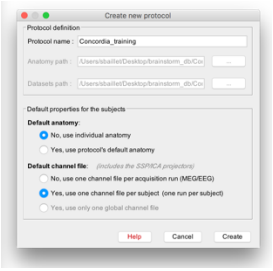
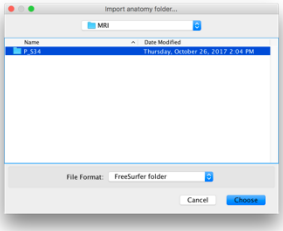
Brainstorm training Concordia University 2018

Welcome (Sylvain Baillet)
From EEG to MEG: the MEG core resources at McGill (Beth Bock)
Lecture: Introduction to Brainstorm (Martin Cousineau)

Data courtesy of the Grova lab (Concordia University)
256-channel EEG
T1-weighted MRI
Left visual grating paradigm (event codes for grating changes: DN2 and DN4)
See detailed description at the end of present document.

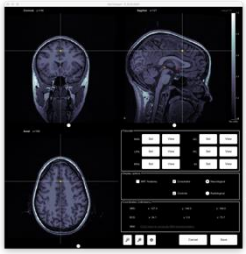


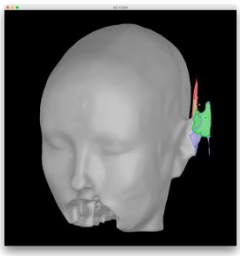
Create a new protocol (protocol = study in Brainstorm jargon)
Pick a name (e.g., Concordia_training)
Anatomy: use individual anatomy
Channel file: use one channel file per subject



Create a new subject
Participant ID: e.g., "P_S34"

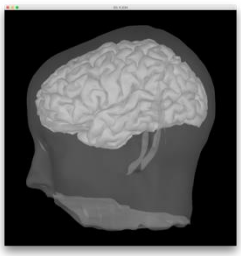
Import anatomy folder
Use Subject view of BST database explorer
Selected from the raw data folder: MRI > P_S34
15,000 vertices
Set the fiducials
In MRI coordinates
NAS: 126 205 95
LPA: 59 111 96
RPA: 196 112 95
AC: 126 132 127
PC: 127 105 130
IH: 127 146 169
Save
Yes to: apply Freesurfer > Brainstorm transform

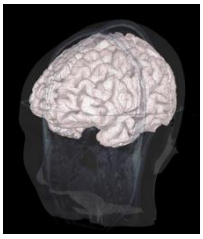
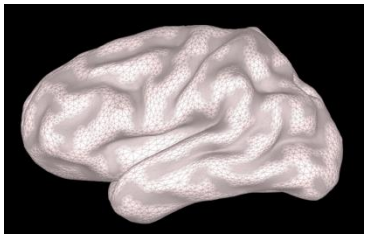




Clean scalp surface (left ear) using the scout functions

Have fun with various ways to visualize MRI / head and brain surfaces



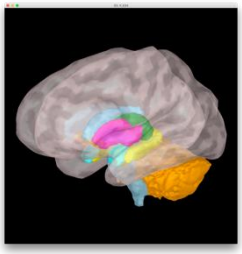



Anatomy view (1st button, on top of the database explorer)

MRI viewer:

The volume (click, mouse wheel, sliders)

Colormaps, colorbar, figure popup menu



Display cortex:

3D figure: rotation, zoom

Predefined views and keyboard shortcuts: Left, right, top, etc.

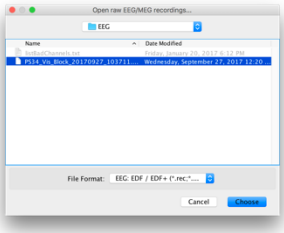
Surface tab: smooth, sulci, edges => <u>smooth 60%</u>

Scouts tab: atlases and scouts

Subcortical atlas ("aseg atlas")

<u>Very useful</u>, any time when using Brainstorm:

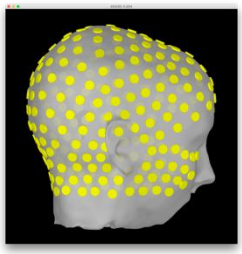
Close all: Big cross on the top-right, close all the figures and empty the memory



Review EEG

Go to functional data viewer (2nd button, on top of the database explorer)

Choose EDF format



Add and view EEG channel locations, consistency with MRI registration

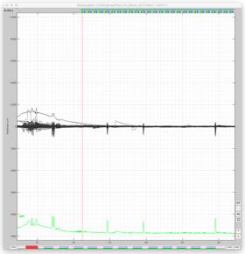
Right-click on channel file

Add EEG positions > Select from file (.pos format)

Do not apply transformation

Display sensors > EEG (Head)

Refine registration with MRI: Project electrodes on head surface



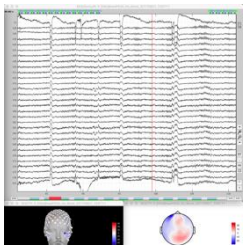
Review raw EEG sensor data:

Average reference

Convert events to "simple events": use Start option

Sensor topography, many display options…

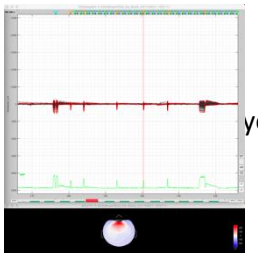
Amplitude gain: Buttons and shortcuts, auto-scaling (button AS)



Options for desktop layout
Tiled, **weighted**, etc.

Detect eye blinks

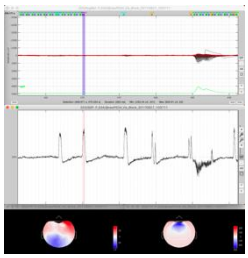
Artifacts > Detect eye blinks
Channel: 21, -25
Event name: e.g., blink



Attenuate blink artifacts

ye Blink with event "blink"
Visualize effect of SSP correction
Visualize SSP topography and time series

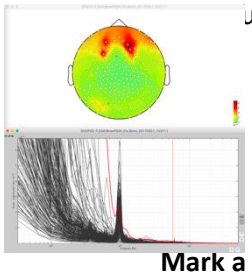
Mark bad segments



Display duration: 10s
Mark bad segments at beginning and end of file

Compute power spectrum density (PSD)

Features the data bucket and process library



uency > Power Spectrum density (Welch)
Use default settings, unless your laptop is slow: limit duration of data for PSD analysis to 90 s (available in process GUI)
Remove a few bad channels (essentially frontal electrodes, as revealed by low-frequency ranges)

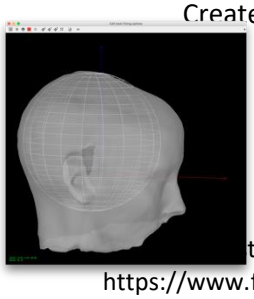
Mark a few more eye blinks and use SSP

Channels 19, -240

Finalize marking of shorter bad segment within presentation blocks

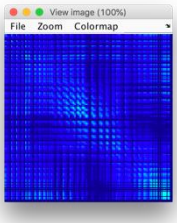
vents DN2 and DN4

-100, +250ms
Use SSP projectors
Remove DC offset (baseline) : -100, 0 ms
Create separate folder for each event type



Head model, Noise & Data covariance and Source models

Head model (at subject root): Cortex surface, 3-shell sphere adjusted to EEG electrodes.

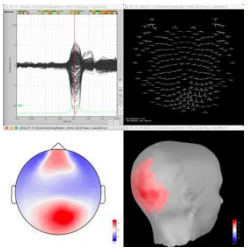


Use DN2 and DN4 single trials to compute noise and data covariances (use process in Source library)

Produce difference source models ([Compute Sources 2018]): Dipole, Beamformer (LCMV), dSPM, etc. with source orientation constrained/unconstrained to cortical surface.

We will use: dSPM with unconstrained orientation in subsequent steps. We'll explore the source maps of the event-related averages (see next step)

Let's build our first pipeline!



Average trials by experimental condition + filter

Process1: Drag and drop all the trials

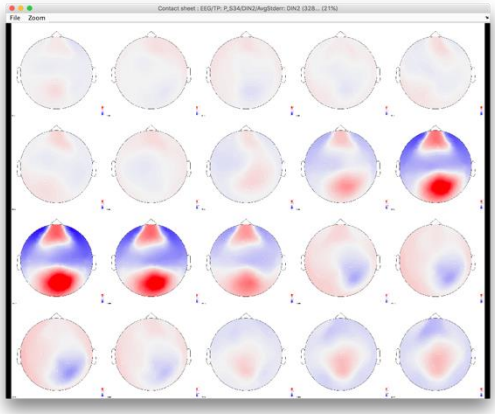
Run > Select the process "Average > Average files"

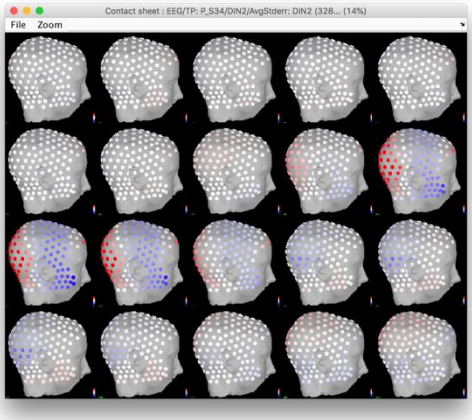
By trial group (folder average), arithmetic average + Standard error

Keep all the event markers from the individual epochs

Add process: Pre-process > Band-pass filter, Lower=0, Upper=80Hz

View filter response, Online tutorial button



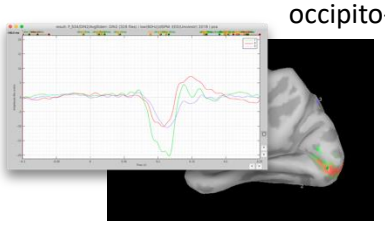


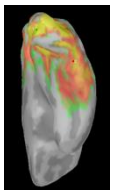
Define Brainstorm scouts (Regions of interest)

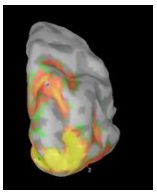
For dSPM source map of DN2 event-related average, low-passed below 80Hz

Set colormap to Custom, with max at about half of global max (e.g., 12)

Select 3 scouts sampling activations at various latencies (e.g., 1=calcarine, 2=ventral occipito-temporal, 3=dorsal parietal)







Visualize scout times series (3 per scout)

PCA of unconstrainted dSPM source map (Process: unconstrained to flat map)

Visualize scout times series of flat map (one per scout)

Visualize single-trial responses from Scout#1 (all or sub-selection of DN2 trials)

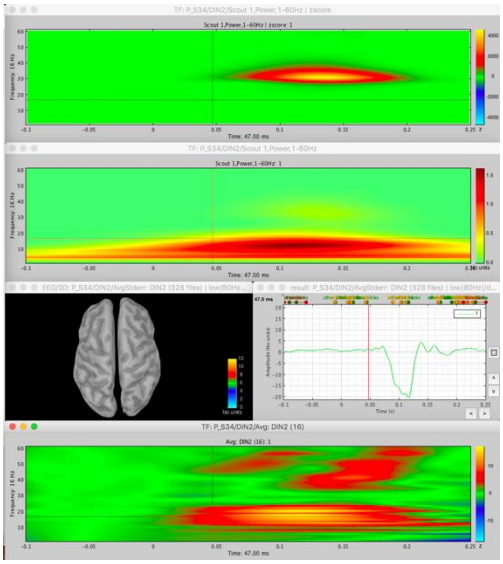
Use process (dSPM source results only)

Time-frequency decompositions

For one or several of the defined scouts

Of event-related average vs. average of time-frequency decompositions of single trial data.

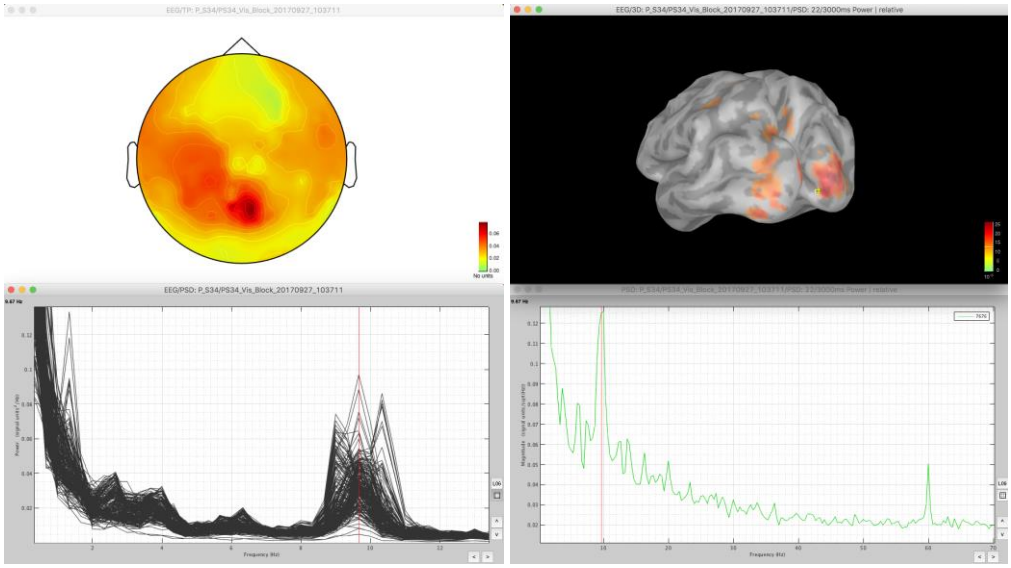
z-score normalization with respect to pre-stim baseline



Compute power spectrum and resample at 300Hz

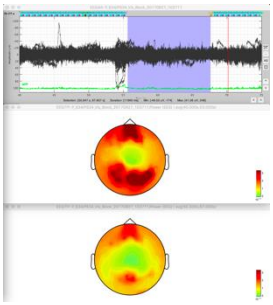
Extract 35s of raw data: 40 to 75 s

Sensors: Process 1: Raw recording > Run > Frequency > Power spectrum density (Welch), 3 sec, 50% overlap
Add process: Standardize > Spectrum normalization > Relative power
Review results.



Sources: Process 1: drop Raw recording [Process sources] > Run > Frequency > Power spectrum density (Welch), 30 secs, 3 s window, 50% overlap, no scouts, default freqs
Add process: Standardize > Spectrum normalization > Relative power
Source power-spectrum – right-click on source

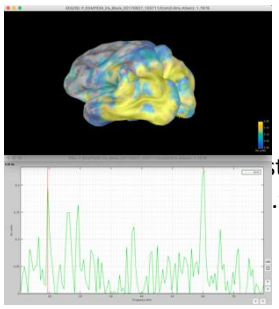
Compute Hilbert transform on 40-53s (stim ON) vs 55-67s (stim OFF)



On sensors, for one or multiple frequency bands (e.g., alpha)
Average across time
Compare the outcome on the two time segments.

Coherence [1xN]: between scout point (s.g. Scout 1) and all other brain sources

In Process1: Raw recording, Click on [Process sources]
Run > Connectivity > *Coherence* [1xN]
MagSquare, MaxRes=1Hz, HighestFreq=30Hz, Save individual
Right-click > Power spectrum
Compute again using *Imaginary coherence*



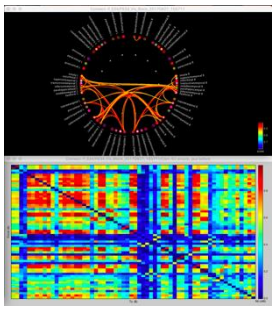
Amplitude Envelope Correlation [1xN]

Run > Connectivity > *Amplitude Envelope Correlation* 1xN

Freq: alpha / 8, 12 / mean

Orthogonalize, Save average

Can be quite greedy, computationally, specify short time window depending on your laptop's performances (CTRL C to interrupt computation in MATLAB's command window)



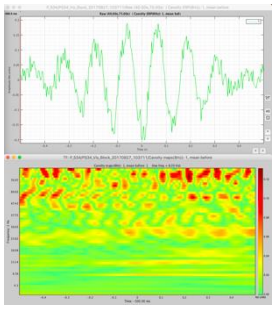
Correlation [NxN] with Mind Boggle atlas

Process 1: DN2 trials or the raw data segment extracted before

Run > Connectivity > *Correlation* [NxN]

Time=All, Select Mind Boggle atlas, Use all scouts

Right-click > Display as graph



Phase-amplitude coupling

From Scout 1

Select fP=8Hz

Extract Canolty maps

Time permitting: scripting, advanced 3D visualization, scout definition in MRI, etc.

Description of tutorial data (Grova lab)

The participant was presented a radial checkerboard in the left-hand side of the screen in 13 blocks of ~25s, with a phase reversal (inversion of colors) of the stimulus every 300ms or 500ms. Between the blocks, the participant had a period of rest of 11-16s. The stimulus presentation and its phase reversal are timed with events 'DIN2' and 'DIN4' respectively.

256-channel EEG, with individual T1-weighted MRI