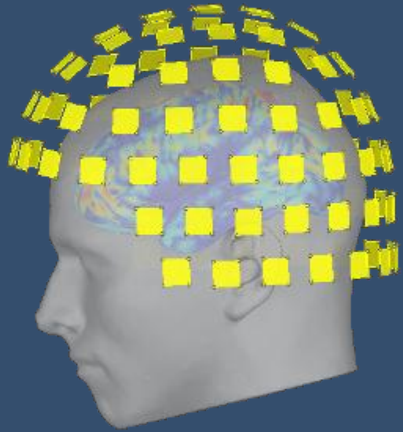
MEG and EEG analysis using

Brainstorm 3.1

http://neuroimage.usc.edu/brainstorm



USC UNIVERSITY OF SOUTHERN CALIFORNIA

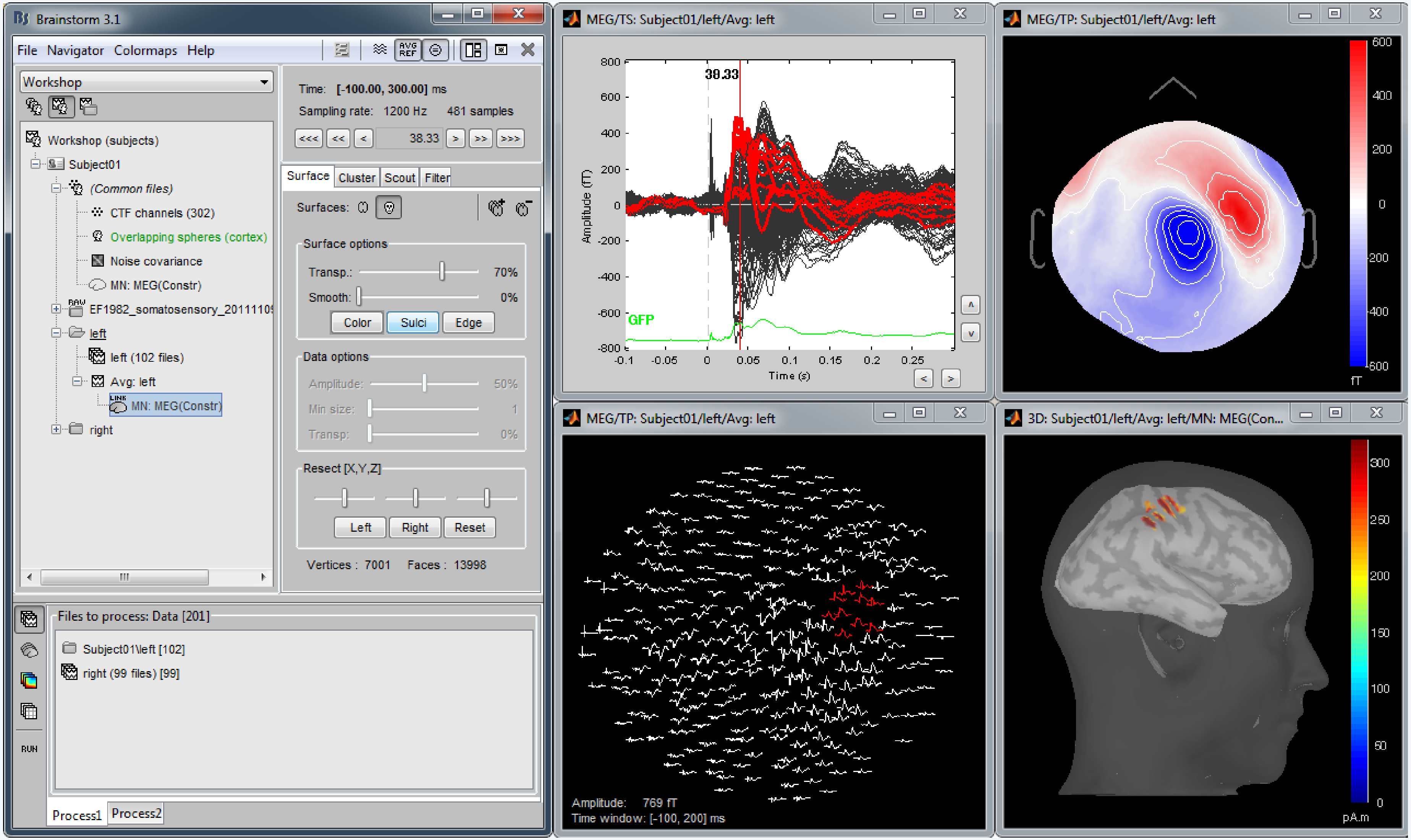
Cleveland Clinic

McGill

neuro

François Tadel
Biomag 2012 – Paris
August 31, 2012

Graphic interface



Brainstorm 3.1

Time: [-100.00, 300.00] ms

Sampling rate: 1200 Hz   481 samples

Transp.: 70%

Smooth: 0%

Amplitude: 50%

Min size: 1

Transp: 0%

Vertices : 7001   Faces : 13998

Files to process: Data [201]

- Subject01\left [102]
- right (99 files) [99]

MEG/TS: Subject01/left/Avg: left

MEG/TP: Subject01/left/Avg: left

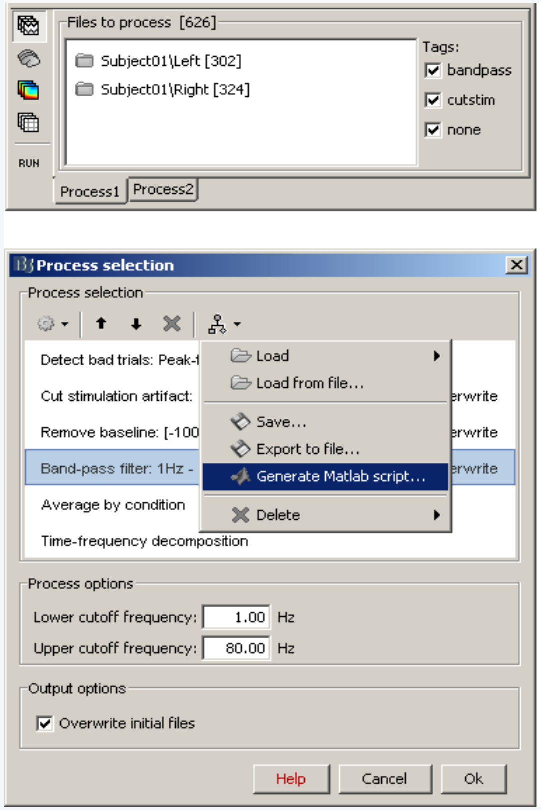
MEG/TP: Subject01/left/Avg: left

Amplitude: 769 fT
Time window: [-100, 200] ms

3D: Subject01/left/Avg: left/MN: MEG(Con...

Scripting environment

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



Files to process [626]

Subject01\Left [302]

Subject01\Right [324]

Tags:
☑ bandpass
☑ cutstim
☑ none

Process selection

Detect bad trials: Peak-t
Cut stimulation artifact:
Remove baseline: [-100
Band-pass filter: 1Hz -
Average by condition
Time-frequency decomposition

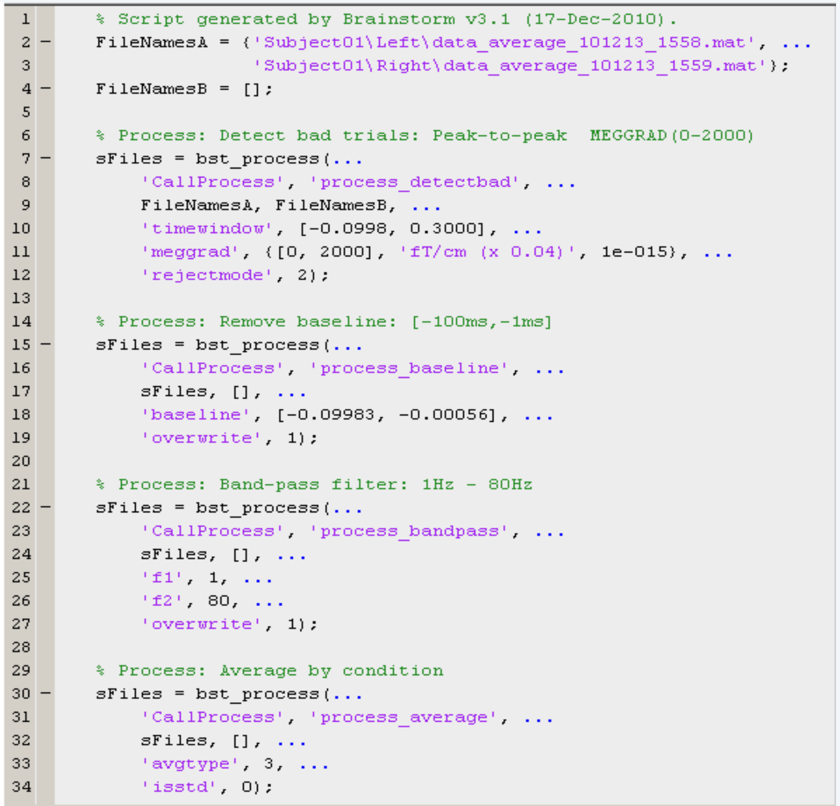
Process options

Lower cutoff frequency: 1.00 Hz

Upper cutoff frequency: 80.00 Hz

Output options

☑ Overwrite initial files



```matlab
% Script generated by Brainstorm v3.1 (17-Dec-2010).
FileNamesA = {'Subject01\Left\data_average_101213_1558.mat', ...
              'Subject01\Right\data_average_101213_1559.mat'};
FileNamesB = [];

% Process: Detect bad trials: Peak-to-peak  MEGGRAD(0-2000)
sFiles = bst_process(...
    'CallProcess', 'process_detectbad', ...
    FileNamesA, FileNamesB, ...
    'timewindow', [-0.0998, 0.3000], ...
    'meggrad', {[0, 2000], 'fT/cm (x 0.04)', 1e-015}, ...
    'rejectmode', 2);

% Process: Remove baseline: [-100ms,-1ms]
sFiles = bst_process(...
    'CallProcess', 'process_baseline', ...
    sFiles, [], ...
    'baseline', [-0.09983, -0.00056], ...
    'overwrite', 1);

% Process: Band-pass filter: 1Hz - 80Hz
sFiles = bst_process(...
    'CallProcess', 'process_bandpass', ...
    sFiles, [], ...
    'f1', 1, ...
    'f2', 80, ...
    'overwrite', 1);

% Process: Average by condition
sFiles = bst_process(...
    'CallProcess', 'process_average', ...
    sFiles, [], ...
    'avgtype', 3, ...
    'isstd', 0);
```

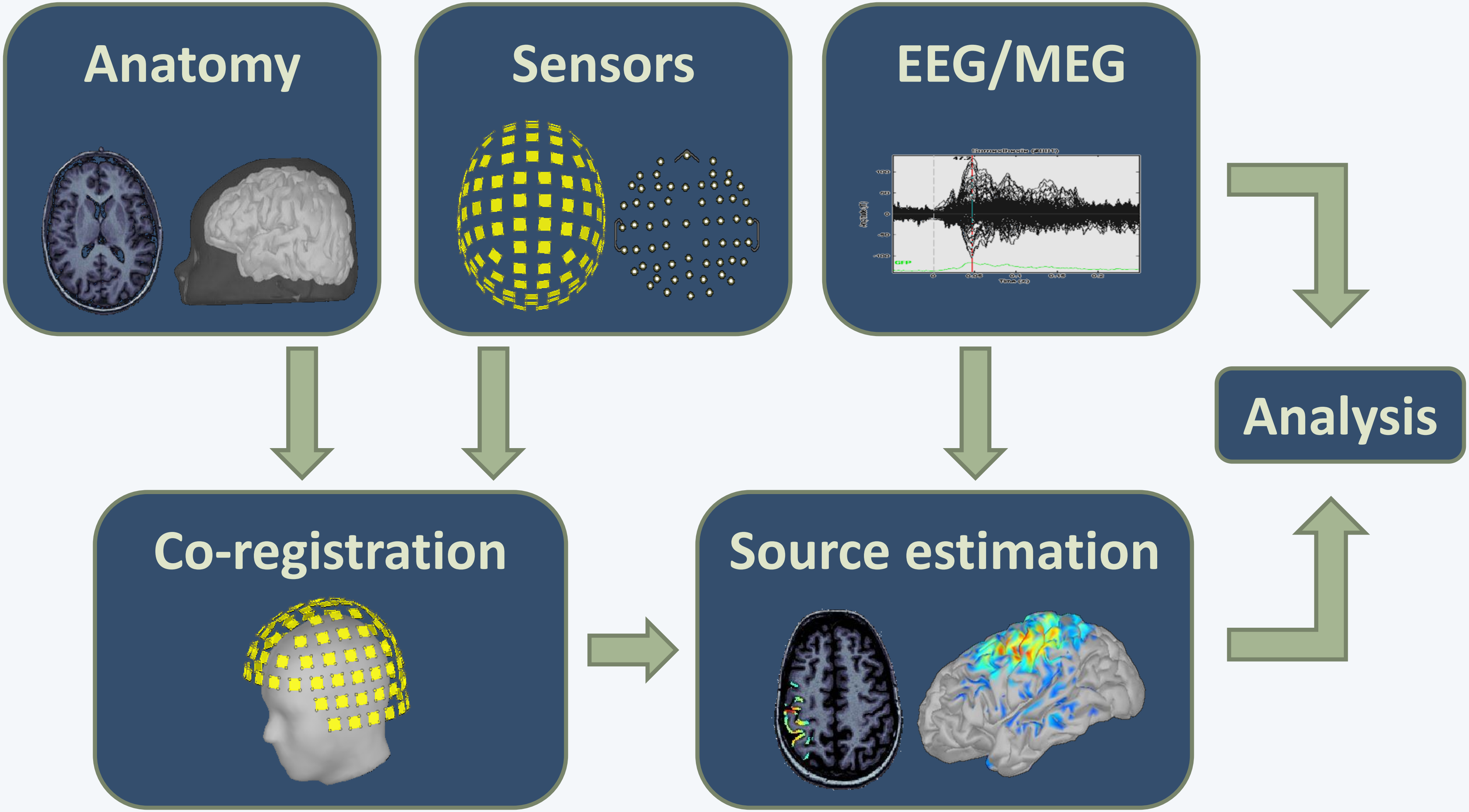
Brainstorm is...

- A free and open-source application (GPL)
- Matlab & Java: Platform-independent
- Designed for Matlab environment
- Stand-alone version also available
- Interface-based: click, drag, drop
- No Matlab experience required
- Daily updates of the software

A bit of history

- 12 years of research and development
- Active collaboration between multiple groups:
  - University of Southern California, Los Angeles
  - La Salpetriere Hospital / CNRS, Paris
  - Neurospin / Inserm / CEA, Paris
  - Los Alamos National Lab, NM
  - Medical College of Wisconsin, Milwaukee
  - Cleveland Clinic, OH
  - Martinos Center / MGH, MA
  - McGovern Institute / MIT, MA
  - Montreal Neurological Institute / McGill, QC
- New interface released in 2009
- Over 7000 user accounts / 60 countries

Workflow



Anatomy

Sensors

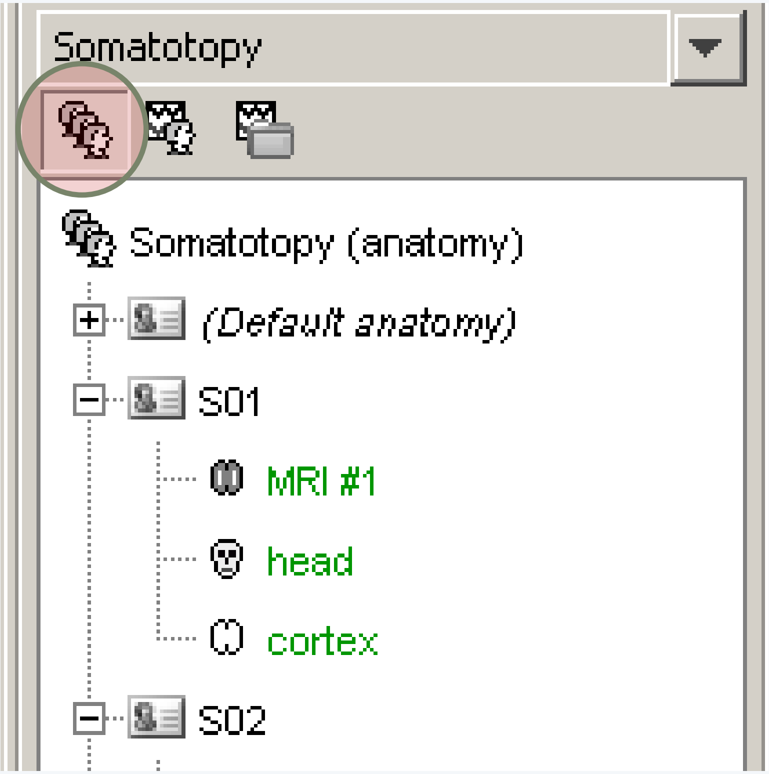
EEG/MEG

Analysis

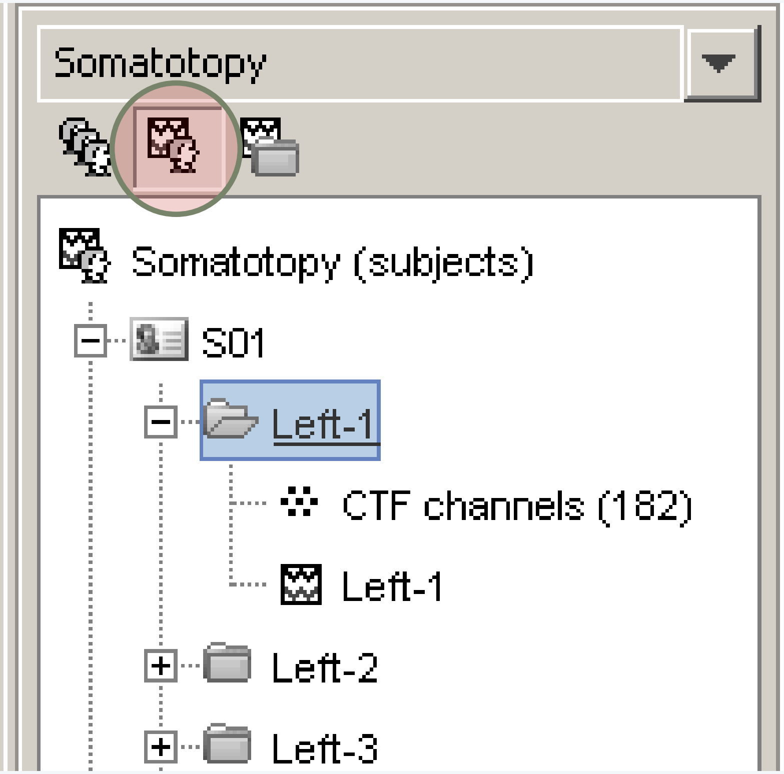
Co-registration

Source estimation

Database


Somatotopy

Somatotopy (anatomy)
- (Default anatomy)
- S01
  - MRI #1
  - head
  - cortex
- S02


Somatotopy

Somatotopy (subjects)
- S01
  - Left-1
    - CTF channels (182)
    - Left-1
  - Left-2
  - Left-3

- Three levels:
  - Protocol
  - Subject
  - Condition

- Popup menus
- All files saved in Matlab .mat
- Same architecture on the disk

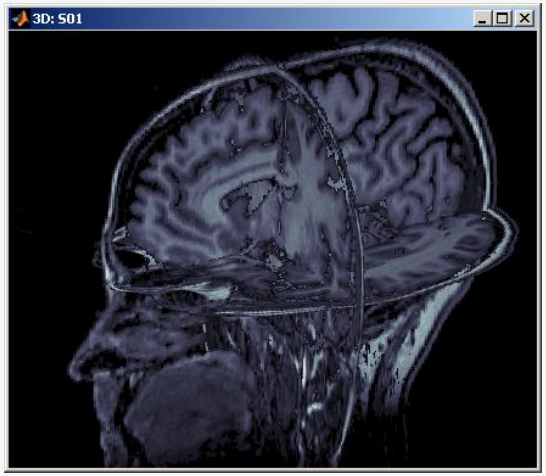
Anatomy

- T1-MRI volume

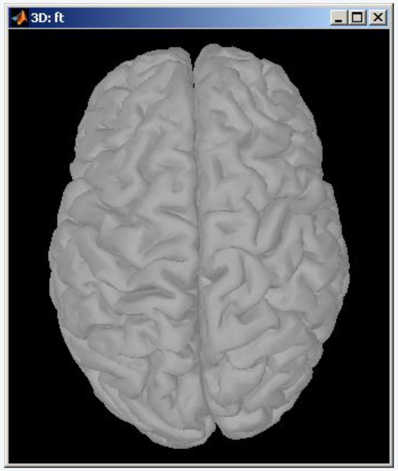
Display options
View: ☑ Crosshai ☑ Sliders
MIP: ☐ Anatomy
Orient: ● Neurological ○ Radiological

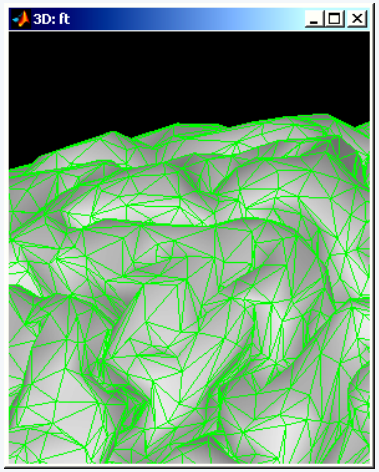
Coordinates (milimeters)

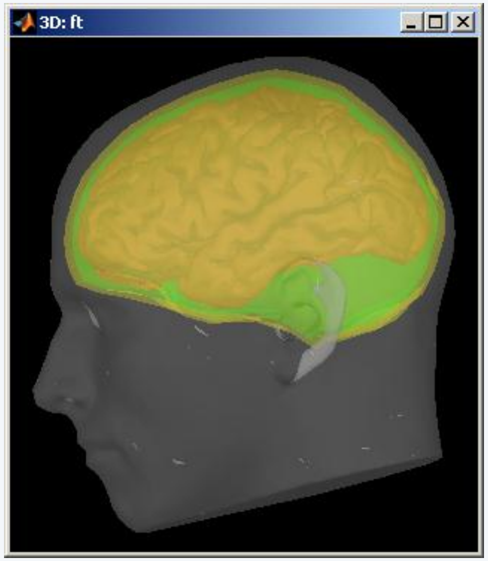
MRI:	x: 120.00	y: 120.00	z: 120.00
SCS:	x: 20.86	y: -7.27	z: 37.19
TAL:	x: 4.18	y: -7.93	z: -13.84



- Surfaces extracted with a dedicated software: BrainVISA, FreeSurfer, BrainSuite

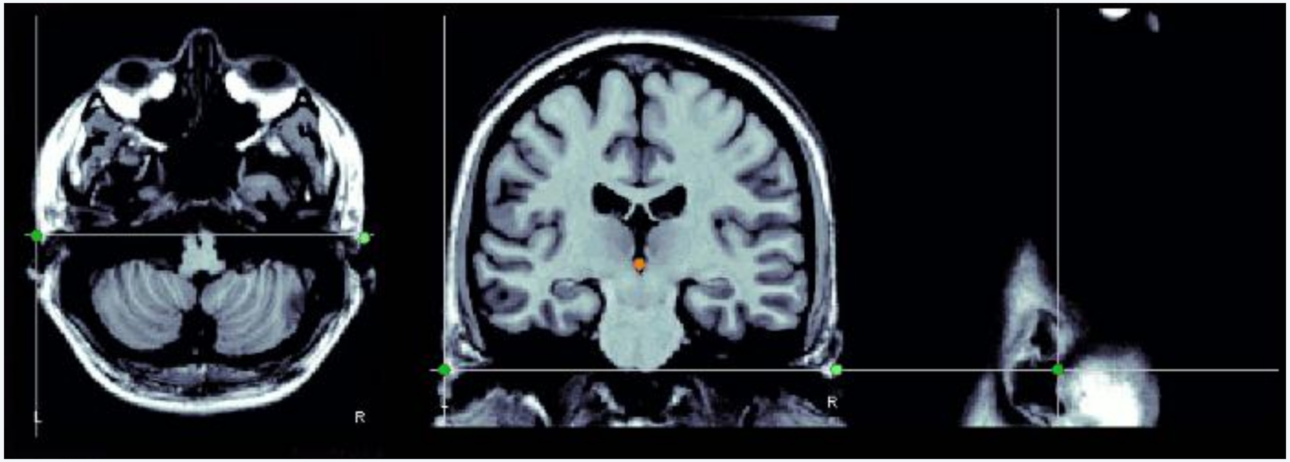






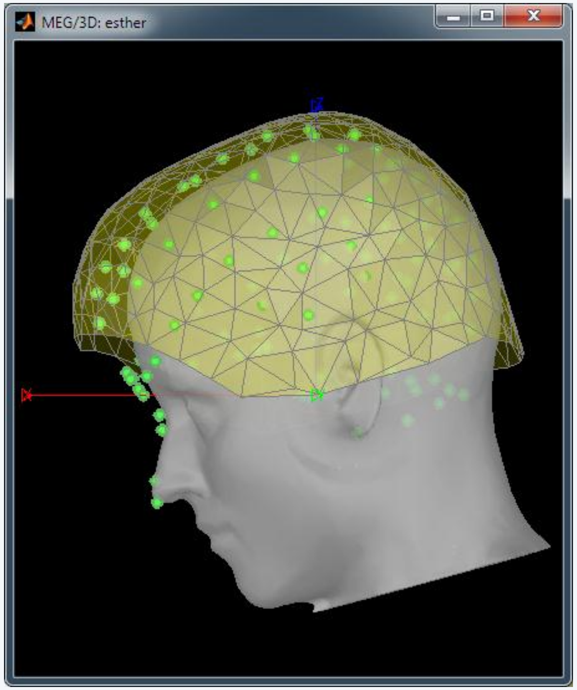
Co-registration MEG / MRI (I)

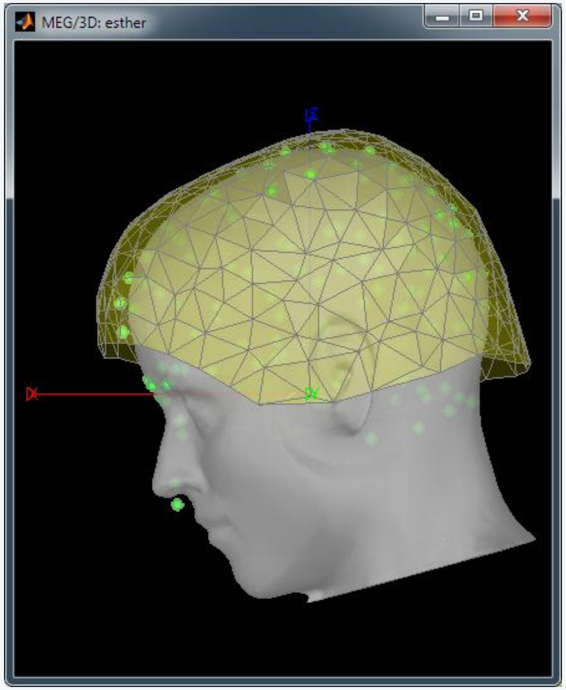
- Basic estimation based on three points (NAS,LPA,RPA)
  - – MRI: Marked in the volume with the MRI Viewer
  - – MEG: Obtained with a tracking system (Polhemus)



Co-registration MEG / MRI (2)

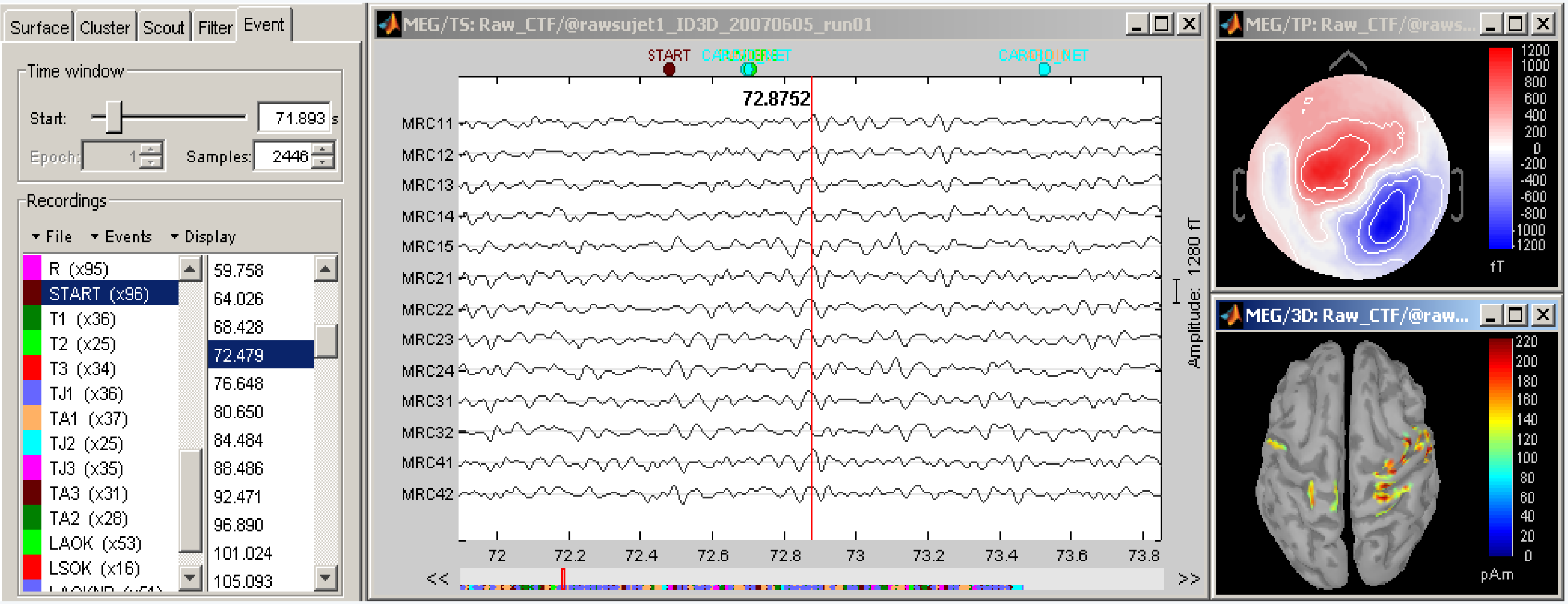
- Automatic adjustment based on head shape
  - Trying to fit the head points (digitized with the Polhemus) with the head surface (from the MRI)
- Final registration must be checked manually





Continuous recordings

- Review continuous file
- Supports most common EEG/MEG file formats
- Edit markers, display 2D projections and sources



Start: 71.893 s

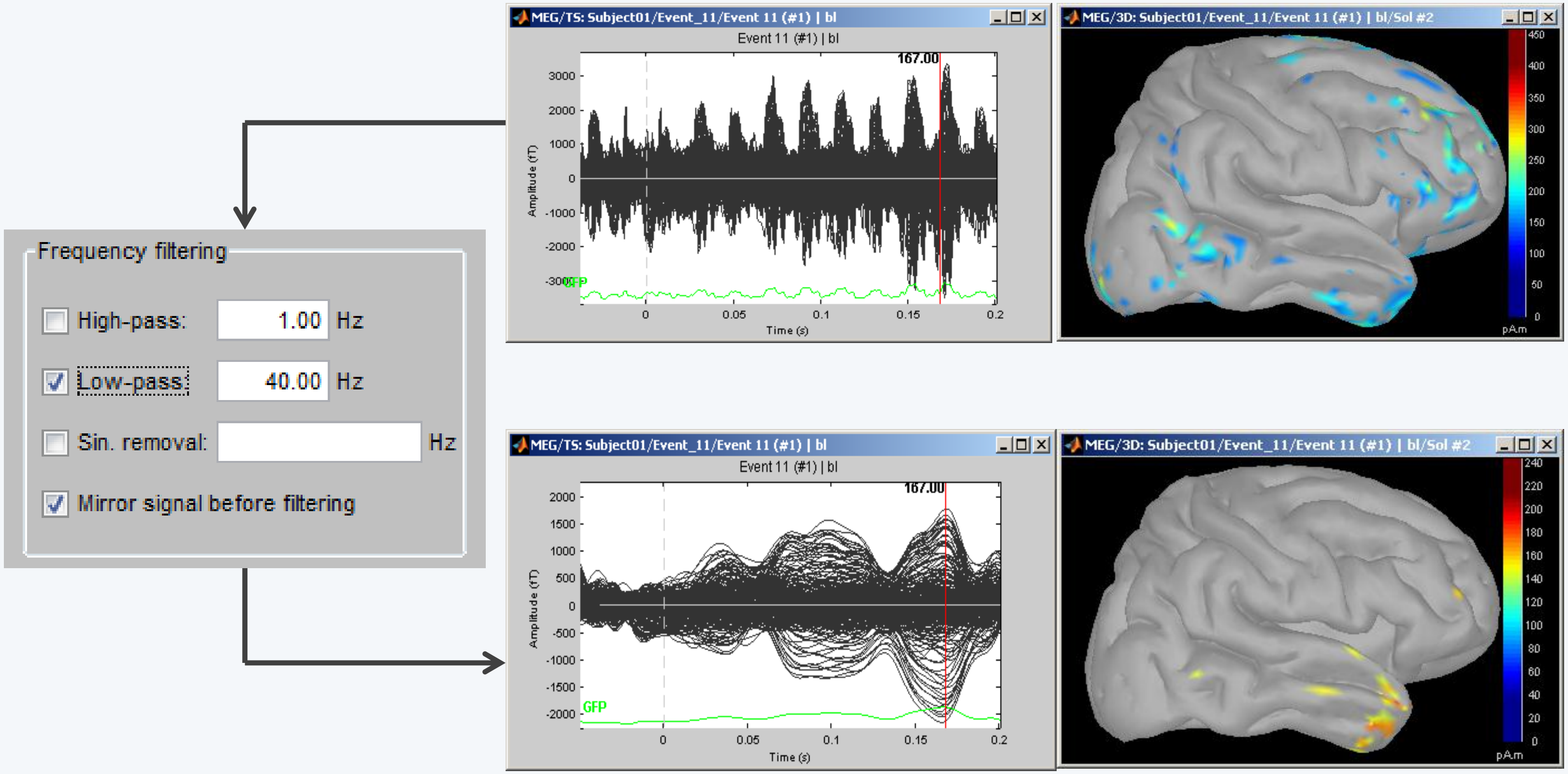
Epoch: 1

Samples: 2446

R (x95) 59.758
START (x96) 64.026
T1 (x36) 68.428
T2 (x25) 72.479
T3 (x34) 76.648
TJ1 (x36) 80.650
TA1 (x37) 84.484
TJ2 (x25) 88.486
TJ3 (x35) 92.471
TA3 (x31) 96.890
TA2 (x28) 101.024
LAOK (x53) 105.093
LSOK (x16)

Pre-processing Filtering

- Frequency filtering



Frequency filtering

☐ High-pass: 1.00 Hz

☑ Low-pass: 40.00 Hz

☐ Sin. removal: Hz

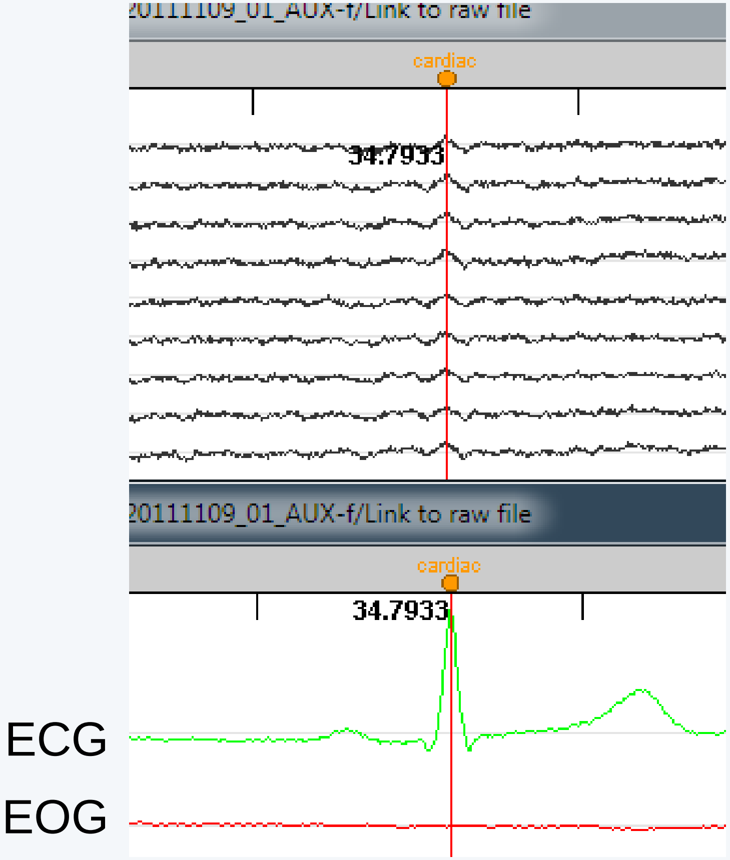
☑ Mirror signal before filtering

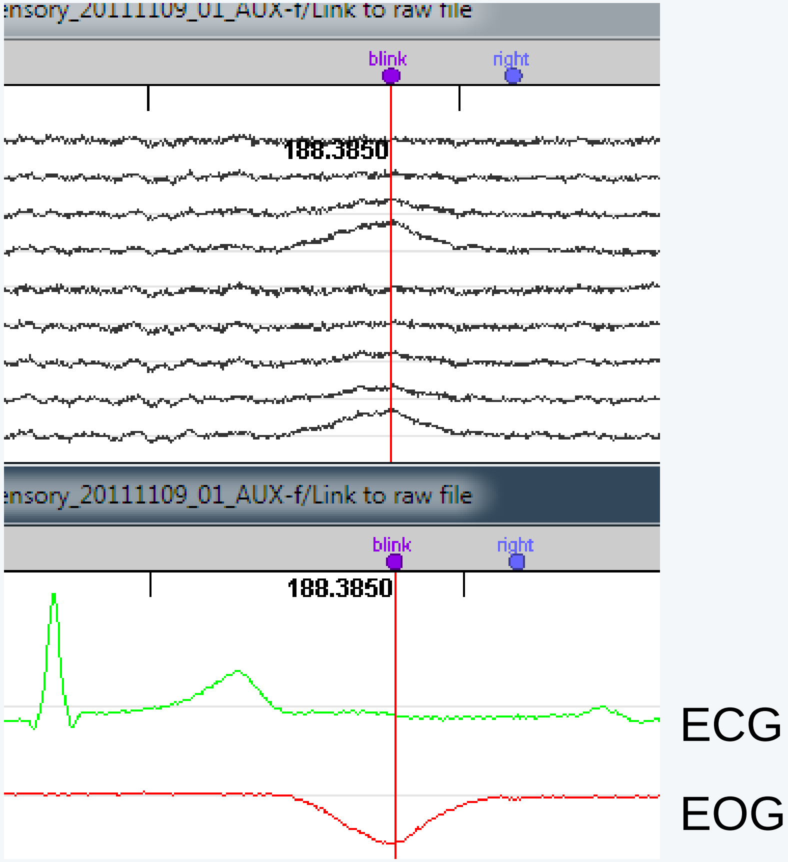
Not filtered

Low-pass 40Hz

Pre-processing Cleaning

- Artifact detection and removal:
  - heartbeats, eye blinks, movements, …





Pre-processing Cleaning

- Two categories of artifacts:
  - Well defined, reproducible, short, frequent:
    - Heartbeats, eye blinks, 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

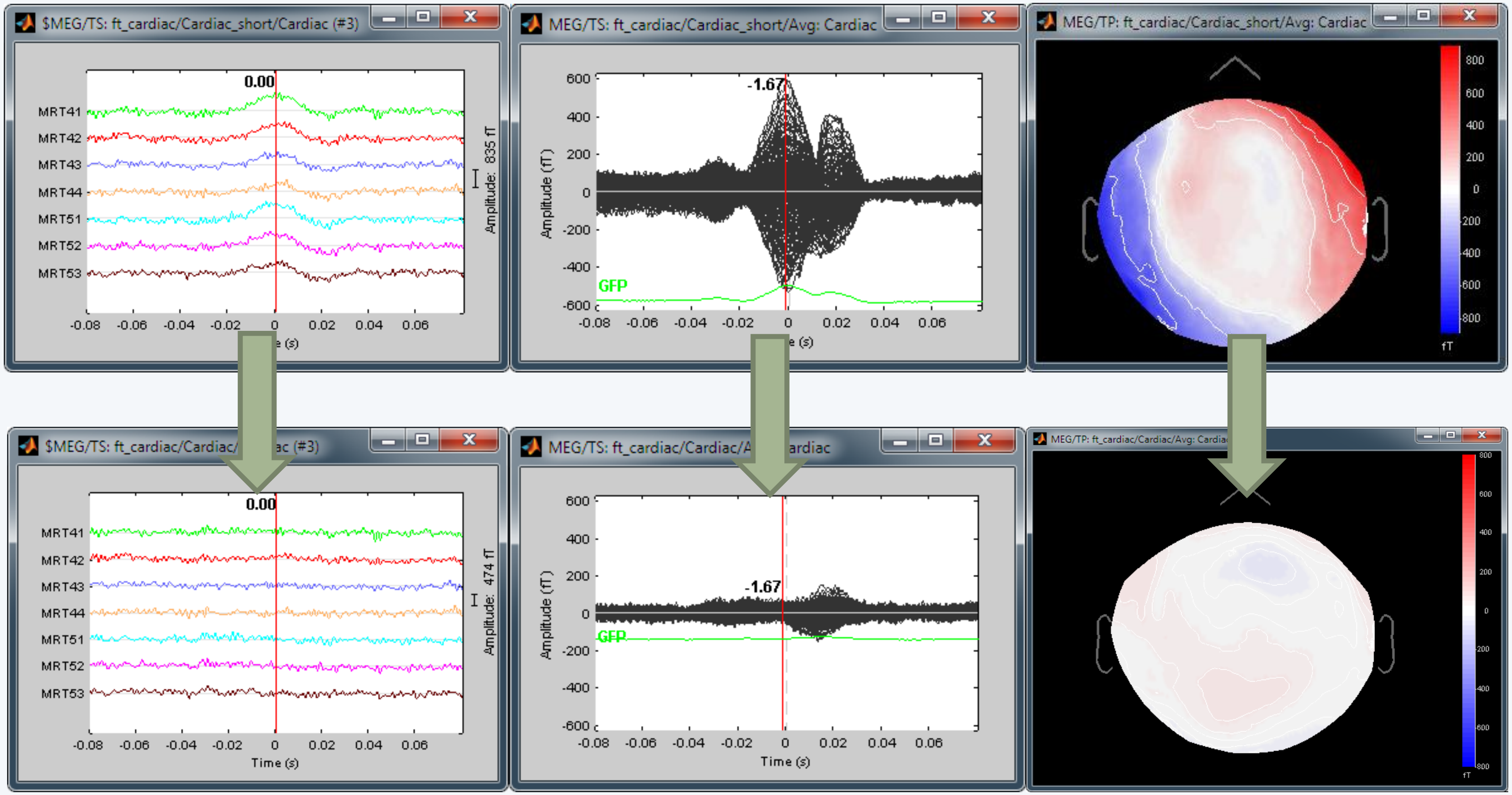
Pre-processing

Cleaning

- Example of the cardiac artifact
  => Computation of a Signal-Space Projection (SSP)

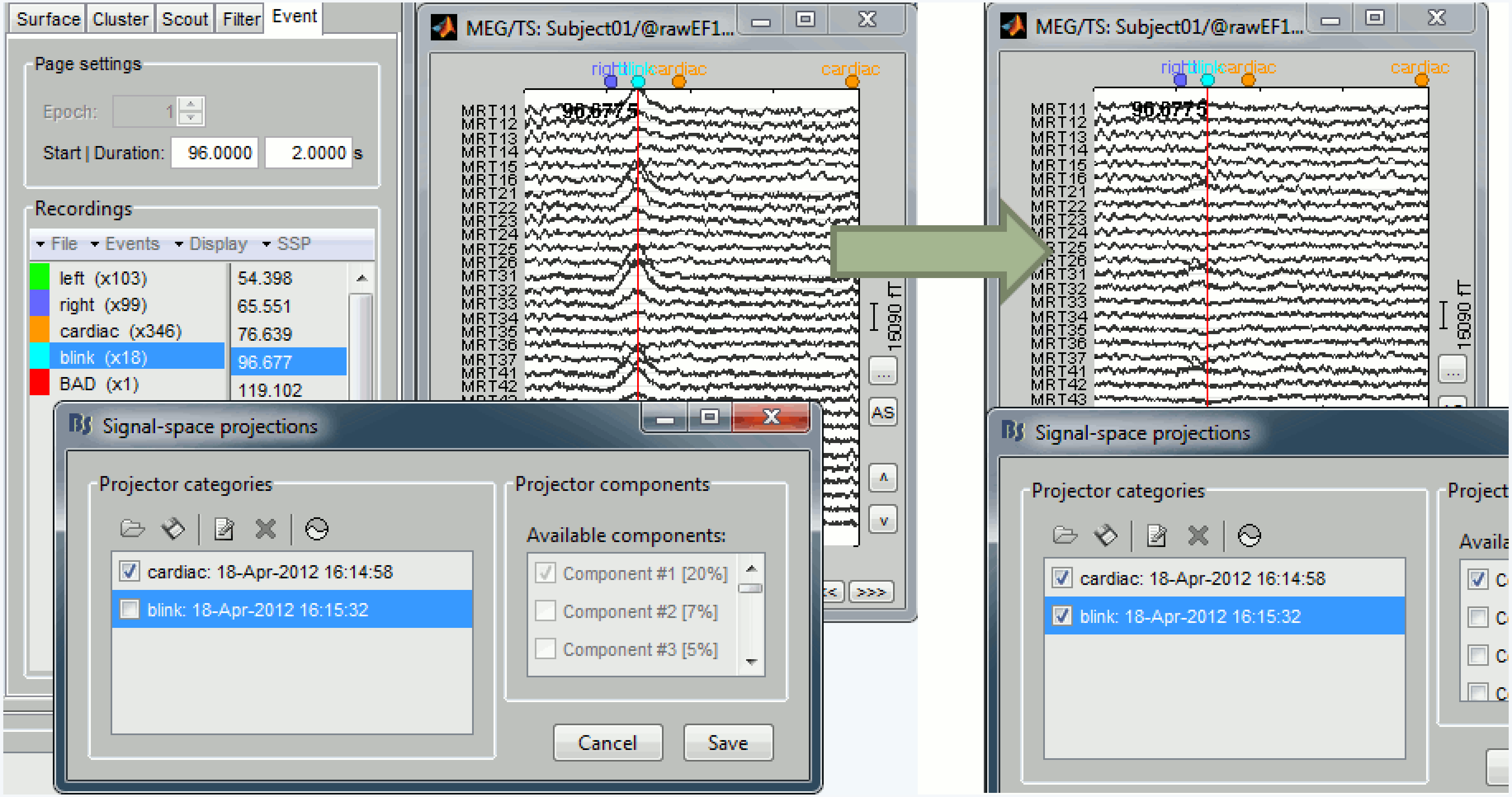
Original

SSP



Pre-processing

Cleaning



Page settings

Epoch: 1

Start | Duration: 96.0000 2.0000 s

Recordings

🟩 left (x103)
🟦 right (x99)
🟧 cardiac (x346)
🟦 blink (x18)
🟥 BAD (x1)

54.398
65.551
76.639
96.677
119.102

Projector categories

☑ cardiac: 18-Apr-2012 16:14:58
☐ blink: 18-Apr-2012 16:15:32

Projector components

Available components:

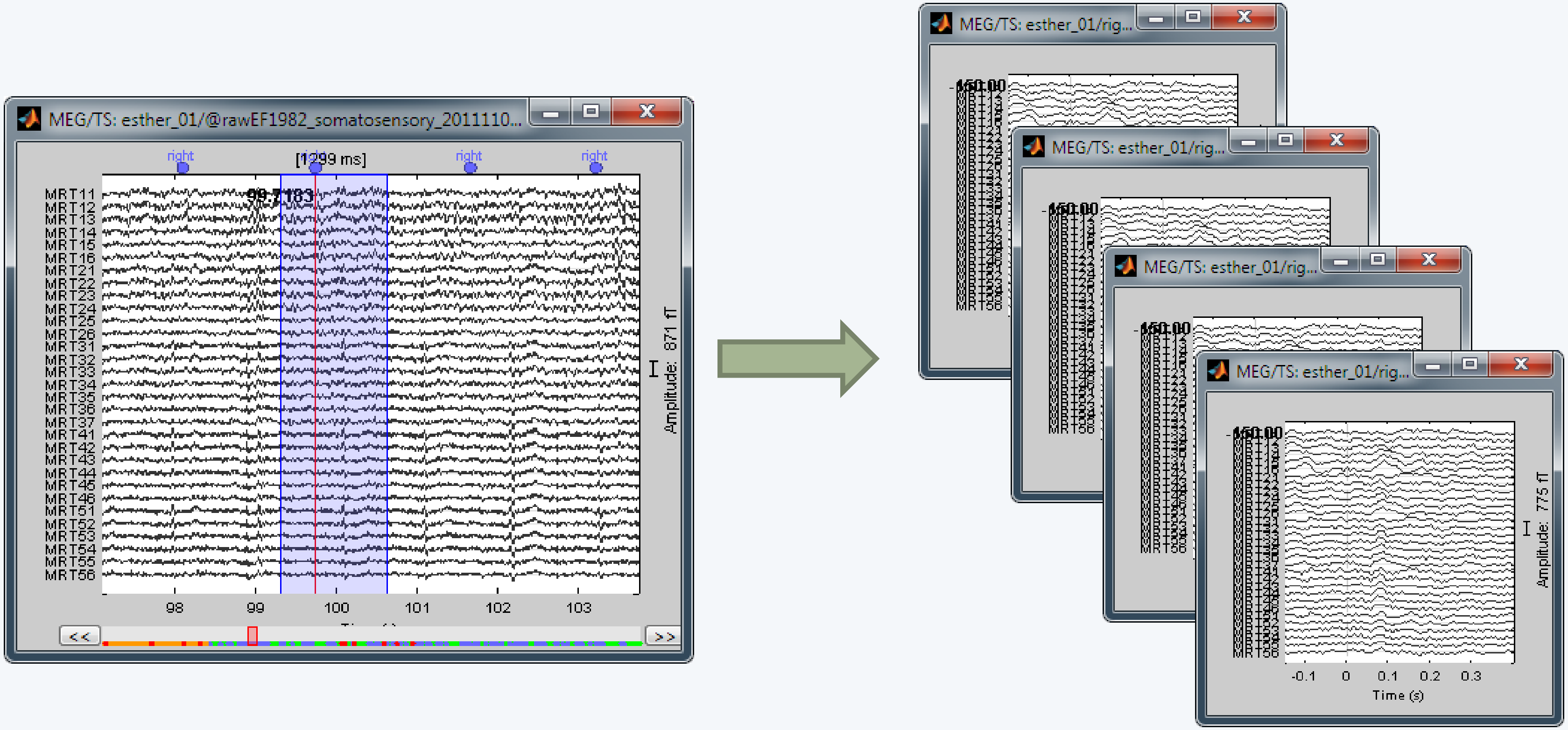
☑ Component #1 [20%]
☐ Component #2 [7%]
☐ Component #3 [5%]

Projector categories

☑ cardiac: 18-Apr-2012 16:14:58
☑ blink: 18-Apr-2012 16:15:32

Pre-processing Averaging

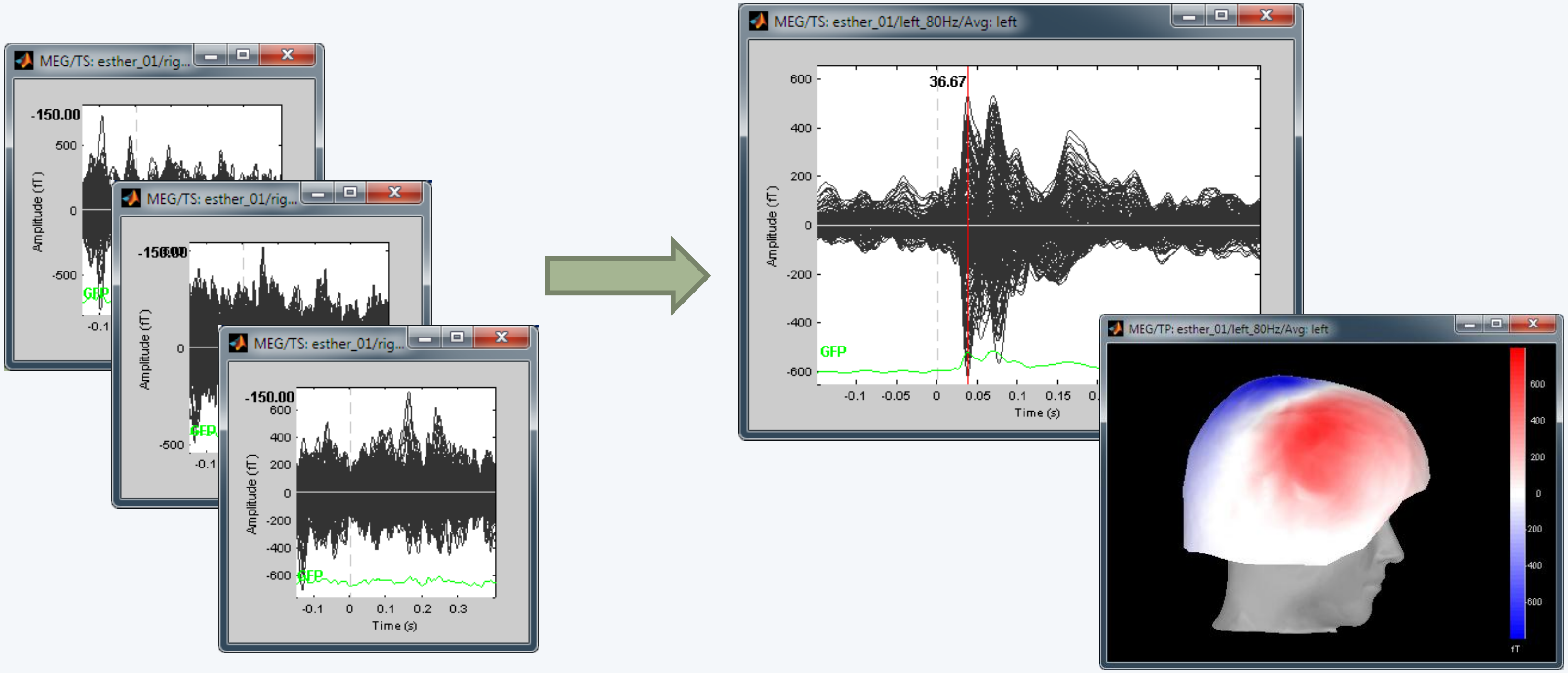
- Epoching: extraction of small blocks of recordings around an event of interest (stimulus, spike…)



Pre-processing Averaging

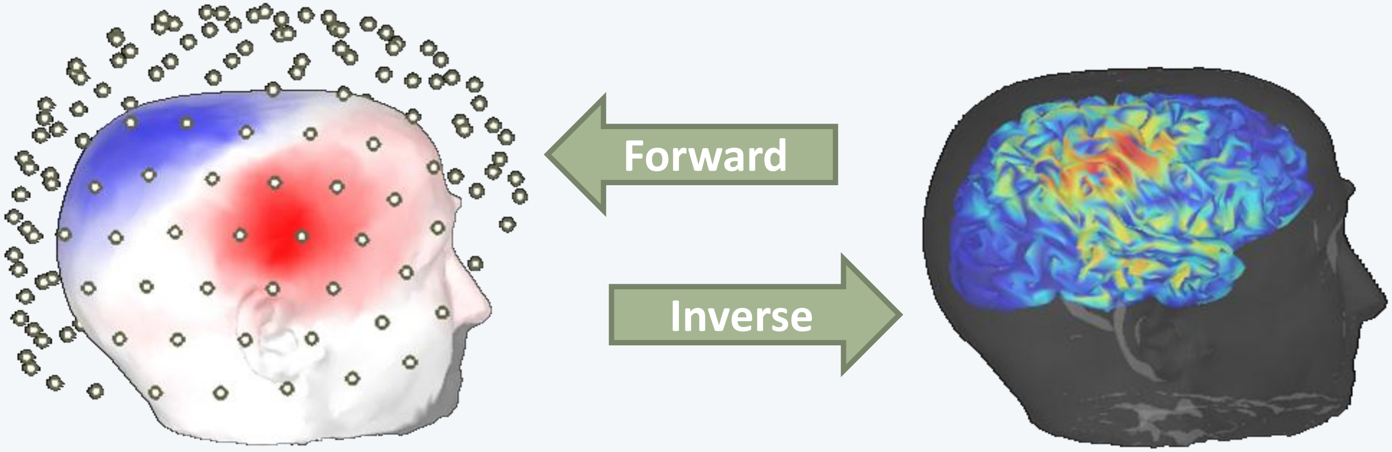
- Averaging all the trials: Reveals the features of the signals that are locked in time to a given event

  => Evoked-response field (or potential)



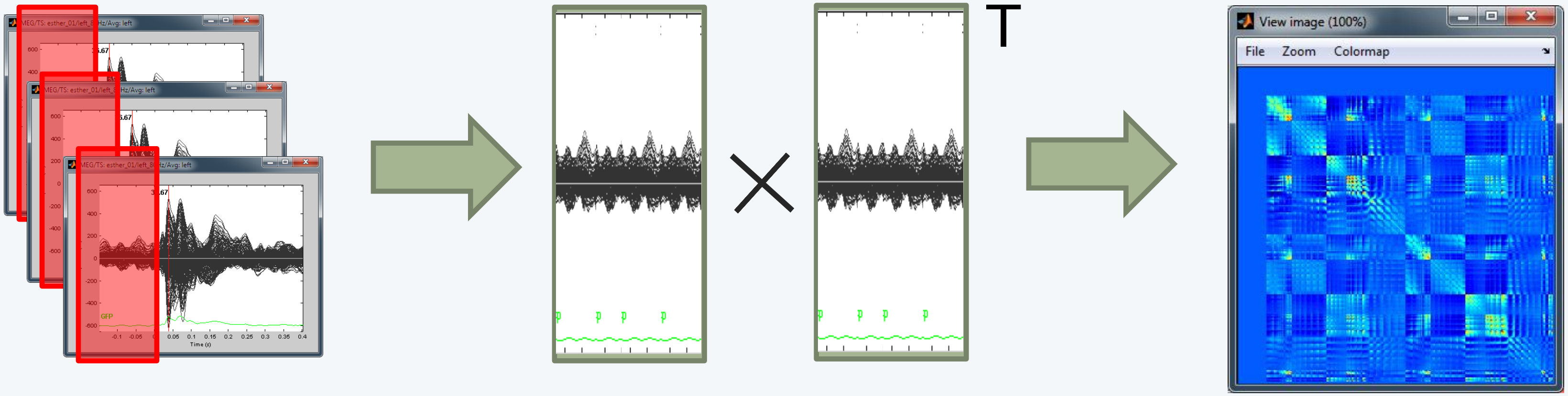
Source estimation

- Source space: cortex surface (or full head volume)
- Forward model = head model
  Sources => Sensors
- Inverse model: Minimum norm estimates
  Sensors => Sources

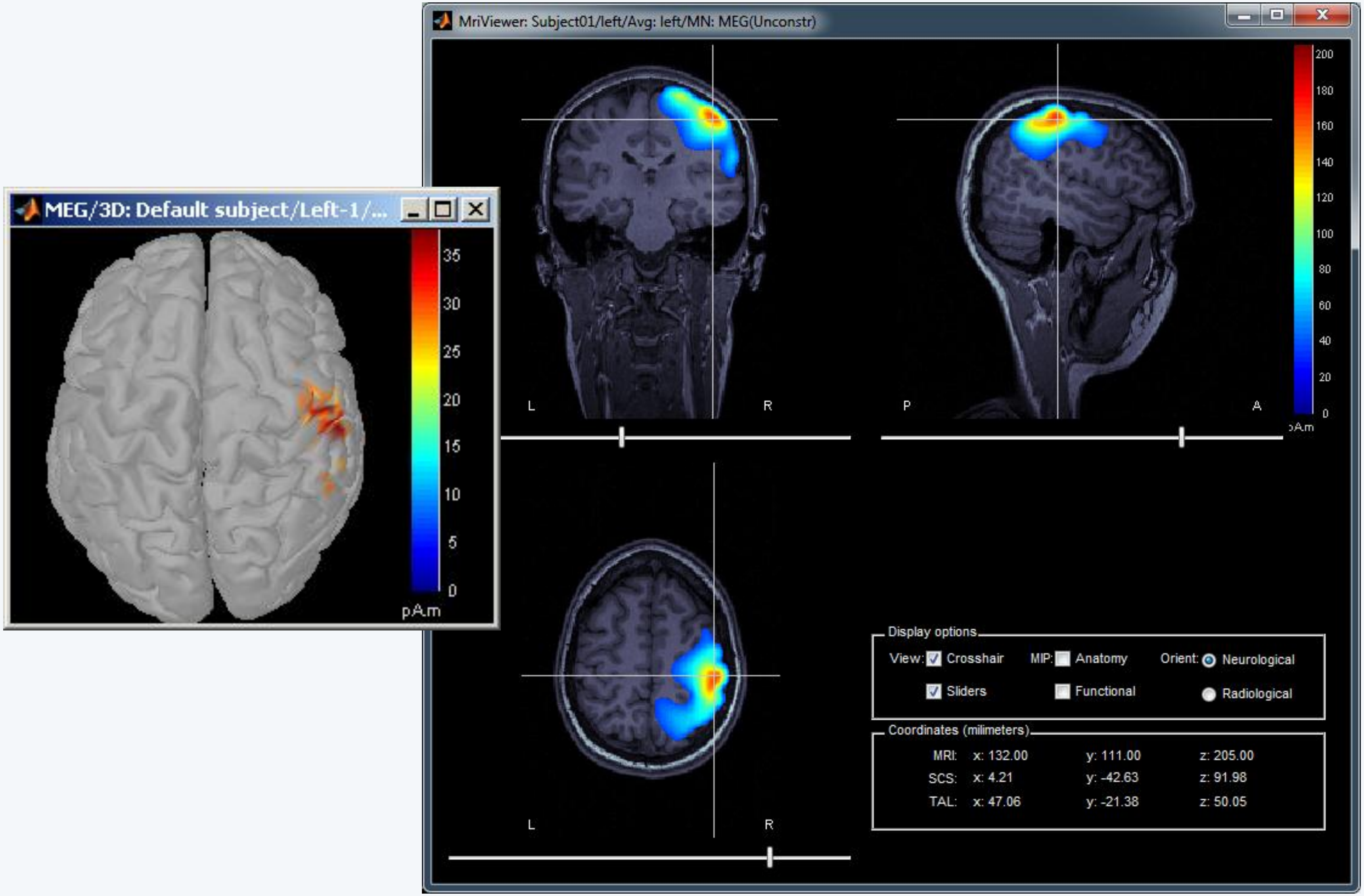


Noise covariance matrix

- Inverse model (minimum norm estimates) requires an estimation of the level of noise on the sensors
- Noise covariance matrix = covariance of the segments that do not contain any “meaningful” data
- Typically: empty room measures, or pre-stim baseline



Sources activity



Display options

View: ☑ Crosshair ☑ Sliders

MIP: ☐ Anatomy ☐ Functional

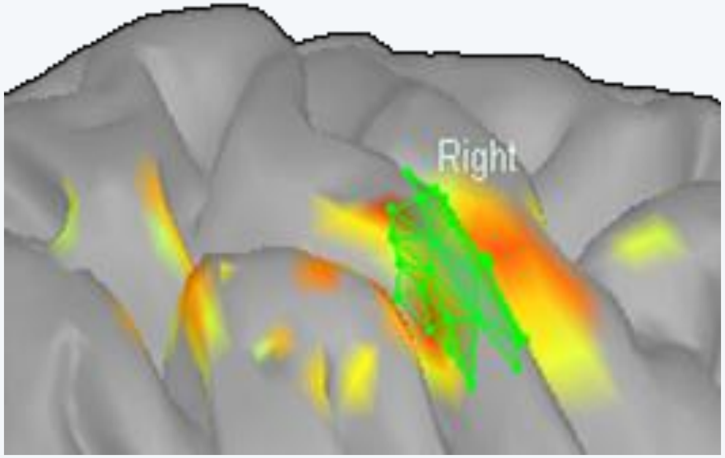
Orient: ● Neurological ○ Radiological

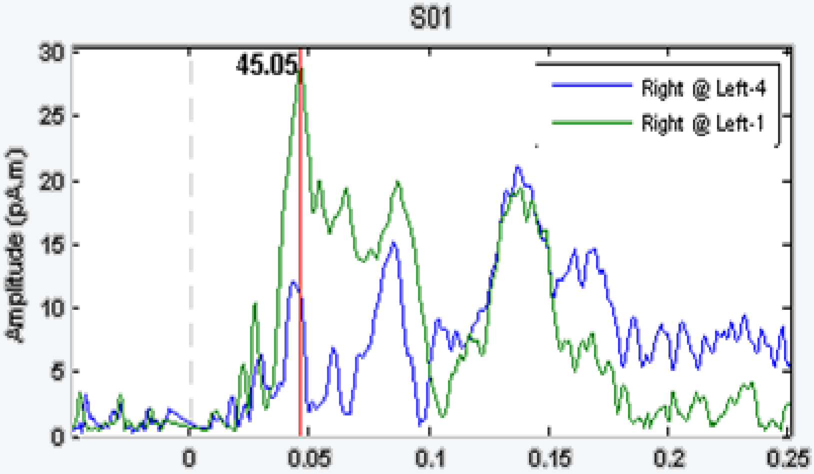
Coordinates (milimeters)

MRI:	x: 132.00	y: 111.00	z: 205.00
SCS:	x: 4.21	y: -42.63	z: 91.98
TAL:	x: 47.06	y: -21.38	z: 50.05

Regions of interest

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



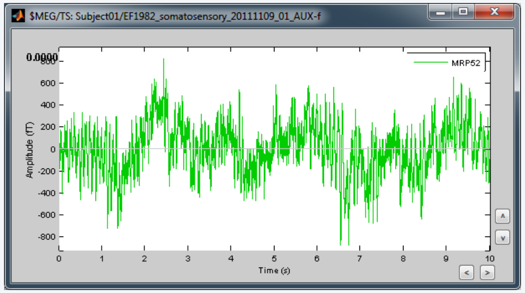


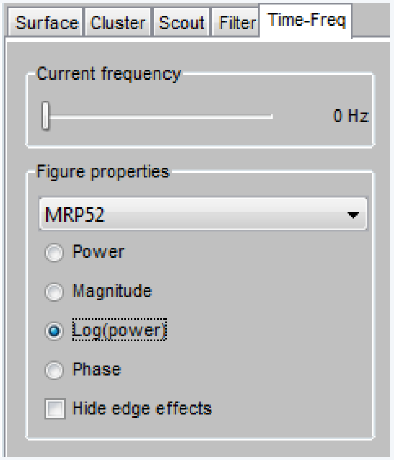
Post-processing

- Noise normalization (z-score)
- Spectral and time-frequency analysis
- Group analysis:
  - Anatomical registration and normalization
  - Statistical inference
- Connectivity measures

Spectral analysis

- Fast Fourier transform (FFT)
- Power spectrum density (PSD)





Current frequency

0 Hz

Figure properties

MRP52

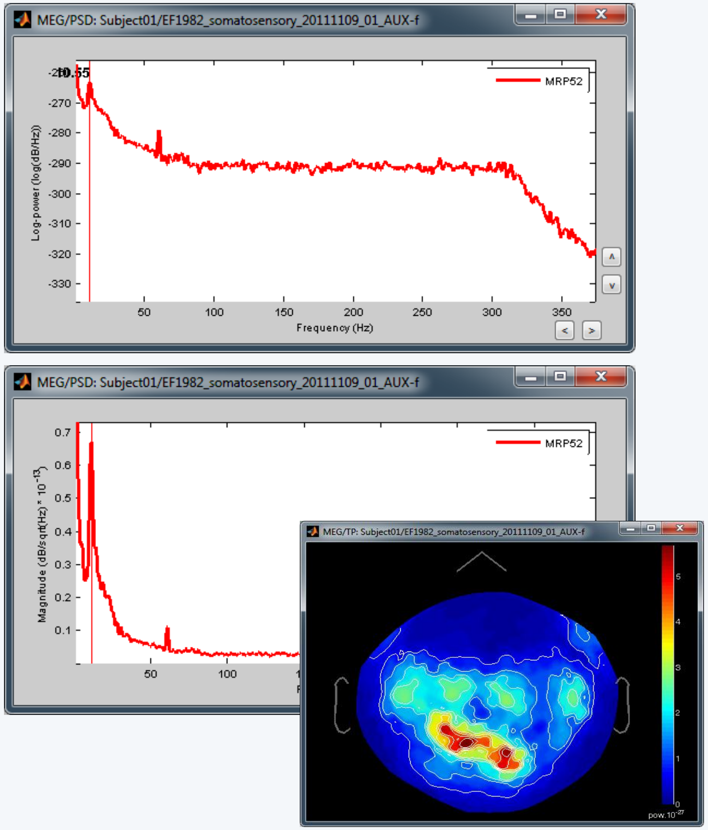
○ Power

○ Magnitude

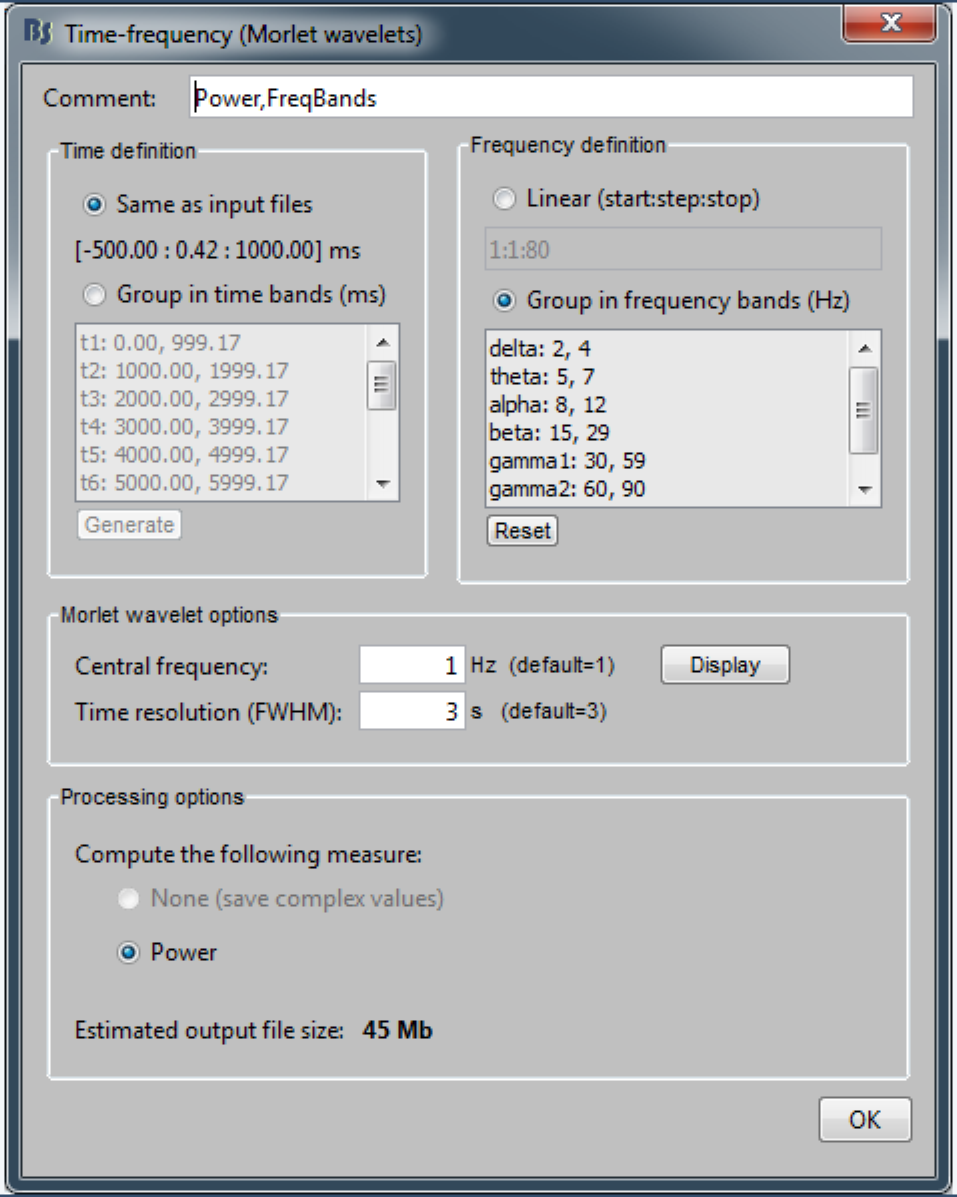
● Log(power)

○ Phase

☐ Hide edge effects



Time-frequency / Hilbert transform



Comment: Power,FreqBands

Time definition

● Same as input files

[-500.00 : 0.42 : 1000.00] ms

○ Group in time bands (ms)

t1: 0.00, 999.17
t2: 1000.00, 1999.17
t3: 2000.00, 2999.17
t4: 3000.00, 3999.17
t5: 4000.00, 4999.17
t6: 5000.00, 5999.17

Frequency definition

○ Linear (start:step:stop)

1:1:80

● Group in frequency bands (Hz)

delta: 2, 4
theta: 5, 7
alpha: 8, 12
beta: 15, 29
gamma1: 30, 59
gamma2: 60, 90

Morlet wavelet options

Central frequency: 1 Hz (default=1)

Time resolution (FWHM): 3 s (default=3)

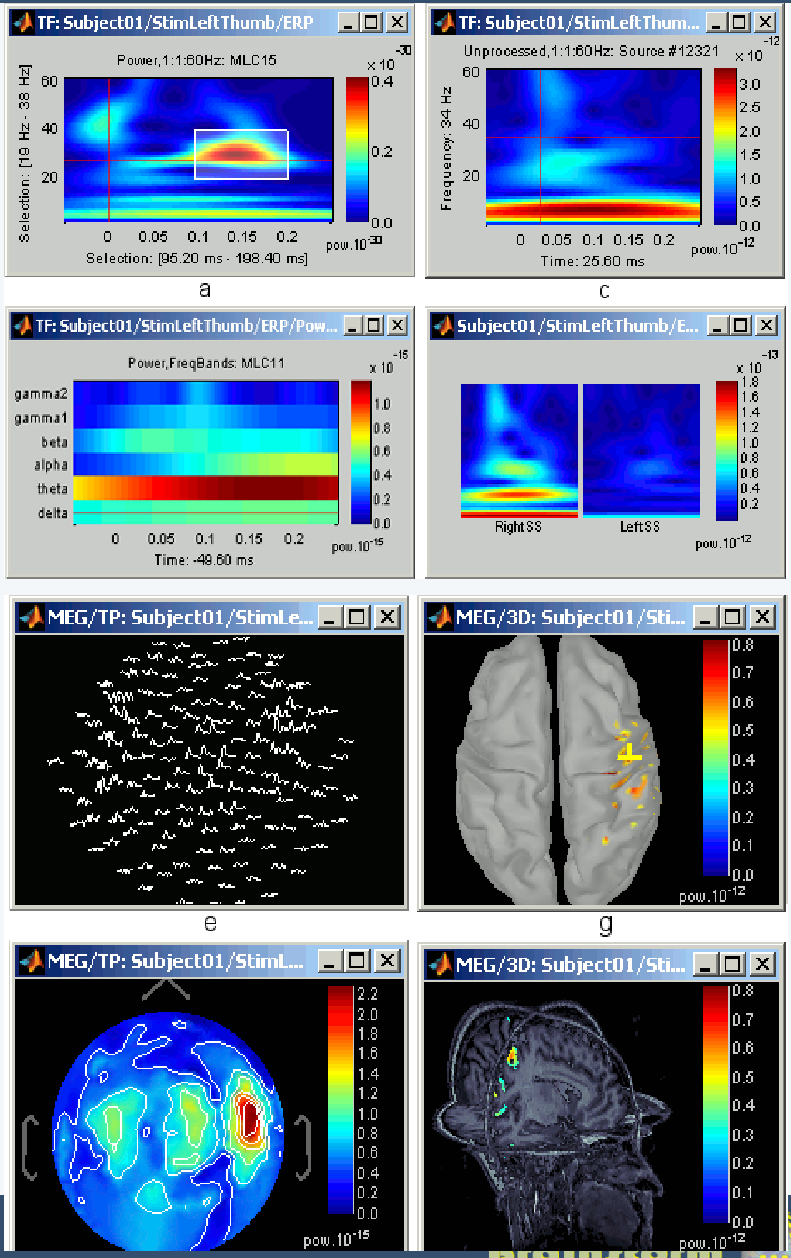
Processing options

Compute the following measure:

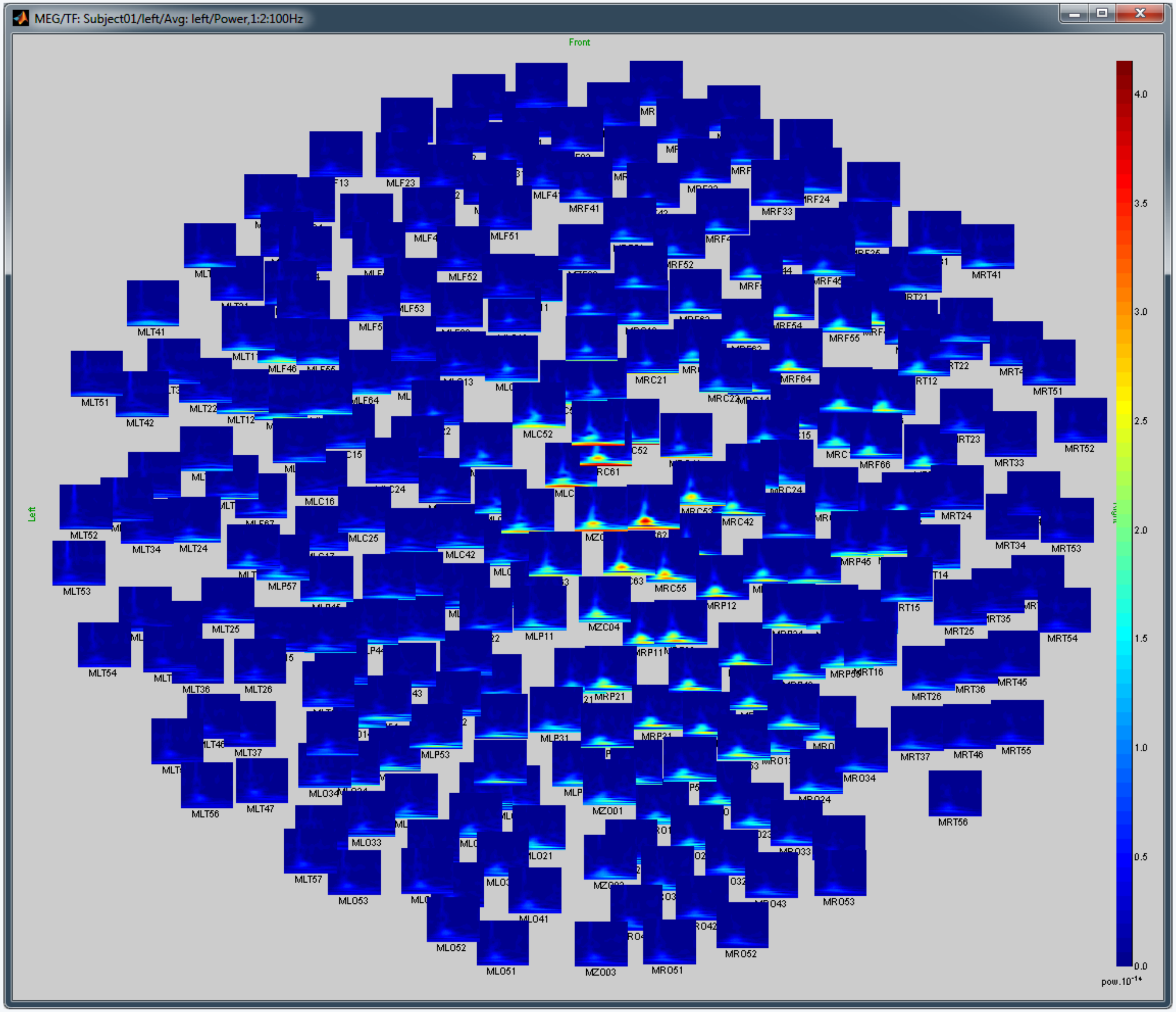
○ None (save complex values)

● Power

Estimated output file size: **45 Mb**



Time-frequency / Hilbert transform

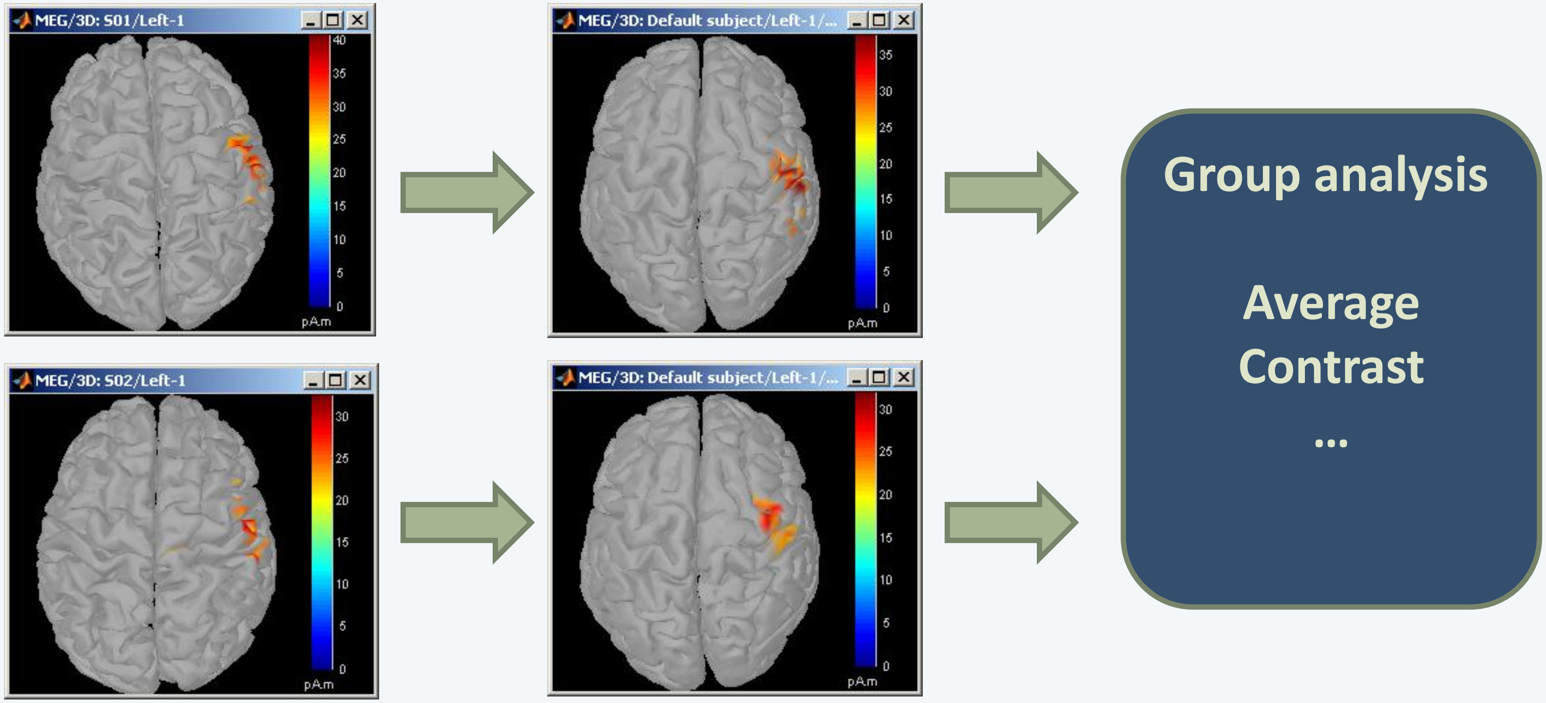


Group analysis — Normalization

- Registration of individual brains on a template

Subject 1

Subject 2



Group analysis

Average

Contrast

...

Individual anatomy

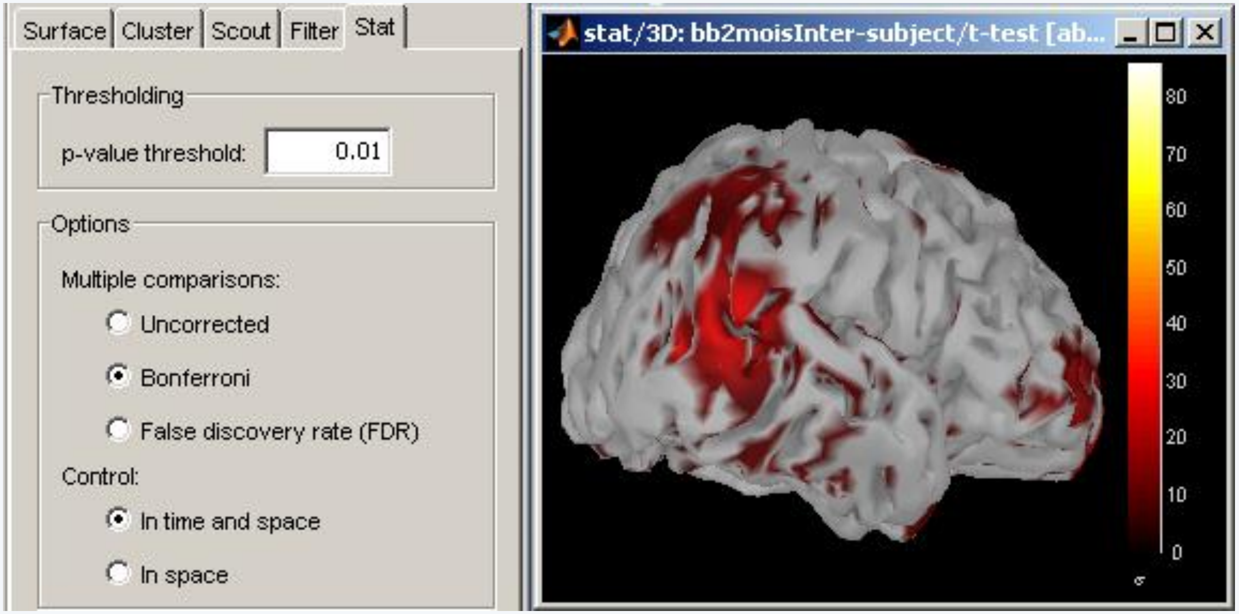
Standard anatomy

Group analysis

Statistics

- Contrasts between subjects or conditions
- Statistical analysis: z-score, t-test
- Quick extraction of measures from complex paradigms

=> Export to: R, Excel, Statistica, SPSS, Matlab…



Thresholding

p-value threshold: 0.01

Options

Multiple comparisons:

○ Uncorrected

● Bonferroni

○ False discovery rate (FDR)

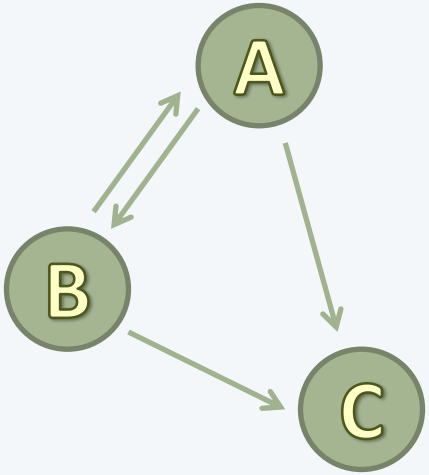
Control:

● In time and space

○ In space

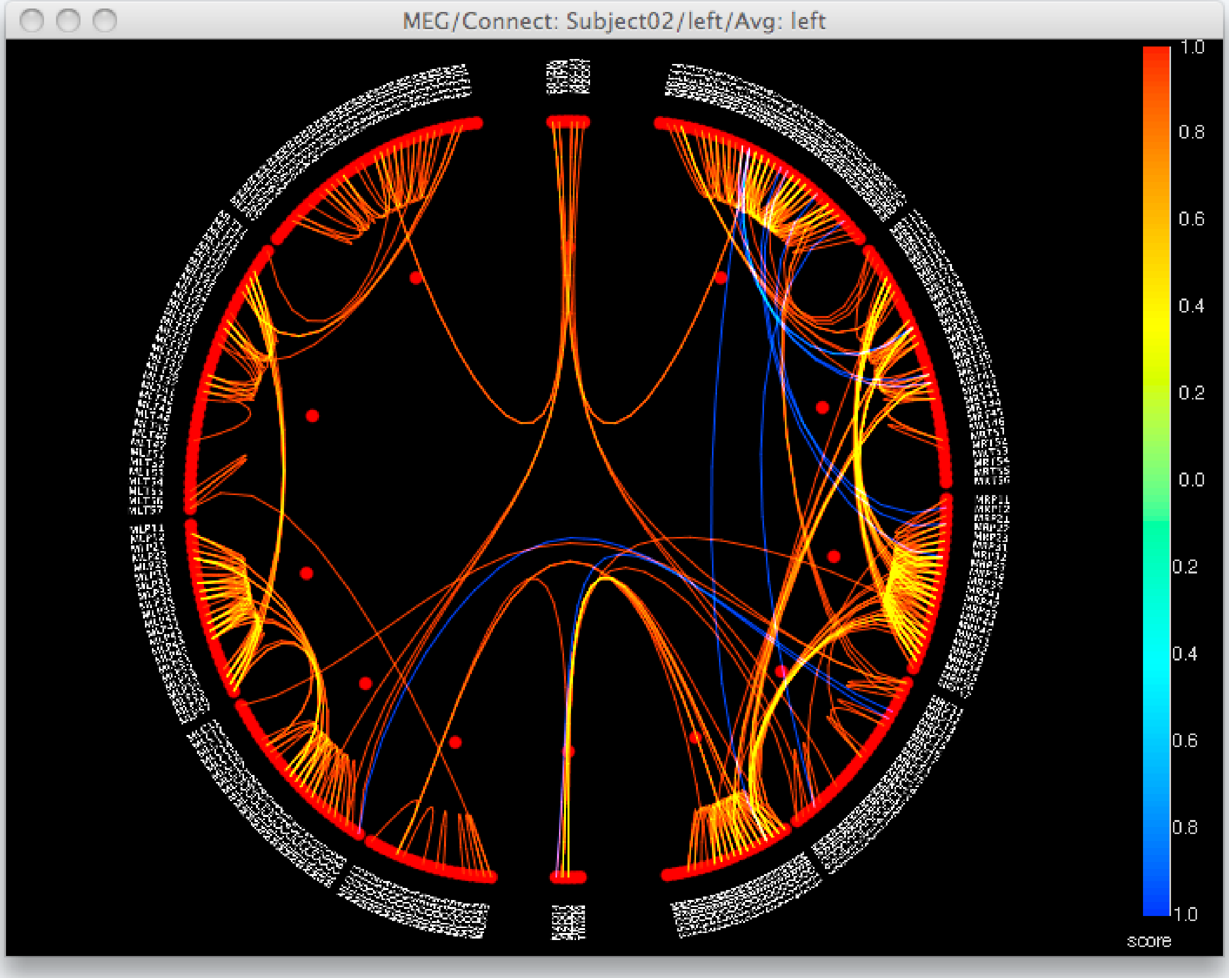
Functional connectivity

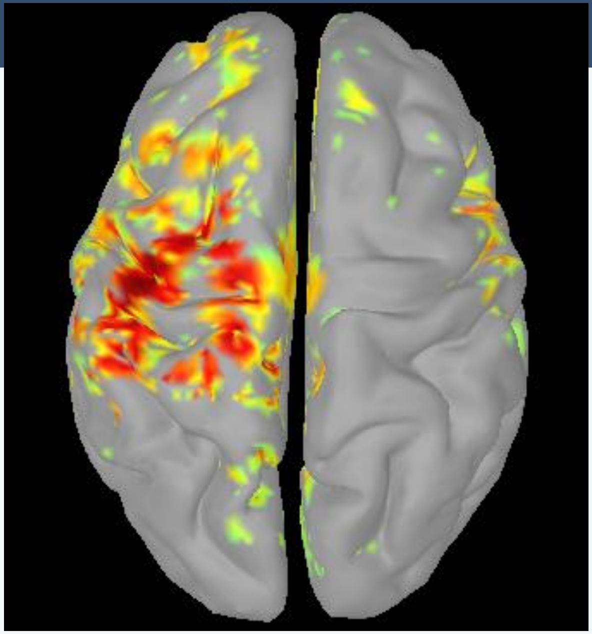
- Objectives: Describe the interaction between two brain regions, identify the brain networks
- Measures:
  - Correlation
  - Coherence
  - Granger causality
  - Phase locking value

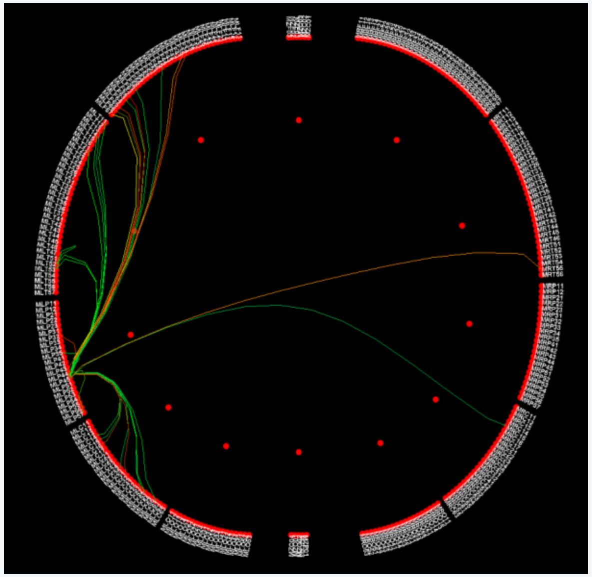


- Both at sensor and source levels

Functional connectivity

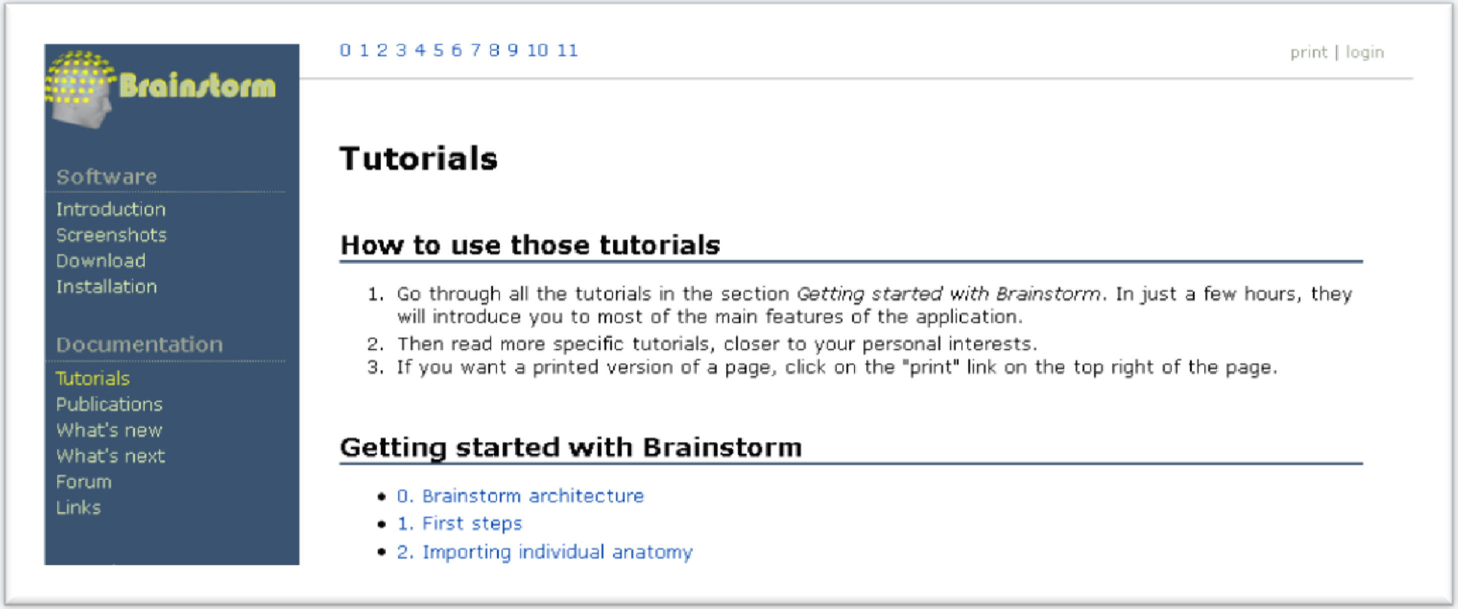

MEG/Connect: Subject02/left/Avg: left





Support

- Brainstorm online tutorials and forum:



Tutorials

How to use those tutorials

1. Go through all the tutorials in the section *Getting started with Brainstorm*. In just a few hours, they will introduce you to most of the main features of the application.
2. Then read more specific tutorials, closer to your personal interests.
3. If you want a printed version of a page, click on the "print" link on the top right of the page.

Getting started with Brainstorm

- 0. Brainstorm architecture
- 1. First steps
- 2. Importing individual anatomy

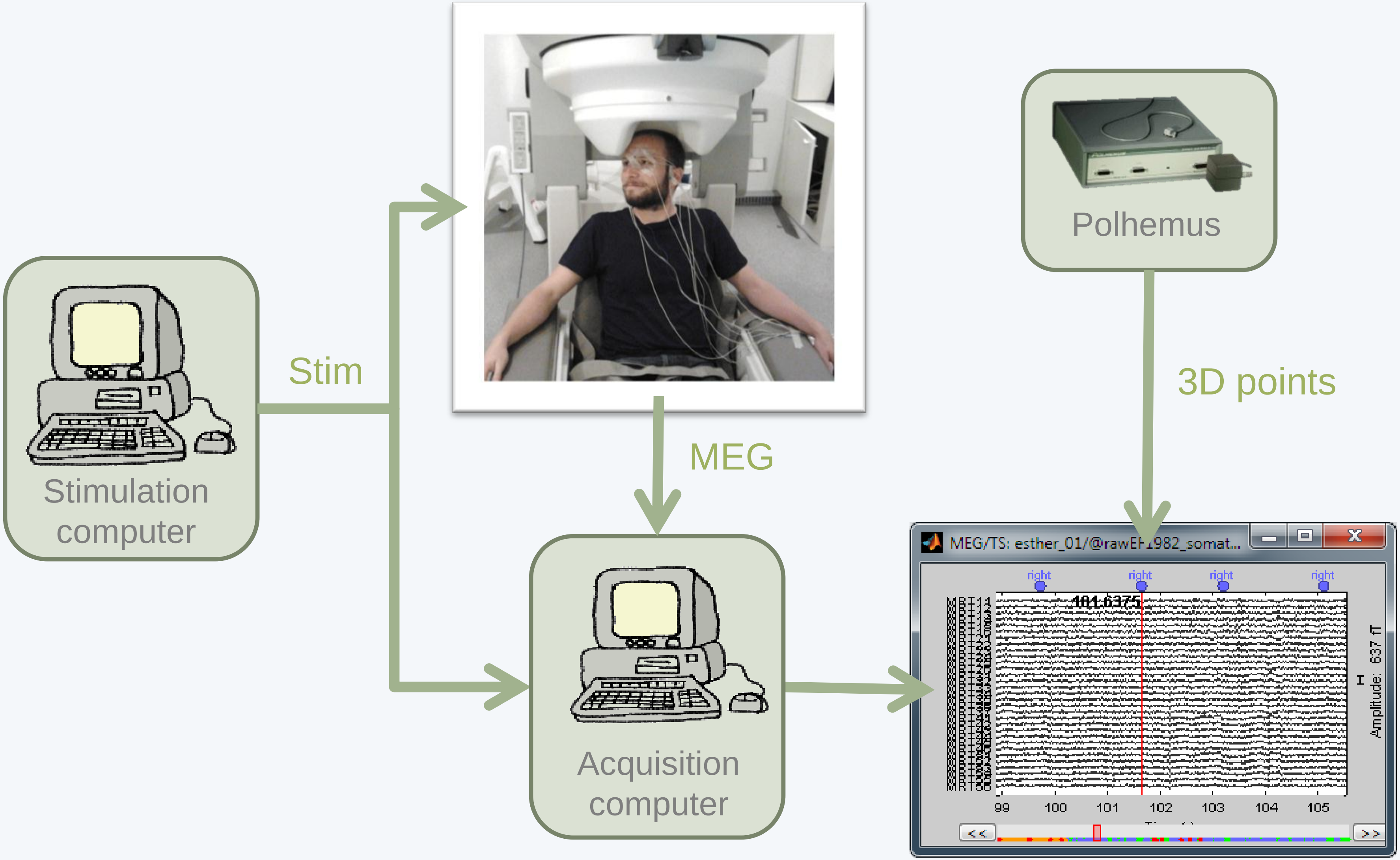
- Contact us for specific questions and requests:
  We will help you adding the features you need

Protocol

- Median nerve stimulation
  (Nov 2011, Montreal Neurological Institute, McGill)
  - Random electric stimulation of both arms
  - ~ 100 trials per arm
  - Acquisition at 1200 Hz
  - Recorded on CTF 275 MEG sensors
    + 26 reference sensors
    + EOG + ECG + STIM + … = 302 channels
  - 6 minutes of recordings, 500 Mb

Sample data

Acquisition setup



Stimulation computer

Stim

MEG

Acquisition computer

Polhemus

3D points

MEG/TS: esther_01/@rawEF1982_somat...

Sample data

To-do list

- Create a protocol, with one subject
- Anatomy
  - MRI and surfaces are already imported
  - 2D / 3D display
- Recordings:
  - Review the continuous file
  - Mark cardiac peaks + eye blinks
  - Remove the ocular artifact (SSP)

Sample data

- Recordings:
  - Import trials: [-100, +300] ms around each stimulus
  - Average the trials (left and right)
  - Explore the average at the sensor level
- Source estimation:
  - Head model
  - Noise covariance matrix
  - Sources time series
  - Review visually the results for left stim
  - Create a couple of regions of interest (scouts)

To-do list

- Advanced analysis:
  - Frequency analysis (Fourier and Hilbert transforms)
  - Registration on default anatomy
  - Anatomical atlases
  - Student’s t-test
  - Warping the default anatomy using head shape
  - Connectivity measures (correlation and Granger causality)

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