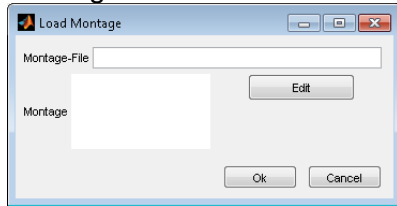
1. Laplacian reference



- Maximal distance (default = 4)
- Weight of maximal distance (default = 5 percent)
- Exclude reference channel

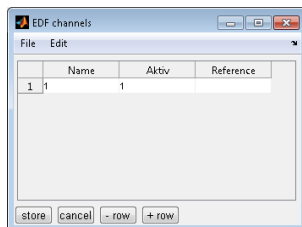
For calculation of laplacian reference the values 'Laplacian Maxdistance' and Laplacian Weight Maxdistance are used. Channel distances are first normalized (minimal distance = 1). The value 'Laplacian Maxdistance' defines the maximal distance of a channel from the active channel to be included as a reference channel, whereas 'Laplacian Weight Maxdistance' defines the weight of that channel compared to the active channel. Knowing that weight sigma is calculated of the gaussian kernel and other weights of surrounding channels are calculated. If a surrounding channel is labeled as bad he is excluded.

2. Montage



Montage-file: Select Montage-file (*.xls / *.xlsx) to load

Edit: Dialog to edit montage is shown



If no montage is loaded and 257 data channels, default EDF-montage (10-10 system) is shown

Montage-file (*.xls / *.xlsx)

	A	B	C	D	E	F	G
1	Montage	257			Field B1: number of channels, the montage file was defined for		
2	ErbRight	active	reference				
3	ErbR_L	AUX1	AUX2				
4	Hwk_ErbL	AUX3	AUX2		reference:	single channel	
5	P1R_ErbL	154	AUX2			multiple channel	
6	P1L_ErbL	78	AUX2			AUX1, AUX2 ...	
7	FL_ErbL	43	AUX2			AVG (average reference)	
8	FCz_ErbL	8	AUX2			LAPL (laplacian reference)	
9	ErbLeft	active	reference				
10	ErbL_R	AUX2	AUX1				
11	Hwk_ErbR	AUX3	AUX1				
12	P1L_ErbR	78	AUX1				
13	P1R_ErbR	154	AUX1				
14	FL_ErbR	197	AUX1				
15	FCz_ErbR	8	AUX1				

Field A1: 'Montage' (must be!)

Field B1: number of eeg/meg channels. Must be the same number as eeg/meg channels in the original eeg/meg input file

Row 2: header first montage {'name' 'active' 'reference'}

A3 ... Ax: names of resulting channels (no spaces, length <= 8)

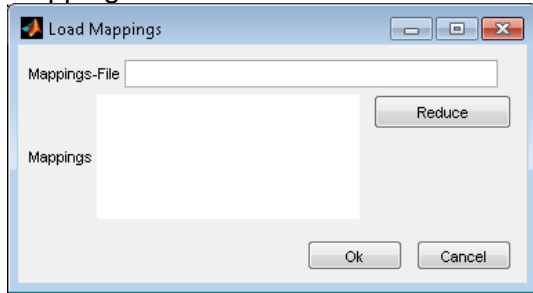
B3 ... Bx: active channels (single channel)

C3 ... Cx: reference channel(s):
 Single channel
 Multiple channels
 AUX1, AUX2, AUX3, AUX4, AUX5, AUX6
 AVG (average reference)
 LAPL (laplacian reference)

Row(x+1): header second montage ...

Warning: For Linux columns D to G must be empty !!!!

3. Mappings



Mappings-file:

Reduce: Reduce channels in mappings
(e.g. if channels are excluded in results and mappings-file is defined for all input channels, the same channels have to be excluded in the mappings-file)

Mappings-file (*.xls / *.xlsx)

- Format (1)

	A	B																												
1	frontal left	16	22	23	24	27	28	29	30	32	33	34	35	36	37	38	39	40	41	42	46	47	48	49	54	55	56	61	252	253
2	frontal right	1	2	3	4	5	6	7	10	11	12	13	14	18	19	20	25	26	207	212	213	214	215	220	221	222	223	224	225	226
3	central left	9	17	43	44	45	50	51	52	53	57	58	59	60	64	65	66	71	72	76	79	80								
4	central right	131	132	143	144	155	164	172	173	181	182	183	184	185	186	194	195	196	197	198	204	205								
5	temporal left	62	63	67	68	69	70	73	74	75	83	84	93	94	95	103	104	112	254											
6	temporal right	178	179	180	188	189	190	191	192	193	200	201	202	203	210	211	218	219	227											
7	parietal left	77	78	85	86	87	88	89	96	97	98	99	100	105	106	109	110													
8	parietal right	128	129	130	140	141	142	152	153	154	161	162	163	169	170	171	177													
9	occipital left	107	108	113	114	115	116	117	118	121	122	123	124	125	134	135	136	146												
10	occipital right	127	138	139	148	149	150	151	156	157	158	159	160	166	167	168	175	176												
11	midline	8	15	21	26	81	90	101	119	126	137	147	257																	
12	no region	31	82	91	92	102	111	120	133	145	165	174	187	199	208	209	216	217	228	229	230	231	232	233	234	235	236			

All channels have to be included. Channels not included in a region, must be noted in the last row with name 'no region'

- Format (2)

[illegible]

Cell A1 must be 'Region'

First column holds region names

4. Detect bad settings

Detect Bad

Read bad channels from file (.txt,.xls,.info)

Set fixed bad channels

Period length for analysis (seconds) Allowed percent bad periods per channel

Frequencies (max percent):

50Hz (0=off)

60Hz (0=off)

spect-range low (0=off) Range (lowfreq highfreq)

spect-range high (0=off) Range (lowfreq highfreq)

Z-value broken (0=off)

Z-value vars (0=off)

Z-value hurst (0=off)

Z-value median (0=off)

Z-value amplitude (0=off)

Z-value kurtosis (0=off)

Z-value topo-corr (0=off) ☒ Laplacian

Z-value eye (0=off) Channel-list

Ecog artifact Ecog channel / heartbeat range

☐ Peak2Min

Markers to exclude (strings / * / all)

☐ Standard deviation in average Std <

☐ Create markers for bad periods Percent of bad channels

Automated bad channels/activations/epochs search is done with a combination of FASTER, Fieldtrip and TAPEEG routines:

Read bad channels from file:

- or if file with bad-information is found, automatic bad-detection is disabled, otherwise automatic-bad-detection is started
- only Bad-detection only by files, automatic detection disabled
- combine Files with bad-information and automatic detection are combined
- disabled Files with bad-information are disregarded, only automatic bad-detection is performed

Set fixed bad chans: Fixed bad channels by default (not included in analysis)

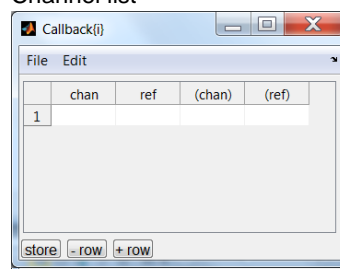
Period length: Files are split in period of ... seconds and every period is labeled good/bad. To set a channel as good-channel a minimum of periods of that channel must be labeled good. This minimum is defined by 'Allowed percent bad...'

Criteria for period-labeling good/bad):
(to disable one of the settings, just set the value to zero)

First a frequency analysis of the periods (pwelch, 80% hanning window) is done. The values 3 - 8 define criteria for bad channels by frequency characteristics:

- Max percent 50Hz: max percent 50Hz (49 – 51Hz) amplitudes of broadband amplitudes
- Max percent 60Hz: max percent 60Hz (59 – 61Hz) amplitudes of broadband amplitudes
- Max percent Spect-range low: max percent low spect range amplitudes of broadband amplitudes
- Spect-range low: spect-range low (e.g. 0-2Hz)
- Max percent Spect-range high: max percent high spect range amplitudes of broadband amplitudes
- Spect-range high: spect-range high (e.g. 15-30Hz)
- Z-value broken: analysis of standard deviation of sum of absolute values, periods with standard deviations > zvalue are labeled 'bad'.
- Z-value vars: simple analysis of variation ('variance'), periods with standard deviations > zvalue are labeled 'bad'.
- Z-value hurst: analysis of Hurst-exponent ('hurst_exponent', B. Davidson 2003), periods with standard deviations > zvalue are labeled 'bad'.
- Z-value median gradient: analysis of median gradient, periods with standard deviations > zvalue are labeled 'bad'.
- Z-value amplitude: analysis of amplitude (max – min), periods with standard deviations > zvalue are labeled 'bad'.
- Z-value kurtosis: analysis of kurtosis exponent, periods with standard deviations > zvalue are labeled 'bad'.
- Z-value topo correlation: analysis of correlation to surrounding electrodes, periods with standard deviations > zvalue are labeled 'bad'.
- Z-value eye: analysis of eye-correlation, periods with standard deviations > zvalue are labeled 'bad'.

Channel list

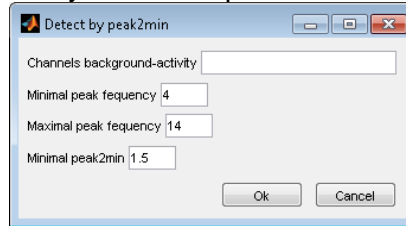


active channel / ref channel /
backup active channel /
backup ref channel

(Backup channels are used, when first channels are labeled bad)

- Ecg-channel/heartbeat-range: ecg-channel-number or heartbeat-range (e.g. 50-120)

- Peak2Min: Analysis of ratio peak to minimal amplitude



- Channels background activity: Channels included in analysis
- Minimal / Maximal peak frequency: Window for peak-search
- Minimal peak2min: Threshold for labeling good/bad

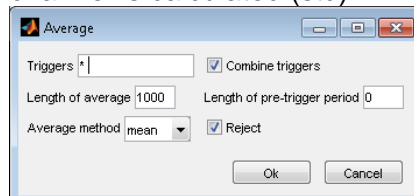
- Markers to exclude: For bad epoch-search markers can be selected, that mark bad-episodes in files. Optimally these markers have a duration of >1 and cover the whole bad episode. Periods including a selected marker are omitted.

* = a window with all found markers is shown for first processed EEG/MEG and one or more markers can be selected)

all = all markers found in file are selected

strings = define one or multiple markers

- Std in average By selecting a marker(s) all channels are averaged, the standard deviation of the average of every channel is calculated (std)



Mode: 'correct bad': channels with std \geq 'Std' are labeled good

'detect bad': channels with std $<$ 'Std' are labeled bad

- Create markers for periods: Markers are generated for bad periods
- Percent of bad channels: Threshold for labeling a period as bad

Note: if enabled, period length is set to 1 second

Note: Code for 'vars', 'hurst', 'median gradient', 'kurtosis' and 'eye' from FASTER-routines; code for frequency characteristics from Fieldtrip routines.

For detection of activations with EOG activity, every activation is compared to EOG's, correlations of all activations are normalized, standard deviations are calculated and activations with standard deviations \geq 'zvalue' are labeled as bad

Automated ECG: QRS-complexes are detected in all activations by comparing to 'ecg-channel' or by detection of regular beats in specified range ('heartbeat-range').

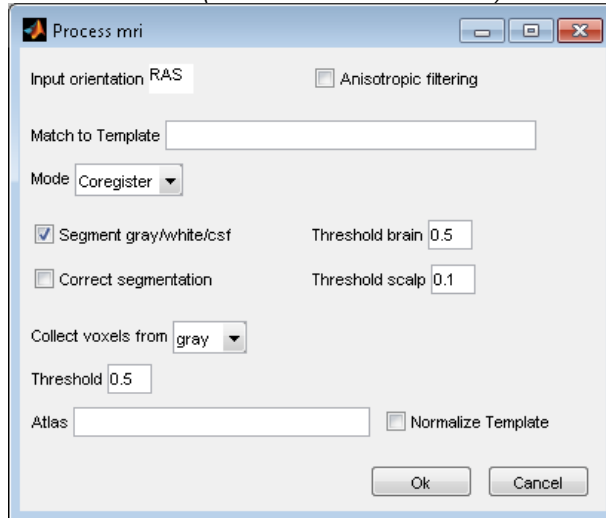
5. Graph measures

Name		Formula	Reference
Average clustering coefficient	Cw	$Cw = mean(C)$ $C_i = \frac{\sum_{k \neq i} \sum_{\substack{l \neq i \\ l \neq k}} W_{ik} W_{il} W_{kl}}{\sum_{k \neq i} \sum_{\substack{l \neq i \\ l \neq k}} W_{ik} W_{il}}$	⁹
Normalized clustering coefficient	Gamma	Cw / Cr (Cr = average of 50 randomized input matrices)	¹⁰
Average shortest path length	Lw	$L = 1/weight$ $L = \infty \text{ (if weight = 0)}$ $Lw = \frac{1}{\frac{1}{N(N-1)} * \sum_{i=1}^N \sum_{j \neq i} (1/L_{ij})}$	⁹
Normalized average path length	Lambda	Lw / Lr (Lr = average of 50 randomized matrices)	¹⁰
Degree correlation	Rw	Rw = Pearson correlation of degrees of pairs of neighbors	¹¹
Degree diversity	Kw	$Kw = \frac{\langle degree^2 \rangle}{\langle degree \rangle}$	¹²
Density		= Fraction of non-zero connections to all possible connections	
Eccentricity	EC	= Maximum of distances to all other vertices from a single vertex	
Radius	Radius	= min(E)	¹³
Diameter	Diameter	= max(E)	
Betweenness centrality	BC	= Fraction of all shortest paths in the network that contain a given vertex	
Efficiency	Eff	= Average of inverse shortest path length	
Eigenvector centrality		= The eigenvector centrality of a vertex i is equivalent to the ith element in the eigenvector corresponding to the largest eigenvalue of the adjacency matrix	
Transitivity		= Ratio of 'triangles to triplets' in the network	
Modularity		= Statistic that quantifies the degree to which the network may be subdivided into such clearly delineated groups	
Matrix Ref		= Pearson-correlation of matrix to a reference matrix	
Minimum spanning tree	MST	Kruskal's algorithm	¹⁴
MST radius	MST-Radius	= min(MST-L)	¹³
MST diameter	MST-Diameter	= max(MST-L)	
MST degree correlation	MST-R	see Rw	
MST degree diversity	MST-Kappa	see Kw	
MST leaf nodes	MST-LeafNodes	= number of nodes with degree of 1	

6. Hidden features

Instead of EEG/MEG-files TAPEEG can also process MRI- and Matrix-files

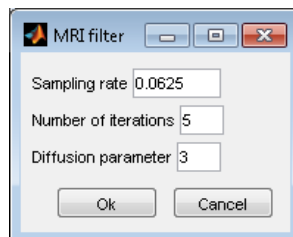
6.1. MRI-Files *(not included in first release)*



Input orientation:

Set input orientation of original mri (settings is defined by a visual interface, showing the mri and asking for the initial orientations)

Anisotropic filter:



function 'segm_aniso_filtering' of Zeynep Akalin Acar, SCCN, 2008 is used

Template:

If a template-mri-file is selected (e.g. MNI-brain), the processed mri will be co-registered to the template before segmentation

Mode:

Select 'Coregister' or 'Normalize' (SPM8-Functions)

Segment gray/white/csf:

Off = only whole brain will be extracted (including csf)

Threshold brain:

Threshold value for brain segmentation (default = 0.5)

Threshold scalp:

Threshold value for scalp segmentation (default = 0.1)

Correct segmentation:

Segmentations are smoothed and holes filled

Collect voxels from:

Select segmentation to collect/count voxels

Threshold collect:

Threshold value for collect (default = 0.5)

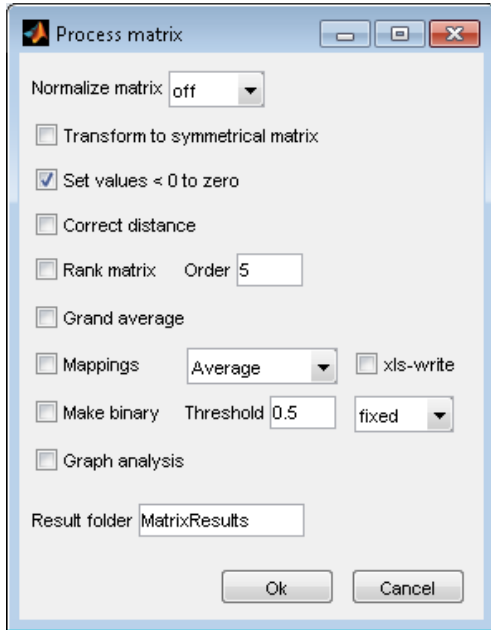
Atlas:

If an atlas-mri-file is selected (e.g. AAL atlas), the processed mri will be co-registered to the atlas and number of voxels are collected for every region

Normalize Template:

To set, provide a Brain-MRI-file corresponding to the anatomy of the Atlas-file. The atlas-file will be normalized to the brain-segment before co-registration.

6.2. Matrix-Files *(not included in first release)*



Normalize matrix:	Normalize matrix to values between 0 and 1
Transform to symmetrical:	Mean values of upper and lower triangles
Set values <0 to zero:	Correct for negative values by setting them to zero
Correct distance:	Correct for direct neighbors (matrix with distance information is needed)
Rank matrix:	Rank matrix: Rank values in lower triangle with values from 1 to $(\text{matrixsize} \times \text{matrixsize} - 1) / 2^{\text{Rank-Order}}$ and transpose to upper triangle
Grand average:	Calculate average matrix of all input matrices
Mappings:	Matrix is reduced according to Mappings-file (Mappings.xls), result is stored as '*_matrix.txt'
	Method: Average = Average connectivity between Mappings
	Degree = Nodes with maximal Degree in every Mapping are selected
	Betweenness = Nodes with maximal Betweenness in every Mapping are selected
Make binary:	Convert matrix to binary matrix with selected threshold
	Threshold: - fixed: Threshold = value
	- std: Threshold = mean +std*value
	- percent: Threshold = value%
Graph analysis:	Perform graph analysis (see Graph analysis)
Result folder:	Folder to store results

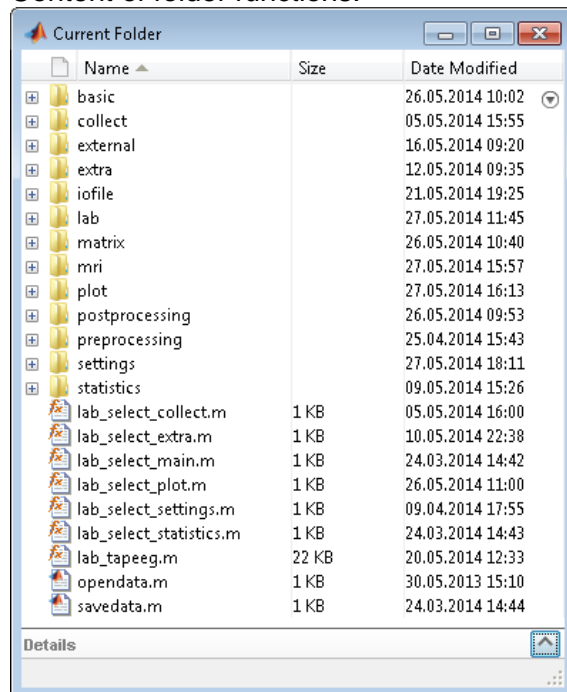
7. Matlab command line

- To start run 'TAPEEG' in the folder 'Code'
- Open any file with the command 'opendata' (only file-formats known to TAPEEG, see folder 'iofile'). When opening a EEG/MEG-file the result will be the variables data/header/cfg in workspace
- Call preprocessings with command

```
[data,header,cfg] = lab_preprocessing(data,header,cfg)
```
- Call postprocessings with command

```
[Result,cfg] = lab_postprocessing(data,header,cfg)
```
- Call *lab_statistics* or *lab_plotting* without any parameters, inputs are Excel-files

Content of folder functions:



The folders are organized according to the menus in TAPEEG

- Extra folders:
 - basic = basic scripts to read data for EEG/MEG processing or statistics/plotting
 - iofile = This folder contains all the scripts for reading files, the script to read a file is selected according to the file-extension (script = *lab_read_extension*)
 - lab = additional scripts used by higher order functions
 - mri = all scripts used to process mri
 - matrix = all scripts used to process matrices
 - settings = all scripts to generate the settings-dialogs for higher order functions. These scripts will be called, if a higher order-script is called without or empty settings

XI. List of included toolboxes

Fieldtrip ¹⁵	BEM-mesh-calculation Calculation of Leadfields (dipoli / openmeeg / simbio) LCMV beamformer, eLoreta, Minimum norm estimate, Dipol fitting Detection of bad channels
Eeglab ¹⁶	Some code for plotting in signal space (headshape, conversion of locs) Runica (independent component analysis) Reading cnt-files Plot EEG Anisotropic filtering (MRI)
FastICA ¹⁷	ICA (independent component analysis)
Brainstorm ¹⁸	BEM-mesh calculation (remesh tessellated volumes)
Nutmeg ¹⁹	Inverse solution: sLoreta
OpenMeeg ²⁰	Calculation of Forward solutions
SPM8 ²¹	Segmentation/Coregistration of MRI
FASTER ²²	Detection of bad channels (adapted code)
AR-model	modified code from Green et al. 2012
Degreecorrelation ²³	Calculation of degree distribution / correlation
MNE toolbox ²⁴	Reading of Elekta-fiff files
Read_mff ²⁵	Read mff file format (enhanced)

Scripts from Mathworks File Exchange:

AdvancedColorMap ²⁶	Create Colormaps
AnDartest ²⁷	Anderson-Darling test
Anova_rm ²⁸	Repeated measures Anova
Brain Connectivity Toolbox ²⁹	Graph analysis calculations
MatlabBGL ³⁰	MST (minimum spanning tree)
BioSig ³¹	Detection of qrs-complex (ecg)
BlandAltman ³²	Bland-Altman-Plots
Colormap and Colorbar utilities ³³	Handling of Colorbars
CronbachAlpha ³⁴	Statistics: Cronbach Alpha
Dijkstra ³⁵	Shortest path calculation
Export_fig ³⁶	Print figures
Findjobj ³⁷	Java object handling
Fleiss ³⁸	Statistics: Fleiss'es kappa
Geom3d ³⁹	Inverse solution: vector/mesh intersections
Graph Theory Toolbox ⁴⁰	Graph analysis: Eccentricity

Hurst_exponent ⁴¹	Calculation of 'Hurst exponent'
ICC ⁴²	Calculation of Intraclass correlation coefficient
ICP ⁴³	Calculation of 'Iterative Closest Point'
Inputsdlg ⁴⁴	Dialogs for settings (modified)
Kappa ⁴⁵	Statistics: Cohen's kappa
Tools for Nifti ⁴⁶	Reading Nifti and Analyze-format MRI
Oscillator ⁴⁷	Oscillator and Signal Generator
Patchline ⁴⁸	3D Line plotting
Phaseran ⁴⁹	Phase randomization of eeg/meg signals
Polygeom ⁵⁰	Helper for channel plotting in signal space
Progressbar ⁵¹	Show progress bar
Randomforest ⁵²	Random Forest Analysis
Regtools ⁵³	Regularization Tools
Rihaczek ⁵⁴	Time-Frequency analysis (modified)
RotateXLabels ⁵⁵	Helper for plotting
Roundn ⁵⁶	Round floating point values
Spear ⁵⁷	Statistics: Spearman rank
SVM ⁵⁸	Decision Boundary using SVM
Swtest ⁵⁹	Statistics: Shapiro-Wilk
Xmltools ⁶⁰	XML parsing
xlwrite ⁶¹	XLS-writing
XTickLabelRotate90 ⁶²	Helper for plotting

XII. References

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