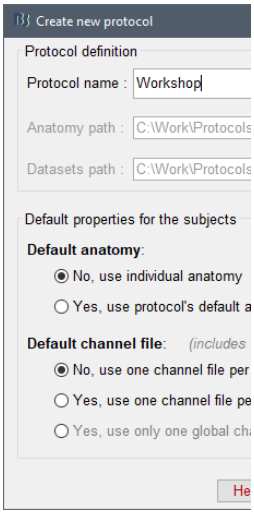
Brainstorm workshop Johns Hopkins - 2019

8:30-9:00 Onsite assistance in installing the material for the training session

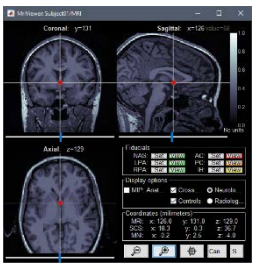
9:00-10:00 Lecture: Introduction to Brainstorm (Martin Cousineau)

10:00-10:45 Import the anatomy 45min

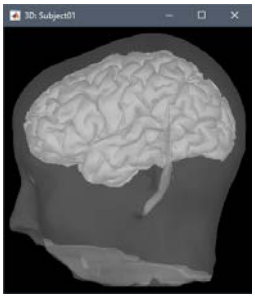


- **CLOSE ALL YOUR APPLICATIONS, INCLUDING WEB BROWSERS**
- Start Brainstorm: from Matlab or stand-alone

- Create new protocol "Workshop"
  - **No**, use individual anatomy
  - **No**, use one channel file per acquisition run (MEG/EEG)
- Introduction to database explorer (list of protocols, exploration modes…)
- Switch to anatomy view (1st button above the database explorer)
- Right-click on protocol top node > New subject: Subject01



- Right-click on Subject01 > **Import anatomy folder**
  - File format: FreeSurfer
  - Select folder: workshop_talca/**anatomy**
  - Number of vertices: **10000** (lower value to make it faster for the training)
  - Introduction to the MRI viewer:
    - Exploring the volume (click, mouse wheel, sliders)
    - Colormaps, colorbar, figure popup menu
  - **Compute MNI transformation (sets all the fiducials automatically)**
    - You need an internet connection to download the SPM atlas
  - Explain the coordinates (MRI, SCS, MNI)

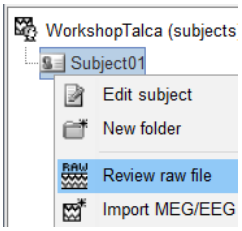


- Display the head and brain surfaces
  - 3D figure: rotation, zoom
  - Predefined views and keyboard shortcuts: Left, right, top, etc.
  - Surface tab: smooth, sulci, edges => **smooth 60%**
  - Scouts tab: atlases and scouts [DEMO ONLY]
  - Subcortical atlas ("ASEG") [DEMO ONLY]

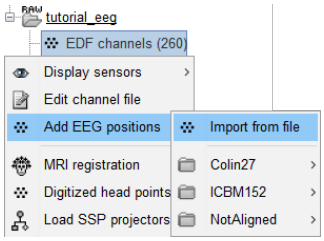
- **Close all**: Cross at the top-right corner to close all the figures and empty the memory

[10:45-11:00] COFFEE BREAK

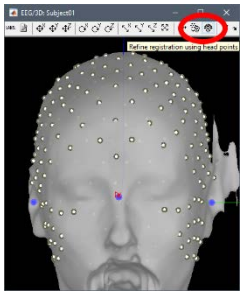
11:00-11:20 Link the recordings 20 min



- Switch to functional view (2nd button above the database explorer)
- Create link to continuous file
  - Right-click on Subject01 > Review raw file
  - Select the file format: "**EEG: EDF / EDF+**"
  - Select the file: workshop_talca/eeg/**tutorial_eeg.edf**
- Load the electrodes positions



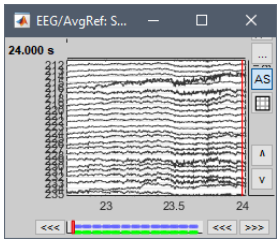
  - Right-click on channel file > Edit channel file: Positions are missing
    This interface allows to change the name, type, comment and order
  - Right-click on channel file > **Add EEG positions** > Import from file
    Select the file format: "**EEG: Polhemus**"
    Select the file: workshop_talca/eeg /**electrode_positions.pos**
    Apply MRI transformation? **NO**
  - Right-click on channel file > Edit channel file > See what changed
  - Double-click on the channel file > Alignment is good but could be better



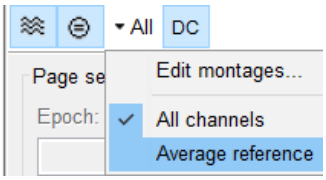
- Adjust the positions of the electrodes
  - Right-click on the channel file > MRI registration > Edit
  - Button: Refine registration using head points
  - Button: Project electrodes on scalp surface
  - Move electrodes 75 and 191 to the scalp (they were projected on the ears)
  - Button: OK to save modifications

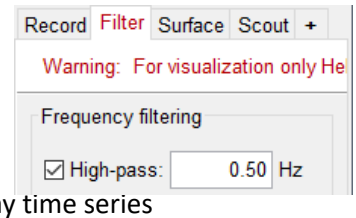
11:20-11:40 Review the recordings 20 min

- Review EEG: Right-click on "Link to raw file" > EEG > Display time series

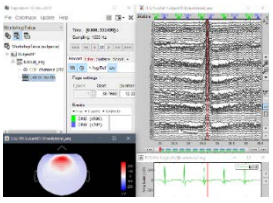


  Time exploration => Display windows of **10 seconds**
  Display in columns: Button [~] in the Record tab
  Amplitude gain: Buttons and shortcuts
  Scroll + Disable auto-scale button [AS]
  Montages: Set to "Average reference"
  Create and edit personal montages + Shortcuts
  Events: List, figure and time bar



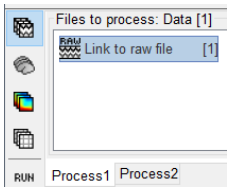


- Online filter: High-pass: **0.5Hz**
- Add other views

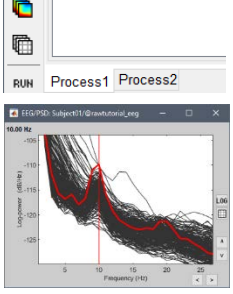


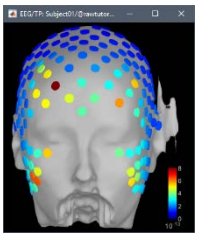
  Add view of **ECG**: Right-click on Link > ECG > Display time series
  Add **topography**: Right-click on Link > EEG > 2D Sensor Cap (or CTRL+T)
  Layout menu: Alternate between Tiled and Weighted (keep **Weighted**)

11:40-12:00 Frequency filters **20 min**



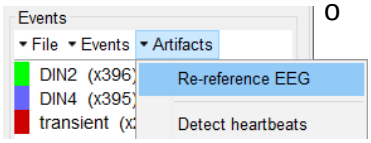
- Drag and drop the "Link to raw file" in Process1
  - Explain the Process1 tab
  - Explain the Filter box
- Run process: "Frequency > Power spectrum density": **[50, 150]s**, win=**2s**, **EEG**
  - Open the PSD file (double-click)
  - Open another view: 3D electrodes
  - Open another view: 2D Sensor cap
  - Display electrodes on the 2D view (right-click on figure > Channels, or Ctrl+E)
  - Explain the noise sources / identify possible bad channels:
  - <3Hz: eyes, 10Hz: alpha, 60/120/180Hz: power lines, 50-80Hz: neck
  - Show the brain in transparency to see what is not recording brain activity



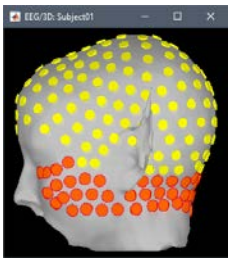


- Run process: "Pre-process > Band-pass filter"
  - Lower cutoff: **0.5 Hz** (High-pass filter)
  - Upper cutoff: **0 Hz** (No low-pass filter)
  - Try button "View filter response"

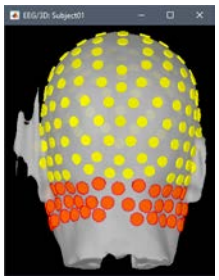
12:00-12:25 Bad channels **25 min**



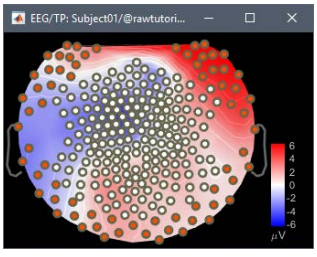
- Re-reference the recordings (the montage is not applied to the file yet)
  - Open the filtered file "Raw | high"
  - Visualization filters: **Disable the high-pass filter** (not necessary any more)
  - Menu: Artifacts > Re-reference EEG: **AVERAGE** + Save + Close
  - Visualization montage: Change the montage back to "ALL"



- Mark as bad: all the electrodes from the face and 3 bottom rows
  - Open 3D Electrodes: Select electrodes with left click
  - Open 2D Sensor cap: Display electrodes (CTRL+E), Select with right-click + drag
  - Press the Delete key to mark the selected electrodes as bad



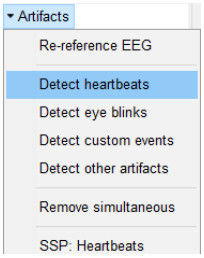
- Alternate solution: Load the list of bad channels from a file
  - Open the file workshop_talca/eeg/**bad_channels.txt** from your file manager
  - Copy the content of the file (CTRL+C)
  - Back in Brainstorm: Close all figures
  - Right-click on "Raw | high" > Good/bad channels > Mark some channels as bad
  - Paste the list (CTRL+V), click OK



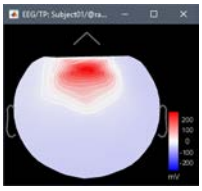
- Display the list of bad channels
  - Montage: In the record tab, select montage "Bad channels"
  - Channel editor: Right-click on the figure > Channels > Edit good/bad channels
  - Database: Right-click on file > Good/bad channels > View all bad channels
  - Interpolation: Possible with "Standardize > Interpolate bad electrodes"

[12:30-13:30] LUNCH

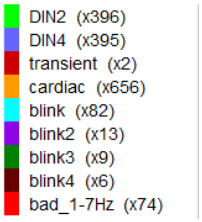
13:30-14:15 Artifacts 45 min



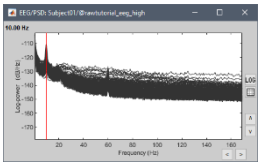
- Detect heartbeats
  - Open EEG for filtered file "Raw | high" (double-click)
  - Add view of **ECG**: Right-click on Link > ECG > Display time series
  - Observe the cardiac artifact (eg. around 55-60s)
  - Menu Artifacts > Detect heartbeats > Channel name: **ECG**



- Detect and compensate for eye blinks
  - Menu Artifacts > Detect eye blinks > Channel name: **25**
  - Menu Artifacts > SSP: Eye blinks
  - Select first 10 components + Display the 2D topography and time series
  - Select component #1: Clearly a blink



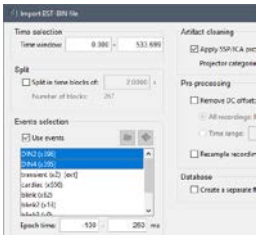
- Artifacts > Detect other artifacts: **1-7Hz**, Sensitivity **5**
  - Review segments with artifacts (with all sensors)
  - Mark the event group 1-7Hz as bad: "**bad_1-7Hz**"
  - Additional bad segments can be marked (select + "Reject time segment")
  - Close all + Save modifications



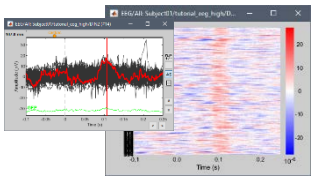
- Compute PSD of the "clean" recordings
  - Process: "Frequency > Power spectrum density": **[50, 150]s**, win=**2s**, **EEG**
  - Open the PSD file (double-click) + Compare it with the previous PSD
  - We could apply a notch filter, but skip it for time consideration

- **Delete** the original non-filtered file (folder "tutorial_eeg"): we won't use it anymore

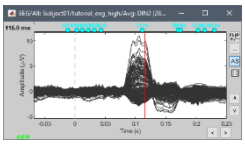
14:15-14:45 Import recordings and average 30 min



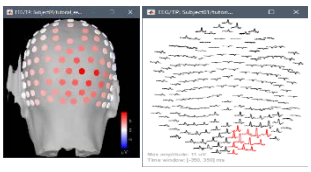
- Right-click on filtered file "Raw | high" > Import in database
  - **Use events**: **DIN2 + DIN4**, Epoch time: **[-100, +250] ms**, Use SSP/ICA
  - **NO** Remove DC offset
  - **NO** Create separate folder for each event type

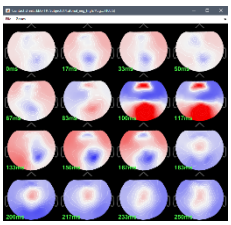


- Review trials:
  - Open the first trial: Switch back to butterfly view (first button in Record tab)
  - Open a 2D topography (CTRL+T) - Enable auto-scale (button [AS])
  - Navigate between trials with F3 / Shift+F3: Users should review all the trials
  - Trials or channels can be marked as bad independently
  - Raster plots: Right-click on group of trials > Display as image > EEG (chan #119)

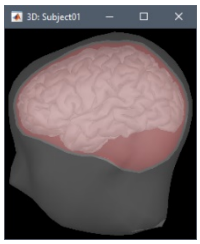


- Average trials
  - Drag and drop **all the DIN2 and DIN4** epochs to Process1
  - Run process "Average > Average files"
  - By trial group (folder average), Arithmetic average, Keep all events
- Review average
  - Open averages DIN2+DIN4 + 2D topography view
  - Review movie of the activity (hold right/left keys)
  - Illustrate 2DLayout / 3D Electrodes
  - Contact sheet topography: **0ms, 250ms, 16 images**





14:45-15:00: START THE FORWARD MODEL COMPUTATION BEFORE THE COFFEE BREAK

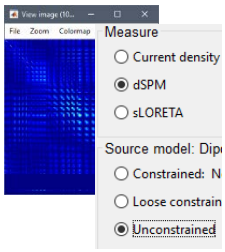


- You will need an internet connection for this step (download of OpenMEEG)
- Do not try if you have a Windows 32bit system (use the "3-shell sphere" model)
- Generate BEM surfaces (from the anatomy view):
  - Right-click on Subject01 > Generate BEM surfaces > **642** / **482** / **482** / **4mm**
- Compute BEM forward model
  - Go back to functional view: Right-click on channel file > Compute head model
  - Leave default options: Cortex surface, OpenMEEG BEM model
- Keep an eye on it during the break, so we can fix it if there is any problem
  - If it crashes: Restart Matlab and try again without "Use adaptive integration"
  - If it crashes again: Use the forward model "3-shell sphere" instead

[15:00-15:30] COFFEE BREAK

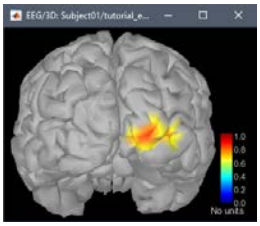
15:30-16:00 Lecture: Source modeling (Sylvain Baillet)

16:00-16:15 Source calculation 15 min

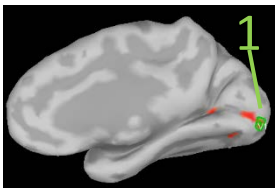


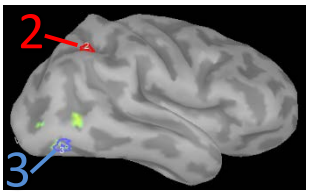
- Noise covariance matrix (from pre-stimulation baselines of all epochs):
  - Select all DIN2+DIN4 trials > Noise covariance > Compute from recordings
- Inverse model:
  - Right-click on head model "OpenMEEG BEM" > Compute sources [2018]
  - Select **Minimum norm, dSPM, <u>Unconstrained</u>**
- Explain inversion kernel / links in database

16:15-16:35 Source display 20 min

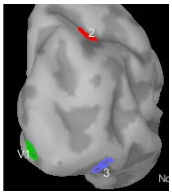


- Average DIN2: Display EEG + 2D topo + dSPM sources
- Add online filter: Low-pass filter at **80Hz**
- Make sure that the atlas selected is "User scouts" (in the Scout tab)
- Explain amplitude threshold at largest peak: t=**105ms**
- Move to beginning: t=**0ms**, Amplitude threshold=**10%**
- Review movie of activity





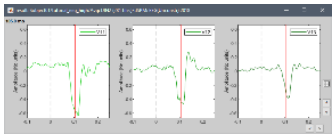
16:35-16:55 Scouts (ROIs) 20 min



- Display sources, t=**105ms**, amplitude threshold=**80%** (Surface tab)
- Get a close and accessible view: Smooth cortex, zoom, rotate, double-click
- Create scout **V1**

  Scout tab: [Select point] (big cross in the toolbar), then point on the brain

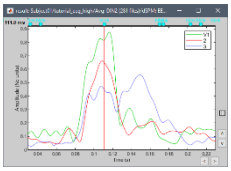
  Grow to **20 vertices**



  Rename to **V1** (double-click on the scout in the list)

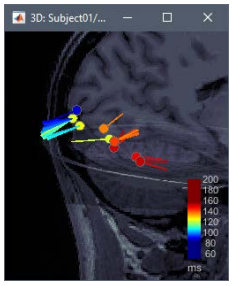
  Review trace: **Absolute values** (norm of the three orthogonal dipoles)

  Relative values (each orientation separately)
- Create other scouts to explore the other sources



  - Decrease the threshold **50%** (Surface tab)
  - Go to **105ms**: Create scout **2** (superior parietal) => Grow to **20v**
  - Go to **150ms**: Create scout **3** (inferior occipital sulcus) => Grow to **20v**
  - Review all the traces, **Absolute values** | **Overlay: Scouts**

[DEMO ONLY] Dipole scanning 10 min



- Scan for best dipoles

  Right-click on average recordings > Compute sources > **Dipole modeling**

  Select the dipole file in Process1

  Run > Sources > Dipole scanning > **[50, 170]ms / Do NOT limit**
- Double-click the dipole file to display it

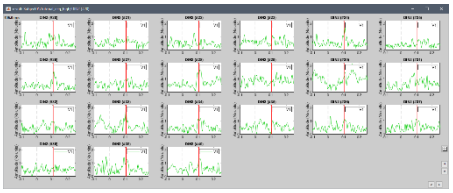
  Display the EEG at the same time

  Explain the Dipoles tab: Sliders, Show all time, Color=Time

  Represent propagation along the ventral stream with Goodness>30%

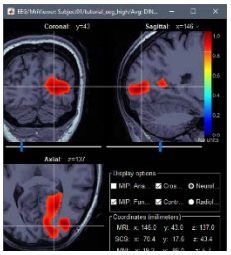
  Scroll in time to show moving dipole (after diabling "Show all time")
- Additional option: FieldTrip dipole fitting function (ft_dipolefitting called from BST)

[DEMO ONLY] Single trial responses in V1 5 min



- Display average sources, select scout **V1** in Scout tab
- Select trials **DIN2 #20-40** in the database explorer
- Right-click on any of the files > Scouts times series

[DEMO ONLY] Sources in MRI 5 min



- Right-click on average sources > Cortical activations > Display on MRI (**MRI Viewer**)

  MIP: Anatomy/Functional (glass brain)
- Right-click on average sources > Cortical activations > Display on MRI (**3D**)

  Introduce the 3D MRI views: move the slices with the mouse, Resect tab

  Locate scout using button in Scout tab in MRI Viewer + 3D figure

DAY 2

9:00-9:30 Lecture: Time-frequency (Sylvain Baillet)

9:30-10:15 Time-frequency decompositions 45min

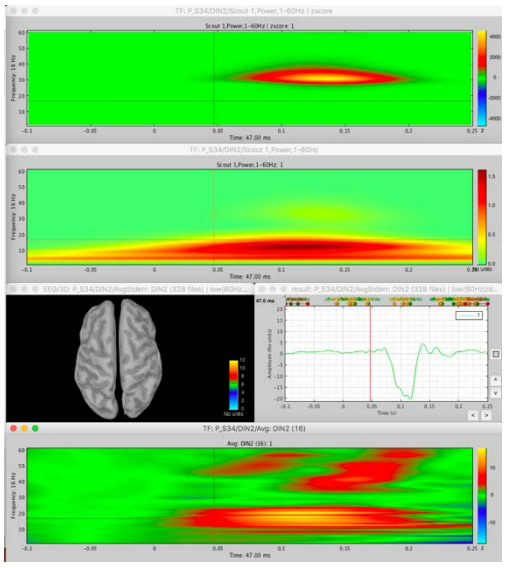
For one of the defined scouts, we will compare the event-related average vs. average of time-frequency decompositions of single trial data.

Event-Related Average

- Drag and drop "Avg: DIN2" in Process1
- [Process sources] -> Run -> Frequency -> Time-frequency (Morlet wavelets)
  Select the V1 scout
  Spectral flattening: **None**
  Explain Morlet wavelet options (leave default)
- Add process: Standardize -> Baseline normalization
  Select "Z-score transformation"

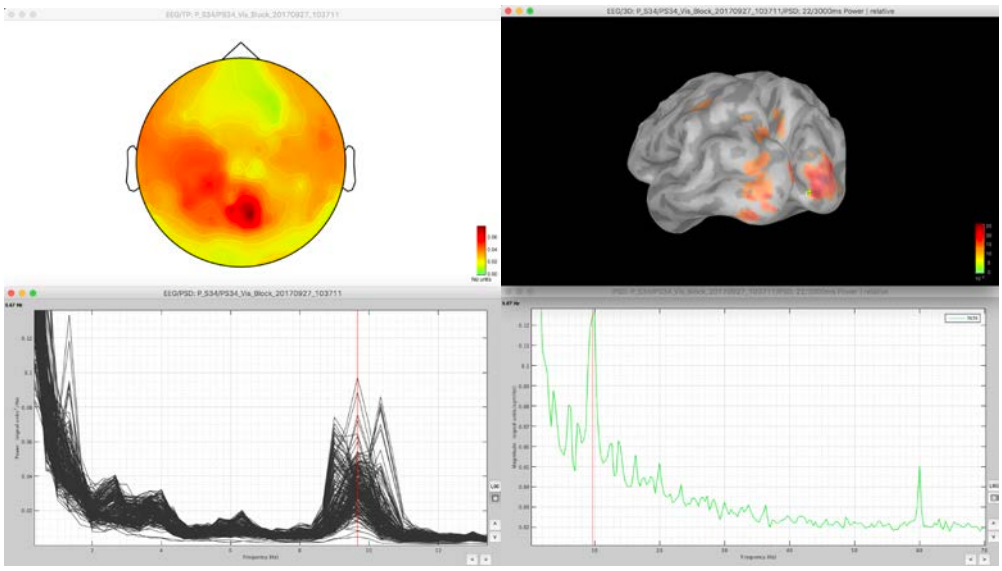
Average of single trial TF decompositions

- Drag and drop all DIN2 trials in the Process1
- [Process sources] -> Run -> Frequency -> Time-frequency (Morlet wavelets)
  Select the V1 scout
  Spectral flattening: **None**
- Edit wavelet options: **Save average time-frequency maps (across trials)**
- Add process: Standardize -> Baseline normalization
  Select "Z-score transformation"
- Compare time-frequency decompositions



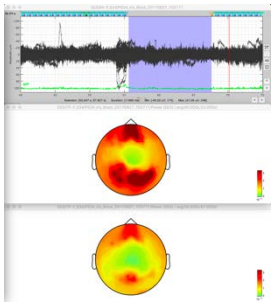
Sensor-level power spectrum

- Right click on “Raw | high” -> Import in database
  Time window: 40 to 75 s
  Uncheck “Use events” and “Remove DC offsets”, but keep projectors
  Resample recordings: 300 Hz
- Right click on new file “Raw (40.00,75.00s)” -> Accept trial
- Drag and drop new file “Raw (40.00,75.00s)” in Process1
- [Process recordings] -> Run -> Frequency -> Power spectrum density (Welch)
  Window length: 3 sec, Overlap: 50%
- Add process: Standardize > Spectrum normalization
  Select Relative power
- Open normalized PSD file (“PSD: Power (EEG) | relative”)
- Right click on figure -> 2D sensor cap to review



Source-level power spectrum

- Drag and drop file “Raw (40.00,75.00s)” in Process1
- [Process sources] -> Run -> Frequency -> Power spectrum density (Welch)
  Window length: 3 sec, Overlap: 50%, No scouts
- Add process: Standardize > Spectrum normalization
  Select Relative power
- Open normalized PSD file (“PSD: Power (EEG) | relative”)
- Right click on vertex of interest in figure -> Source: Power
- Review and compare results.



Hilbert transform

- Drag and drop file "Raw (40.00,75.00s)" in Process1
- [Process recordings] -> Run -> Frequency -> Hilbert transform
  Spectral flattening: **None**
- Edit options: Keep only **alpha** in frequency bands (alpha / 8, 12 / mean)

Stim ON vs Stim OFF

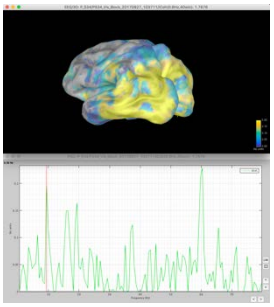
- Drag and drop Hilbert transform "Power (EEG)" in Process1
- Run -> Average -> Average time, 2 times
  - First run: 40 to 53s (stim ON)
  - Second run: 55 to 67s (stim OFF)
- Right click on both output files ("Power (EEG) | avg") -> 2D sensor cap
- Compare the outcome on the two time segments (make sure colormap is the same).

10:15-10:45 Lecture: Connectivity (Sylvain Baillet)

[10:45-11:00] COFFEE BREAK

11:00-12:00 Connectivity 45min

Note: This section can be quite slow on a laptop. It is recommended to specify shorter time windows depending on your laptop's performance. (You can press CTRL+C to interrupt computation in MATLAB's command window and try again with a shorter window) It is fine not to reproduce the results yourself, simply follow the presenter.

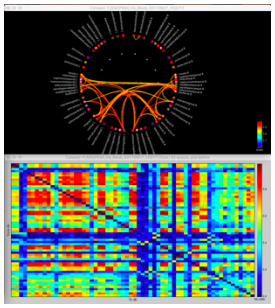


Coherence [1xN]

- Drag and drop "Raw (40.00s,75.00s)" in Process1
- [Process sources] -> Run -> Connectivity -> Coherence [1xN]
  Scout: V1, Measure: Magnitude-squared
  Maximum frequency: 1Hz, Highest frequency: 30Hz
  Save individual results
- Double click on "Coh(0.6Hz,40win)" to view output
- Right click on vertex of interest in figure -> Source: Power spectrum
- Compute again with Measure: imaginary

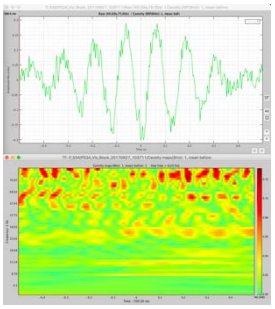
Amplitude Envelope Correlation [1xN]

- Drag and drop "Raw (40.00s,75.00s)" in Process1
- [Process sources] -> Run -> Connectivity -> Amplitude Envelope Correlation [1xN]
  Scout: V1, Frequency: keep only **alpha** (alpha / 8, 12 / mean)
  Orthogonalize signal pairs
- Double click on "AEC: V1" to view output



Correlation [NxN] with Mind Boggle atlas

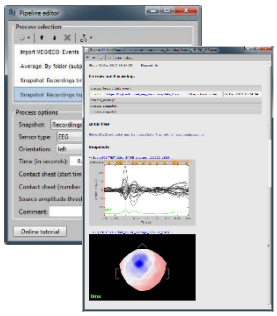
- Drag and drop "Raw (40.00s,75.00s)" in Process1
- [Process sources] -> Run -> Connectivity -> Correlation [NxN]
  Select the Mind Boggle atlas, use all scouts
- Right click on "Corr: 62 scouts" -> Display as image
- Right click on "Corr: 62 scouts" -> Display as graph



Phase-amplitude coupling

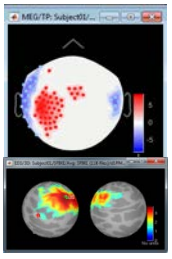
- Drag and drop "Raw (40.00s,75.00s)" in Process1
- [Process sources] -> Run -> Frequency -> Canolty Maps
  Use scout: V1, Nesting frequency: 8Hz
  Save averaged low frequency signals
- Double click on "Canolty maps(8Hz)"
- Double click on "Raw (40.00s,75.00s) | Canolty ERP(8Hz)"

[DEMO ONLY] Batching and scripting **15min**



- Create analysis pipeline: (TutorialIntroduction)
  - Import recordings > MEG/EEG:Events: Event=**deviant** [-100,500]ms
  - Average > Average file
  - File > Save snapshot : Recordings time series, **MEG**
  - File > Save snapshot : Recordings topography, **MEG / 0s**
- Save / Load script in user preferences + Generate Matlab (.m) script
- Report viewer + Snapshots
- Various ways to run personal code on files in the Brainstorm database:
  - Plugins: Flexible, exchange between users, external contributions
  - Process: "Pre-process > Run Matlab command"
  - Direct interaction with files: File>Export/Import, or load/save .mat
  - Online tutorials with many detailed examples

Additional topics can be discussed, based on participants' requests and time available.



- Statistics: Illustrate with a different protocol (TutorialIntroduction)
  - Select deviant (A) and standard trials (B). Test –> Parametric test: Independent
  - View output (+ topo). Stat tab: Correction for multiple comparison / p-threshold
  - Non-parametric statistics available with FieldTrip functions
- Project sources on default anatomy
- Template warping: Generation of pseudo-individual anatomy using Polhemus headpoints
- Mixed source models: Integration of deep brain structures in the inverse model computation

[12:30-13:30] LUNCH

Participants can have a short lunch and start working on their own without waiting for the group.

Data courtesy of the Grova lab (Concordia University)

Left visual grating paradigm:
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 - EGI HydroCel net
Individual T1-weighted MRI, processed with FreeSurfer