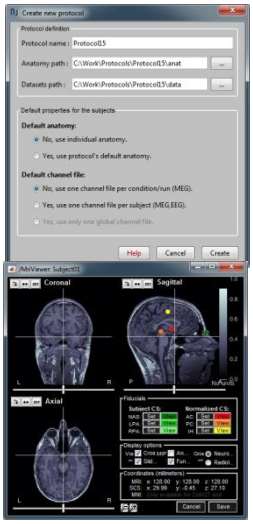
# Brainstorm workshop — Montreal, April 2018

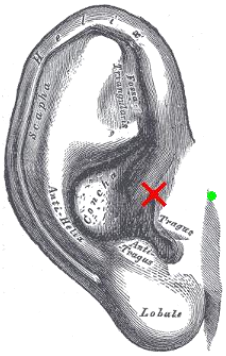
- **9:00-9:30** Onsite assistance in installing the material for the training session
- **9:30-9:45** Lecture: Overview of the MEG program at the MNI (Elizabeth Bock)
- **9:45-10:45** Lecture: Introduction to Brainstorm (Martin Cousineau)

**[10:45-11:00] COFFEE BREAK**

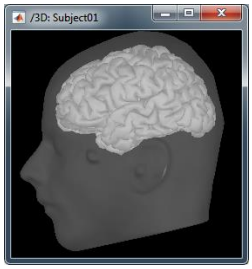
- **11:00-11:30** Import anatomy: **30min**



- **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)
- Introduction to database explorer (list of protocols, exploration modes…)
- Switch to anatomy view (1st button, on top of the database explorer)
- Right-click on protocol top node > New subject: Subject01
- Right-click on Subject01 > Import anatomy folder > File format: FreeSurfer
  - Select folder: **sample_introduction/anatomy**
  - Number of vertices: **15000** (default value)
  - Introduction to the MRI viewer:
    - Exploring the volume (click, mouse wheel, sliders)
    - Colormaps, colorbar, figure popup menu
  - **Compute MNI transformation** **(defines AC/PC/IH automatically)**
    > You need an **internet connection** for this step (to download of SPM atlas)
  - Select the fiducial points for the registration with MEG (NAS, LPA, RPA):
    NAS [127, 213, 139] LPA [52, 113, 96] RPA [202, 113, 91] +/- 5mm
  - Explain the coordinates (MRI, SCS, MNI)

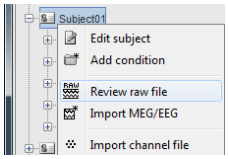


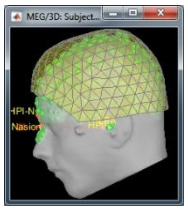

- **Crash**: If the import of the anatomy crashes before creating the head surface (win32)
  - We will have to copy manually an imported version on your computer
- Display cortex:
  - 3D figure: rotation, zoom
  - Predefined views and keyboard shortcuts: Left, right, top, etc.
  - Surface tab: smooth, sulci, edges => **smooth 60%**
  - Scouts tab: **atlases and scouts** **[DEMO ONLY]**
  - **Subcortical atlas** **[DEMO ONLY]**

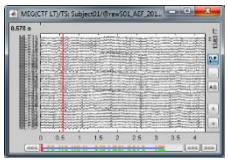



- **Close all**: Big cross on the top-right, close all the figures and empty the memory

- **11:30-12:00** Review RAW recordings: **30 min**



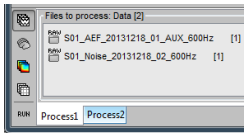



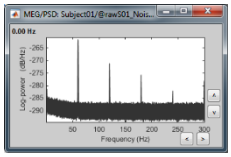


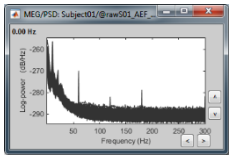
- Switch to functional view (2nd button, on top of the database explorer)
- Create link to RAW file
  - Right-click on Subject01 > Review raw file > File format: **MEG/EEG CTF**
    Select **all** the folders in: sample_introduction/**data/*.ds**
  - Yes, refine registration
- Convert all the files to "**continuous**" display mode:
  - Right-click on Link to raw file > Switch epoched/continuous
- Channel file: MEG CTF Coils
  - Right-click on channel file > Display sensors > CTF coils (all)
- Review MEG: Right-click on "Link to raw file" > MEG > Display time series
  - Display in columns + channel selection => Shift+D (Left Temporal)
  - Time => display windows of **5s**
  - Events: List, figure and time bar
  - Amplitude gain: Buttons and shortcuts
  - Disable auto-scaling (button AS)

**[12:00-13:00] LUNCH**

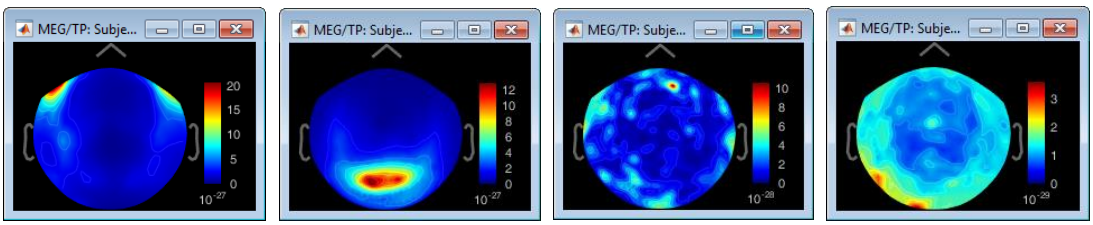
- **13:00-13:10** Line noise: **10 min**



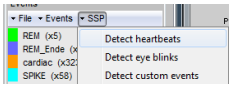


- Drag and drop all the datasets in Process1
  - Explain the Process1 tab
  - Filter box (just mention, do not test)
- Run > Frequency > Power spectrum density: **[0, 100]s**, win=**2s**, **MEG**, **no average**
  - Open the two PSD files
  - Display topography for subject's recordings (right-click or CTRL+T)
  - Close the noise PSD file
  - Explain the noise sources:
    3Hz: eyes, 10Hz: alpha, 60/120/180Hz: power lines, 50-80Hz: neck muscles
- We should do:
  - Run a notch filter to remove the line noise (60 120 180 Hz)
  - Run a high-pass filter and/or a low-pass filter
  - Write down the name of the noisy sensors for further evaluation

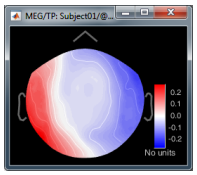


- **13:10-13:40** Artifacts: **30min**

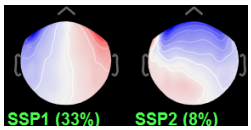

  - Open MEG sensors, **CTF LT** (double-click)
    - Add view of **EOG**: Right-click on Link > EOG > Display time series
    - Add view of **ECG**: Right-click on Link > EOG > Display time series
  - Set page duration to **3s**
  - Layout menu: Alternate between Tiled and Weighted (keep **Weighted**)
  - Scrolling for blinks: **20.8s** (In this window, observe cardiac and ocular artifacts)



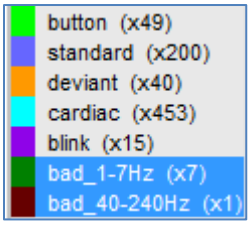

  - Artifacts > Detect heartbeats > ECG
  - Artifacts > Detect eye blinks > VEOG
  - Artifacts > Remove simultaneous > cardiac / blink / 250ms




  - Artifacts > SSP: Heartbeats
    - Display 2D topography for the first spatial component
    - Select component #1: It is clearly a cardiac component
    - Show the influence of the projector on the sensors LT

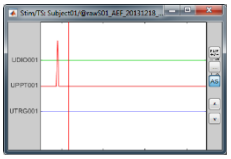


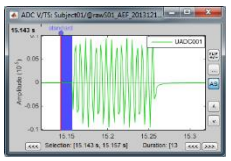

  - Artifacts > SSP: Eye blinks **DO NOT USE EXISTING SSP**
    - Display the 2D topography for the first spatial components
    - Select component #1: Clearly a blink
    - Component #2 could be used to remove saccades
    - Show the influence of the projector on the sensors LT




  - ICA decompositions can be done in a similar way, but very slow with 275 channels
  - Artifacts > Detect other artifacts: Default options
    - Review segments with artifacts (with all sensors)
    - Events -> Mark the two groups as bad: "**bad_1-7Hz**" and "**bad_40-240Hz**"
    - Additional bad segments can be marked (select + "Reject time segment")
  - Close all, save modifications

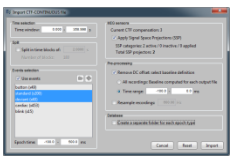
- **[OPTIONAL]** Correction of stimulation delays



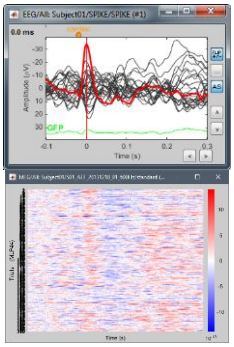




  - Describe the marker problems: repeated markers and equipment delays
  - Show delay between audio (ADC V) and triggers (Stim) - Time window **0.3s**
    - Open **Stim**, then open **ADC V**
    - Go to any standard event, observe the delay
    - Delays: 12-15ms (jittered) + 5ms (fixed)
  - We could do:
    - Read the triggers from the stim channel ("Read events from channel")
    - Generate accurate markers using the audio signal ("Detect analog triggers")
    - We recommend doing this for all audio and visual stim (micro / photodiode)

- **13:40-13:55** Import recordings: **15 min**

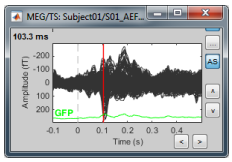


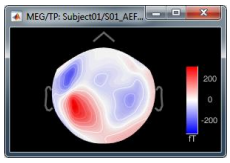
  - Right-click on "Link to raw file" > Import in database
    - **Use events**: standard/deviant, Epoch time: **[-100, +500] ms**, **Use SSP**
    - **Remove DC offset**, Time range = **[-100, 0]ms**
    - **Do not create separate folders**

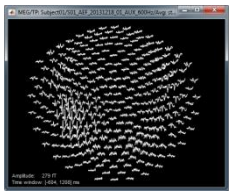


- Review trials:
  - Show bad trials (marked with a red sign in the database explorer)
  - Open the first trial: Switch back to butterfly view (first button in Record tab)
  - Display all the channels again (Drop-down menu in the Record tab)
  - Navigate between trials with F3 / Shift+F3: Users should review all the trials
  - Trials or channels can be marked as bad independently
- Display trial images per sensor: **[OPTIONAL]**
  - Right-click on standard **trial group** > Display as image > MEG (MLP44)

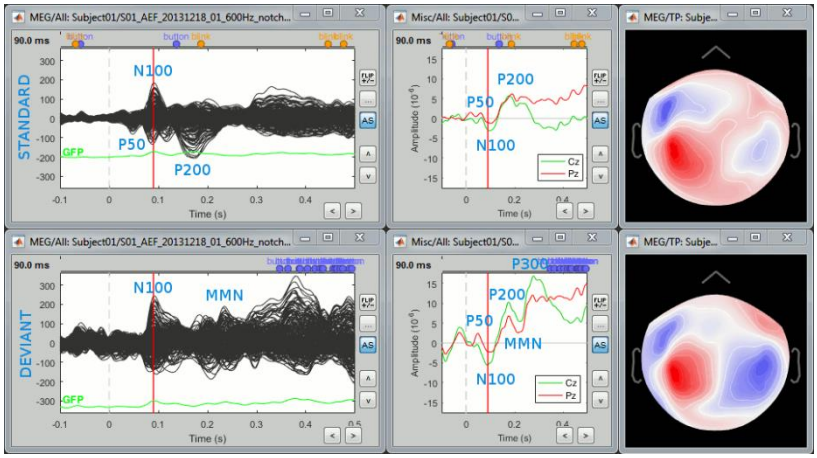
- **13:55-14:15** <u>Average trials</u>: **20 min**
  - Average trials by experimental condition:
    - Process1: Drag and drop all the trials (total files: 232 files)
    - Run > Select the process "Average > Average files"
    - By trial group (folder average), Arithmetic average, **Keep events**





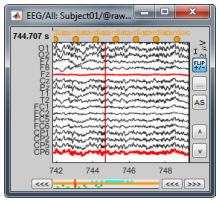


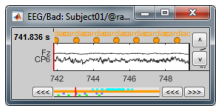
  - Review average **<u>STANDARD</u>**
    - Delete cardiac events
    - Open MEG + topography view
    - Open **EEG** (channels **MISC**) + Button "Flip sign"
    - Online filter: Add a **low-pass at 40Hz**
    - Components of the evoked response: P50, N100, P200
      - P50: 65ms, bilateral auditory response (in both conditions).
      - N100: 110ms, bilateral auditory response (in both conditions).
      - P200: 180ms, in both conditions but much stronger in standard.
  - Review average **DEVIANT**: MEG + MEG topo + EEG
    - Delete cardiac event
    - Panel Record: Button "**EQUAL amplitudes**"
    - Different waves: MMN, P300 + motor response
      - MMN: 250ms, detection of an abnormality.
      - P300: 300ms, decision making in preparation of the button press.
  - **Close all**

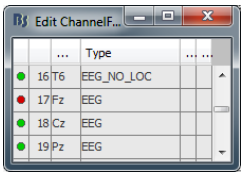


- **[OPTIONAL]** Compare conditions:
  - Stat: t-test on the sensors, deviant vs. standard
    - Process2: Select ALL the deviants trial (A) + ALL the standards trials (B)
    - Run > Test > Parametric test: Independent
      > All file, All channels, **T-test equal variance**, Two-tailed
    - Open MEG signals + 2D topography
    - Correction: p<0.05, FDR, Signals + Time
  - Non-parametric tests are available, but requires FieldTrip to be installed
  - Close all

- **[OPTIONAL]** Bad channels:

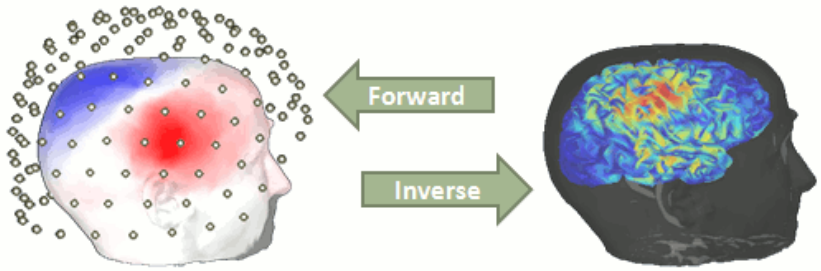




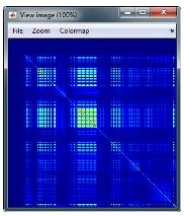



  - Pick any trial: Open MEG recordings + 2D Topo (CTRL+T) + Sensors (CTRL+A)
  - Marking some bad channels for the example:
    - Select a few channels in any figure by clicking on them (highlighted in red)
    - Right-click + select bloc of sensors from the 2D topography
    - Right-click > Channels > Mark selected as bad (or Delete key)
  - To 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 files > Good/bad channels > View all bad channels
    - Interpolation: Possible with "Standardize > Interpolate bad electrodes", but only once the recordings are imported in the database.
  - Mark all channels as good: Right-click on the file > Good/bad channels > …

- **[OPTIONAL]** Source modeling theory:
  - See tutorial page and references: http://neuroimage.usc.edu/brainstorm/Tutorials/



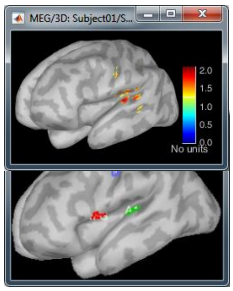

- **14:15-14:30** Source calculation: **15 min**
  - Forward model:
    - Right-click on channel file > **Compute head model**
    - Leave default options: Cortex surface, Overlapping spheres



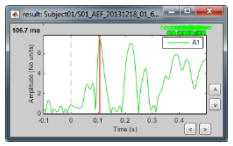
  - Noise covariance matrix (from noise recordings):
    - Right-click on noise Link > Noise covariance > **Compute from recordings**
    - Leave default options: [0, 120]s, block by block
      - Produces a numChannels x numChannels symmetric matrix

- Right-click on noise covariance > Copy to other folders
- Inverse model:
  - Right-click on head model "Overlapping spheres" > **Compute sources [2016]**
  - Select: Minimum norm / dSPM / Constrained
    - Minimum Norm: Most versatile and stable. Based on L2 regularization.
- Explain inversion kernel / links in database

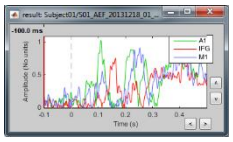
- **14:30-15:00** Source Display and Scouts (ROIs): **30 min**



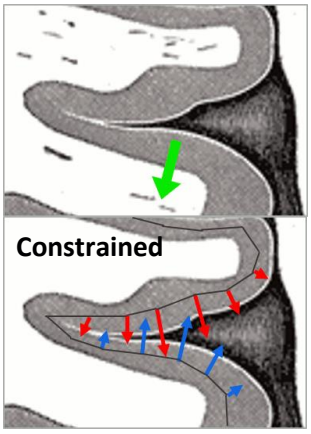

- Display of MEG time series and source of Avg DEVIANT
- Make sure that the atlas selected is "User scouts" (in the Scout tab)
- Display sources for deviant: t=**108ms**, amplitude threshold=**50%**
- Get a close and accessible view: Smooth cortex, zoom, rotate, double-click
- Create scout **A1** (primary auditory cortex):
  - In the scout tab, select point (big cross in the toolbar)
  - Click on point in the brain
  - Grow to ~**20 vertices**
  - Rename to **A1** (double-click on the scout in the list)



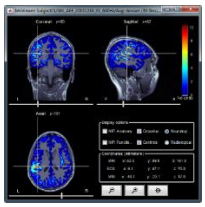

- **Review trace for scout A1**
- Explain the scout function
- Create IFG (inferior frontal gyrus): **155ms**, 40%, ~**20 vertices**
- Create M1 (motor cortex): **455ms**, 65%, ~**20 vertices**




- Review all the signals, **overlay: scouts**
- Review movie of activity (hold the left/right keys)
  - Also show contact sheet / movie (Right click -> Snapshot)
- Explain why constrained sources have signed values.
  - Right click -> Colormap: Sources -> Absolute values
- Compare smoothed surface and original folding (discuss spatial accuracy)
- Close all



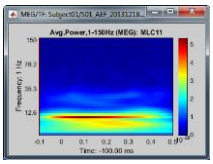

- **[OPTIONAL]** Sources in MRI:



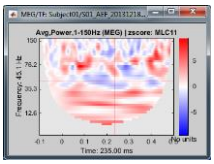
- Open **Deviant** dSPM sources in MRI viewer
  - Right click -> Cortical activations -> Display on MRI (MRI Viewer)
- Right-click on figure > Overlay Options > Smooth (3)
- Maximum intensity projection (MIP): Anatomy/Functional (glass brain)
- Locate scout in MRI viewer using button (Center MRI on scout) in Scout tab

**[15:00-15:30] COFFEE BREAK**

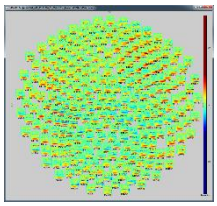
- **15:30-16:00** Time-Frequency analysis: **30 min**
  - **RECORDINGS**: Select all the **deviant** trials [**Process recordings**]



  - Run > Frequency > Time-frequency (Morlet wavelets)
    - Select all sensors, **Log 1:40:150**, Power, **Save average,** NO 1/f compensation
  - Double-click on TF file to display it:
    - Explain the time-frequency plane and frequency cursor
      - Click on the 11 Hz row -> Right click -> Time series
    - Nothing visible because the power in the lower frequencies is too high



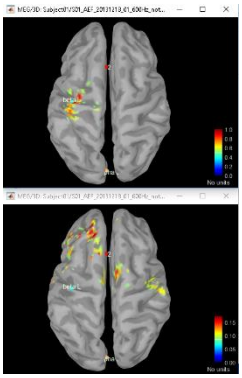
  - Select TF file: Run > Standardize > Baseline normalization > [-100, 0] ms , **Z-score**
  - Double-click on TF file:
    - Set the colormap to "jet". Play with the colormap contrast and brightness
    - Smooth display
    - Hide edge effects : **Cannot estimate below 8 Hz**
      - The epoch is too short: you need longer segments to do a proper TF analysis



  - Right-click on TF|zscore file > **2D Layout (maps)**
    - Click on one image to display the sensor
    - Observe the event-related + button click responses
      - Show figures synchronization (time series + sensor cap + time-freq)
  - Right-click on TF|zscore file > **2D Sensor cap**
    - Scroll in time and scroll in frequency
    - It gets complicated to explore a 3D volume of data [signals x time x freq]

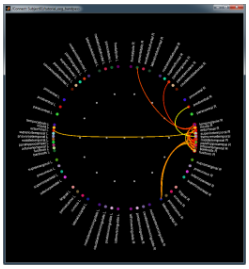
  - **SCOUTS**: Select all the **deviant** trials again
  - Select the [**Process sources**] button
  - Run > Frequency > Time-frequency (Morlet wavelets)
    - Select all the scouts, **Log 1:40:150, After, Save average**
    - **Mean, Do NOT apply 1/f compensation**
  - **Add process**: Run > Standardize > Baseline normalization > [-100, 0] ms , Z-score
    Double-click – display the three scouts

**16:00-16:50** Connectivity: **50 min** (Warning: Takes a long time on slow computers)



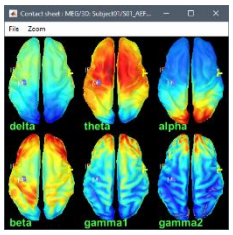
  - Right-click on the continuous file S01_AEF (Link to raw file) > Import in database :
    - Time: **[0, 50] s**, No events, **Remove DC Offset: ALL**, Create=**NO**
  - Coherence [1xN]: M1 motor scout vs all other sources
    - In Process1: Raw (50s), Click on [Process sources]
    - Run > Connectivity > Coherence [1xN]
    - Time window = [0,30s], Use motor (**M1**) scout, Function = **PCA / Before**
    - MagSquare, MaxRes=**1Hz**, HighestFreq=**30Hz**, **Save individual**
    - Display on cortex: (Observe beta band around 20 Hz)
      - Minimum norm contaminates around seed
      - Solution: Imaginary Coherence or Amplitude Envelope Correlation
  - Compute again using Imaginary coherence

- Amplitude Envelope Correlation [1xN]: M1 motor scout vs all other sources
  - In Process1: Raw (50s), Click on [Process sources]
  - Run > Connectivity > Amplitude Envelope Correlation [1xN]
  - Time window = [0,10s], Use motor (**M1**) scout, Function = **PCA / Before**
  - Freq: beta / 19,23 / max, **Orthogonalize**, **Save individual**
  - Run again for auditory scout **A1** (14.5Hz)
    - Freq: beta / 13, 16 / max
    - Observe how A1 is correlated to other parts of motor cortex
- Correlation [NxN] with Mind Boggle atlas



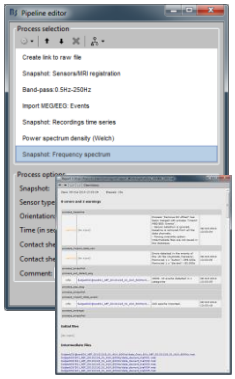
  - Process 1: Raw (50s), Click on [Process sources]
  - Run > Connectivity > Correlation [NxN]
  - Time=All, Select **Mind Boggle** atlas, Use all scouts, **PCA/BEFORE**
  - Click Run.
    - NxN means comparing all 15000 sources with each other
    - Using an atlas allows us to group all these signals in 60 regions
    - PCA extracts the most meaningful signal from regions before correlation
  - Double-click on connectivity matrix > No interesting data…
  - Right-click > Display as graph > Explain the graph
    - Explain display thresholds and buttons

- **16:50-17:00** Power maps Resting-state analysis **10 min**




- Right-click on the continuous file S01_AEF (Link to raw file) > Import in database :
  - Time: **[0, 50] s**, No events, **Remove DC Offset: ALL**, Create=**NO**
- Select file Raw (0.00s,50.00s) , select [Process sources]
- Run > Frequency > Power spectrum density (Welch)
  - Window length: 4s, No scouts, Group in frequency bands
- **Add process**: Standardize > Spectrum normalization > Relative power
- Double-click on normalized PSD to open it (set the amplitude threshold to 0%)
  - Study different frequency bands, e.g. alpha activates in occipital lobe

- **17:00-17:15** Batching and scripting **[DEMO]** **15 min**



- Create a new subject: Subject03 **USE DEFAULT ANATOMY**
- Start a full analysis for the same run
  - Import recordings > Create link to raw file **NO ALIGN WITH HEADPOINTS**
  - Import recordings > Convert to continuous
  - File > Snapshot > Sensors/MRI registration
  - Events > Detect eye blinks [All file]
- Processes: plugins, flexible, exchange between users, external contributions
- Save script in the user preferences
- Generate Matlab script | Run the analysis pipeline | Report viewer