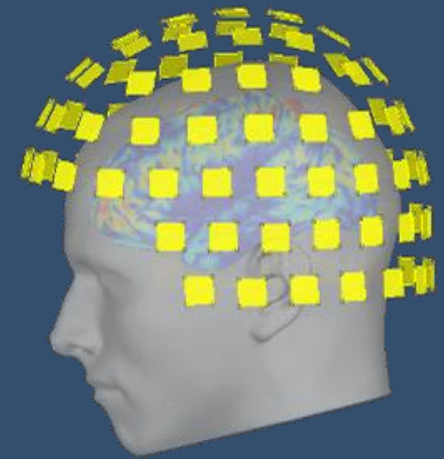
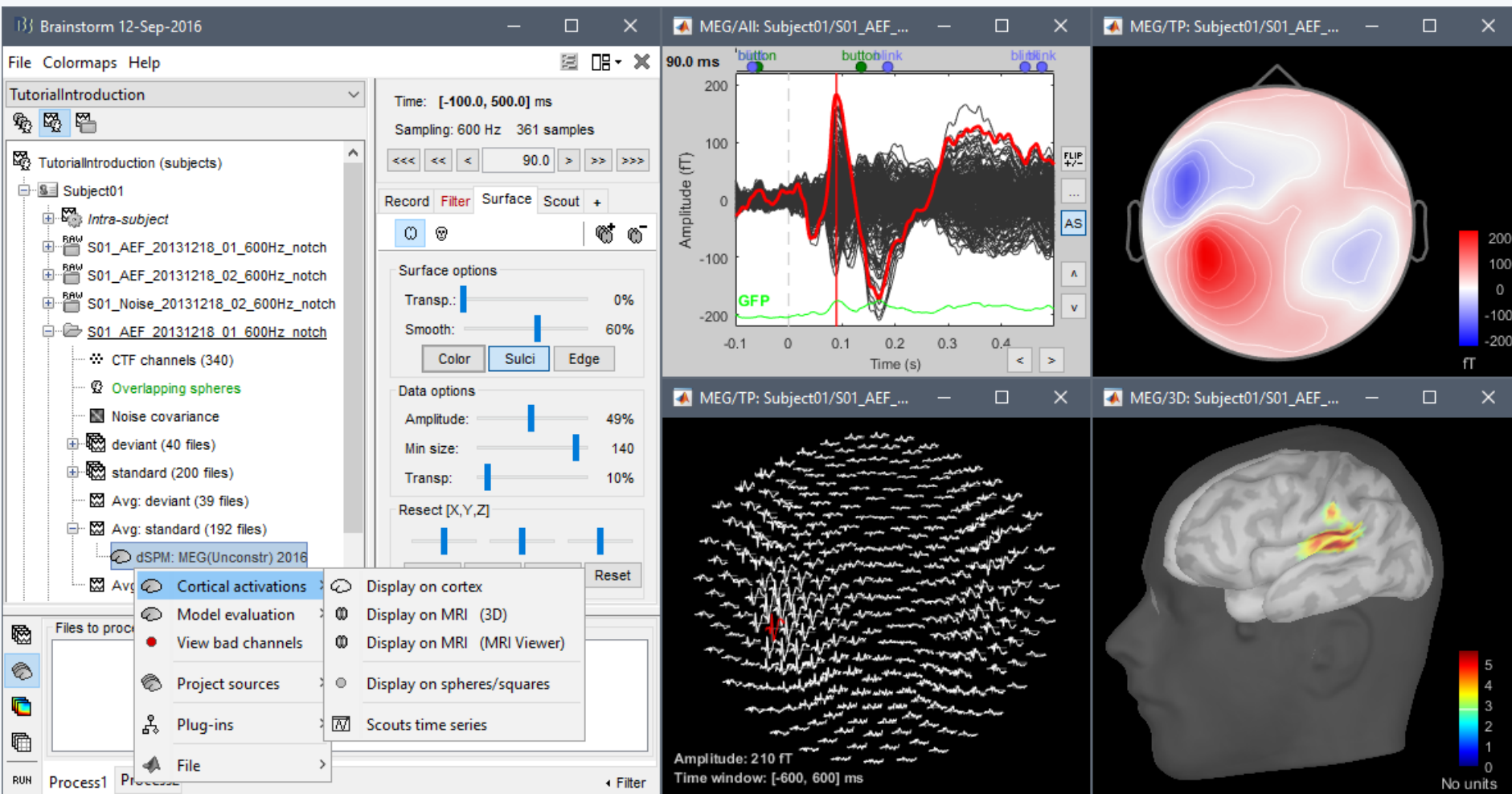


MEG and EEG analysis using
Brainstorm
<http://neuroimage.usc.edu/brainstorm>



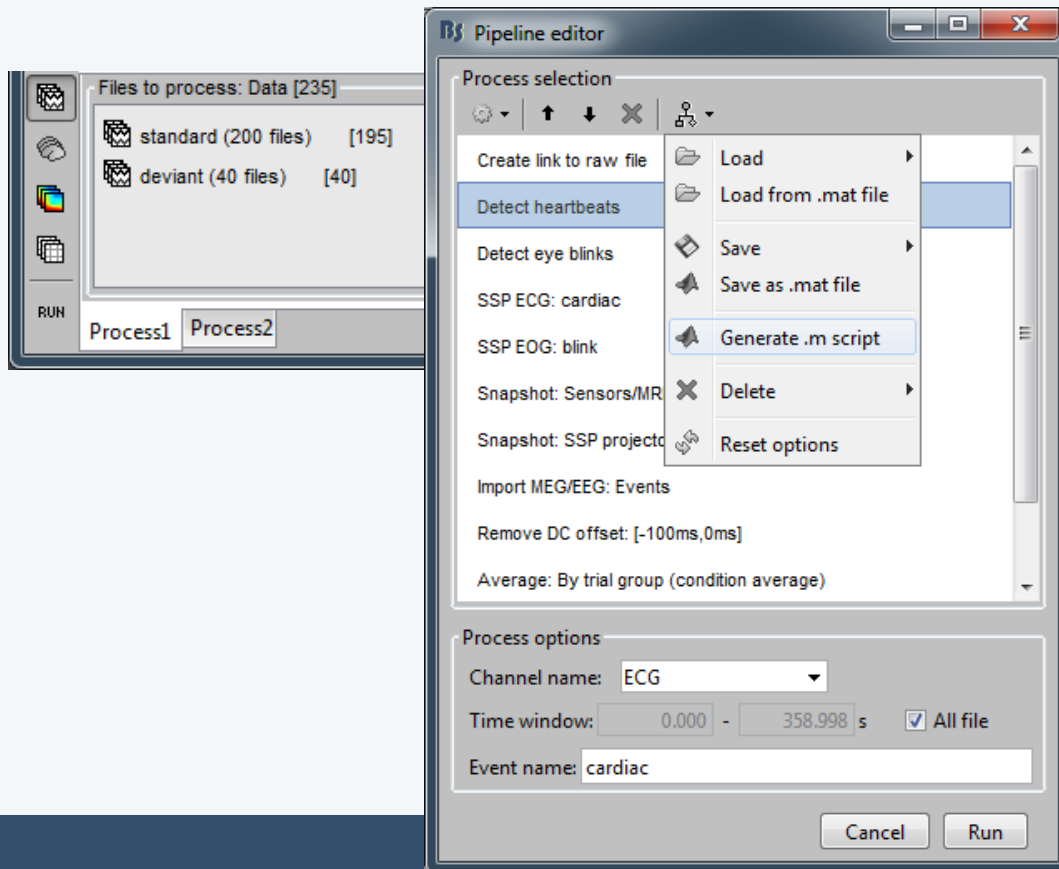
Cambridge, June 2017
Francois Tadel
Sylvain Baillet

Graphic interface



Scripting environment

- Rapid selection of files and processes to apply
- Automatic generation of Matlab scripts
- Plug-in structure: easy to add custom processes



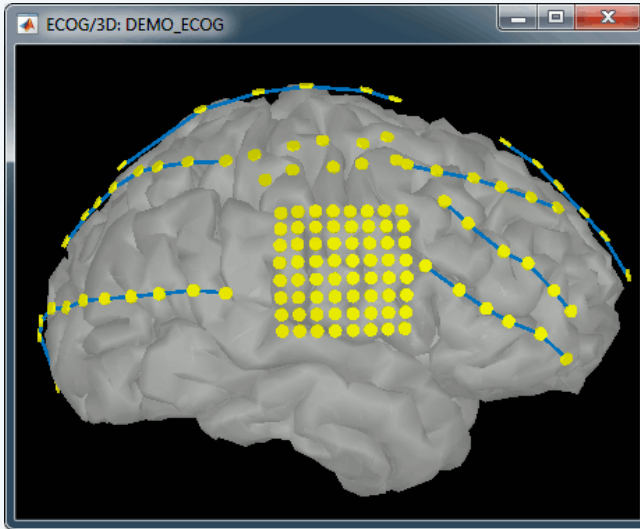
```
1 % Script generated by Brainstorm v3.1 (17-Dec-2010).
2 FileNamesA = {'Subject01\Left\data_average_101213_1558.mat', ...
3               'Subject01\Right\data_average_101213_1559.mat'};
4 FileNamesB = [];
5
6 % Process: Detect bad trials: Peak-to-peak MEGGRAD(0-2000)
7 sFiles = bst_process(...
8     'CallProcess', 'process_detectbad', ...
9     FileNamesA, FileNamesB, ...
10    'timewindow', [-0.0998, 0.3000], ...
11    'meggrad', {[0, 2000], 'fT/cm (x 0.04)', 1e-015}, ...
12    'rejectmode', 2);
13
14 % Process: Remove baseline: [-100ms,-1ms]
15 sFiles = bst_process(...
16     'CallProcess', 'process_baseline', ...
17     sFiles, [], ...
18     'baseline', [-0.09983, -0.00056], ...
19     'overwrite', 1);
20
21 % Process: Band-pass filter: 1Hz - 80Hz
22 sFiles = bst_process(...
23     'CallProcess', 'process_bandpass', ...
24     sFiles, [], ...
25     'f1', 1, ...
26     'f2', 80, ...
27     'overwrite', 1);
28
29 % Process: Average by condition
30 sFiles = bst_process(...
31     'CallProcess', 'process_average', ...
32     sFiles, [], ...
33     'avgttype', 3, ...
34     'isstd', 0);
```

- Free and open-source application
- Matlab & Java: Platform-independent
- Designed for Matlab
- Stand-alone version available
- Interface-based: click, drag, drop
- No programming experience required
- Daily updates of the software
- Supports most common file formats

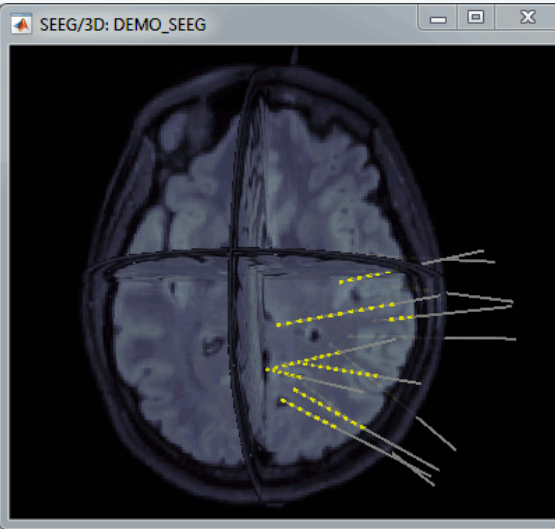


Multi-modal imaging

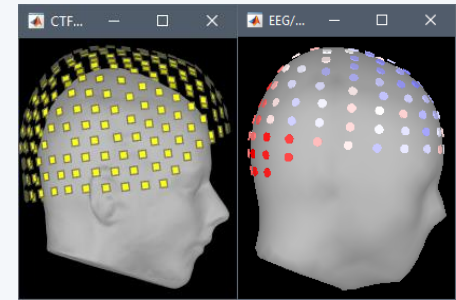
ECoG



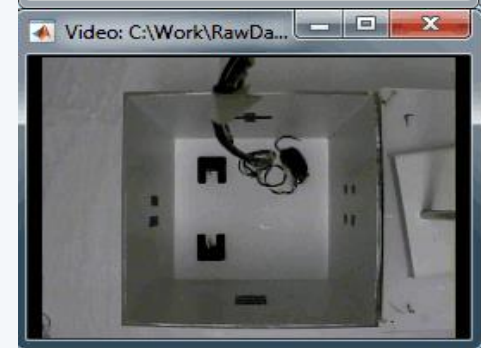
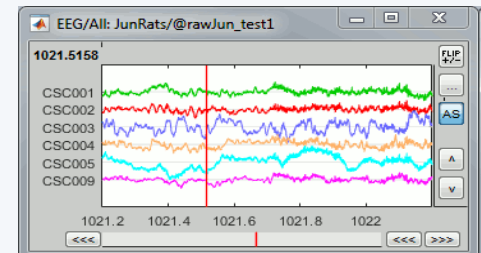
Depth electrodes



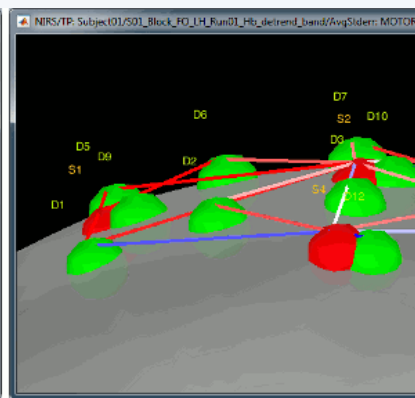
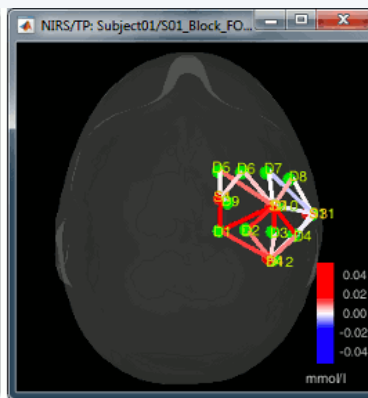
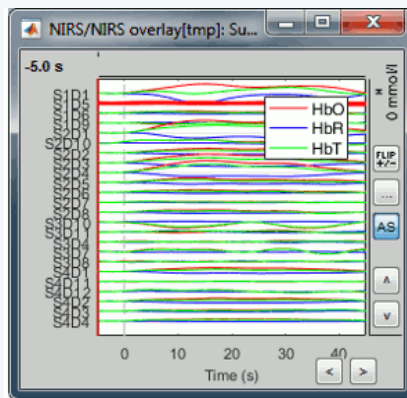
MEG/EEG



Electrophysiology



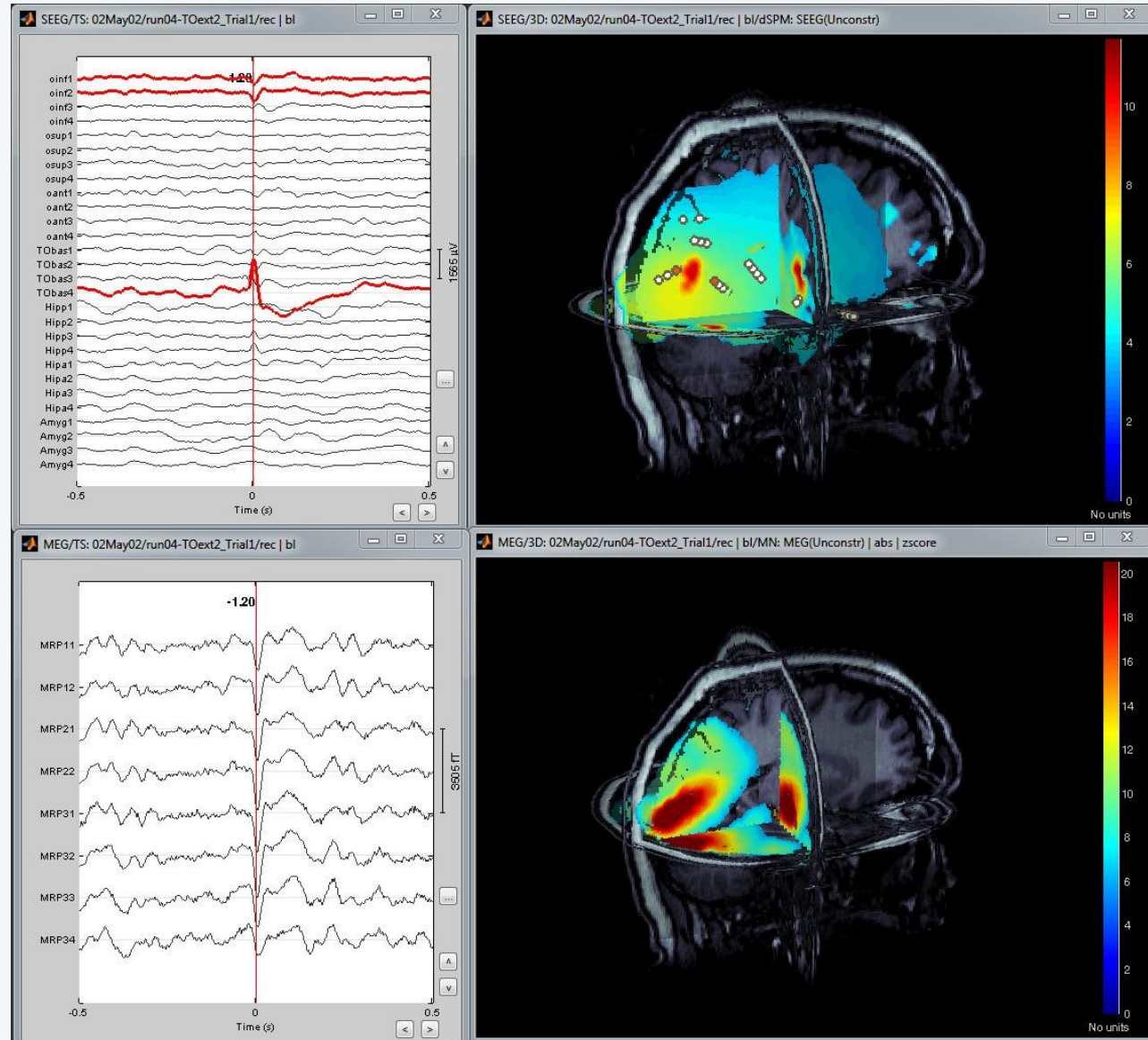
fNIRS



Multi-modal imaging

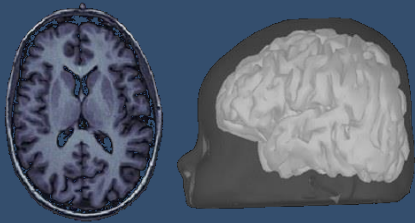
Easy integration of:

- MEG
- EEG
- ECoG
- SEEG
- Animal LFP
- NIRS

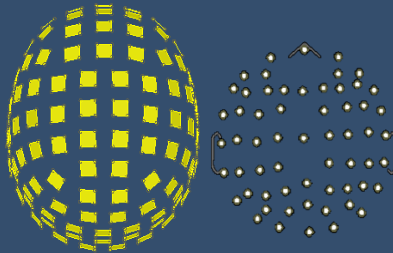


Workflow

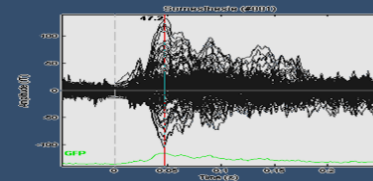
Anatomy



Sensors



EEG/MEG



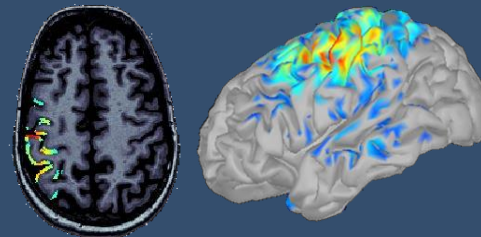
Analysis

Averages
Contrasts
Group analysis
Time-frequency
Connectivity

Co-registration



Source estimation



Single subject

Anatomy
Link recordings
MRI registration

Importing

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Pre-processing

Markers
Epoching
Averaging
Sources
Time-frequency

Analysis of the experimental data

Loop:
all acquisition runs
all subjects

Anatomy

Link recordings
MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

Epoching

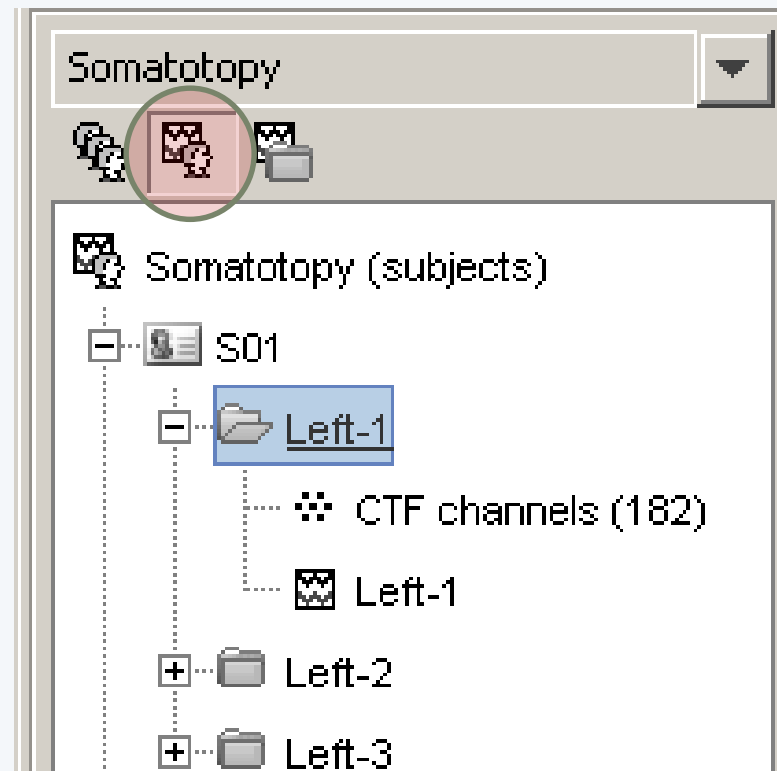
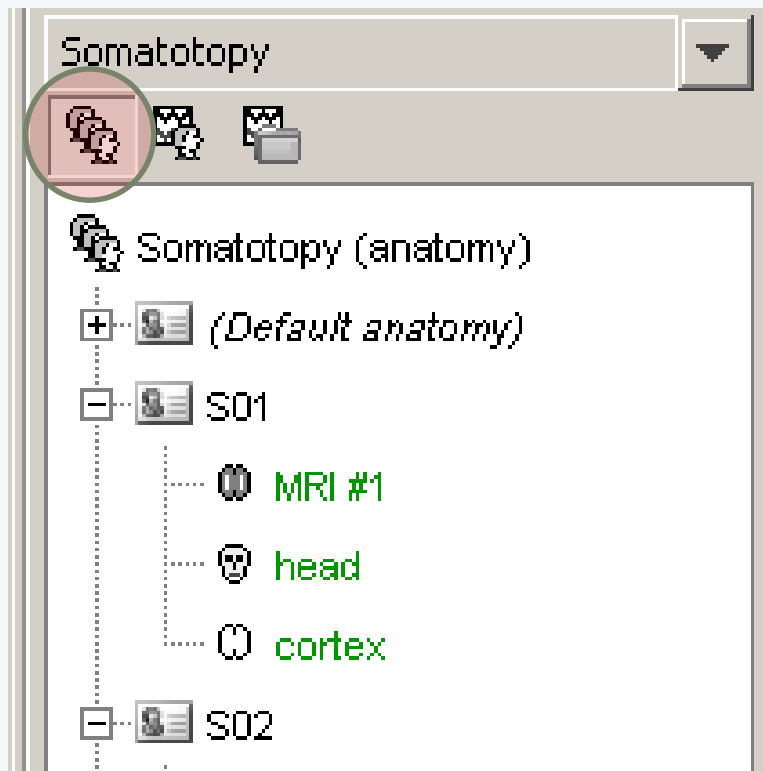
Averaging

Sources

Time-frequency

- One-click import of the T1 segmentation: FreeSurfer, BrainSuite, BrainVISA, CIVET
- Import and place fiducials in the MRI (N,L,R)





- Three levels:
 - Protocol
 - Subject
 - Condition
- Popup menus
- All files saved in Matlab .mat
- Same architecture on the disk

Import

Anatomy

Link recordings

MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

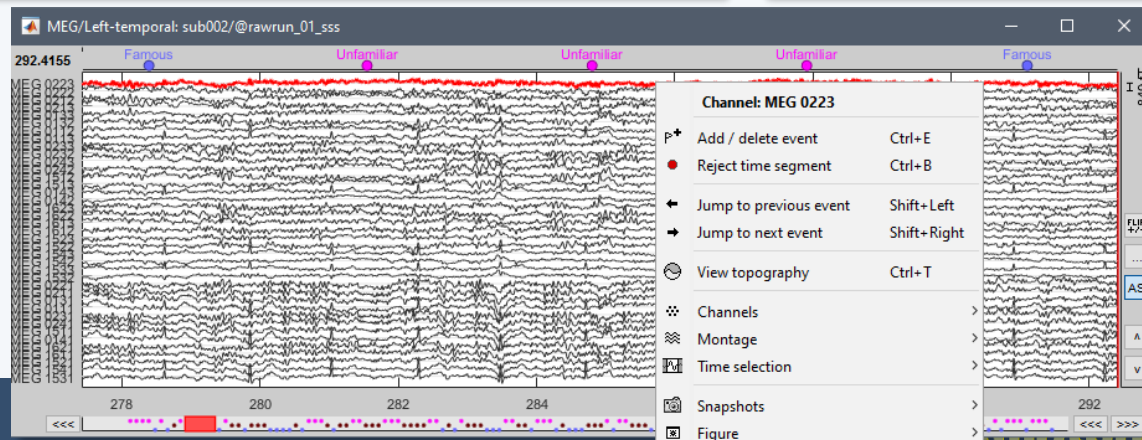
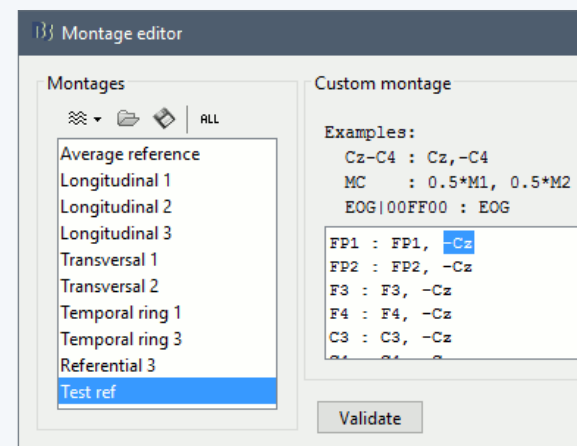
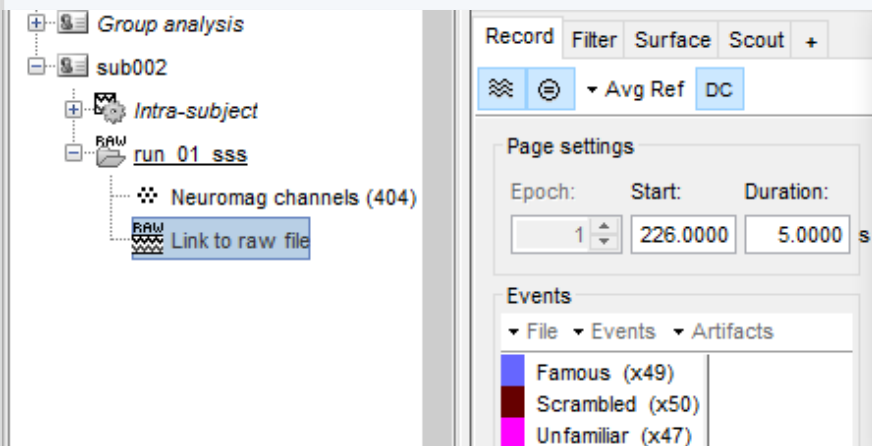
Epoching

Averaging

Sources

Time-frequency

- Original files linked to the database (no copy)
- Rich data viewer with flexible montage editor
- Optimized reading functions



Co-registration MEG / MRI (I)

Anatomy

Link recordings

MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

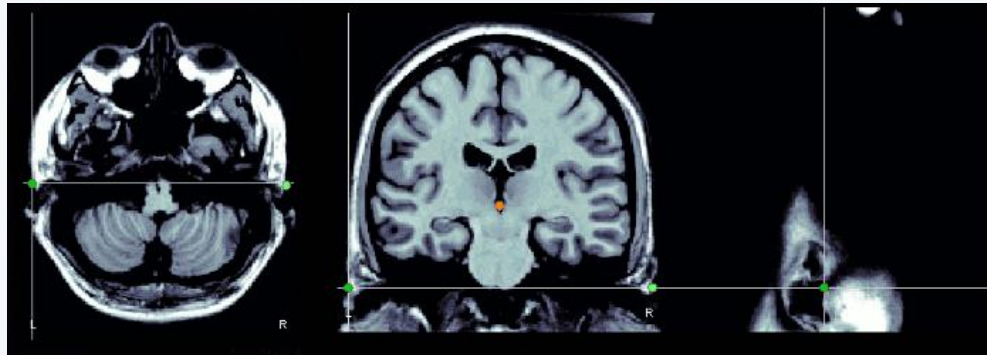
Epoching

Averaging

Sources

Time-frequency

- Basic estimation based on three points: Nasion (NAS), Left ear (LPA), Right ear (RPA)
- MRI: Marked in the volume with the MRI Viewer
- MEG: Obtained with a tracking system (Polhemus)



Co-registration MEG / MRI (2)

Anatomy

Link recordings

MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

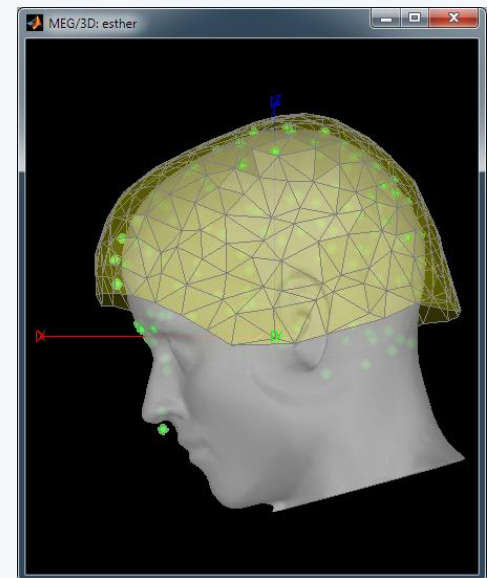
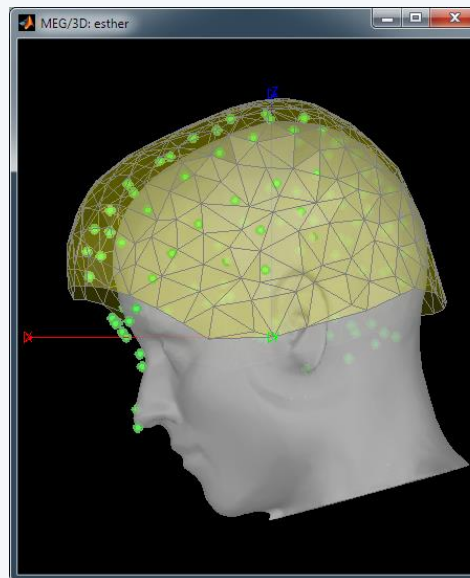
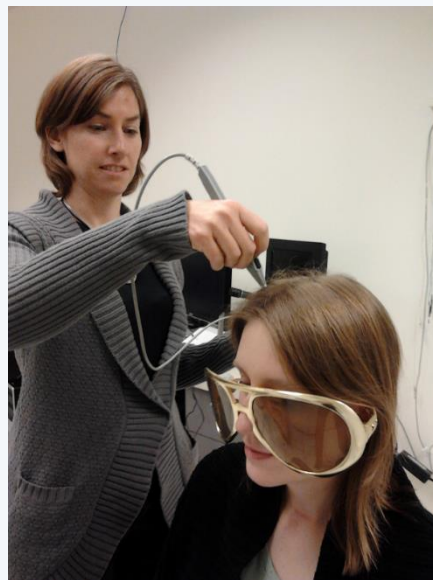
Epoching

Averaging

Sources

Time-frequency

- Automatic adjustment based on head shape: Fitting Polhemus points on the MRI head surface
- Final registration must be checked manually
- Polhemus driver included in Brainstorm



Quality control

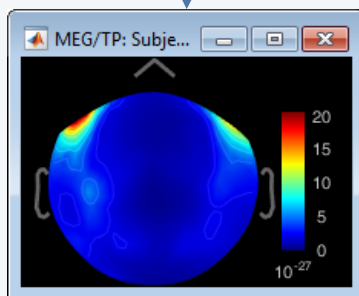
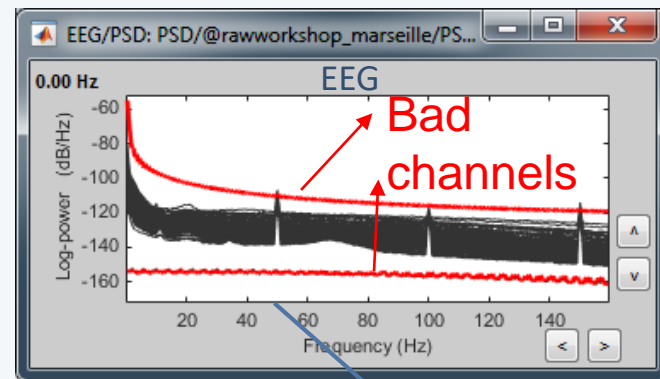
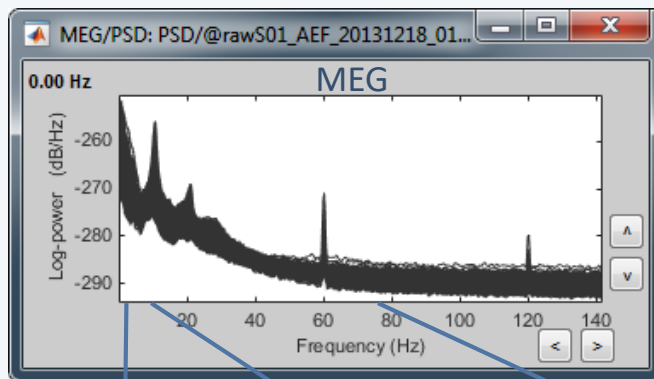
Anatomy
Link recordings
MRI registration

PSD

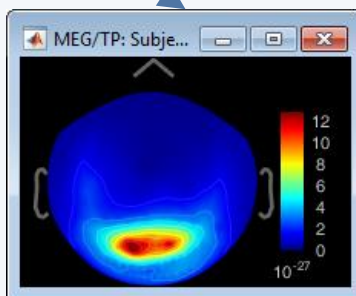
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

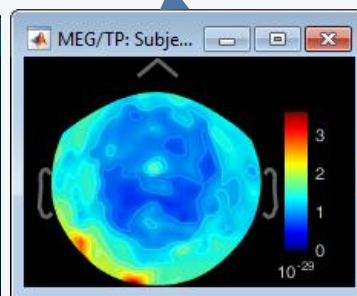
- Power spectrum density for quality control



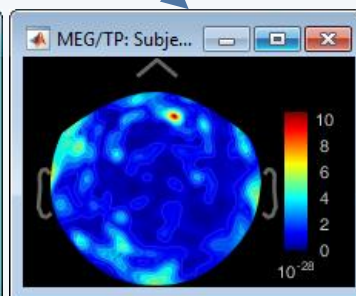
< 3Hz: Eyes



10Hz: Alpha



> 40Hz: Muscle



50/60Hz

Pre-processing

Anatomy
Link recordings
MRI registration

PSD

Filters

Bad channels
Artifacts
Correction
Bad segments

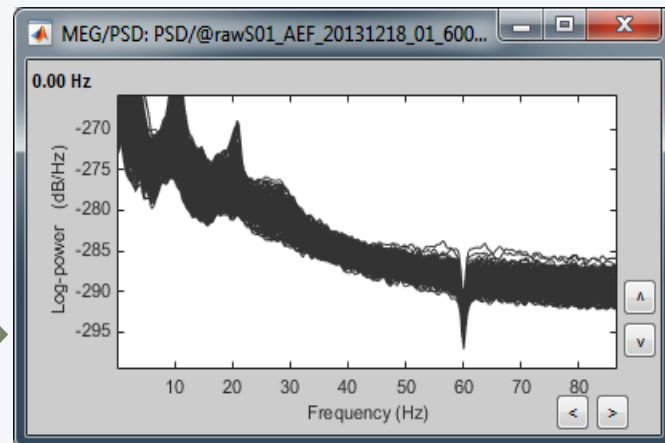
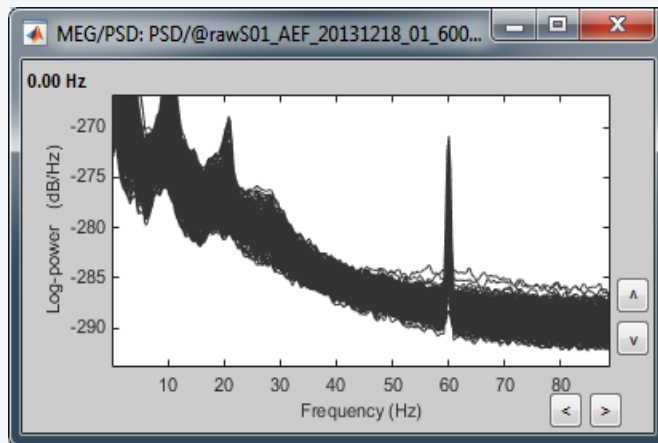
Markers

Epoching
Averaging
Sources

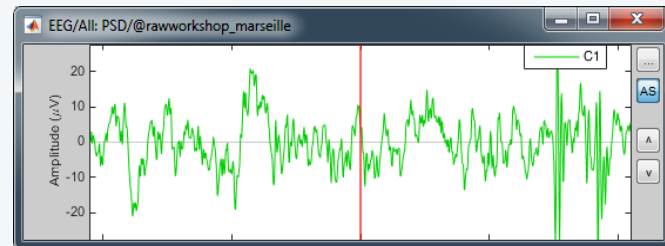
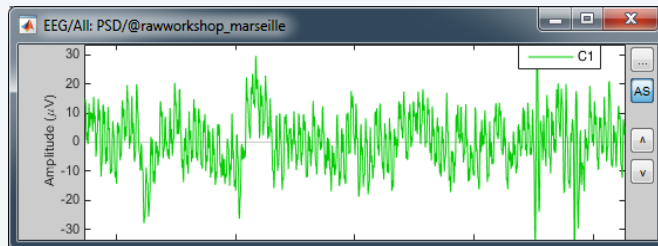
Time-frequency

- Notch filter: Removes 50Hz/60Hz power line noise (and harmonics)

PSD



Signal



Pre-processing

Anatomy
Link recordings
MRI registration

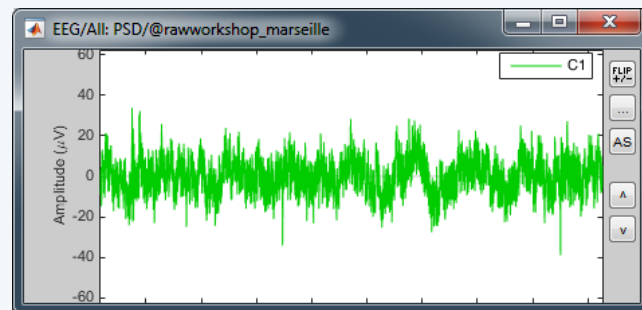
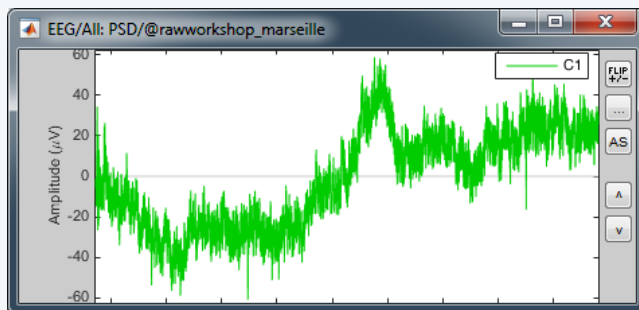
PSD

Filters

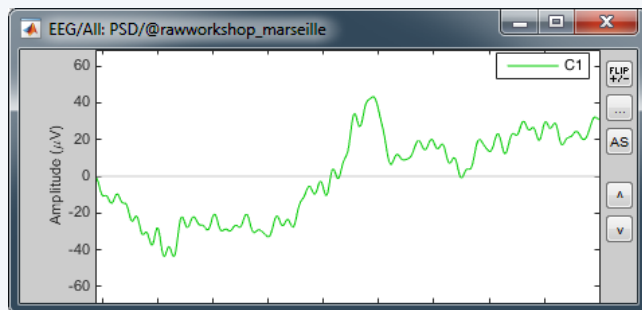
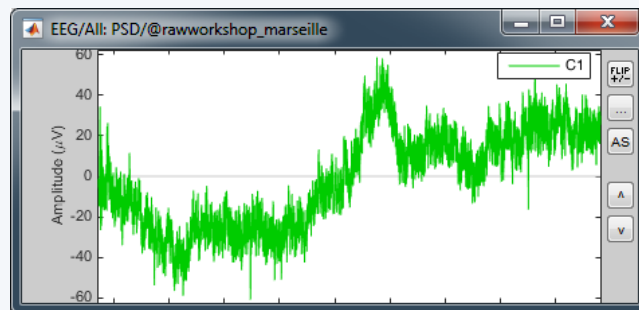
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- High-pass filter: Removes slow components (eye movements, breathing, sensor drifts...)



- Low-pass filter: Remove high-frequencies



Pre-processing

Anatomy
Link recordings
MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

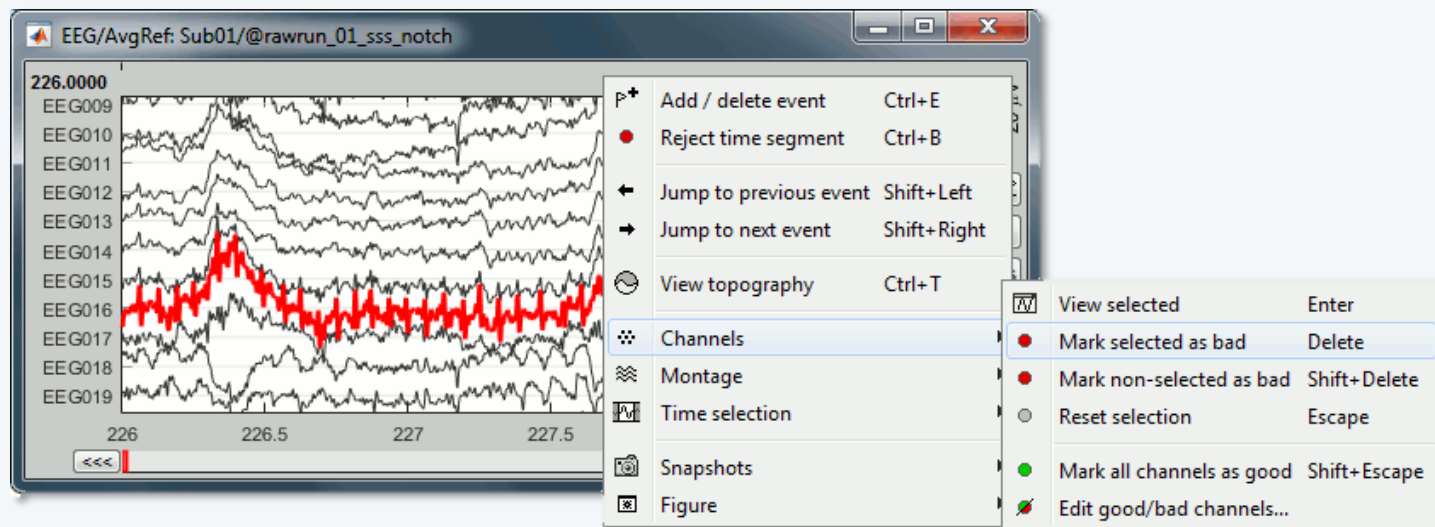
Epoching

Averaging

Sources

Time-frequency

- Manual inspection of the recordings
- Interactive selection of bad channels
- Re-reference the EEG if necessary (Average ref)



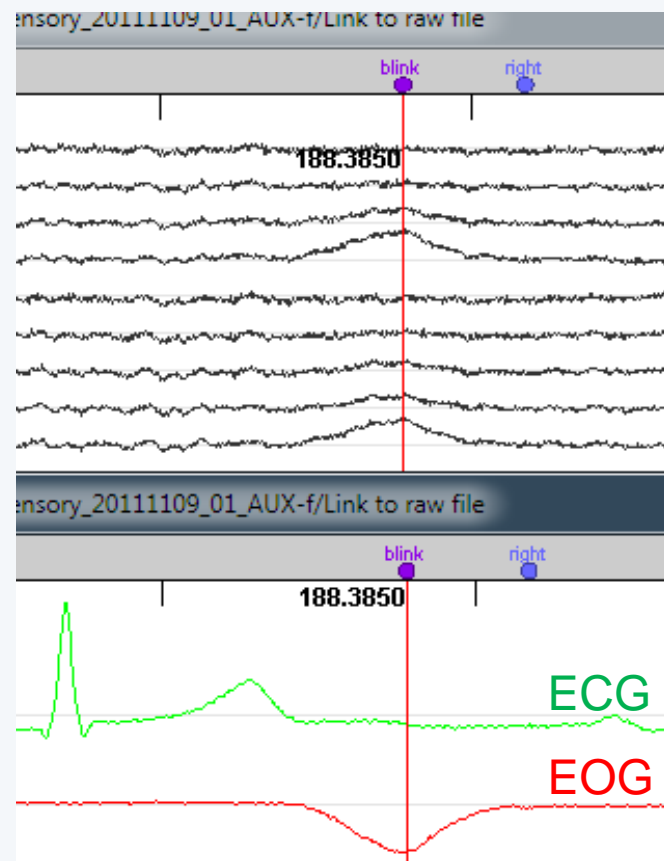
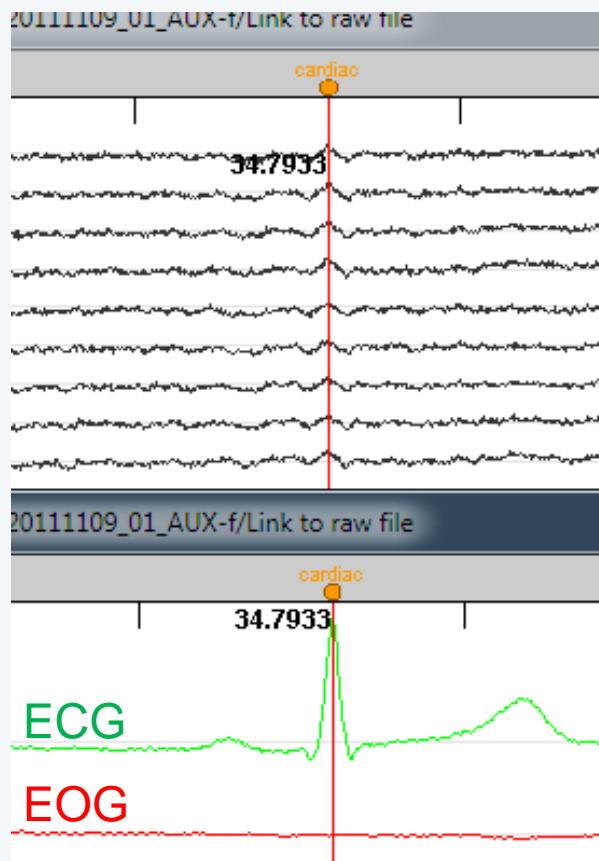
Pre-processing

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- Automatic detection of blinks and heartbeats (peak detection, or explicit amplitude threshold)



- Two categories of artifacts:
 - Well defined, reproducible, short, frequent:
 - Heartbeats, eye blinks, eye movements, some stimulators
 - Unavoidable and frequent: we cannot just ignore them
 - Can be modeled and removed from the signal efficiently
 - All the other events that can alter the recordings:
 - Movements, building vibrations, metro nearby...
 - Too complex or not repeated enough to be modeled
 - Safer to mark them as bad segments, and ignore them

Pre-processing

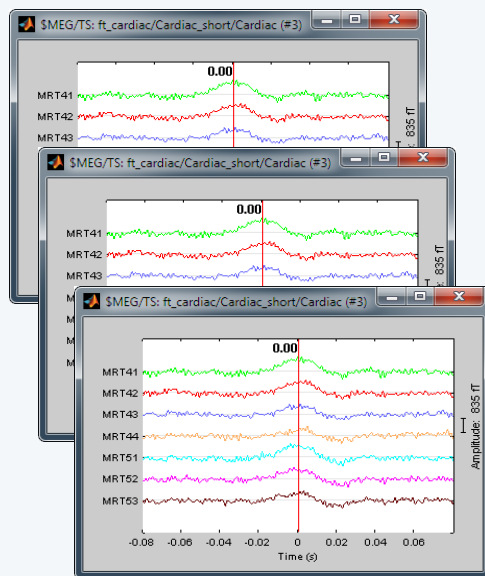
Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- Correction with Signal Space Projections (SSP)

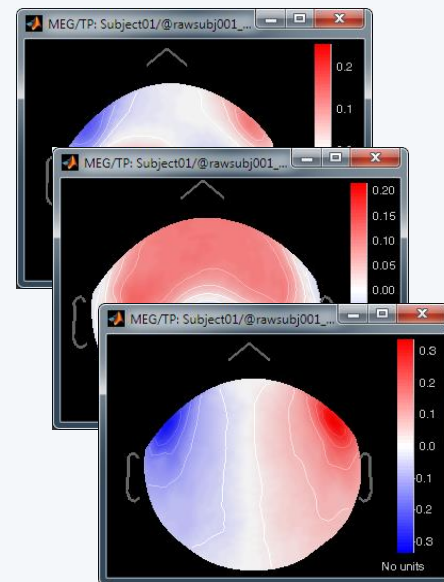
Detect artifacts



PCA



Spatial components



Select components and compute a linear projector to remove their contribution from the recordings

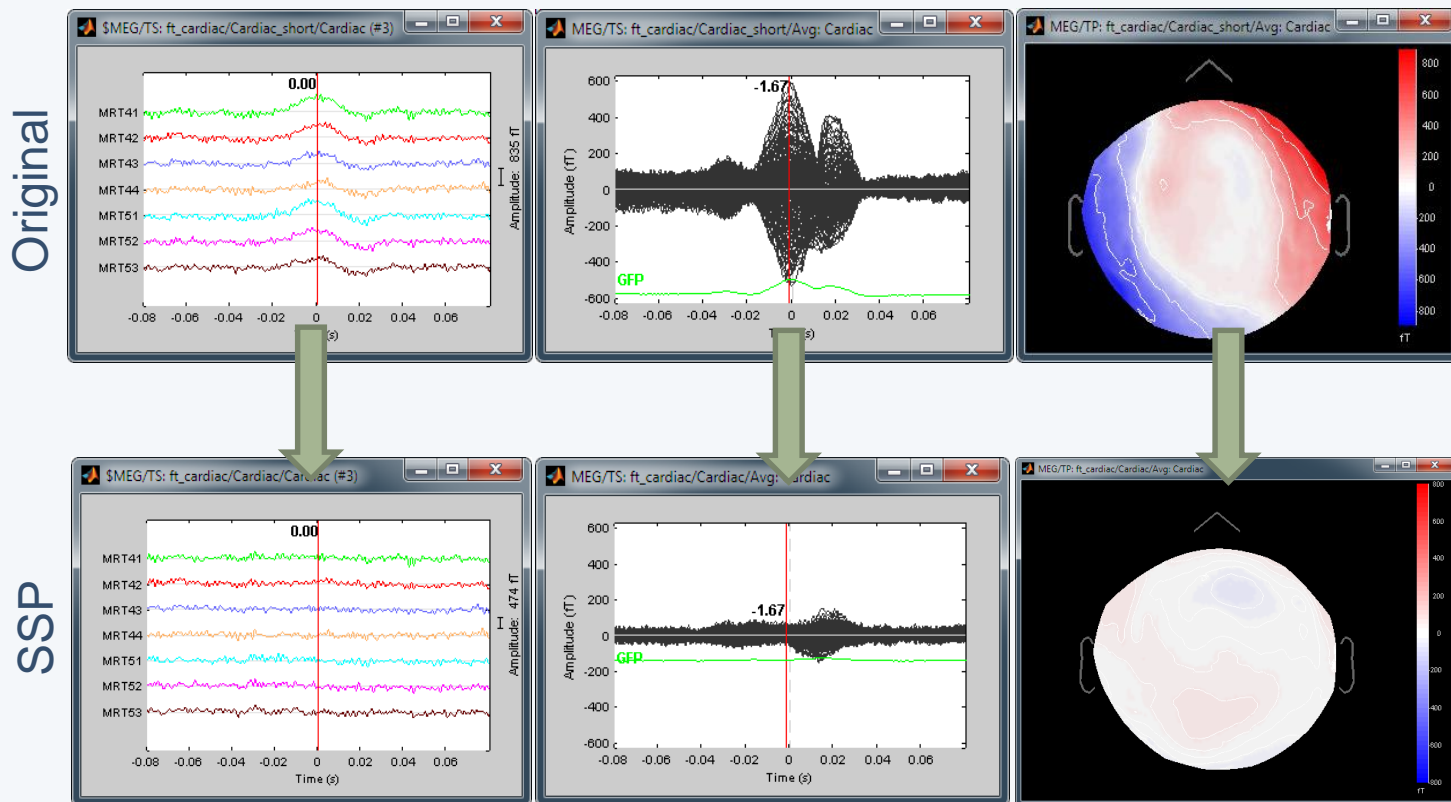
Pre-processing

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

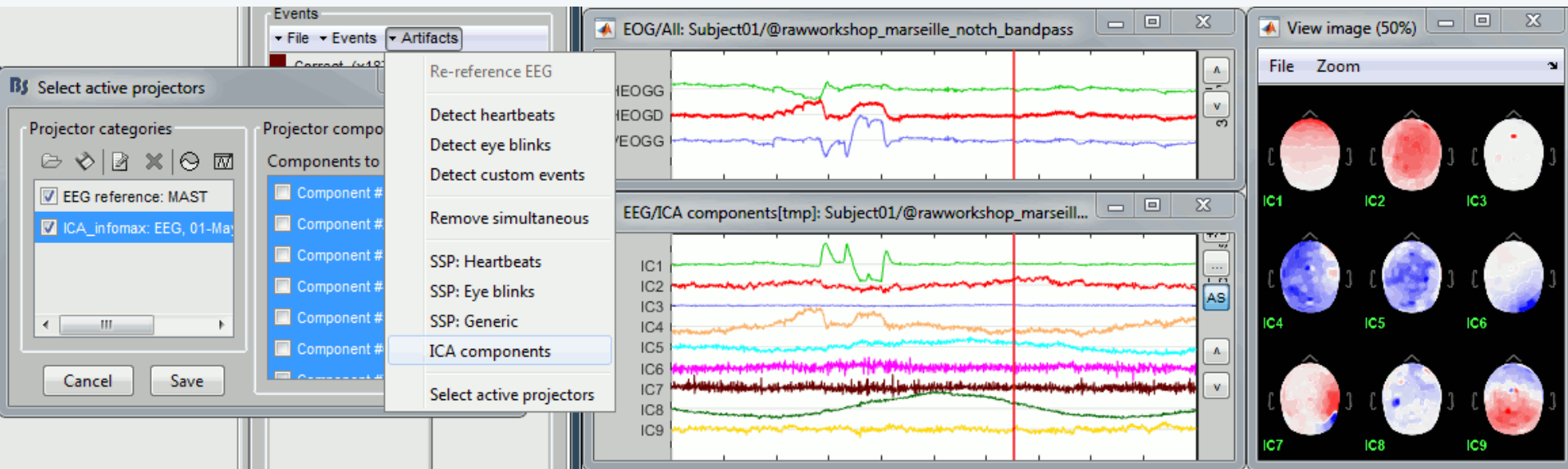
Markers
Epoching
Averaging
Sources
Time-frequency

- Example: Cardiac artifact



Pre-processing

- Independent component analysis (ICA):
 - Popular in the EEG literature
 - Alternative to SSP for low number of sensors
 - Already implemented: Infomax and JADE (EEGLAB)



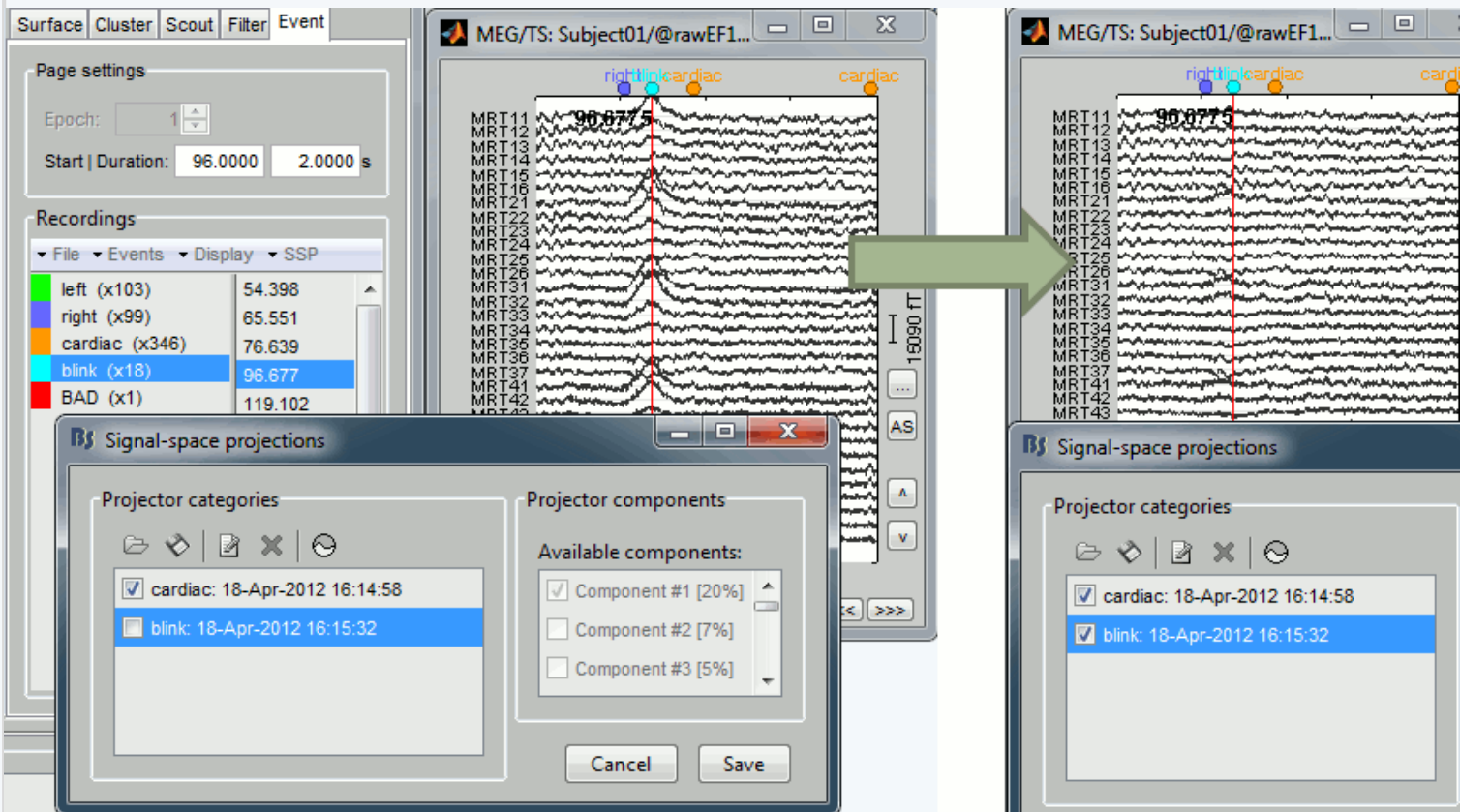
Pre-processing

Anatomy
Link recordings
MRI registration

PSD
Filters
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Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- Example: Blink



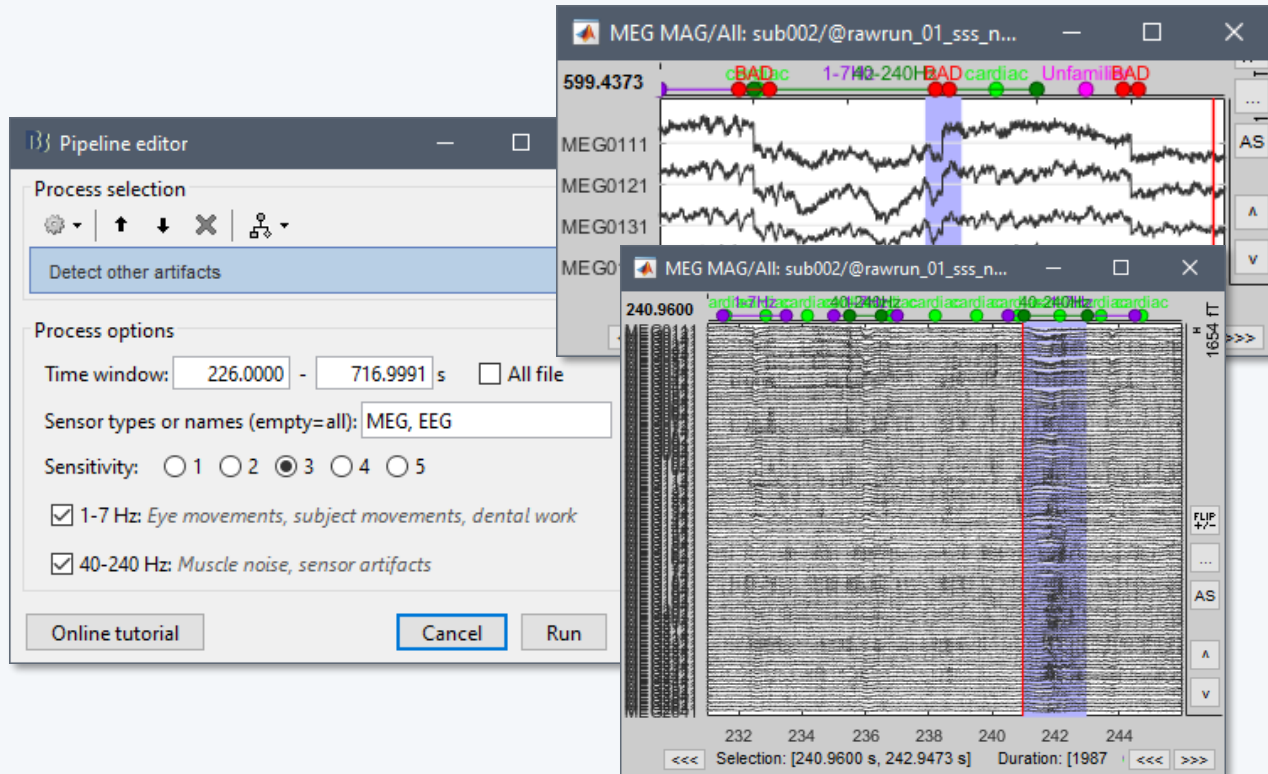
Pre-processing

Anatomy
Link recordings
MRI registration

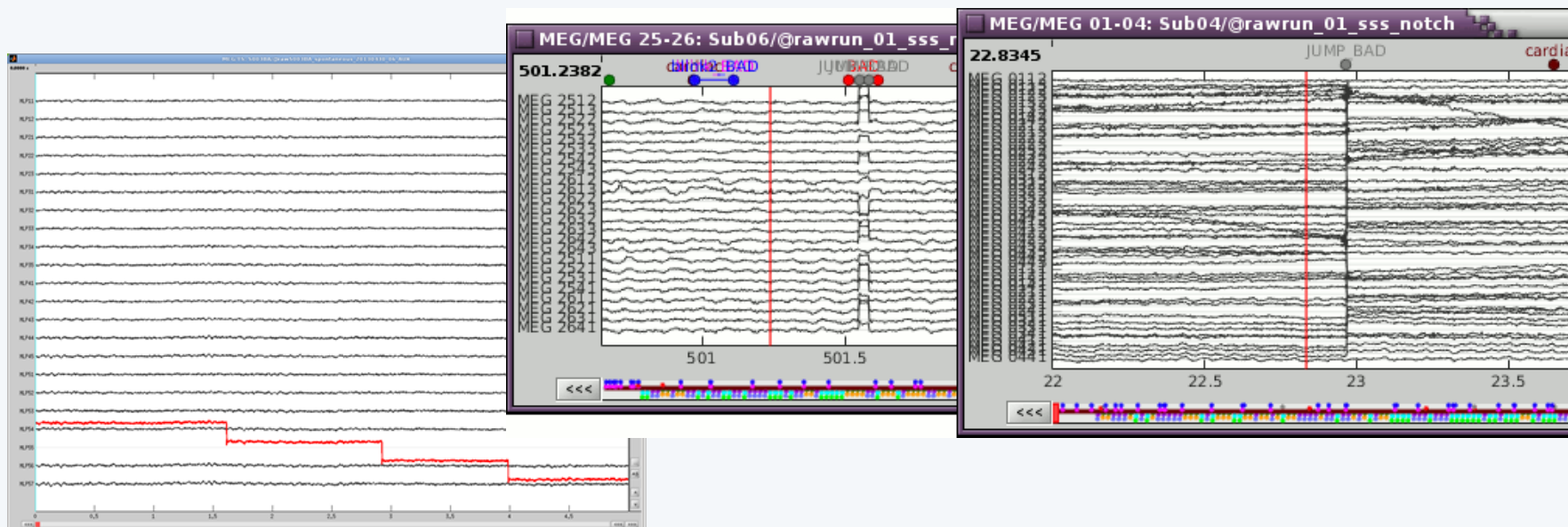
PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- Automatic detection of artifacts (RMS-based)
- Manual screening of all the recordings is advised (scroll all the sensors by pages of 10-20s)
- Exclude: Blinks, movements, SQUID jumps



- Sharps steps followed by a change of baseline value
- Mark the channels as bad before running MaxFilter
- Or mark the segments as bad in Brainstorm



Epoching

Anatomy
Link recordings
MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

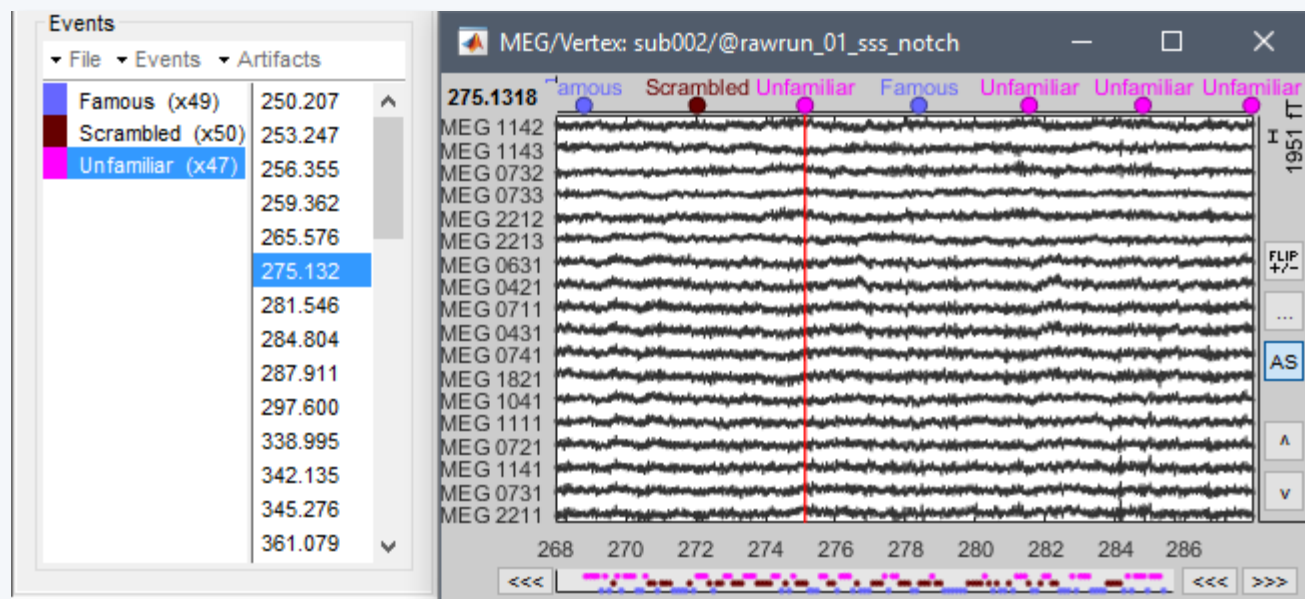
Markers

Presentation

Sensor

Manual

- Two types of experiments:
 - Steady-state or resting-state (ongoing activity)
 - Event-based (stimulus, response, spike...)
- How to get event markers in the recordings?



Epoching

Anatomy
Link recordings
MRI registration

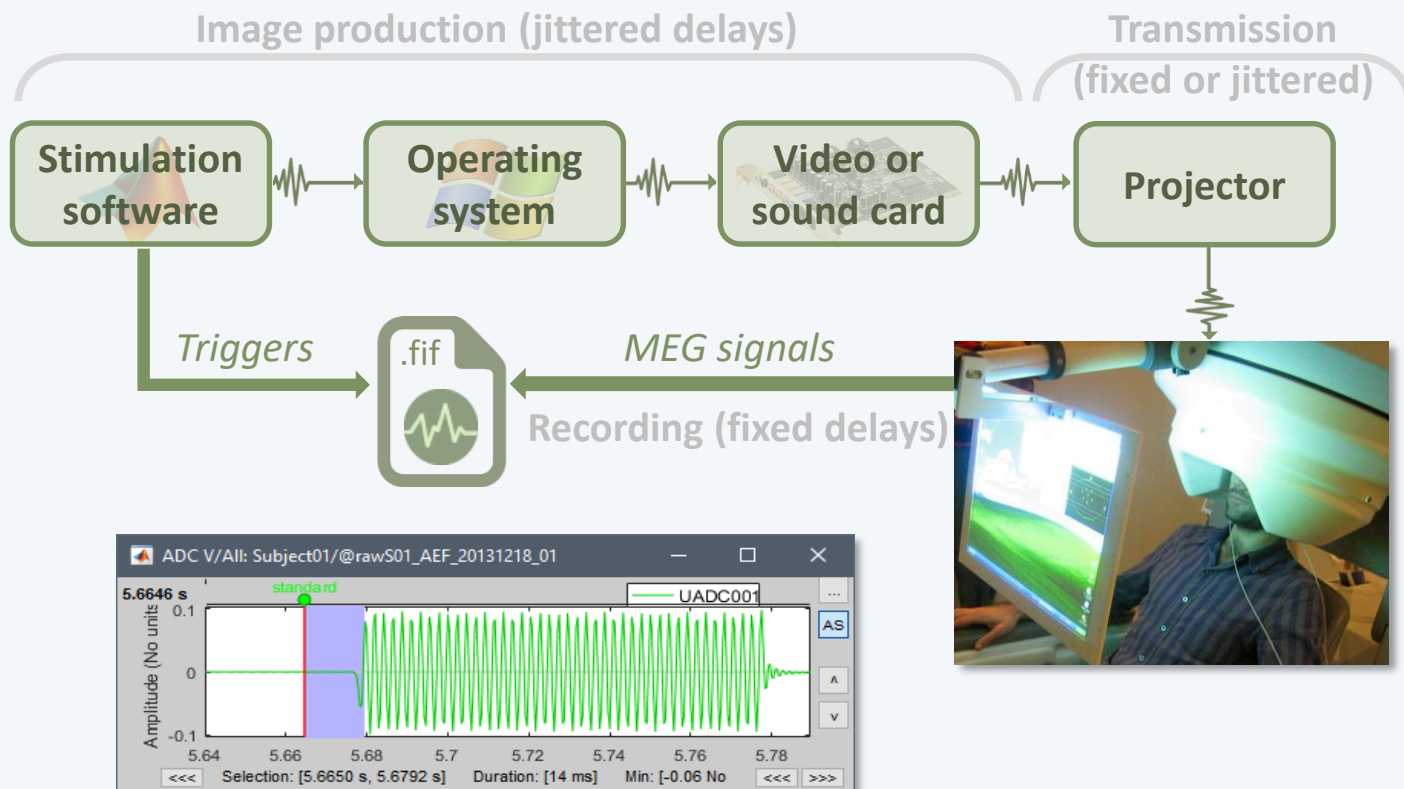
PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers

Presentation

Sensor
Manual

- Reading the triggers saved by the presentation software (includes jittered OS delays)



- File triggers are never aligned with the real stim

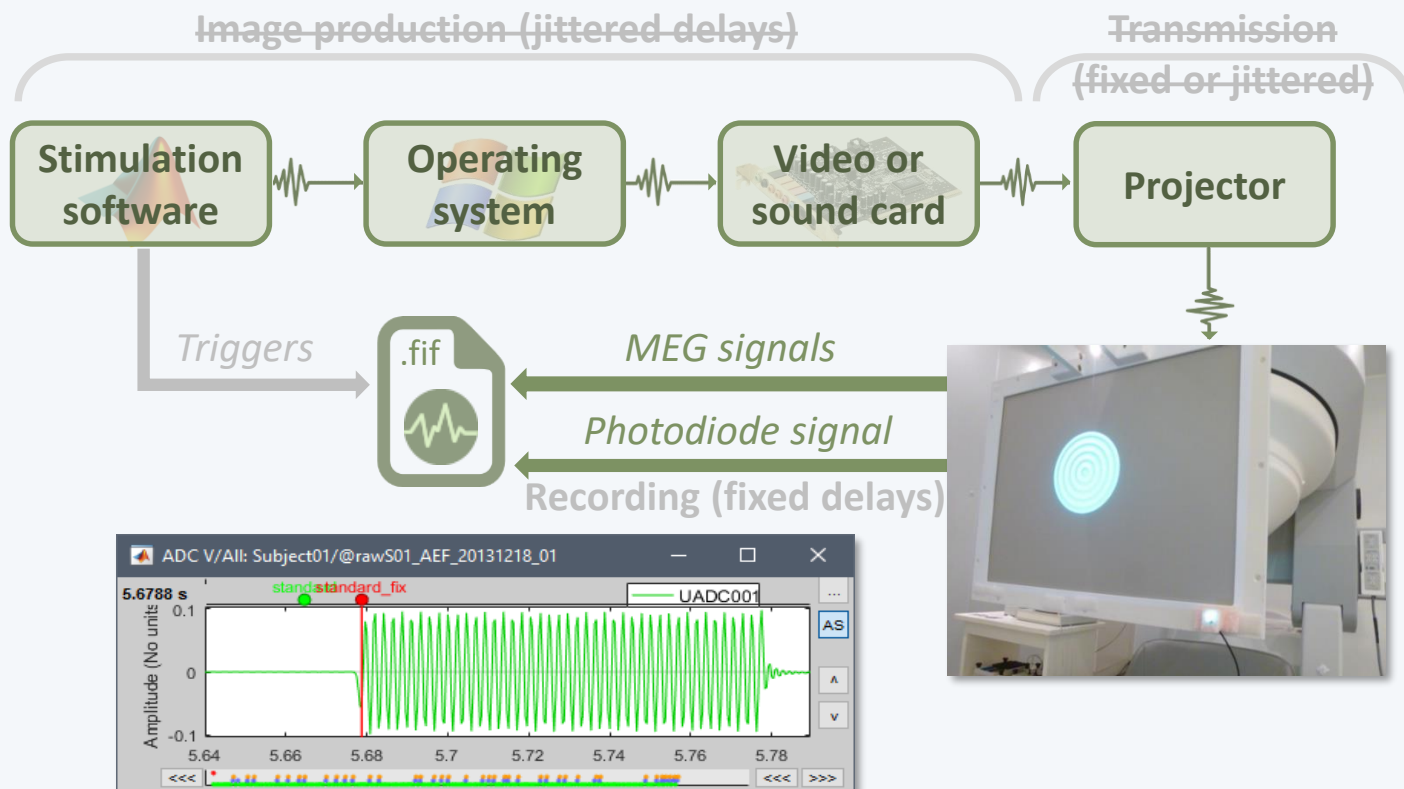
Epoching

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Presentation
Sensor
Manual

- Reading information recorded on the subject side (photodiode, microphone, response box...)



- Avoids most uncontrollable jittered delays

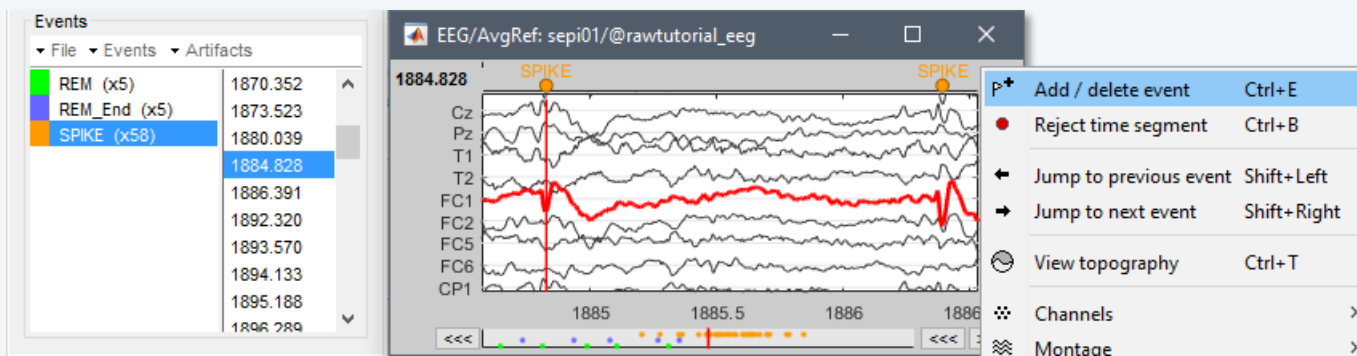
Epoching

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Presentation
Sensor
Manual

- Reading the triggers saved by the presentation software (includes jittered OS delays)
- Reading information recorded on the subject side (photodiode, microphone, response box...)
- Manual or automatic marking of biological or behavioral events, post-acquisition (epileptic spikes, sleep spindles, rat position in a box...)
- Optimized workflow for clinicians (keyboard and mouse shortcuts, workspace...)



Epoching

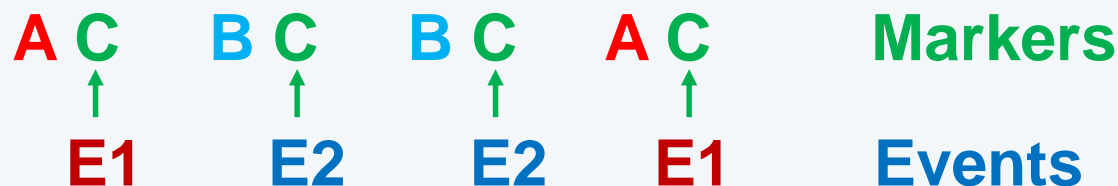
Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Combine
Extract
Length
Process

- In some experiments, the event of interest is a combination of presentation markers.

- Example: Priming experiments



- In Brainstorm, the events of interest are saved as new marker types in the continuous files.
- In other environments, the events are sometimes defined only at the epoching time and not saved in the continuous file.

Epoching

Anatomy
Link recordings
MRI registration

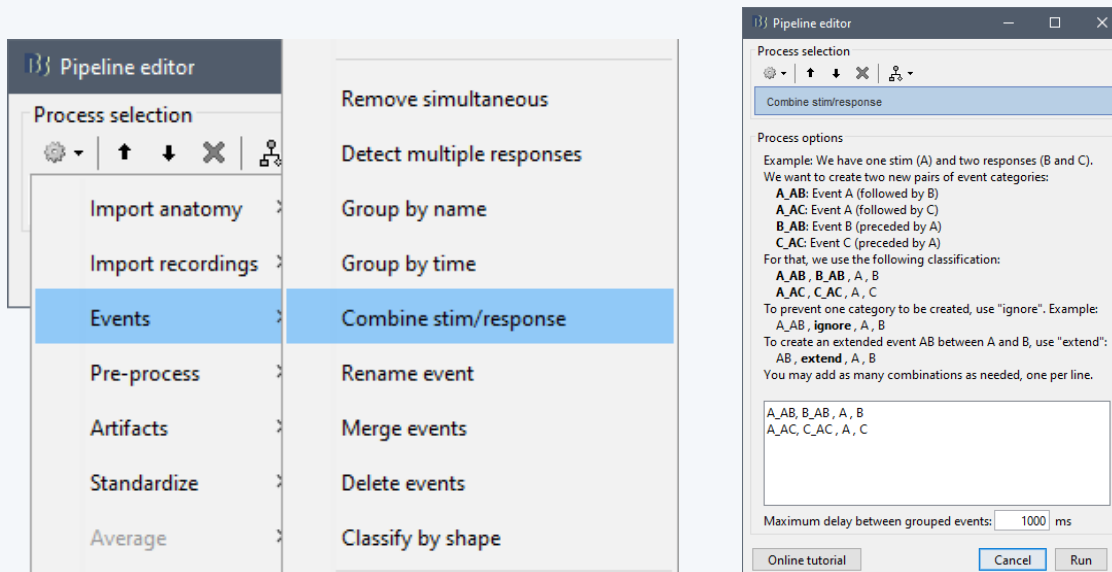
PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching

Combine

Extract
Length
Process

- In Brainstorm, the events of interest are saved as new marker types in the continuous files.



- In other environments, the events are sometimes defined only at the epoching time and not saved in the continuous file.

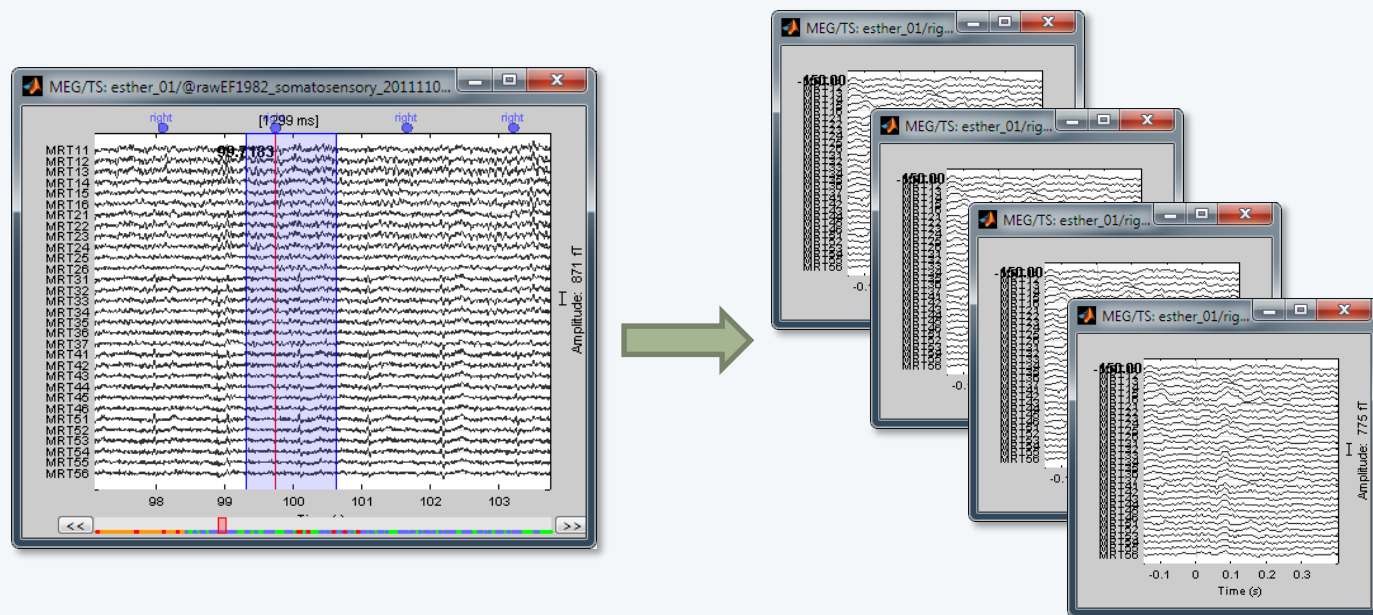
Epoching

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Combine
Extract
Length
Process

- Epochs = Trials = Short blocks of recordings around an event of interest.
- Epoching = Extracting epochs from the continuous recordings and saving them.



Epoching

Anatomy
Link recordings
MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

Epoching

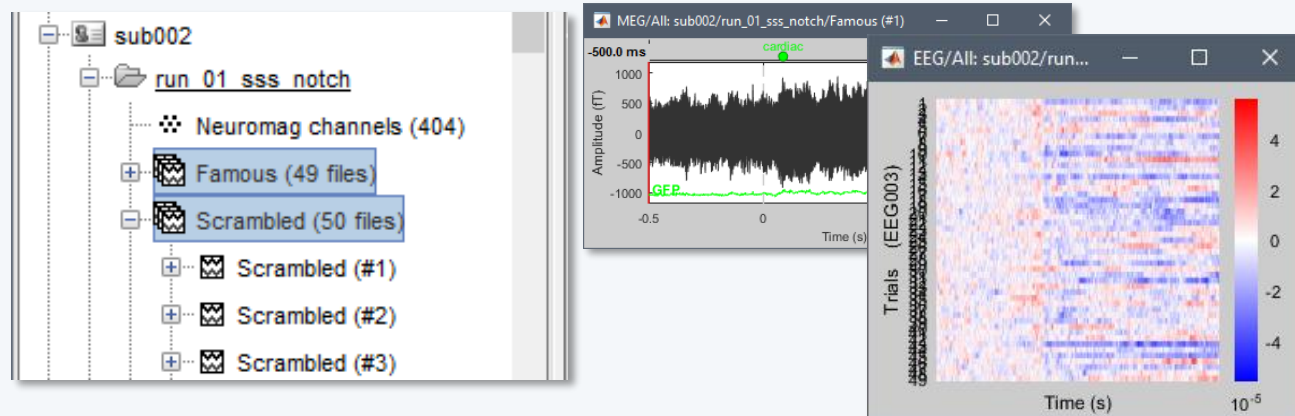
Combine

Extract

Length

Process

- In Brainstorm, each imported epoch is an independent file in the database.
- Accessible by event type or individually.



- In other programs, all the epochs from one run are saved in one single file (one file per event type, or one file with all the events).

Epoching

Anatomy
Link recordings
MRI registration

PSD

Filters

Bad channels

Artifacts

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Bad segments

Markers

Epoching

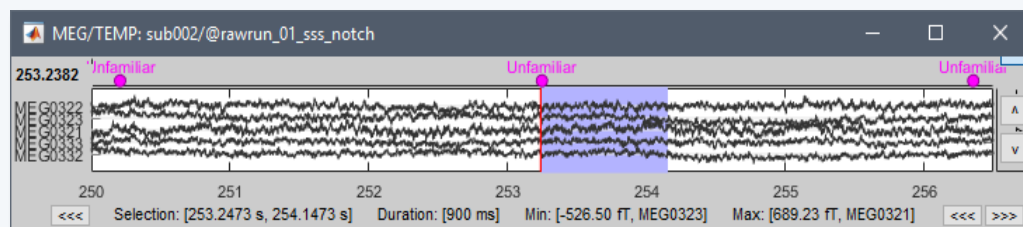
Combine

Extract

Length

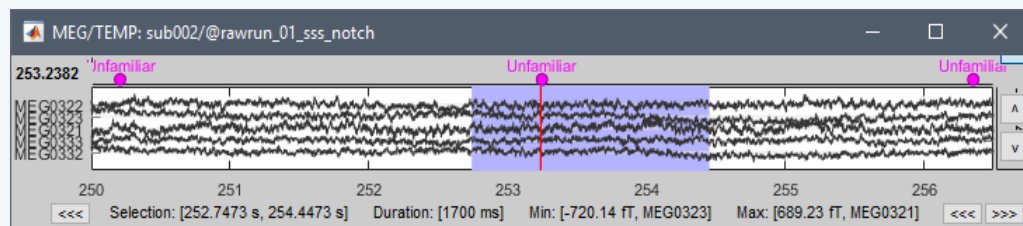
Process

- How to define the optimal epoch length ?
- Experimental design:
Expected effect duration, inter-stimulus interval



[0,900] ms

- Analysis: Frequency filters and amplitude normalizations may require longer epochs



+ 200ms baseline
+ 300ms filters
= [-500, 1200] ms

- Computational limitations: Size and time

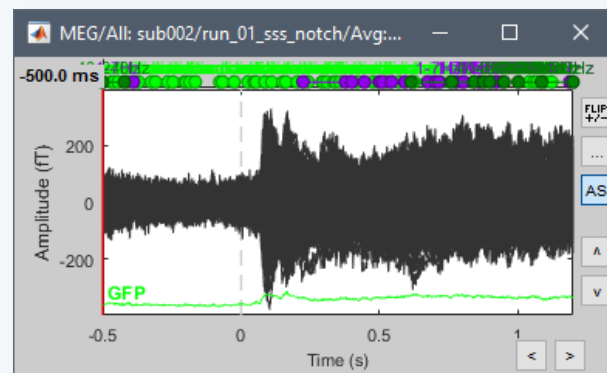
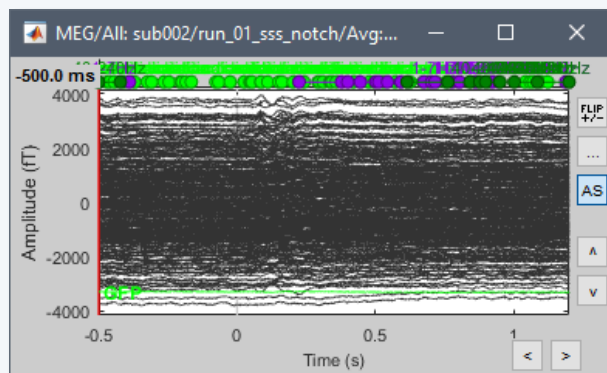
Epoching

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Combine
Extract
Length
Process

- Processing steps that can be applied on epochs:
 - **DC offset correction:** Subtract the average estimated over a baseline period
 - **Detrending:** Subtract a linear trend estimated over a reference period
 - **Resampling:** Decrease the sampling rate
- This dataset: DC correction, baseline= $[-500,0]$ ms



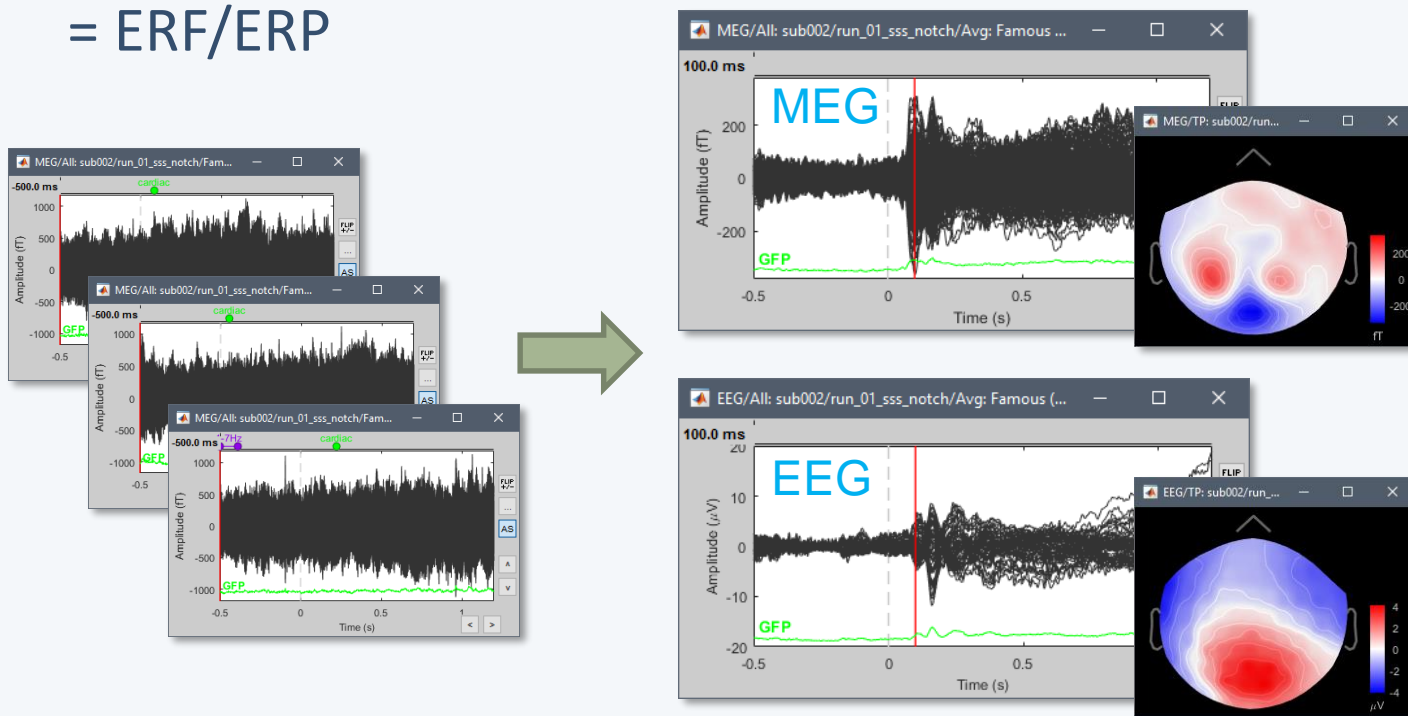
Single subject

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- Averaging the trials: Reveals the features of the signals that are locked in time to a given event
 - = Event-related field / potential
 - = Evoked response
 - = ERF/ERP



Single subject

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Link recordings
MRI registration

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Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- **EEG:** Averaging data across runs and subjects OK.
- **MEG:** Averaging across runs is not always accurate
 - Head shapes differ between subjects.
 - Head positions different between runs.
 - One sensor does not record the same thing in two different runs.
 - Coregistration of runs with Elekta MaxFilter helps but modifies a lot the recordings.
Never use this to average across subjects.
 - Recommended: Estimate the sources for each run separately, then average in source space.

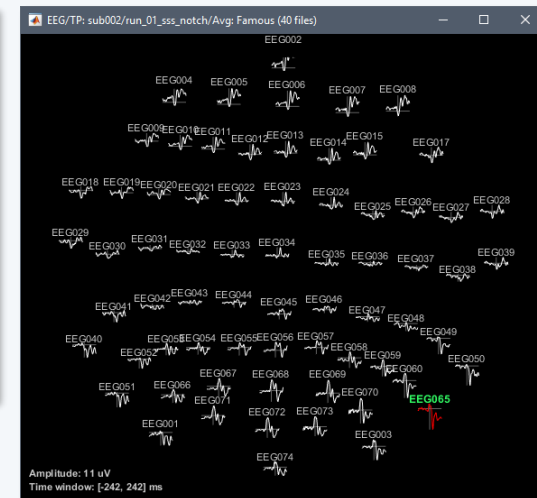
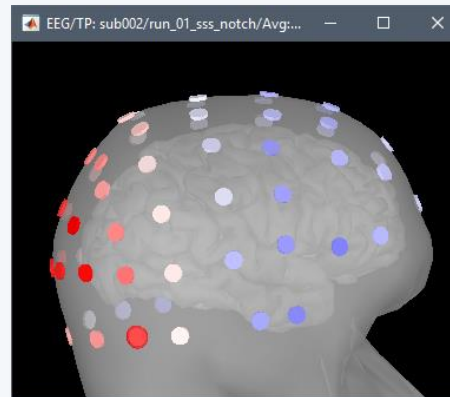
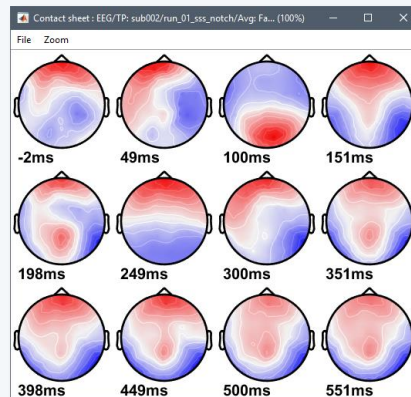
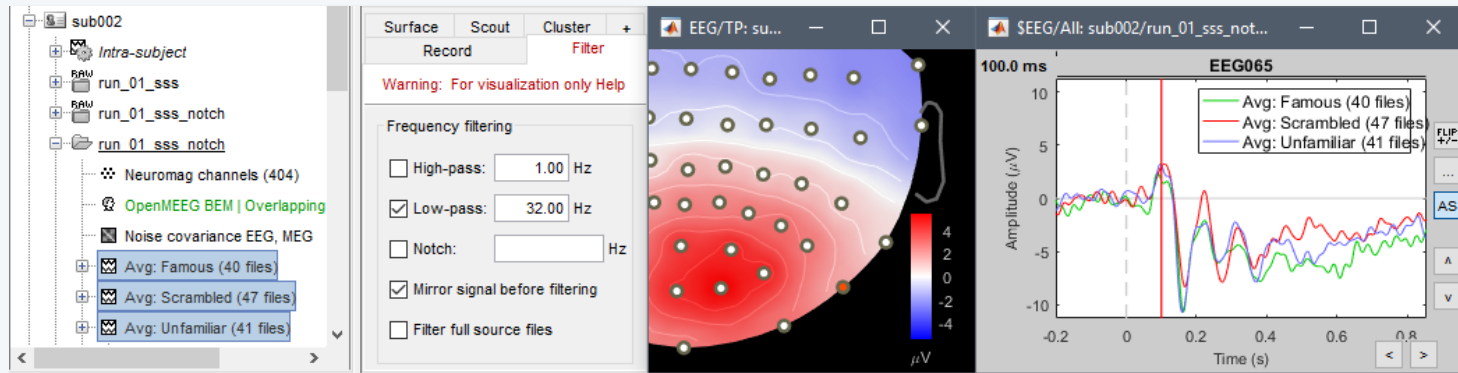
Single subject

Anatomy
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MRI registration

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Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- EEG ERP: Famous faces



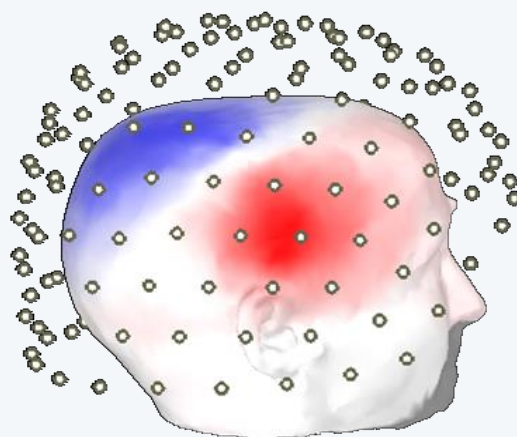
Single subject

Anatomy
Link recordings
MRI registration

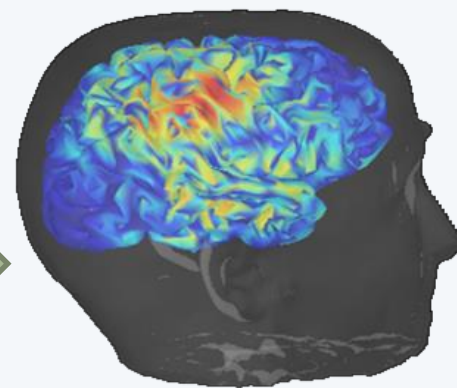
PSD
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Artifacts
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Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

- Source space: Cortex or full head volume
- Forward model: Overlapping spheres (MEG)
OpenMEEG BEM (EEG)
- Inverse model: **Minimum norm estimates**
Beamformers
Separately for MEG and EEG



Sensor space



Source space

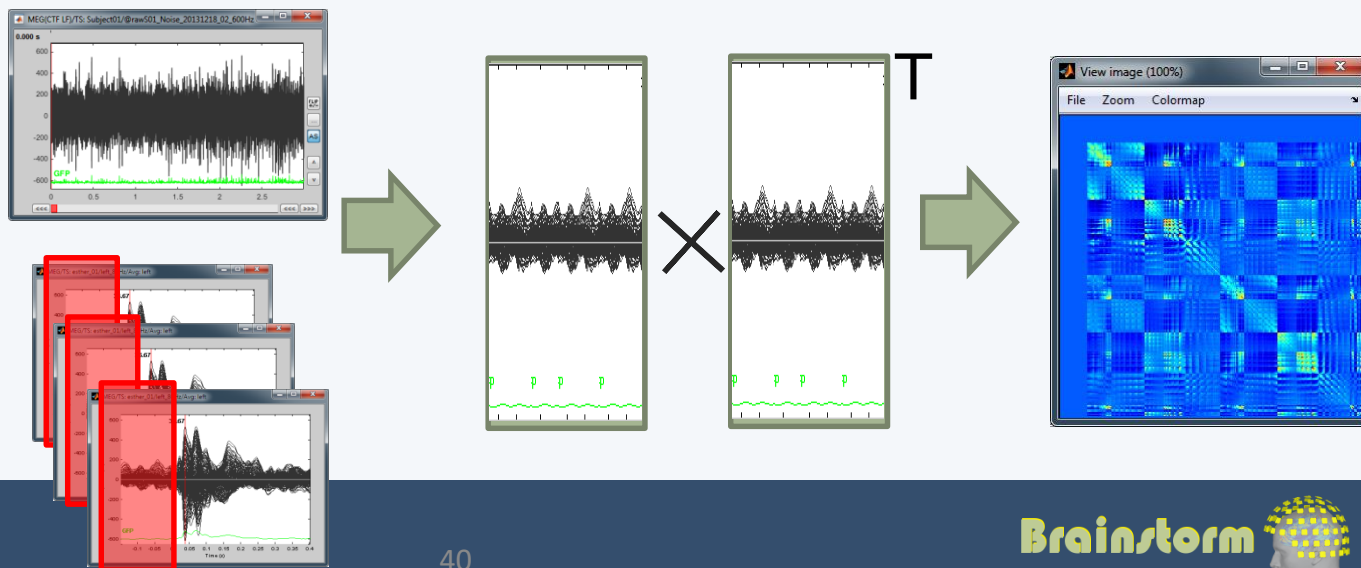
Single subject

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- The MNE model requires an estimation of the level of noise of the sensors
- Noise covariance matrix = covariance of segments that do not contain any “meaningful” data
- Empty room, pre-stim baseline, resting



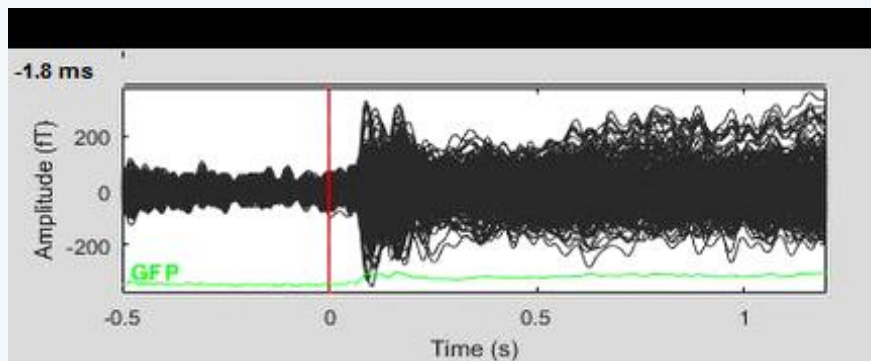
Single subject

Anatomy
Link recordings
MRI registration

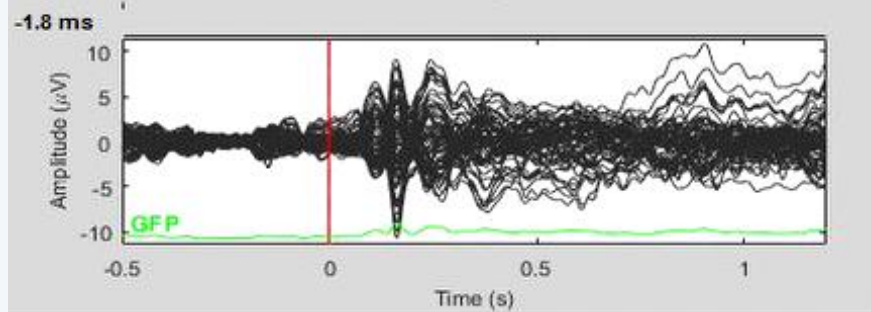
PSD
Filters
Bad channels
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

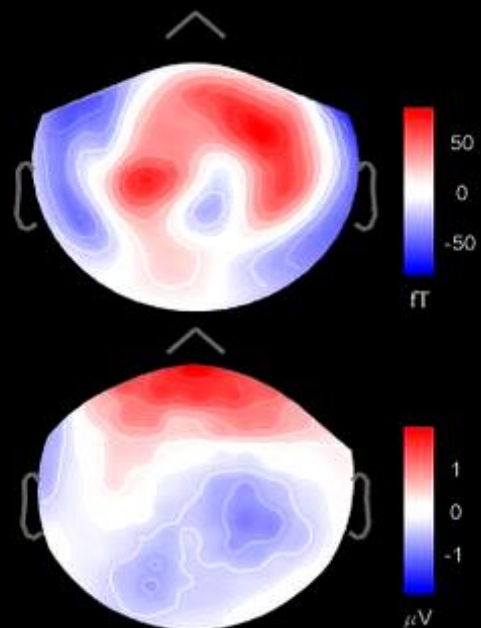
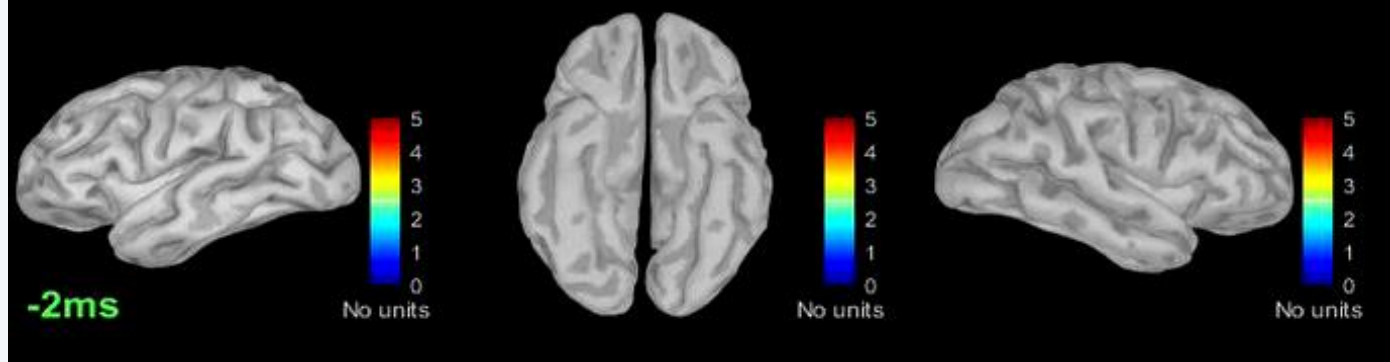
MEG



EEG



MEG sources



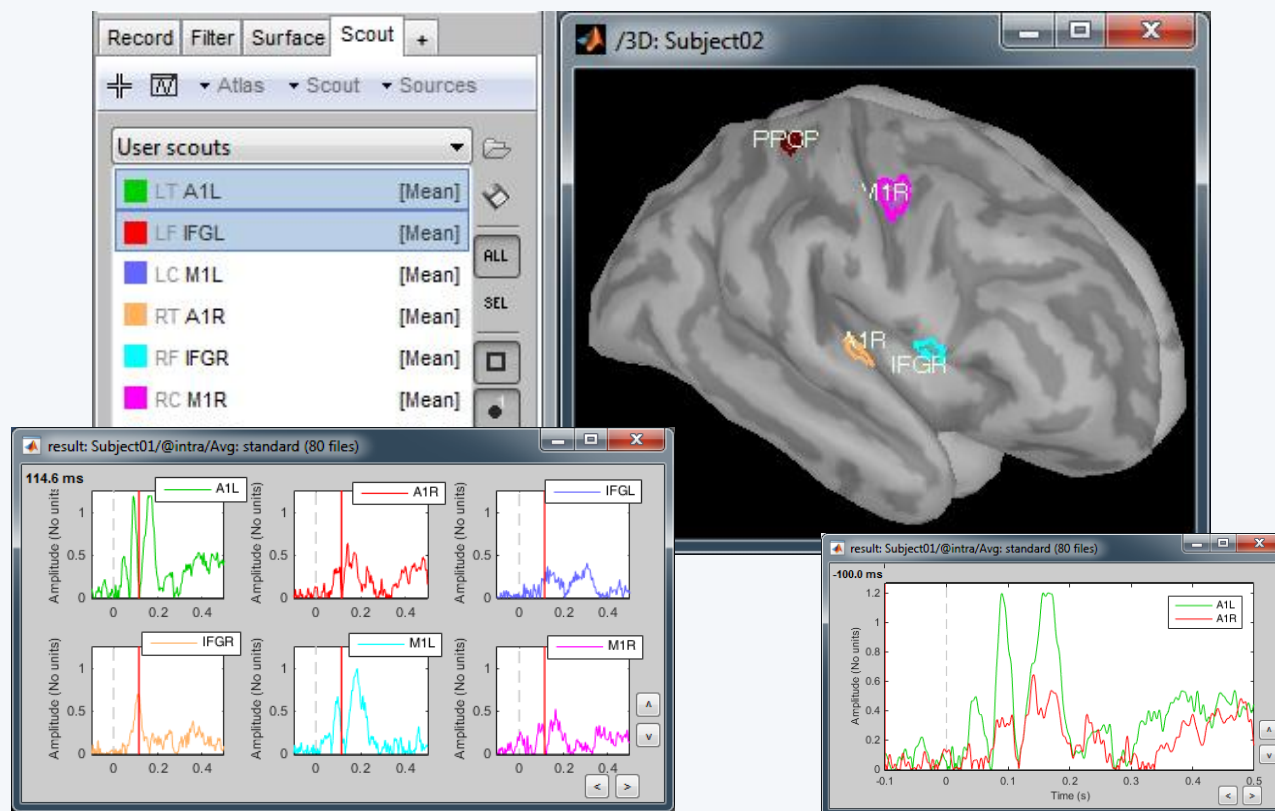
Single subject

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Markers
Epoching
Averaging
Sources
Time-frequency

- Regions of interest at cortical level (scouts)
 - = Subset of a few dipoles in the brain
 - = Group of vertices of the cortex surface



Single subject

Anatomy

Link recordings

MRI registration

PSD

Filters

Bad channels

Artifacts

Correction

Bad segments

Markers

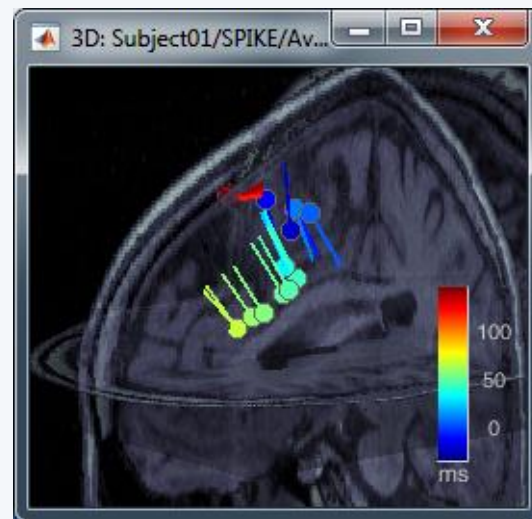
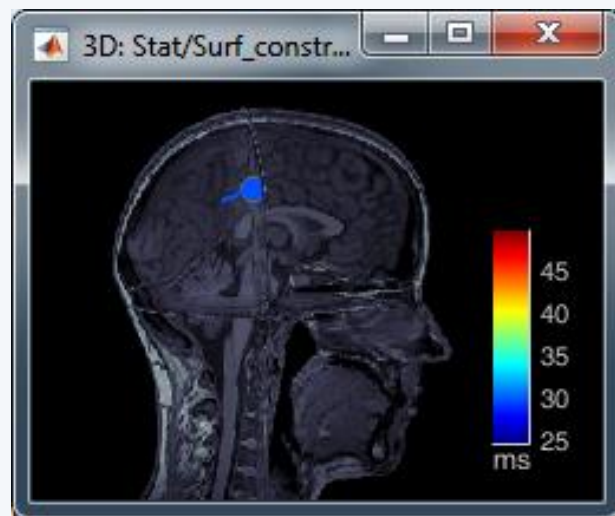
Epoching

Averaging

Sources

Time-frequency

- **Dipole scanning**
Compute a distributed source model, then find the most significant dipole at each time sample.
- **Dipole fitting (FieldTrip)**
Non-linear search of the dipoles that minimizes the residuals (data explained - recordings)



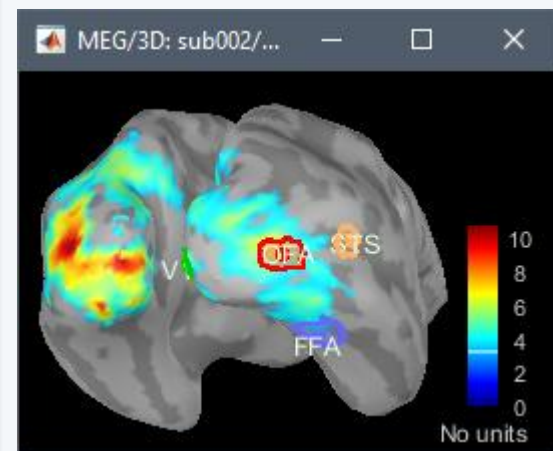
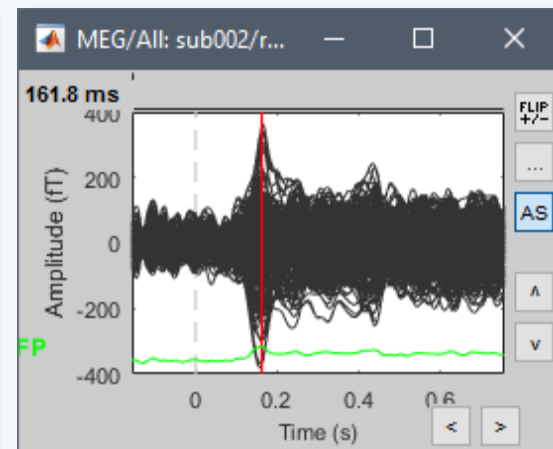
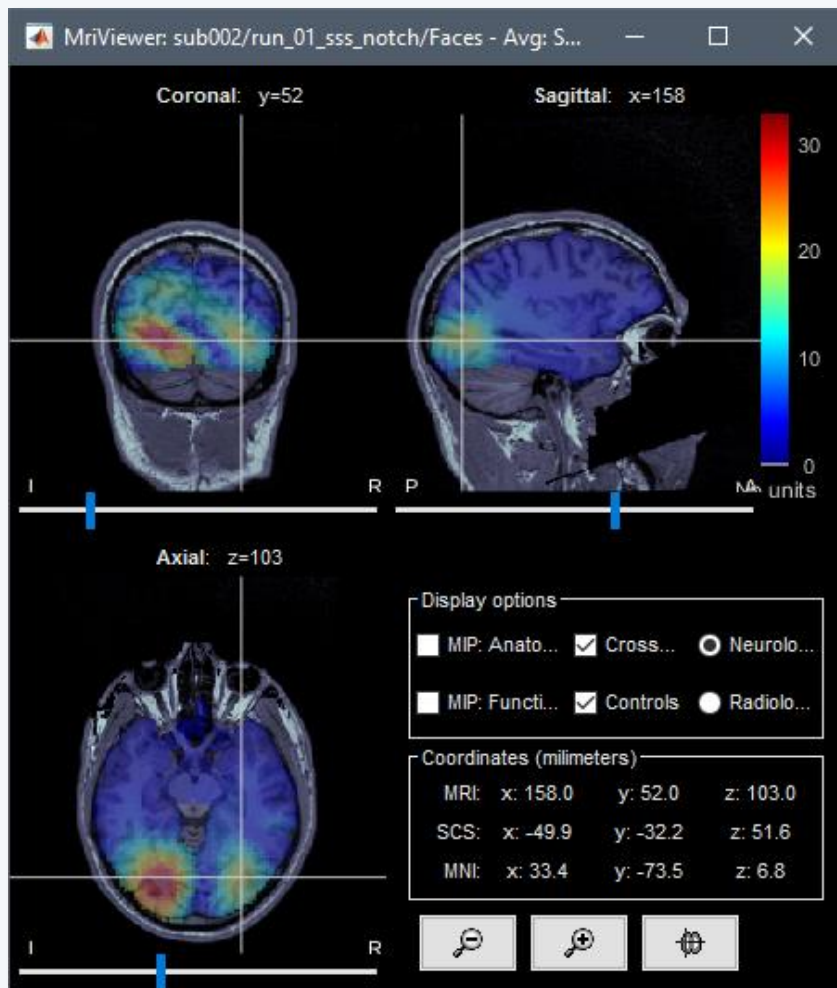
Single subject

Anatomy
Link recordings
MRI registration

PSD
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Bad channels
Artifacts
Correction
Bad segments

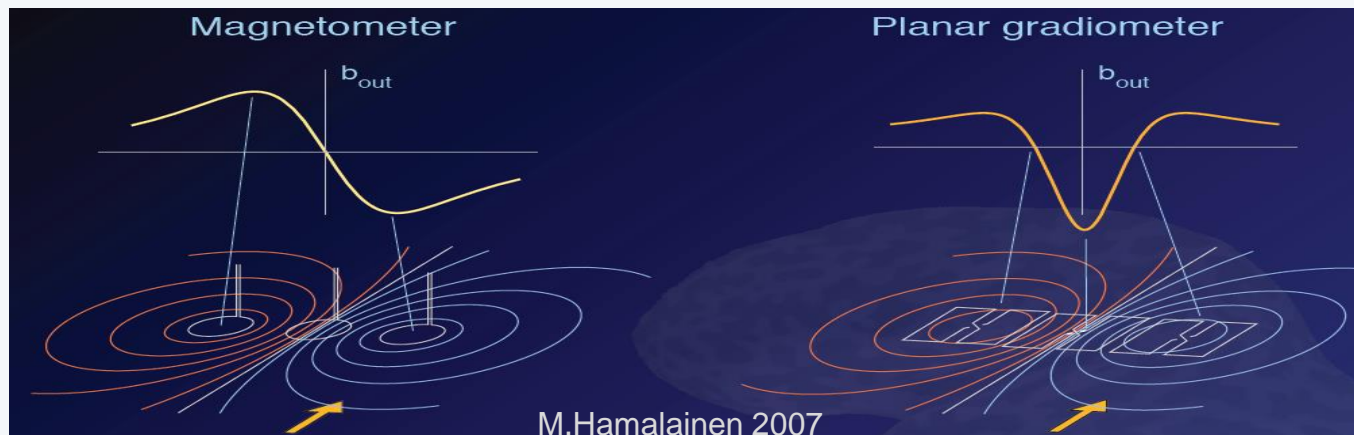
Markers
Epoching
Averaging
Sources
Time-frequency

- Faces – Scrambled, 160ms



Source estimation: MEG

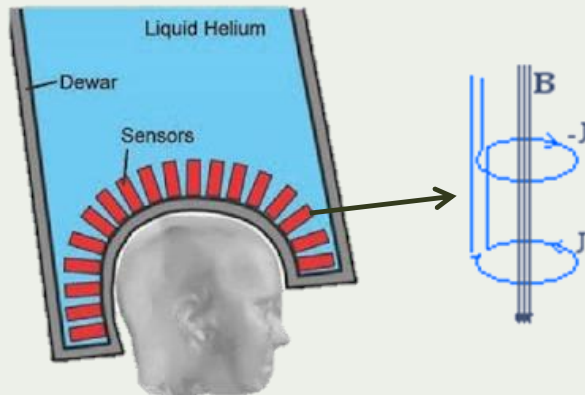
- Recommended in MEG analysis:
 - The subject head can move in the helmet
 - One sensor is not corresponding to one brain region
 - Different types of sensors (magneto / gradiometers)
 - Difficult to read, reproduce or compare
- Converting to source space helps solving those issues





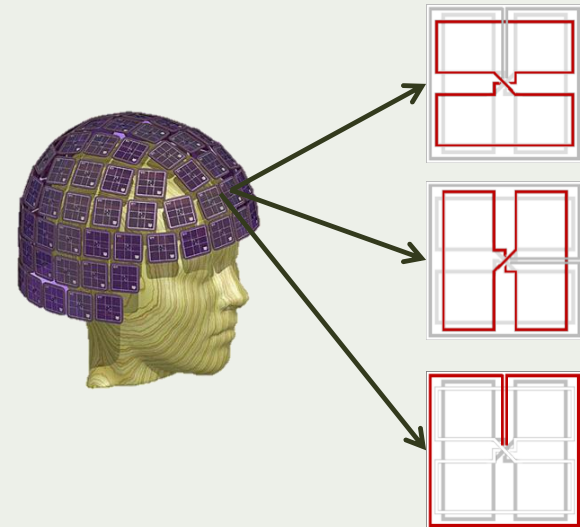
CTF (MNI)

275 axial gradiometers



Elekta (MIT)

204 planar gradiometers
102 magnetometers



Source estimation: EEG

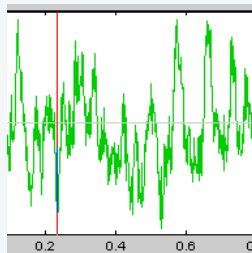
- In EEG, those problems don't exist:
 - Electrodes positions are fixed and known
 - More reproducible signal shapes and topographies
 - Clinicians are trained to work at the sensor level
- But the source reconstruction is still interesting:
 - Localize the signal generators in the brain
(epilepsy and pre-surgical functional mapping)
 - Spatial separation of simultaneous sources

Single subject

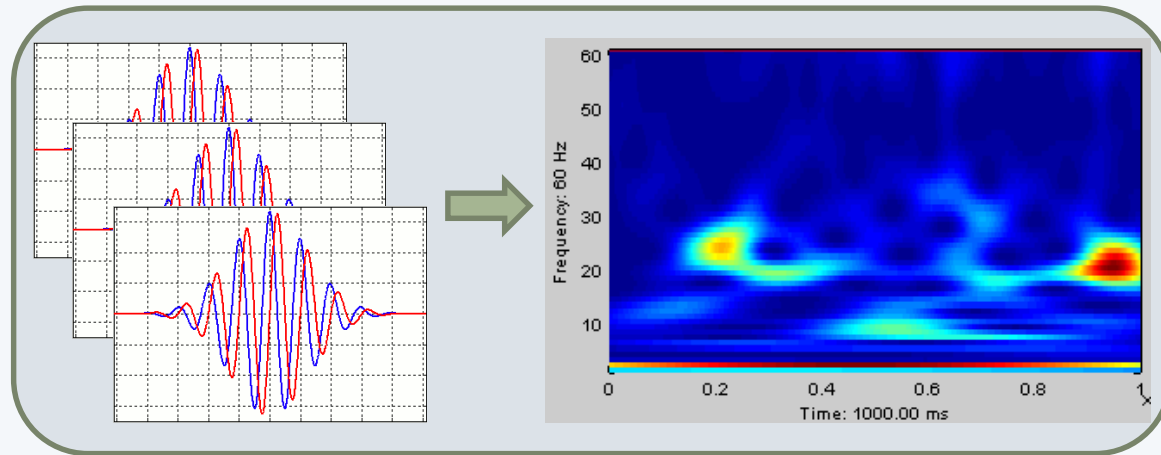
Anatomy
Link recordings
MRI registration

PSD
Filters
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Artifacts
Correction
Bad segments

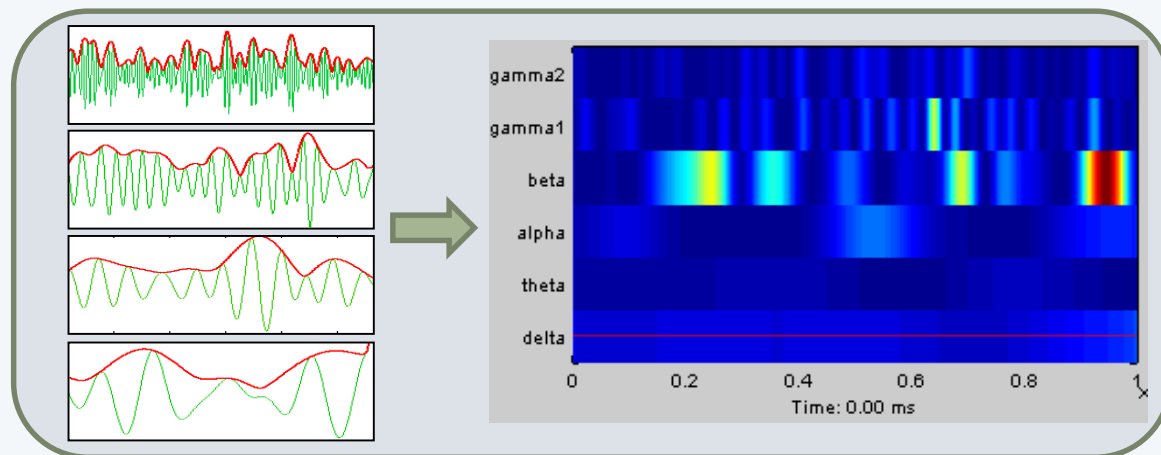
Markers
Epoching
Averaging
Sources
Time-frequency



Morlet wavelets



Hilbert transform + band-pass filter

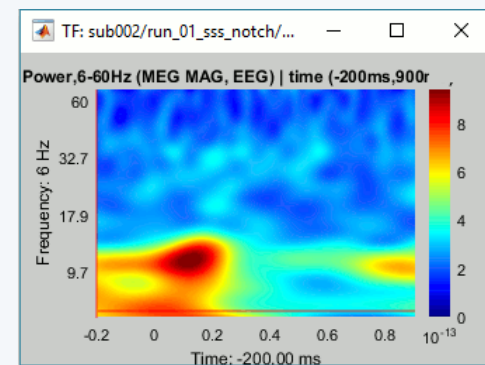
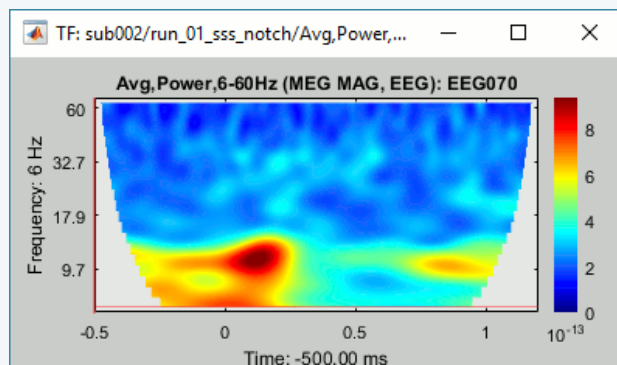


Anatomy
Link recordings
MRI registration

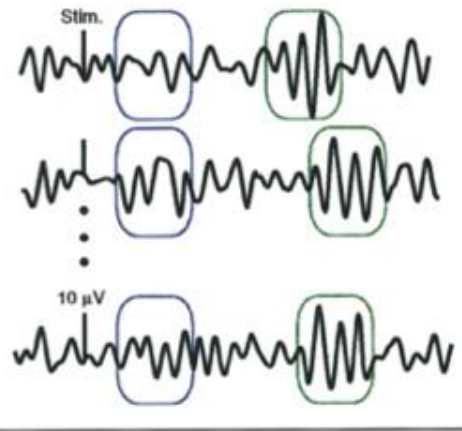
PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency

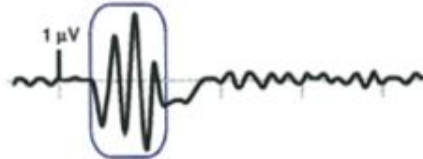
- Make sure you know the transient periods for all the frequency bins, and do not include them in your analysis.
- An easy solution is to cut them out immediately after the computation.



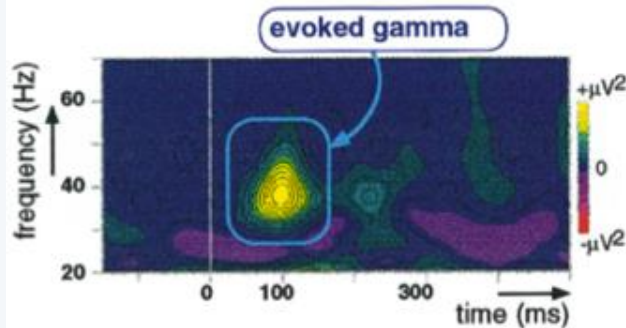
A Single-trials



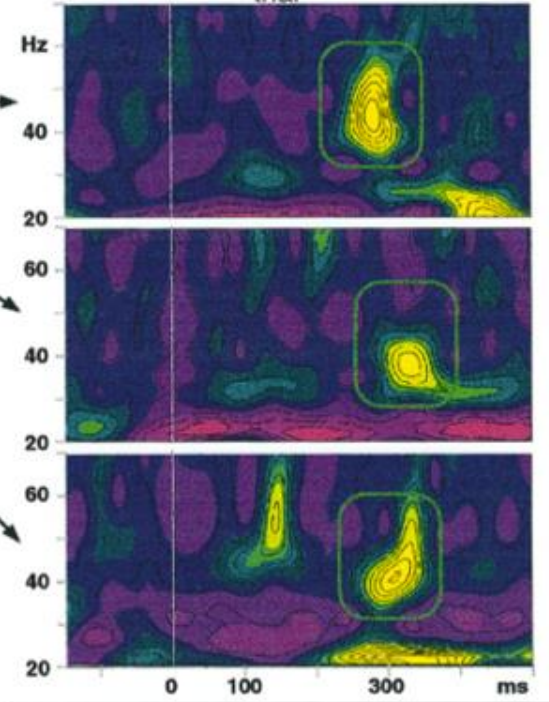
B Time average : evoked potential



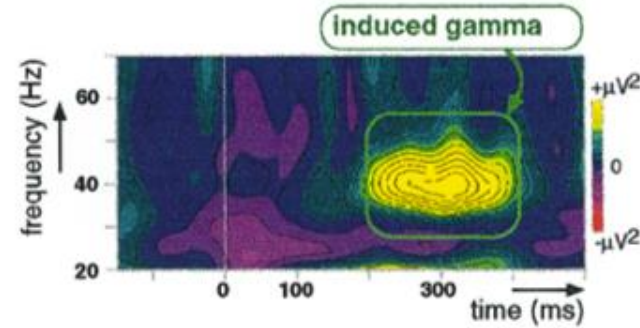
C Time-frequency power of the evoked potential



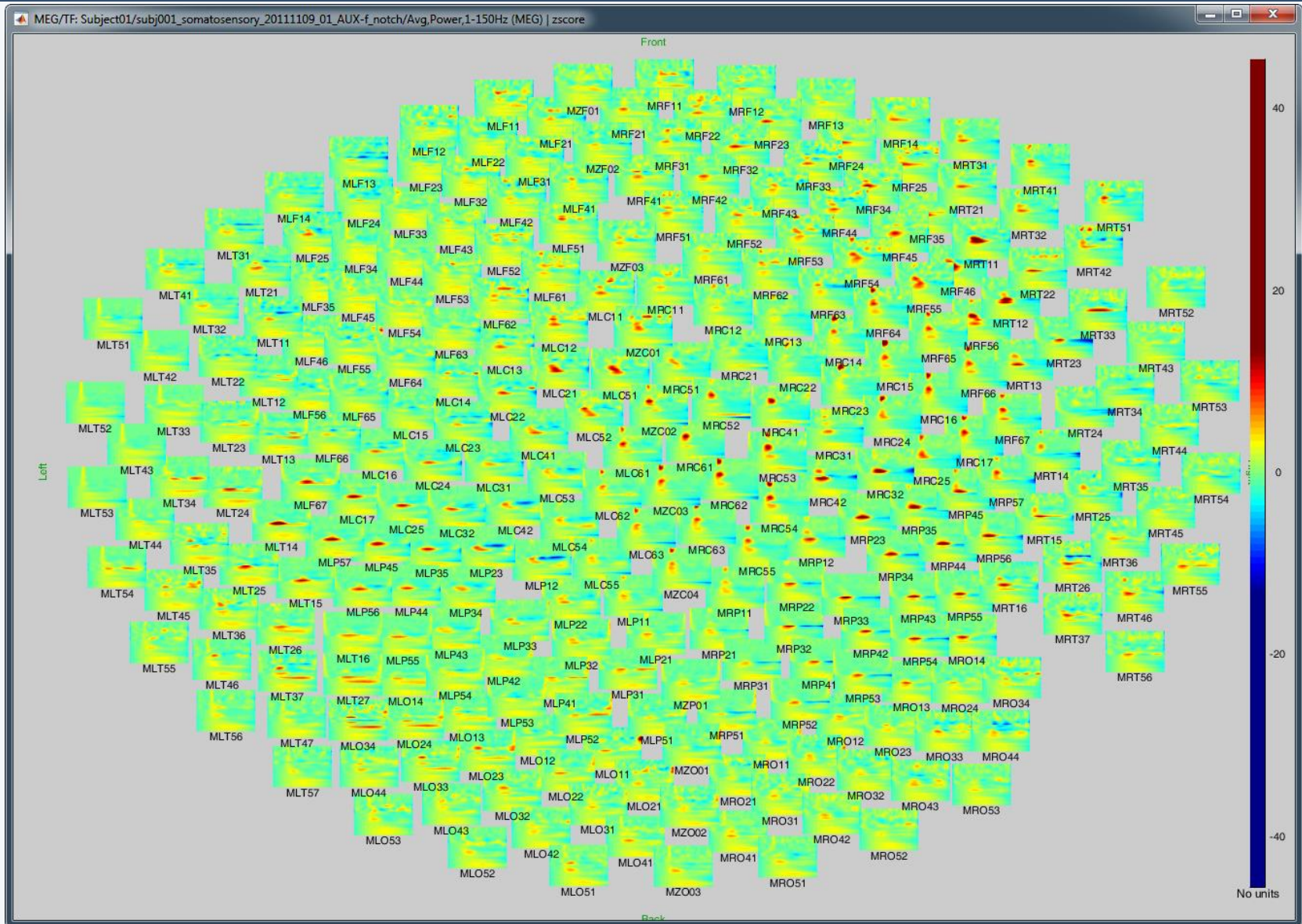
D Time-frequency power of each single trial



E Time-frequency power average



Time-frequency



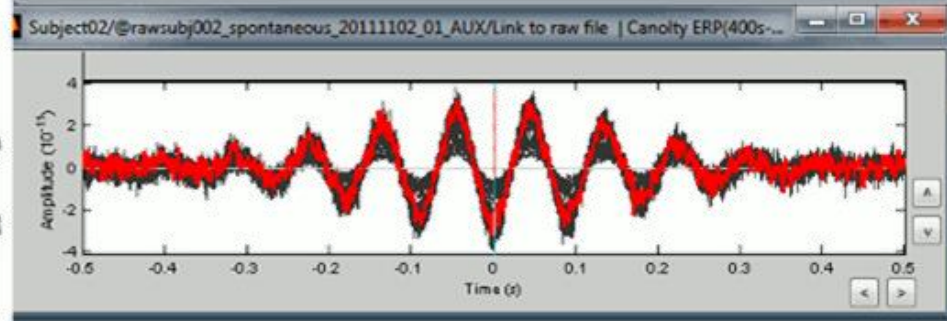
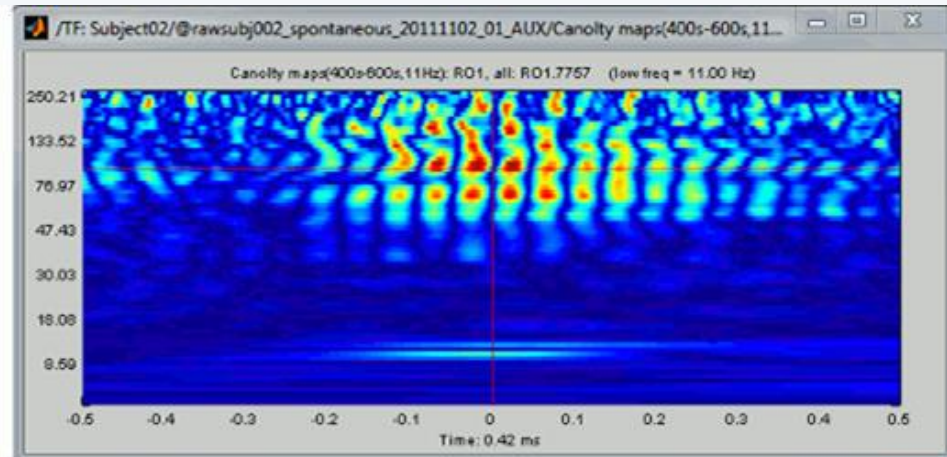
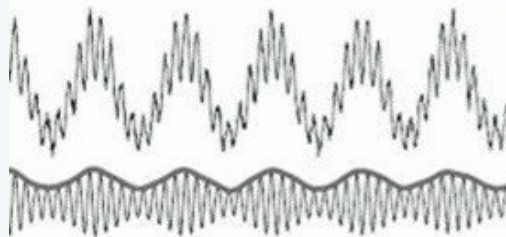
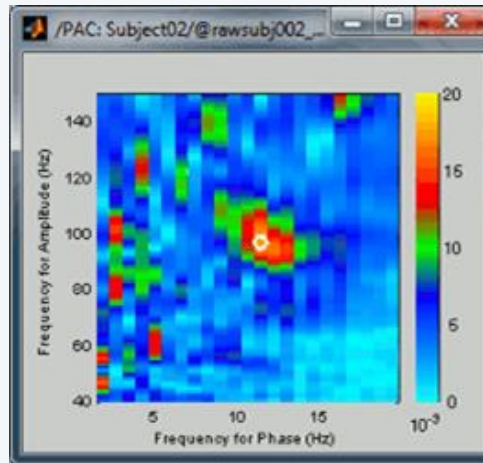
Single subject

Anatomy
Link recordings
MRI registration

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Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency
Other measures

- Phase-amplitude coupling



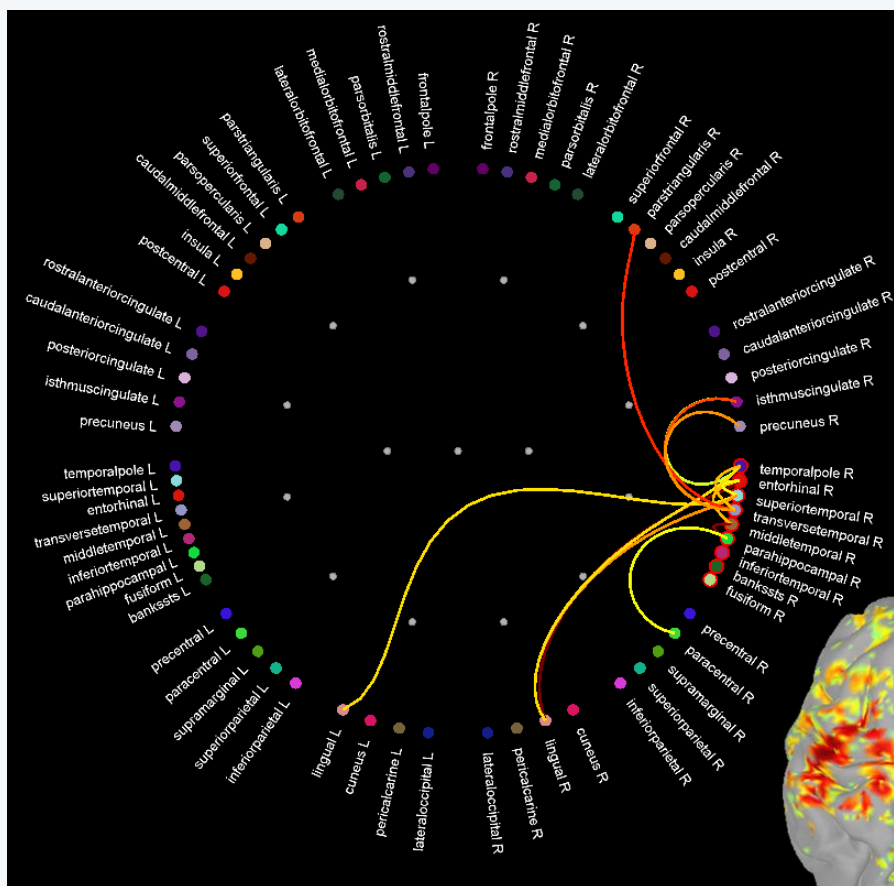
Single subject

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Bad segments

Markers
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Averaging
Sources
Time-frequency
Other measures

- Connectivity measures



- Correlation
- Coherence
- Phase locking value
- Granger causality

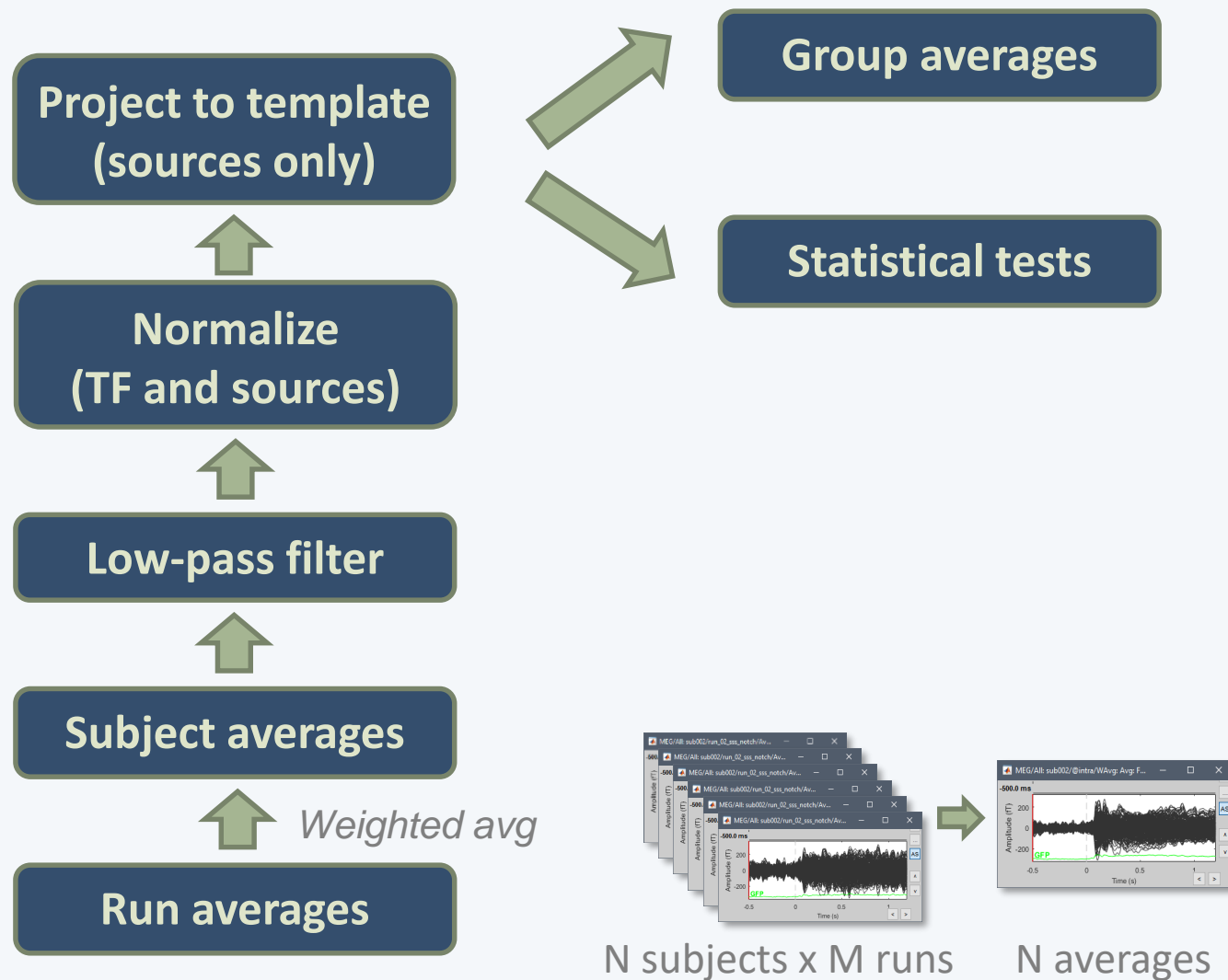


Group analysis

Anatomy
Link recordings
MRI registration

PSD
Filters
Bad channels
Artifacts
Correction
Bad segments

Markers
Epoching
Averaging
Sources
Time-frequency



Group analysis

Subject averages

Low-pass

Normalize

Project

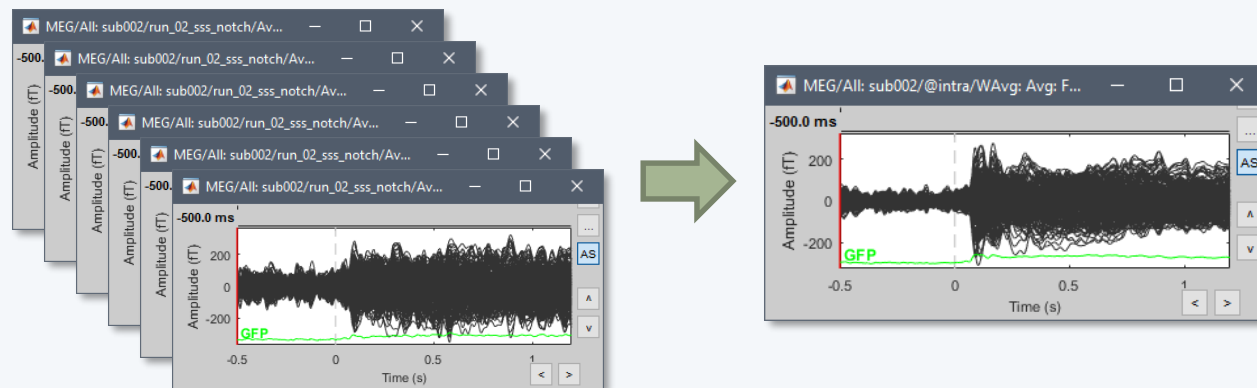
Group averages

Group statistics

Quality control

Workflow

- Weighted average of 6 runs per subject (recordings, sources MEG/EEG, time-frequency)



- Sources: Compute within-subject differences
 - (Faces - Scrambled) and (Famous - Unfamiliar)
 - The sign of the MNE source amplitude is ambiguous, we will apply an absolute value before comparing between subjects

Group analysis

Subject averages

Low-pass

Normalize

Project

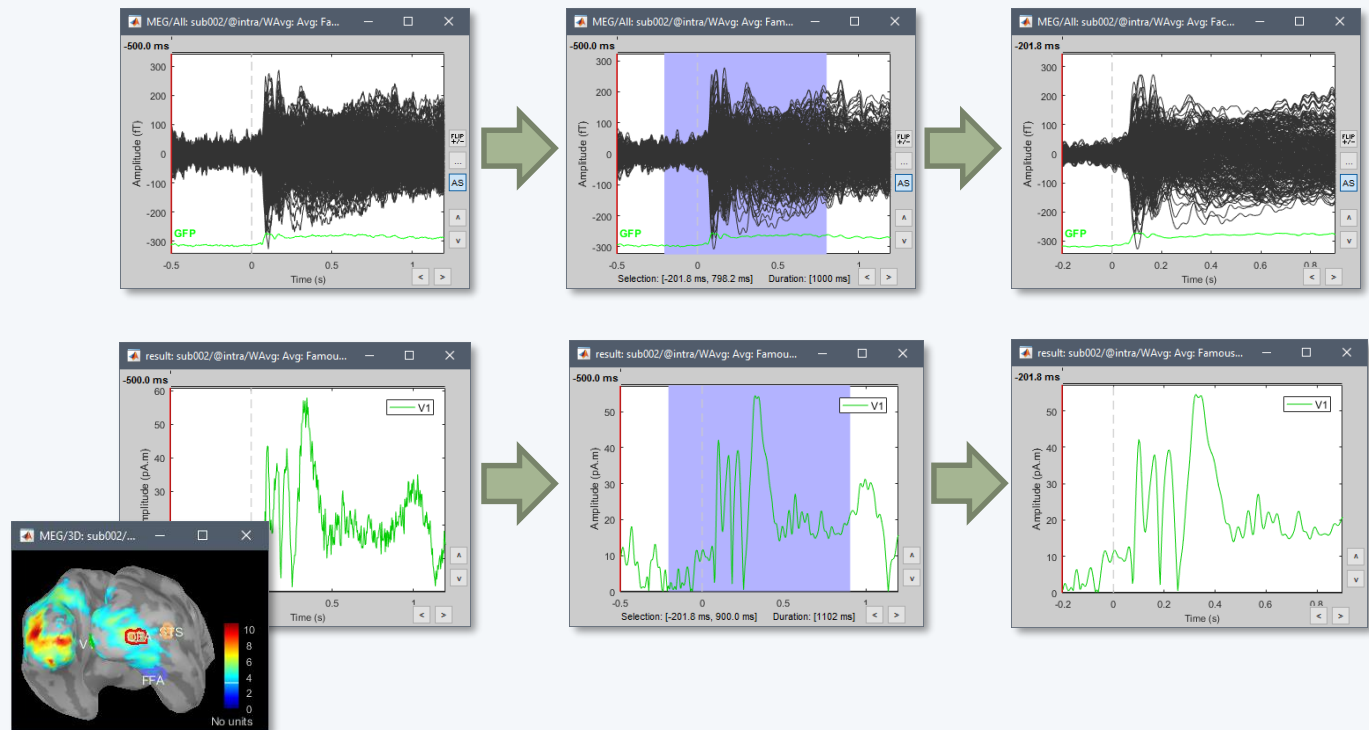
Group averages

Group statistics

Quality control

Workflow

- Low-pass filter the subject averages: 32Hz
- Remove 300ms on each side (edge effects)



Group analysis

Subject averages

Low-pass

Normalize

Project

Group averages

Group statistics

Quality control

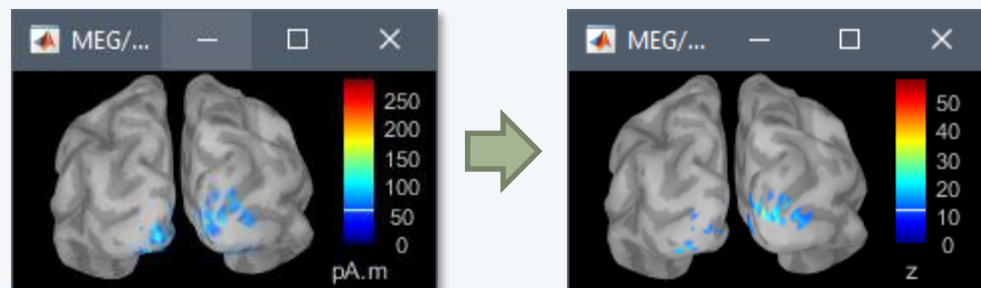
Workflow

- Amplitude normalization before group analysis

Baseline = [-200,0]ms

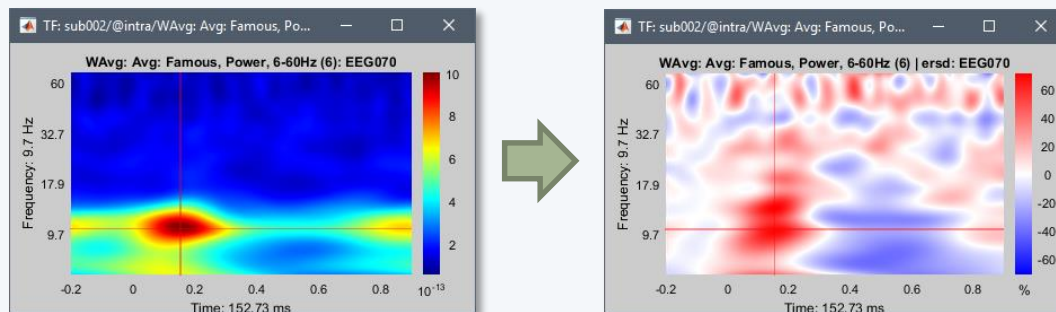
- Sources: Z-score normalization wrt baseline

$$S = (S - \text{mean}(\text{baseline})) / \text{std}(\text{baseline})$$



- Time-frequency: Event-related sync/desync

$$TF = (TF - \text{mean}(\text{baseline})) / \text{mean}(\text{baseline}) * 100$$



Group analysis

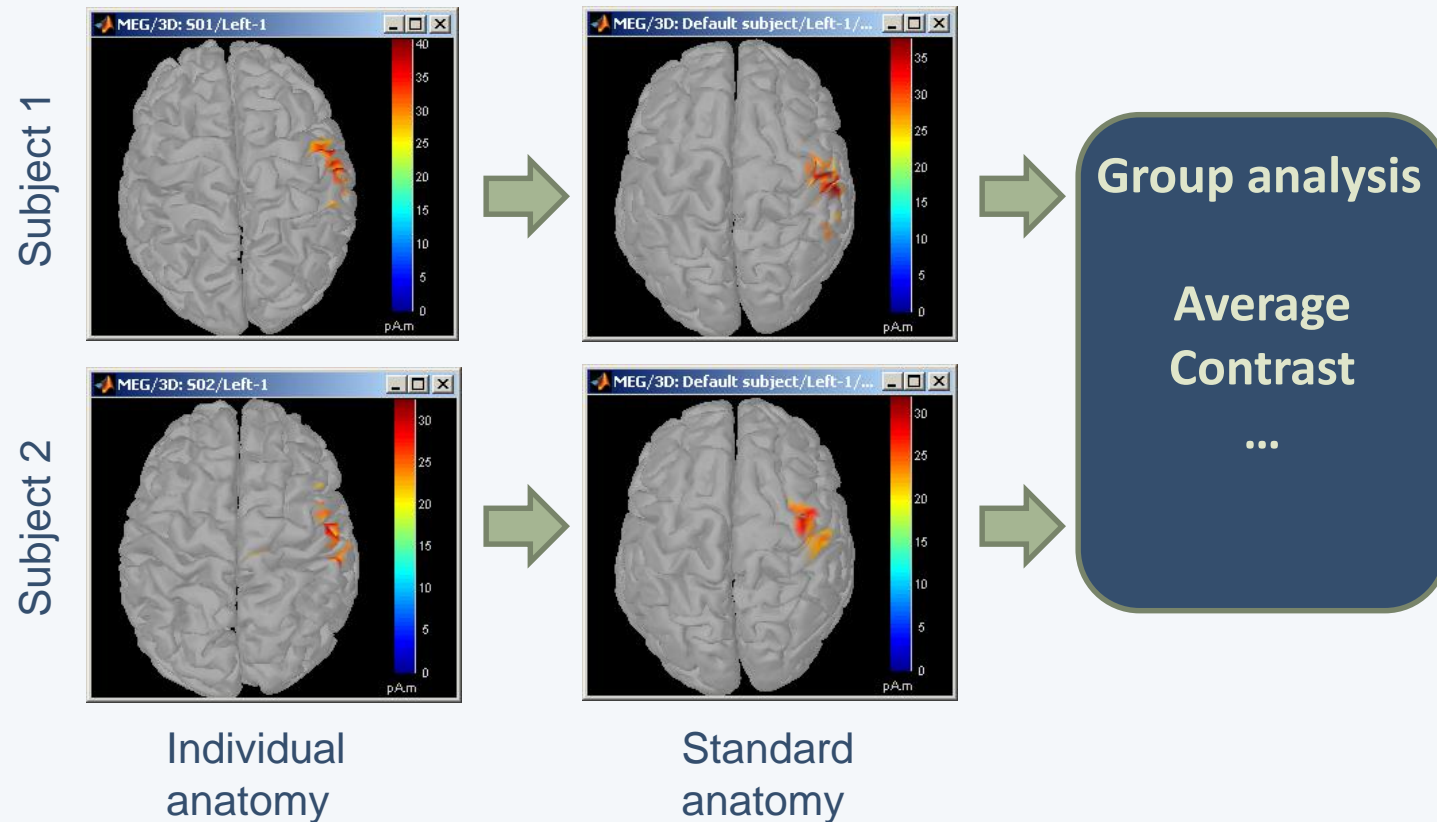
Subject averages
Low-pass
Normalize

Project

Group averages
Group statistics

Quality control
Workflow

- Registration of individual sources on a template (ICBM152, Colin27, DNI, infants...)



Group analysis

Subject averages

Low-pass

Normalize

Project

Group averages

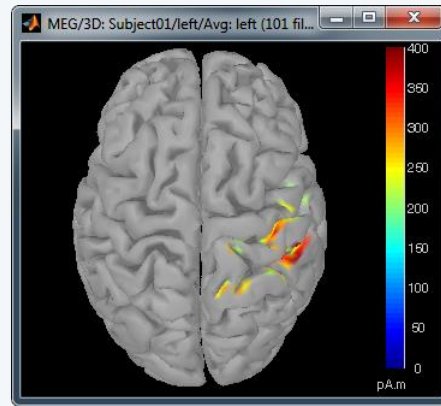
Group statistics

Quality control

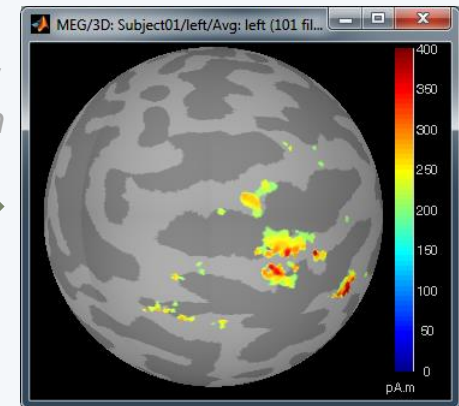
Workflow

- Using FreeSurfer registration

Subject



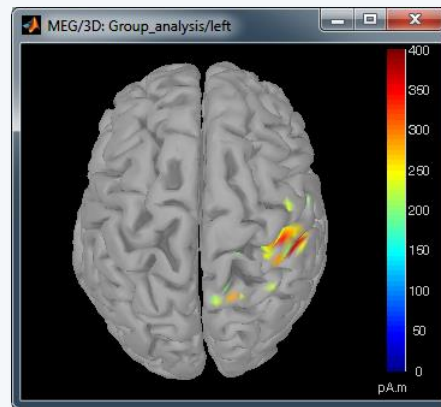
*FreeSurfer
registration*



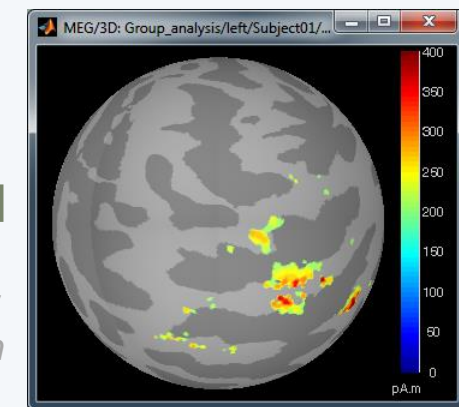
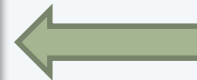
3D interpolation



Template



*FreeSurfer
registration*



Group analysis

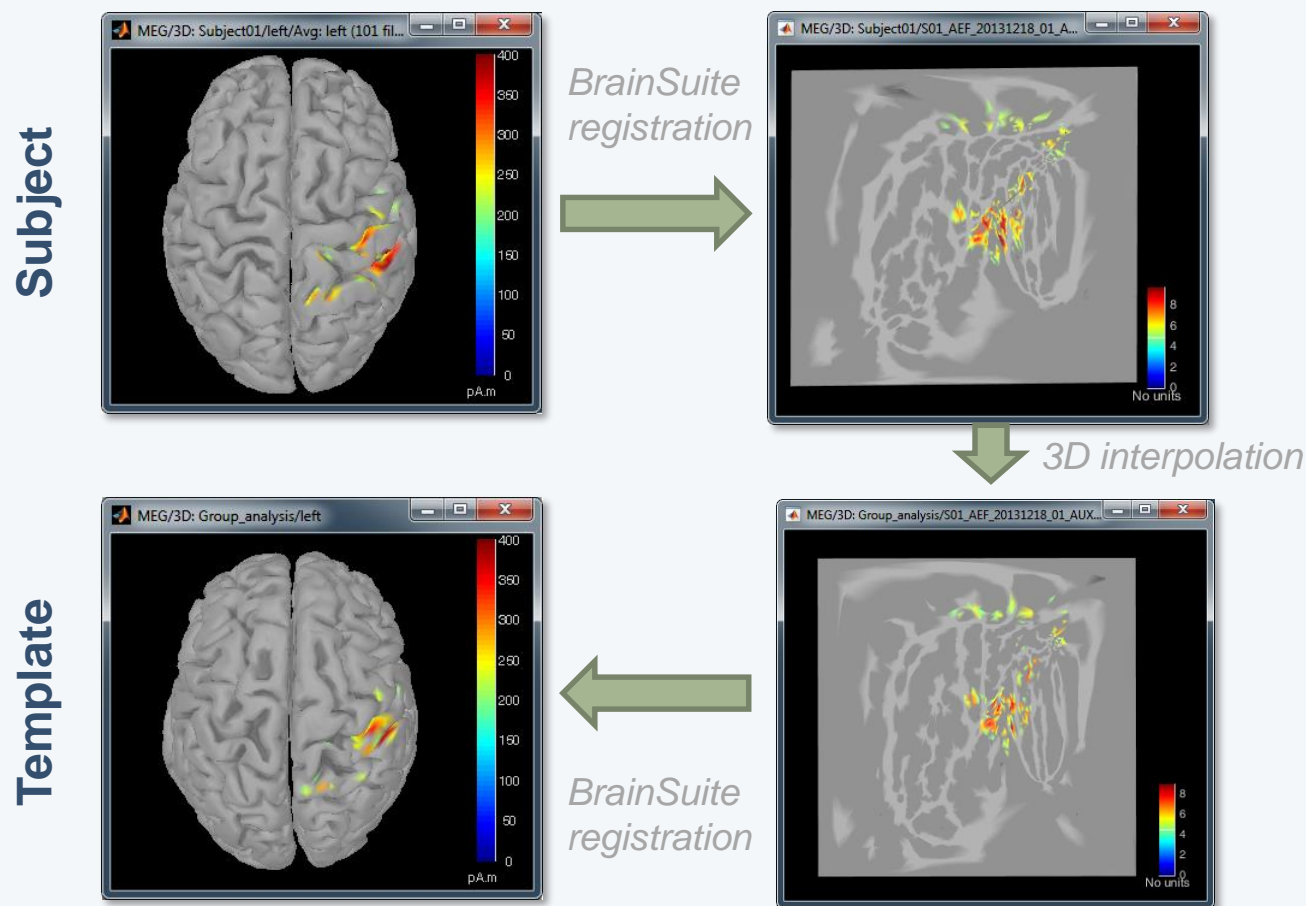
Subject averages
Low-pass
Normalize

Project

Group averages
Group statistics

Quality control
Workflow

- Using BrainSuite registration



Group analysis

Subject averages

Low-pass

Normalize

Project

Group averages

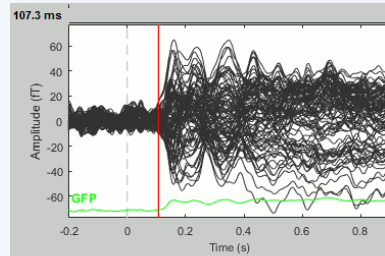
Group statistics

Quality control

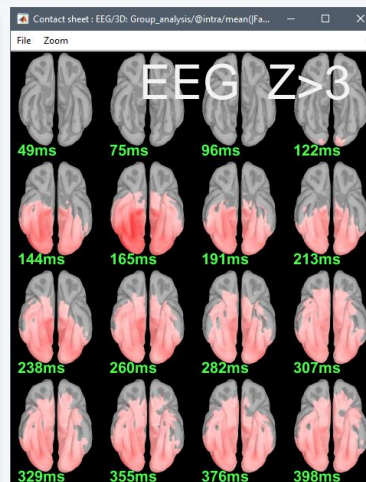
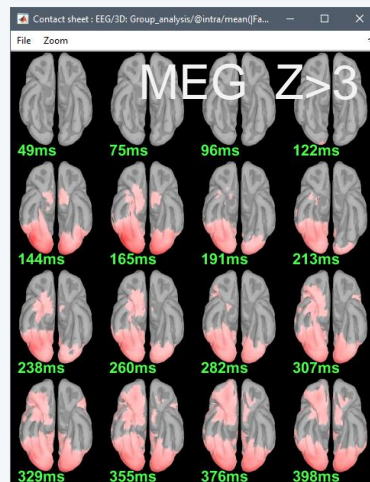
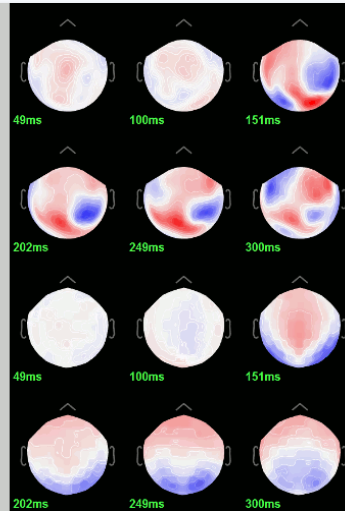
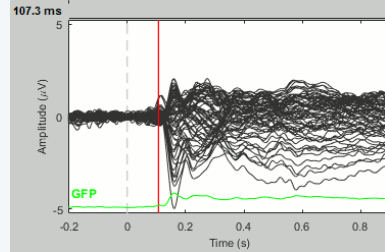
Workflow

- **Faces - Scrambled**

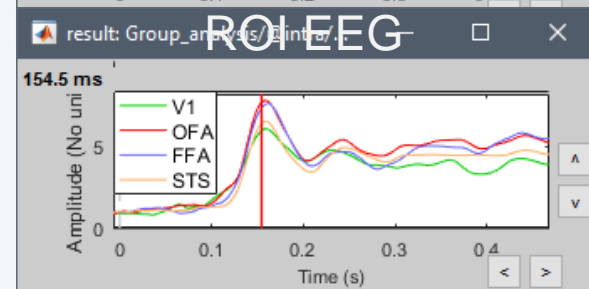
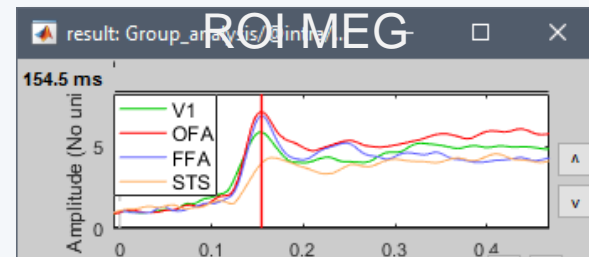
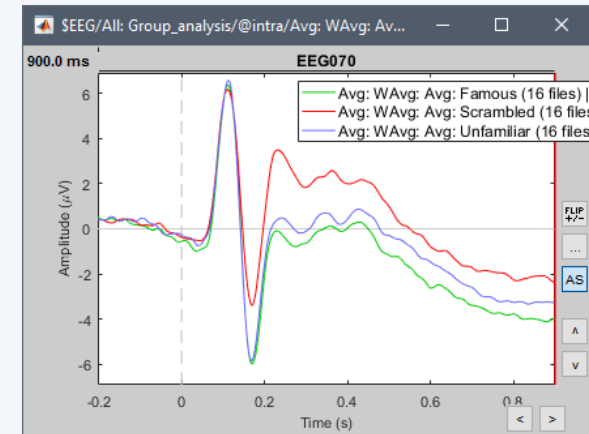
MEG



EEG



EEG 070



Group analysis

Subject averages

Low-pass

Normalize

Project

Group averages

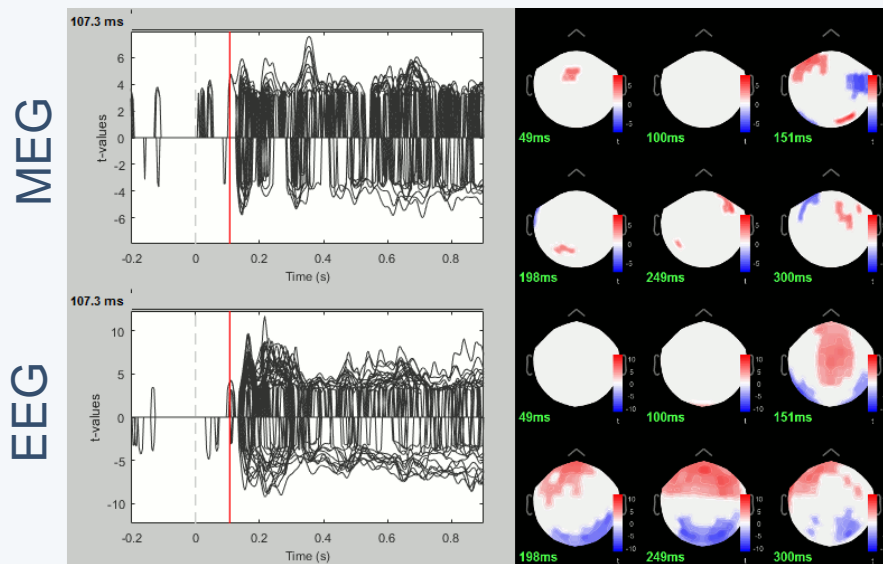
Group statistics

Quality control

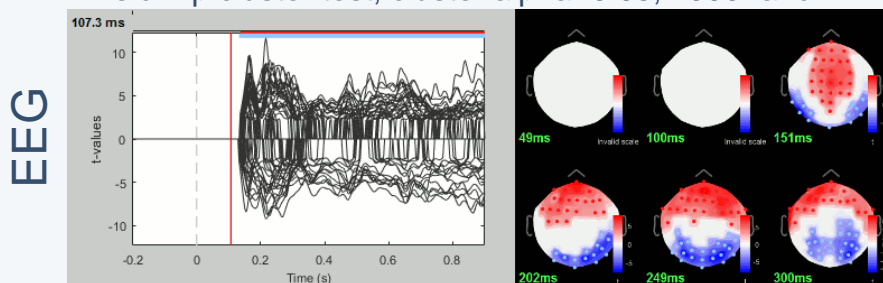
Workflow

- **Faces - Scrambled**

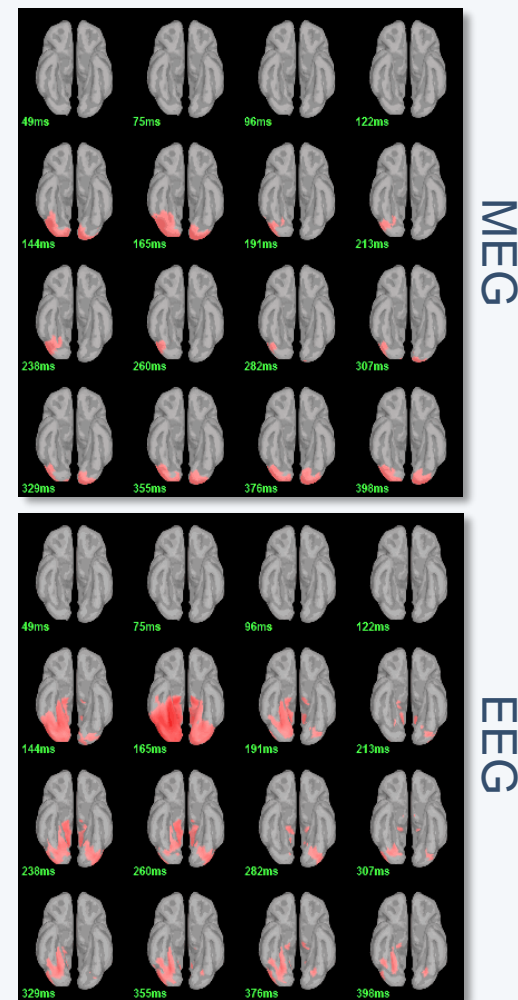
Permutation t-test, 1000 rand, $p < 0.05$ FDR-corrected



FieldTrip cluster test, cluster alpha=0.05, 1000 rand



Parametric Chi2-test
 $\log(|\text{Faces-Scrambled}|)=0$
 $p < 0.05$ FDR-corrected



Group analysis

Subject averages

Low-pass

Normalize

Project

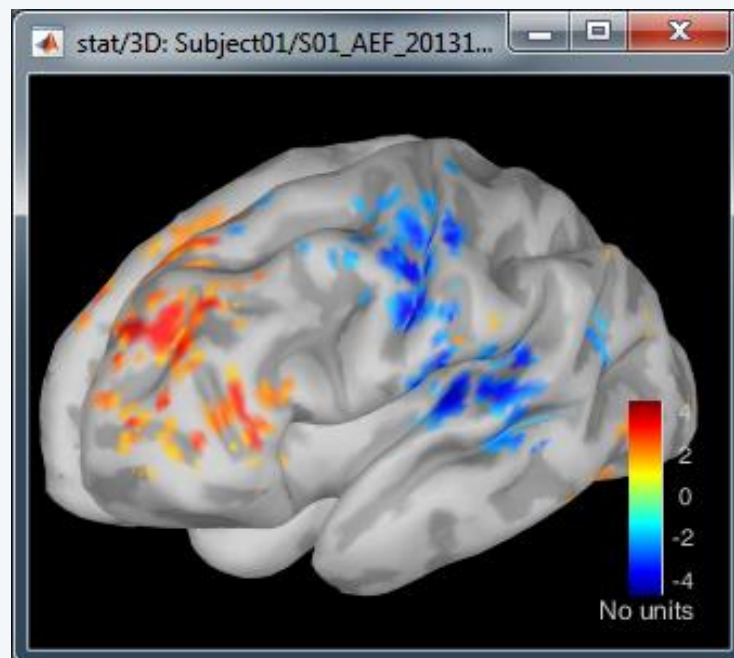
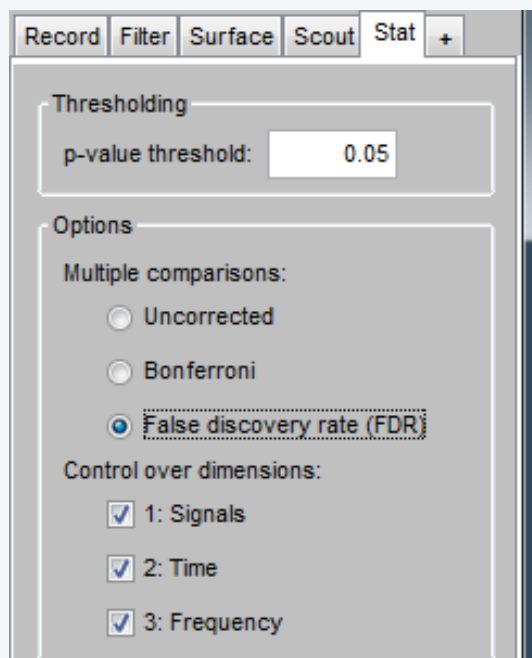
Group averages

Group statistics

Quality control

Workflow

- Contrasts between subjects or conditions
- Parametric or non-parametric t-test
- Cluster-based non-parametric tests
- Export to: **SPM**, R, Excel, SPSS, Matlab...



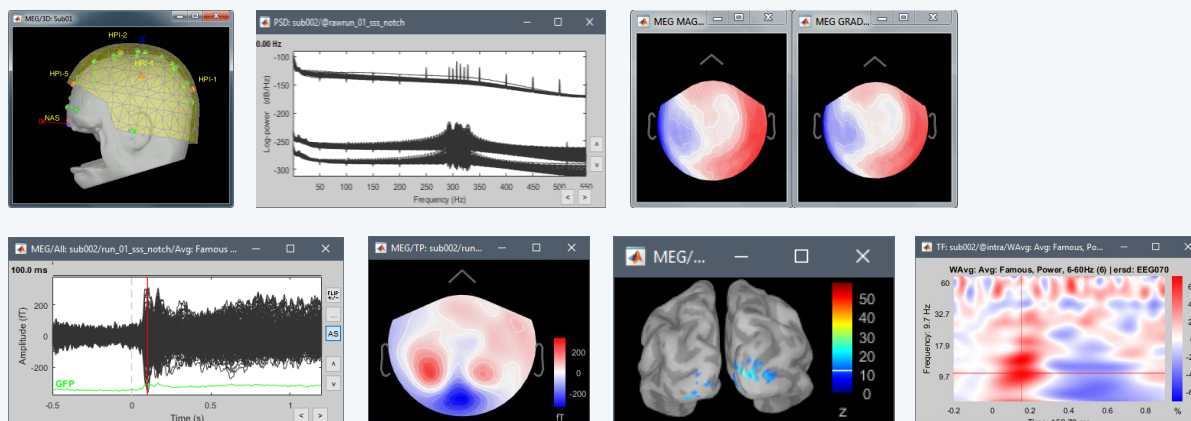
Group analysis

Subject averages
Low-pass
Normalize
Project

Group averages
Group statistics

Quality control
Workflow

- When scripting the analysis, we recommend you always check visually the following items for each run separately:
 - MRI/sensors registration
 - PSD before and after filters
 - SSP and ICA component topographies
 - ERP/ERF: Sensors time series
 - ERP/ERF: Sensors topo of primary response
 - ERP/ERF: Sources of primary response
 - Any other metric of interest



Group analysis

Subject averages

Low-pass

Normalize

Project

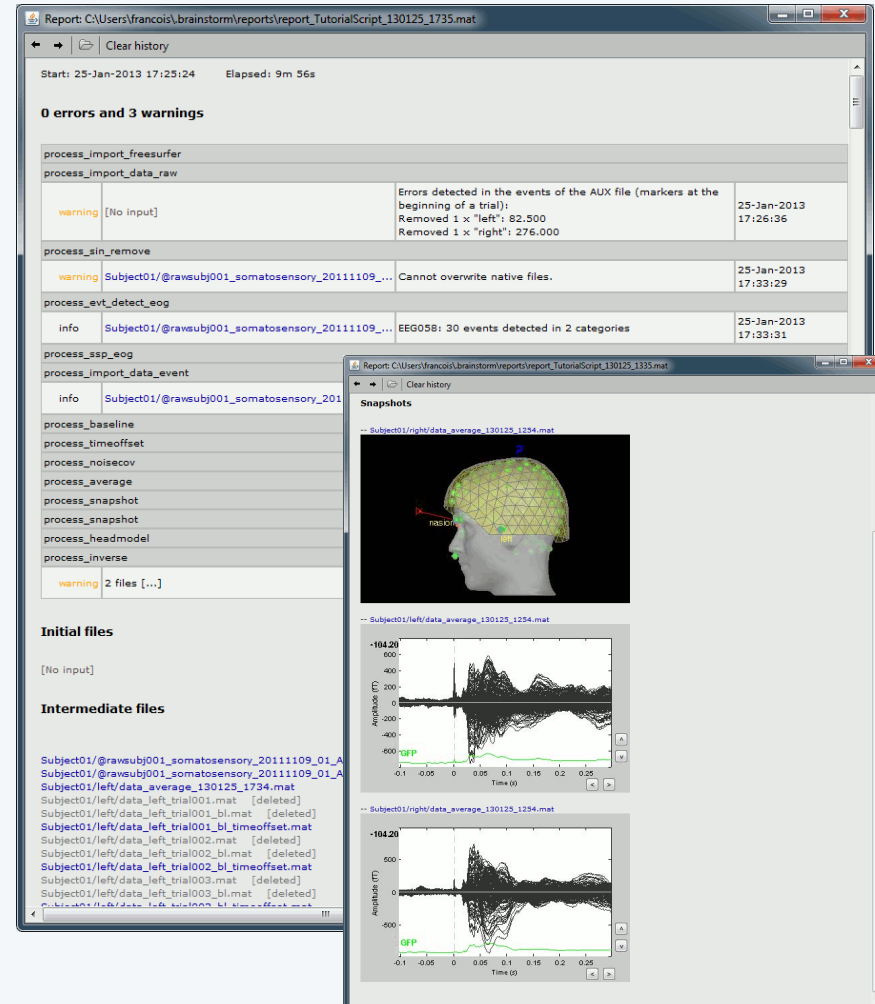
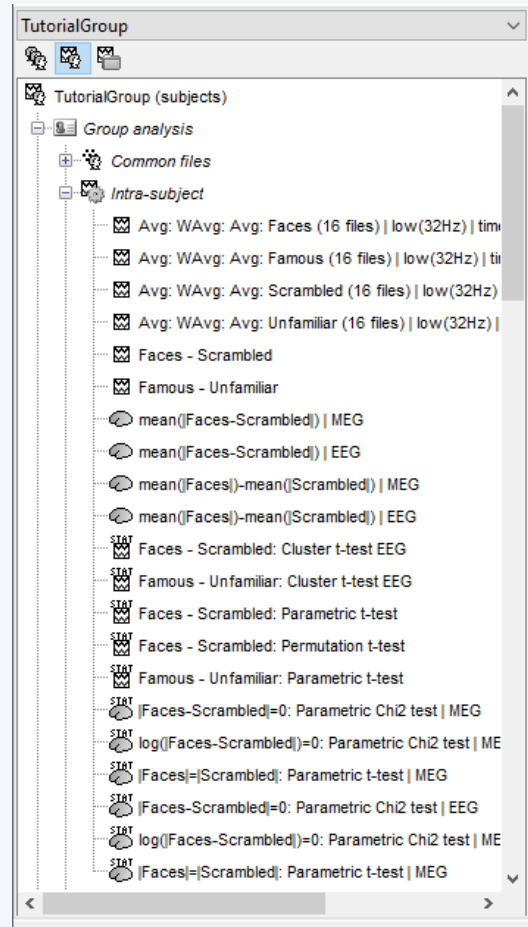
Group averages

Group statistics

Quality control

Workflow

- Execution reports with snapshots saved in HTML



Group analysis

Subject averages

Low-pass

Normalize

Project

Group averages

Group statistics

Quality control

Workflow

- Prototype the analysis interactively with one subject.
Write down all the parameters to reproduce with a script.
- Set the anatomical fiducials for all the subjects.
- **Script #1:** Import the anatomy for all the subjects
- **Script #2:** Pre-processing (loop on subjects)
 - Link the raw files, register with MRI, compute PSD
 - Detect or import event markers
 - Pre-processing: Filtering, detect artifacts, SSP, ICA
- **Manual inspection:**
 - Check the execution reports for script 2
 - Fix the SSP/ICA (re-compute, manual selection)
 - Mark bad channels and bad segments

Group analysis

Subject averages

Low-pass

Normalize

Project

Group averages

Group statistics

Quality control

Workflow

- **Script #3:** Subject-level analysis (loop on subjects)
 - Importing and averaging
 - Source estimation
 - Time-frequency
- **Manual inspection:**
 - Check the execution reports for script #3
 - Define regions of interest
- **Script #4:** Group analysis
 - Subject-level averages
 - Group-level averages
 - Statistics
 - Anything that involves regions of interest

Add your code to Brainstorm

- Direct manipulation of the files in Matlab
- Use the menu “Run Matlab command”
- Write a plugin:
 - Well documented API
 - Lots of example (170 functions written as plugins)
- Examples of recent external contributions:
 - MVPA decoding (Oliva, MIT)
 - Microstate segmentation (Cacioppo, UChicago)
 - Eyetracker/EEG synchronization (Uni Freiburg)

User community

- 16,000 users registered on the website



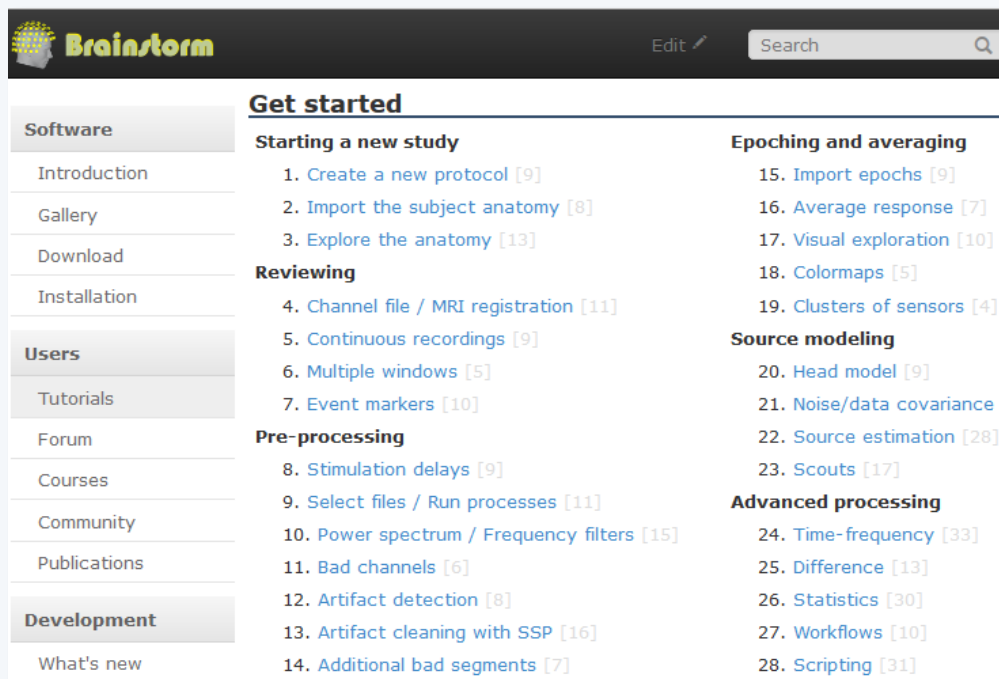
Find users next to you

Location:

josiannebertrand	UQAM, Montreal	EEG	post-doc	2013
timothynest	Montreal, McGill	MEG, fNIRs	research	2013
Clara Moreau	Montreal	MEG	stagiaire	2013

User support

- Online tutorials: 30-hour self-training program
- Active user forum: 150 posts/month
- Daily updates: 750 downloads/month



Brainstorm Edit Search

Software

- Introduction
- Gallery
- Download
- Installation

Users

- Tutorials
- Forum
- Courses
- Community
- Publications

Development

- What's new

Get started

Starting a new study

1. Create a new protocol [9]
2. Import the subject anatomy [8]
3. Explore the anatomy [13]

Reviewing

4. Channel file / MRI registration [11]
5. Continuous recordings [9]
6. Multiple windows [5]
7. Event markers [10]

Pre-processing

8. Stimulation delays [9]
9. Select files / Run processes [11]
10. Power spectrum / Frequency filters [15]
11. Bad channels [6]
12. Artifact detection [8]
13. Artifact cleaning with SSP [16]
14. Additional bad segments [7]

Epoching and averaging

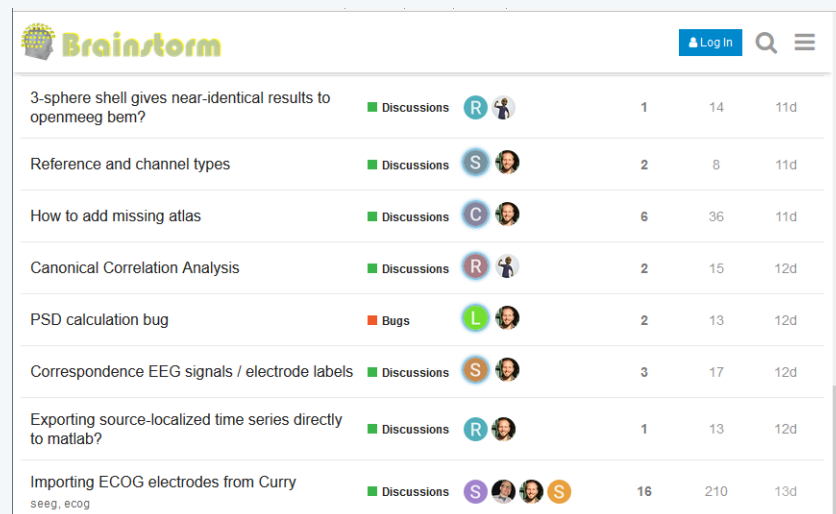
15. Import epochs [9]
16. Average response [7]
17. Visual exploration [10]
18. Colormaps [5]
19. Clusters of sensors [4]

Source modeling

20. Head model [9]
21. Noise/data covariance
22. Source estimation [28]
23. Scouts [17]

Advanced processing

24. Time-frequency [33]
25. Difference [13]
26. Statistics [30]
27. Workflows [10]
28. Scripting [31]



Brainstorm Log In Search

3-sphere shell gives near-identical results to openmeeg bem?	Discussions	R	1	14	11d
Reference and channel types	Discussions	S	2	8	11d
How to add missing atlas	Discussions	C	6	36	11d
Canonical Correlation Analysis	Discussions	R	2	15	12d
PSD calculation bug	Bugs	L	2	13	12d
Correspondence EEG signals / electrode labels	Discussions	S	3	17	12d
Exporting source-localized time series directly to matlab?	Discussions	R	1	13	12d
Importing ECOG electrodes from Curry seeg, ecog	Discussions	S	16	210	13d



Contributors

Investigators



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Geeks



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Inserm Grenoble



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And...

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Antoine Ducorps
Denis Schwartz
...

MEG @ McGill



Elizabeth Bock
MEG engineer



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Post-doc



Soheila Samiee
PhD student



Jeremy Moreau
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Peter Donhauser
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Key collaborators



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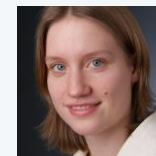
Alexandre Gramfort
Telecom / Neurospin



Anand Joshi
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USC



Esther Florin
Univ Hosp Cologne



Anne-Sophie Dubarry
Aix-Marseille Univ



Rey Ramirez
UW

Epilepsy recordings: Localization of frontal spikes

- Patient recorded at the Epilepsy Centre of the University Hospital in Freiburg, Germany
- Focal epilepsy with focal sensory, dyscognitive and secondarily generalized seizures since the age of eight years
- Histological analysis revealed a focal cortical dysplasia
- One hour of sleep recordings
- Neurofile NT EEG system, sampled at 256Hz
- 58 epileptic spikes marked by the epileptologists in Freiburg
- MRI processed with FreeSurfer 5.3