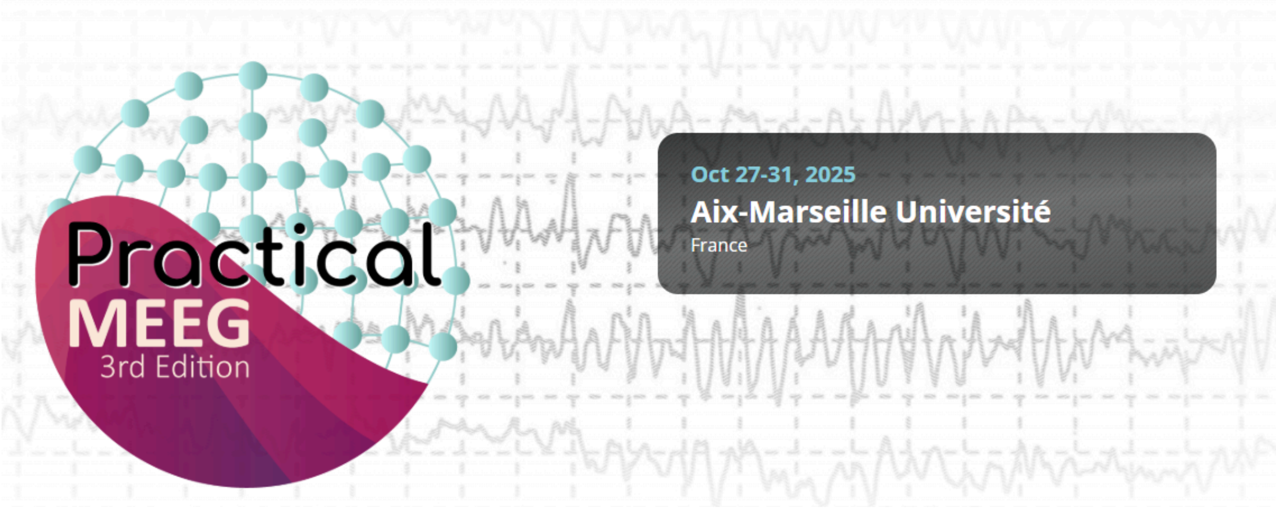

BRAINSTORM TRAINING

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Dear Brainstorm participants,

As the 3rd edition of the Practical MEEG event approaches, we would like to share some important information to help you prepare in advance.

Preparation Before the Workshop:

To ensure a smooth and productive experience, please complete the following tasks before your arrival:

1. Install MATLAB
    - If needed, a free trial version of MATLAB is provided by the PracticalMEEG team for the Hands-On sessions.
    - Please make sure it is fully installed and activated before the workshop.
    - We recommend to add the “Signal Processing Toolbox”
2. Install Brainstorm software:
    - Register on the Brainstorm website: Brainstorm Registration.
    - Download and install the latest version by following the Brainstorm Installation Guide.
    - Please ensure the software is fully installed and thoroughly tested.
2. Download the dataset:
    - Please download the datasets in advance to avoid delays during the sessions:
        - Pruned version of the dataset (~1Go) <download from Zenodo>
        - Brainstorm processed data 16 participants (~20Go) <download from Brainstorm>
3. Prepare your laptop:
    - Ensure both MATLAB and Brainstorm are installed and tested.
    - Have the datasets ready for immediate use.
    - Bring your own computer, charger, mouse, and electrical adaptor if needed.
    - We also highly recommend bringing an external mouse for better usability.

We kindly ask all participants to complete the installations and downloads before the event. If you encounter any issues, please post your questions here so the team can assist you.

A detailed walkthrough will be posted here in the coming days.

We look forward to seeing you soon and hope you enjoy an engaging and hands-on experience at Practical MEEG!
Best,

Takfarinas and Guiomar for the Brainstorm team
==

Updates to be posted on the forum:

📦 PracticalMEEG 2025 — Data Package Updates

We have **pruned and reorganized the data** to include only the essential files required for the workshop.
All necessary datasets are now provided in a **smaller, ready-to-use folder** that includes the **Zenodo data** and complementary materials.
The following material folder contains: (size ~5Go)

- **ds000117_pruned.zip** — Pruned version of the original dataset, including T1 MRI and DWI data.
- **femmat_tensors.mat** — Realistic FEM head model with mesh and conductivity tensors (from DWI).
- **PracticalMEEG_sub-01_3-runs.zip** — Preprocessed data for subject *sub-01* with 3 runs (sensor, forward, source, and TF data).
- **PracticalMEEGGroup_pruned.zip** — Group-level data from 16 subjects (6 runs each), containing intra-subject folders only; MEG source maps for *Face–Scramble* retained.
- **Readme.txt** — Overview and instructions for the PracticalMEEG 2025 workshop materials.

Introduction

The aim of these hands-on sessions is to guide participants through a comprehensive MEG/EEG preprocessing and analysis pipeline using Brainstorm. The workflow will go from raw data preprocessing to source estimation, group-level statistics, and results visualization, following best practices for open and reproducible neuroimaging research. The workflow presented contributes to a community-wide initiative to document and harmonize MEG/EEG analysis pipelines, as featured in the Frontiers Research Topic “From Raw MEG/EEG to Publication: How to Perform MEG/EEG Group Analysis with Free Academic Software,” where the Brainstorm pipeline was featured in Tadel et al. (2019).

The main goal is to introduce Brainstorm to new users. Some of the operations and the analysis presented here are not detailed. For in-depth explanations of the interface and theoretical foundations, please refer to the introduction tutorials.

Dataset

We will use the W&H dataset, which has been recently reformatted according to the Brain Imaging Data Structure (BIDS) standard. BIDS ensures consistent data organization and facilitates interoperability across neuroimaging analysis tools. The dataset comprises simultaneous MEG and EEG recordings from 16 participants performing a simple visual recognition task that involves the presentation of famous, unfamiliar, and scrambled faces.

You can download the data here: [don't download all the data, please read all instructions first]

- **Original** raw data (~180Go) <Zenodo> or <OpenNeuro (ds000117)>
- **Pruned** version of the dataset (~1Go) <download from Zenodo (ds000117_pruned)>
- **Brainstorm processed** data for the 16 participants (~20Go) <download from Brainstorm>
- **PracticalMEEG 2025: Data Package Final(~5Go) <PracticalMEEG2025_FinalMaterials.zip>**

References

This dataset is made available under the Creative Commons Attribution 4.0 International Public License. Please cite the following reference if you use these data:

- *Wakeman DG, Henson RN, A multi-subject, multi-modal human neuroimaging dataset, Scientific Data (2015).*

Please cite the following reference if you use the Brainstorm analysis pipeline:

- *Tadel F, Bock E, Niso G, Mosher JC, Cousineau M, Pantazis D, Leahy RM, Baillet S, MEG/EEG Group Analysis With Brainstorm, Frontiers in Neuroscience (2019)*
- *Tadel F, Baillet S, Mosher JC, Pantazis D, Leahy RM, Brainstorm: A user-friendly application for MEG/EEG Analysis Comput Intell Neurosci (2011)*

Notes

This dataset is formatted according to the BIDS-MEG specifications (Niso et al. 2018); therefore, we can import all relevant information (MRI, FreeSurfer segmentation, MEG+EEG recordings) in just one click, with the menu **File > Load protocol** > **Import BIDS dataset**. Please follow the online tutorial MEG resting state & OMEGA database.

If your data does not follow the BIDS standard, this tutorial provides a step-by-step guide to the manual import process. We also include additional steps required due to **data anonymization** (defaced MRIs and missing acquisition dates). We will work on importing and processing the **first run of subject #01**. The same procedure applies to all other participants and runs.

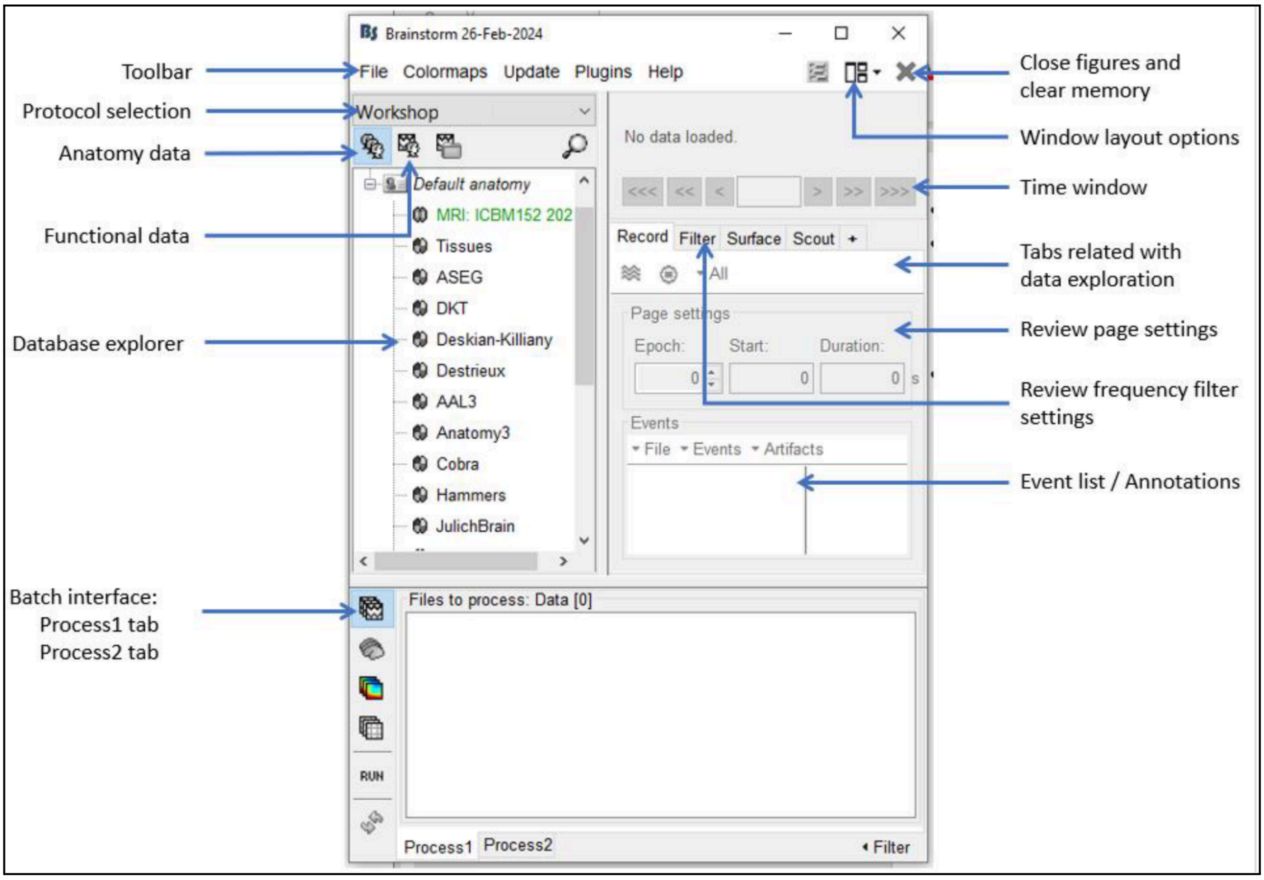
Brainstorm download and installation

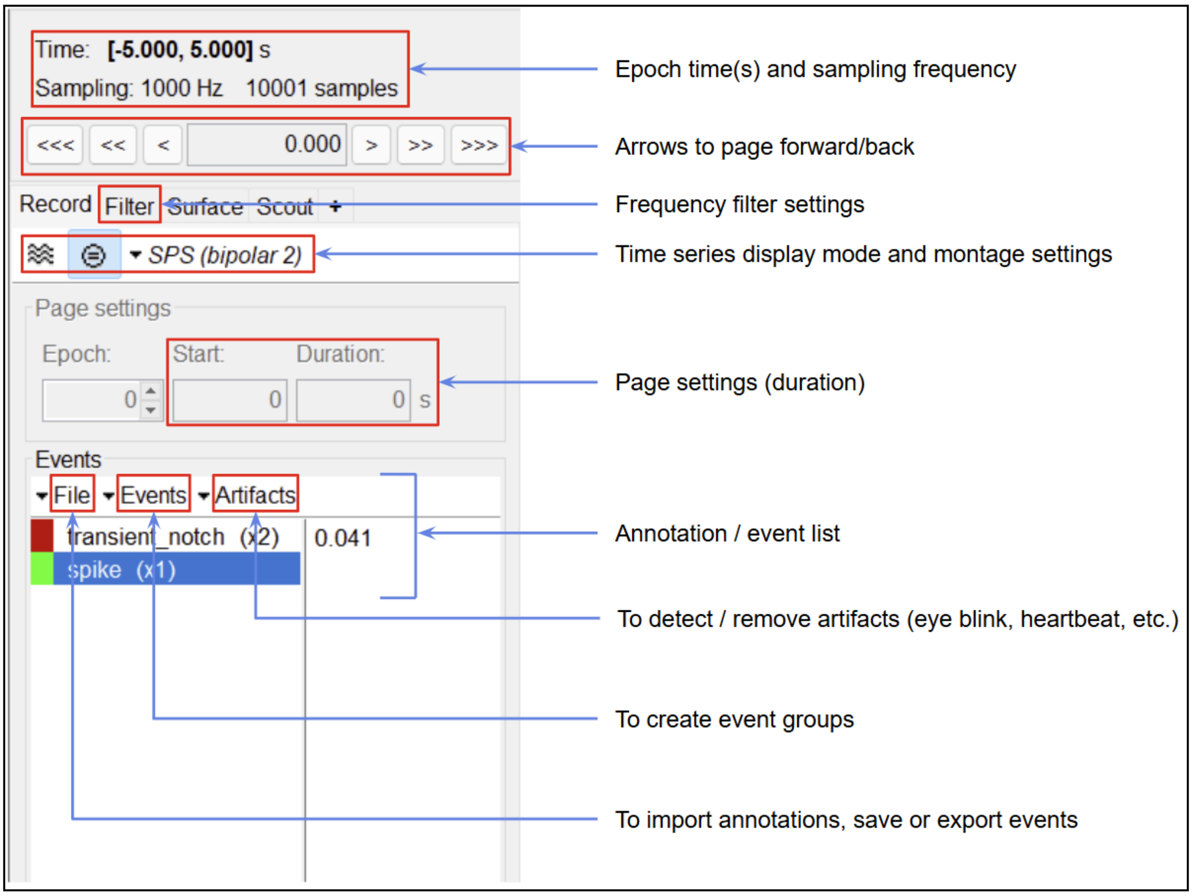
Brainstorm is available in both an open-source MATLAB application (MATLAB license required) and a standalone Java executable (free). Please follow the installation instructions for a complete installation and configuration: https://neuroimage.usc.edu/brainstorm/Installation. For the workshop, we will use the MATLAB version[check the post on the forum].

⚠ **Having any issues**: ☞https://neuroimage.usc.edu/brainstorm/WorkshopGeneralInstall

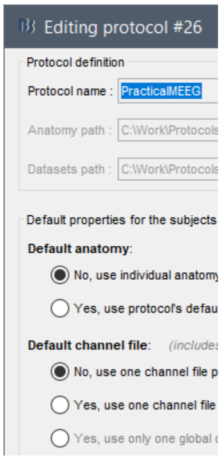
Introduction to Brainstorm Interface

CLOSE ALL YOUR APPLICATIONS, INCLUDING WEB BROWSERS





DAY1: Tuesday, Oct 28 – AM Session
Get to know your data



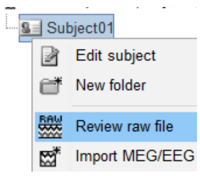
10:10-10:35 Introduction to Brainstorm (lecture)

10:35-11:00 Review recording

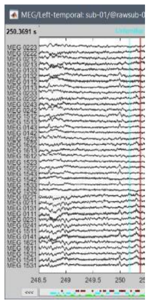
- Create a new protocol. File > **New protocol**: "PracticalMEEG"
  - **No**, use individual anatomy
  - **No**, use one channel file per acquisition run (MEG/EEG)
- Introduction to database explorer (list of protocols, exploration modes…)
- Right-click on protocol top node > **New subject** >sub-01
  - Leave the default options you defined for the protocol.

📜You can find more details here: https://neuroimage.usc.edu/brainstorm/Tutorials/CreateProtocol

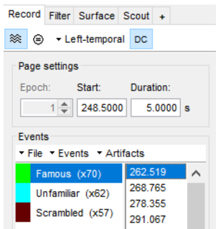
- Switch to functional view (2nd button above the database explorer)
- Create a link to the continuous file:
  - Right-click on sub-01 > **Review raw file**
  - File format: MEG/EEG: Elekta-Neuromag (*.fif)
  - Select folder: ds000117_pruned/derivatives/meg_derivatives/sub-01/ses-meg/meg/
  - File: ***sub-01_ses-meg_task-facerecognition_run-01_proc-sss_meg.fif***
  - Select option: Event channel > STI101



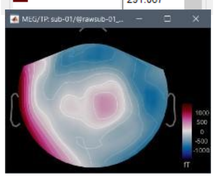
- Edit the channel types:
  - Right-click on the Neuromag channel file > Edit channel file
  - Change the types: EEG061>Misc, EEG062>EOG, EEG063>ECG, EEG064>Misc.
  - Close and save
- Review MEG: Right-click on "Link to raw file" > MEG (all) > Display time series
  - Display in columns + channel selection (click or montage) => Left Temporal
  - Time: Display windows of **5s**
  - Amplitude: Buttons and shortcuts
  - Scroll to detect the beginning of the continuous head localization (248s), Online filters
  - Events: List, figure, time bar, display modes (dots or lines)



- Edit/combine events
  - Select **5+6+7**: Events > Merge groups > **Famous**
  - Select **13+14+15**: Events > Merge groups > **Unfamiliar**
  - Select **17+18+19**: Events > Merge groups > **Scrambled**
  - Delete all the other categories of events
  - Events > **Add time offset**: Famous, Unfamiliar, Scrambled **34.5ms** (delay)



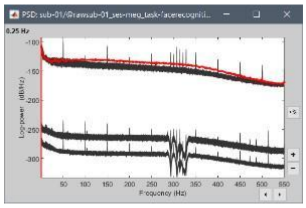
- Add other views
  - **EEG:** Right-click on "Link to raw file" > EEG > Display time series
  - **ECG:** Right-click on "Link to raw file" > ECG > Display time series
  - **EOG:** Right-click on "Link to raw file" > EOG> Display time series
  - **Topography**: Right-click on "Link to raw file" > EEG > 2D Sensor Cap (or CTRL+T)
  - Layout menu: Alternate between Tiled and Weighted (keep Weighted)



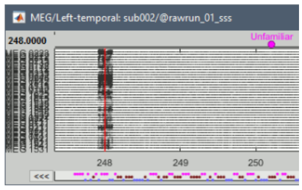
- Close all + Save modification

11:00-11:15 Spectral inspection and filtering

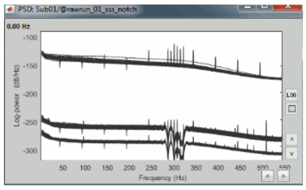
- Drag and drop the "Link to raw file" in Process1
  - Explain the Process1 tab + Filter box
- Run process: "Frequency > Power spectrum density (Welch)":
  - Time window: **[250, 300]**s, Window length: **4s**, Sensor type: **MEG, EEG,** PSD options: **Edit… > OK**. Click Run. Open the PSD file (double-click)



Open topography: EEG > 2D Sensor cap
Open topography: MEG (mag) > 2D Sensor cap
Open topography: MEG (grad norm) > 2D Sensor cap
Explain the noise sources / identify possible bad channels:
(~10Hz:alpha, 50Hz: power, ~300Hz: HPC(248s), EEG016 bad)

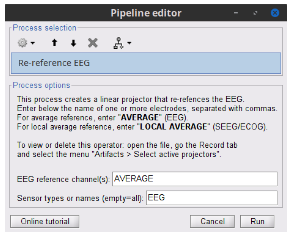


- **Optional: remove line noise** (later low-pass filter at 40 will be applied)
  Keep the "Link to raw file" in Process1.
  Select process Pre-process > Notch filter (50, 100, 150, 200).
  Add the process Frequency > Power spectrum density (Welch)
  Double-click on the PSD for the new continuous file to evaluate the quality of the correction.
- Run process: “Pre-process > Band-pass filter”:
  MEG, EEG Lower cutoff: 0 Hz (No high-pass filter)
  Upper cutoff: 40 Hz (Low-pass filter)

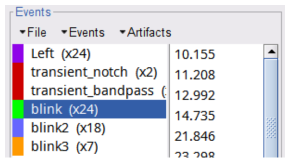


📜 Most filters cause edge effects, i.e. unreliable segments of data at the beginning and the end of the signal. When applied to short epochs, they might contaminate all the data of interest. Learn more about filters here:
Epoch_length: https://neuroimage.usc.edu/brainstorm/Tutorials/Epoching#Epoch_length
What filters to apply:
https://neuroimage.usc.edu/brainstorm/Tutorials/ArtifactsFilter#What_filters_to_apply.3F

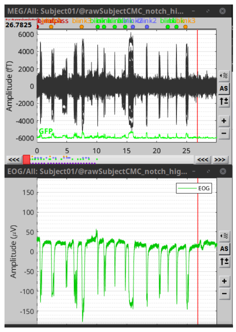
11:15-11:45 Artifacts detection and cleaning



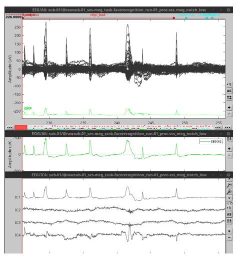
- Bad channels & Re-reference the EEG recordings
  Right click on “Raw | low” > EEG > Display time series
  Mark EEG016 as bad
  Record tab: Artifacts > Re-reference EEG: **AVERAGE**
- Detect eye-movement events
  Open the time series for MEG and EOG
  In the Record tab, select *Artifacts > Detect eye blinks*:
  Channel name = **EEG062**, *Time window* = **All file**,
  Event name = **blink**
  Display MEG signals (along EOG) and see some blink occurrences
  Merge all the **bink** event groups in a **blinks** group



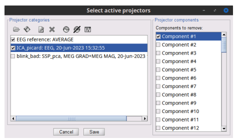
- Detect heartbeat events
  Open the time series for MEG and ECG (set Duration to 1 s)
  In the Record tab, select *Artifacts > Detect heartbeats*, and use the parameters:
  Channel name = **EEG063**, *Time window* = **All file**, *Event name* = **cardiac**

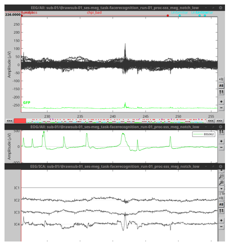


- Handle simultaneous events
  In the Record tab, select *Artifacts > Remove simultaneous:*
  Remove events named: **cardiac**
  When too close to events: **blinks**
  Minimum delay between events: **250 ms**
- Remove heartbeat artifacts from MEG with SSP
  Open the time series for MEG
  In the Record tab, select *Artifacts > SSP: Heartbeats*, and use the parameters:
  Event name = **cardiac**, *Sensors* = **MEG** *Compute using existing* = **Check**
  In the *Select active projectors* window, **uncheck** all components
  Highlight the first two and plot them (📈)
  Open MEG (all) and ECG time series, and disable **auto scaling** in the 3 plots
  Check **Component #1** to verify the impact of removing it from the MEG signal
  Click on Save, and close all figures



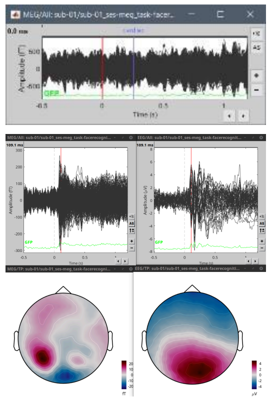
- **Optional: Remove blink artifacts from the EEG with ICA**
  Open the time series for EEG
  In the Record tab, select *Artifacts > ICA components*, and use the parameters:
  Time window = **[226- 400]**, *Sensor type*: **EEG,** *Band-pass filter* = **[0, 0]**, *Resample* = **0**



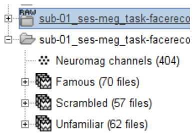


ICA algorithm = **Picard**, *Number of ICA components* = **0**
Sort components based on correlation with = **EOG, ECG**
In the *Select active projectors* window, **uncheck** all ICA components.
Highlight a few and plot them.
Open EEG and EOG time series and disable **auto scaling** in the 3 plots (check the shape)
Check **Component #1** to verify the impact of removing it from the EEG signal
Click on Save, and close all figures

<u>**11:45-12:00 Epoching and single trials reviewing**</u>



- Right-click on the pre-processed file (Raw | low) > *Import into database*
  - *Time window* = **226.0 - 716.99 s** (this is set automatically)
  - Uncheck **Split**
  - Check **Use events** and select **Famous, Unfamiliar,** and **Scrambled**
  - *Epoch time* = from **-500 ms** to **1200 ms**
  - Check **Apply SSP/ICA projectors**
  - Check **Remove DC offset**, select **Time range [-500, 0]**
  - Uncheck **Create a separate folder for each type**
  - Click on **Import**
  - A new folder without the **'raw'** indication is created

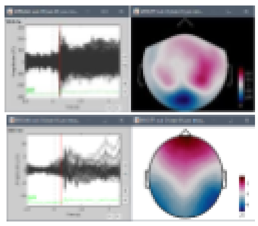


<u>DAY1: Tuesday, Oct 28</u> – PM Session
Sensor-level Analysis & frequency space analysis

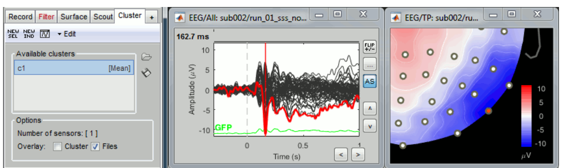
<u>**15:15-15:45 Sensor level averages (ERP/ERF)**</u>

- Review trials:
  - Open the first trial MEG+EEG: Switch back to butterfly view, ALL sensors. Open a 2D topography (CTRL+T)
  - Enable auto-scale (button [AS]). Navigate between trials with F3 / Shift+F3 (Fn + F3 on Mac)
  - Trials or channels can be marked as bad independently

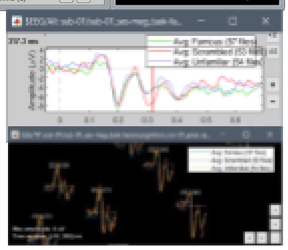
📜 Read more about the keyboard shortcuts:
https://neuroimage.usc.edu/brainstorm/Tutorials/ExploreRecordings#Keyboard_shortcuts



- Raster plots: Right-click on trials > Display as image > EEG (EEG065)
  - You can change the selected sensor with the drop-down menu in the Display tab, or use the up/down arrows on your keyboard
  - The bad trials are already marked, but if they were not, this view could help you identify them easily.
- Average trials
  - Drag and drop all the trial groups in Process1
  - Run process "Average > Average files": By trial group (folder average)
- Review average
  - Open Famous average: MEG + 2D topography view + EEG Review movie of the activity (hold right/left keys/ filter tab)
  - Display with a low-pass filter at 32Hz



- Channel Cluster/Single channel
  - Close all and open EEG: Signals + all topography modes.
  - Open the Cluster tab and create a cluster with the channel **EEG065** (button [NEW IND]). Overlay EEG065 for 3 averages with Cluster tab (NEW IND). Overlay averages with 2DLayout
  - Display Mean + Std : "Edit > Set Cluster function > Mean"



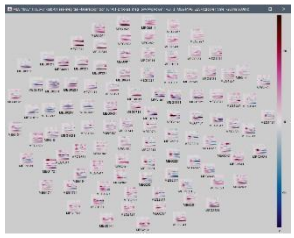
📝 Plot the trial average time series for electrode EEG056

📜 Read more here about Clusters:
https://neuroimage.usc.edu/brainstorm/Tutorials/ChannelClusters

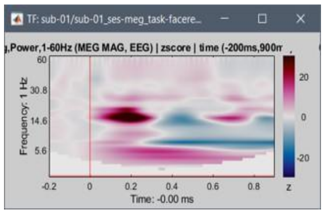
Snapshot > Time contact sheet topography with 2D Disc:
0ms, 500ms, 16 images Movies…

- Basic observations for ERP EEG065 (right parieto-occipital electrode):
  Around 170ms (N170): greater negative deflection for Famous than Scrambled faces.
  After 250ms: difference between Famous and Unfamiliar faces.

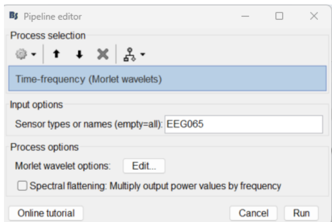
15:45-16:45 TF Wavelets Analysis



- **Wavelets**
  Drag-drop all the **Famous** trials in Process1
  Add process: *Frequency > Time-frequency (Morlet wavelets)*
  Click on ***Edit…***
  Time definition = **Same as input files,**
  Frequency definition = **Linear: 5 : 2 : 60**
  Central freq = **1 Hz,** *Time resolution* **3 s**
  Measure = **Power**, Select **Save individual**
  Add process: *File > Add tag*
  Tag to add = **Famous**, Select **Add to file name**
  Display time-frequency average:
  Smooth display and **hide edge effects** for channel **EEG056**

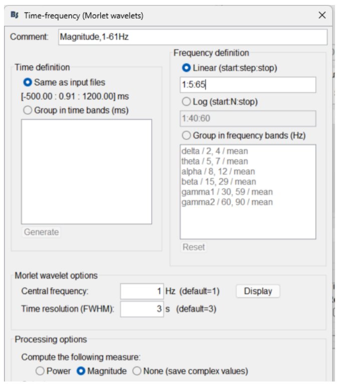


- **Explore time-frequency results**
  Display 2D Layout (maps): Select a few sensors
  Change colormap: Maximum -10/+10, colormap type
  Add views: time series + power spectrum + all the other options



- **Processing the time-frequency results**
  Run process: Standardize > Baseline normalization > Z-score: [-200, 0]ms
  Add process: Extract > Extract time: [-200, 900]ms, Overwrite.
  [To remove the section of the data with edge effects]

📜 Check this link for more information:
https://neuroimage.usc.edu/brainstorm/Tutorials/VisualSingle#Time-frequency_analysis
https://neuroimage.usc.edu/brainstorm/Tutorials/TimeFrequency



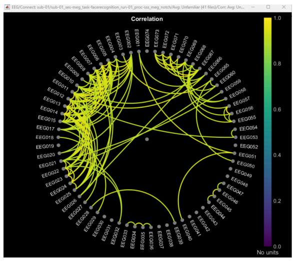
- **Optional: Hilbert transform and Multitaper**
  Select all the **Famous** trials in Process1
  - Add process *Frequency > Hilbert transform*:
    Sensor type = **MEG** only
    Morlet wavelet options:
    Time definition = **Same as input files**, *Frequency definition =* **Group [Reset]**
    Measure = **Power**, Select **Save average**
  - Add the process: *File > Add tag*
    Tag to add = **Famous**, Select **Add to file name**

  Display both time-frequency representations (from wavelets and Hilbert transform):
  Smooth display and **hide edge effects**

📜 Read more here Multitaper (through Fieldtrip):
https://neuroimage.usc.edu/brainstorm/Tutorials/Epileptogenicity#Time-frequency_analysis_.28pre-onset_baseline.29

Optional: Connectivity sensor level *[not described in the original data/paper]*
Select all the **Famous Average** trials in Process1
Run process: Connectivity> Correlation NxN > 100-500ms, EEG,
Right-click on the connectivity node, Display as Graph or as Image

Check more options for the graph here:
https://neuroimage.usc.edu/brainstorm/Tutorials/ConnectivityGraph



📜 Read more about connectivity in Brainstorm here:
https://neuroimage.usc.edu/brainstorm/Tutorials/Connectivity
PAC/source level here: https://neuroimage.usc.edu/brainstorm/Tutorials/Resting

Discussions:

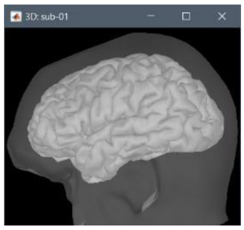
Brainstorm beyond the GUI

- Interaction with other toolboxes: FieldTrip, MNE-Python, EEGLAB, SPM
- Plugins: available plugins
- GitHub: repo and collaboration

DAY2: Wednesday, Oct 29 – AM Session
Source level estimation I: Getting to source level maps

10:10-10:45 Import anatomy

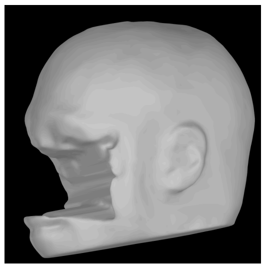
- Switch to anatomy view (1st button above the database explorer)
- Right-click on sub-01 > Import anatomy folder File format: FreeSurfer
  Select folder: derivatives/**freesurfer**/sub-01/ses-mri/anat
  Number of vertices: 10000 (lower value to make it faster).
- Introduction to the MRI viewer:
  Exploring the volume (click, mouse wheel, sliders),
  Colormaps, colorbar, figure popup menu
- Compute MNI transformation, maff8 (sets all the fiducials automatically)
- Check the positions of NAS / LPA / RPA
  Explain the coordinates (MRI, SCS, MNI)
  Click save, this will create the "cortex" file



📜 The MNI transformation automatically sets default NAS/LPA/RPA fiducials based on MNI coordinates. Since MEG-MRI coregistration will use digitized head points, precise fiducial placement isn't critical, unless there's no good head shape or the coregistration looks poor, in which case the fiducials should be manually marked following the MRI acquisition convention.

Head Model Generation

📜 The forward models depend on the subject's anatomy, including head size and geometry, tissue conductivity, the computational method, and sensor characteristics. In the following sections, we will present the two approaches available in Brainstorm for constructing the head model for EEG: the Boundary Element Method (BEM) and the Finite Element Method (FEM). However, only the BEM method is used in the subsequent sections. For the MEG, we will use the overlapping spheres. For more detailed documentation, please refer to: https://neuroimage.usc.edu/brainstorm/Tutorials/HeadModel



Generate BEM head surfaces from the MRI:

- Switch to anatomy view: (1st button, on top of the database explorer)

Optional: Right-click on **sub-01 > MRI segmentation > Generate head surface > OK**
This will generate a surface file named *"head mask"* estimated from the T1 MRI.

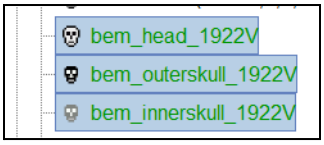
- Right-click on **sub-01 > MRI segmentation > Generate BEM surfaces**
  Select Brainstorm
  Number of vertices: Scalp = **642**, Outer skull = **642,** and Inner skull = **642**
  Thickness of layers, Skull (mm)= **4**
  Click OK [This process will take ~2min]

This will generate three surfaces (head, outer skull, and inner skull)

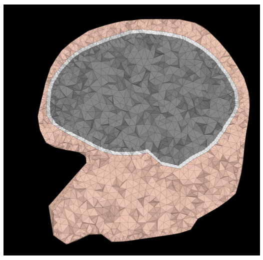
Demo: Generate FEM from BEM surfaces (simplified model):

- Press and hold "Ctrl", then select with the mouse the BEM surfaces

- Right-click on the selected surfaces **> Generate FEM Mesh**
  > Iso2mesh (default 2021) > MergeMesh > Keep default values > OK
  The Iso2Mesh plugin will be installed automatically
  Other tools are also available; Iso2Mesh is recommended
  Once completed, a new node will appear on the anatomy tab
  Double-click to display the FEM mesh

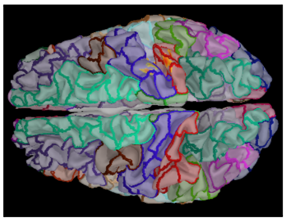


- **Set the default cortex to be used as the source space**
  Double-click on **cortex** to make it the default cortex (in green), or *right-click> set surface type> Cortex*.



- Display cortex and the other surfaces:
  - Double-click or right-click **> Display**
  - 3D figure: rotation, zoom, transparency
  - Predefined views and keyboard shortcuts: left, right, top, etc
  - Surface tab: smooth, sulci, edges
- Close all figures (✖ button at top-right)

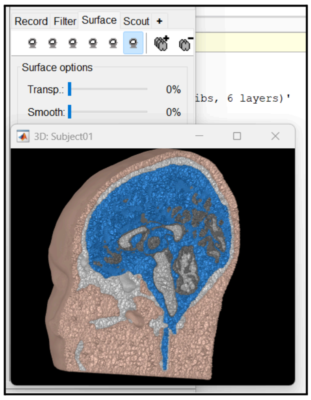
Atlases and Scouts



- Display scouts on the Cortical surface
  - Right-click on cortex **> Display on cortex**
  - In the **Scout** tab, use the drop-down to select different Atlases
  - Display **Desikan-Killiany** and **Destrieux**
- Display the head and brain surfaces
  3D figure: rotation, zoom
  Predefined views and keyboard shortcuts (1,2,3…) Surface tab: smooth, sulci, edges => smooth 60% Scouts tab: atlases and scouts

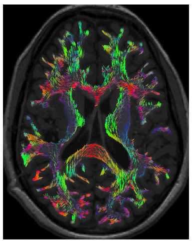
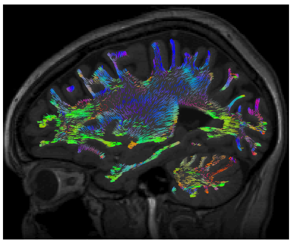
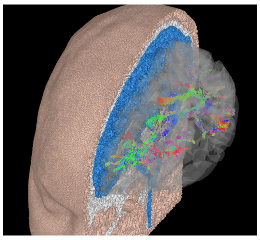
Demo: Generate FEM from MRI data (realistic model)

- From the material folder, load "femmat_tensors" to MATLAB, from the Brainstorm: anatomy folder
  >right click on subject>import from Matlab>femmat_tensors

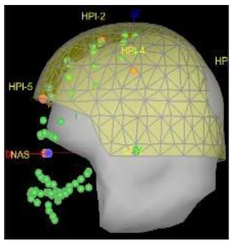


Demo: Defacing MRI data (anonymize the subject)

Demo: Diffusion data processing and conductivity tensors

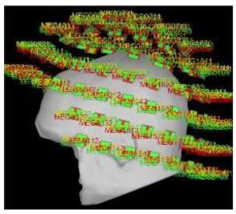
  

📜 *Read more about FEM modeling here:*
https://neuroimage.usc.edu/brainstorm/Tutorials/FemMesh



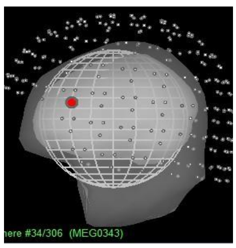
10:45-11:15 Registration MRI-sensors

- Switch to functional view (2nd button above database explorer)
- In the folder with epochs:
  Right-click on the channel file > **MRI registration** > MEG: Check
- Channel file: Digitized head points > **Remove points below nasion**
- Channel file: MRI registration > MEG: Edit > **Refine registration using head points**
- Channel file: MRI registration > EEG: Edit > **Project electrodes on surface**
  Save and close
- Channel file > **Display sensors** > **Vectorview306 coils (ALL)**



11:15-11:30 Forward model

- In the folder with epochs: Right-click on the channel file > **Compute head model**
  MEG: Overlapping spheres EEG: 3-shell sphere

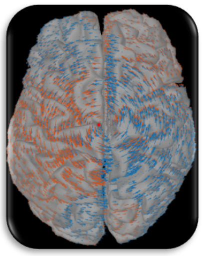


- Display locally fitted spheres

Demo: View Leadfield vectors

Optional: FEM Method with Duneuro

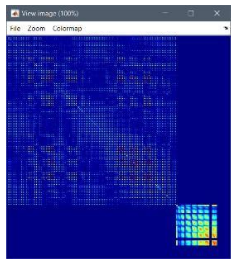
The forward model can also be computed using the FEM method with the DUNEuro plugin => use default options



11:30-11:30 Noise Modeling

- Noise covariance: MEG=empty room recordings, EEG=pre-stim baselines
  Apply the same signal processing steps for noise / same as data
- Import noise recordings:
  Right-click on **sub-01** > **Review raw file**
  File format: MEG/EEG: Elekta-Neuromag (*.fif)
  Select file:

  ds000117_pruned/derivatives/meg_derivatives/sub-emptyroom/ses-20090409/meg/*.fif.
  Ignore all the questions and warnings: indeed, there is no subject in the MEG
- Filter noise recordings:
  Select it in Process1, run process Pre-process > Band-pass filter: 0-40Hz

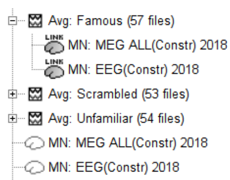


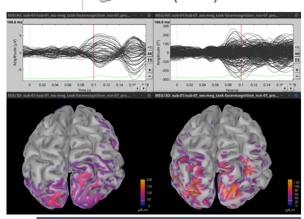
- Compute noise covariance for MEG:
  Right-click on sub-emptyroom/Raw|Low > Noise cov > Compute from recordings> keep default options
  Baseline = all **time window**, *Sensors* = **MEG GRAD** and **MEG MAG**
  Select **Block by block**
  Right-click on noise covariance > Copy to other folders
- Compute noise covariance for EEG:
  Select all epochs Famous+Unfamiliar+Scrambled > Noise cov > Compute from recordings
  Baseline: **[-500,0]ms**, **EEG** only,
  Merge with existing noise covariance > this will merge the EEG covariance matrix with the MEG

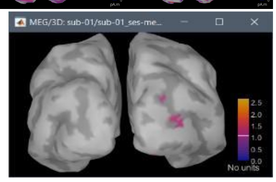
Start source level analysis II, if time allows.

DAY2: Wednesday, Oct 29 – PM Session
Source level analysis II: Analysing source time-series

15:15-15:45 Inverse modeling: Distributed sources / minimum norm estimation



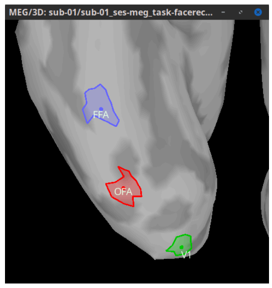




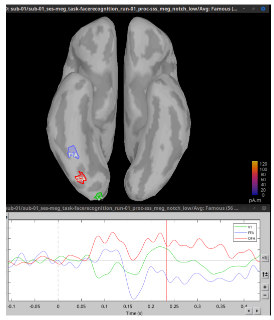
- Compute inverse model (MEG)
  Right-click on the head model > *Compute sources*, use these parameters:
  Select **Minimum norm imaging**
  Select the **Current density map**
  Select **Constrained: Normal to the cortex**
  Sensors = **MEG GRAD** and **MEG MAG**
- Compute inverse model (EEG)
  Right-click on the head model (   ) *Compute sources*, use these parameters:
  Select **Minimum norm imaging**
  Select the **Current density map**
  Select **Constrained: Normal to the cortex**
  Sensors = **EEG**
- Explanation of the inversion kernel ( ) and link ( ) files in the database
- Explore the **Famous** average
  Display EEG and MEG **time series** (butterfly mode)
  Display the **sources** derived from EEG and from MEG data
  Set time to **100 ms**
  Set *Smooth* = **30%** and **Amplitude** threshold to **20%** (both in Surface tab)

15:45-16:45 Atlases and Scouts

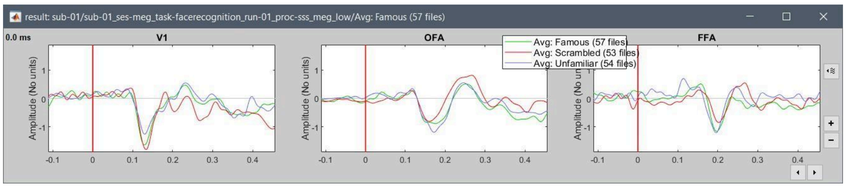
- Display the **sources** derived from MEG data
  - In the Scout tab, use the drop-down to select different Atlases
  - Operations with Atlases and Scouts



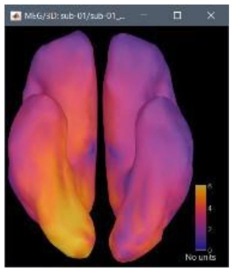
- Create Scouts
  - Open the sources (from MEG) for the **Famous** average, bottom view
  - Move to beginning: t=0ms, Colormap Max Custom = **[0, 5]**
  - Amplitude threshold=**20%**
  - Select the **User Scouts** atlas
  - Go to Time **85 ms**, Amplitude threshold **80%** Smooth = **80%**
  - Create the scout **V1** (primary visual cortex) on the right hemisphere
    - Scout tab: Click on *Select point*, then point on the brain's most active zone
    - Grow Scout to 20 vertices
    - Rename to V1 (double-click on the scout in the list)
    - Review trace: Absolute values, then relative values



- Create other scouts to explore the other sources
  - Decrease the threshold by 40% (Surface tab)
  - Go to **130 ms**: Create scout **OFA** (occipital face area), grow to 20 vertices
  - Go to **165ms**: Create scout **FFA** (fusiform face area), grow to 20 vertices
- Review all the traces, Absolute values| **Overlay: Scouts** | Online filter

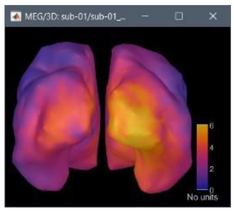


📝 In which scout of the Desikan-Killiany atlas are the vertices of our FFA scout?
Demonstrate Left-click and Drag on the color bar to select the appropriate Brightness and Contrast
📜 Read more here: https://neuroimage.usc.edu/brainstorm/Tutorials/Colormaps



Optional: LCMV Beamformer

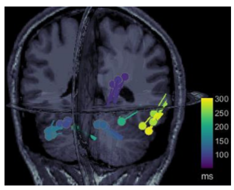
- Compute data covariance:
  - Select all epochs > Data cov > Compute from recordings Baseline: **[-500,0]ms**, Data: **[0,500]ms,** All sensors
- Right-click on head model > **Compute sources [2018]**:
  - LCMV beamformer, Pseudo NAI, Unconstrained, MEG GRAD + MAG
- Right-click on head model > **Compute sources [2018]**:
  - Minimum norm, dSPM, Unconstrained, MEG GRAD + MAG
- Open both source maps (e.g., Famous): review in time
  - Unconstrained: Smoother, nicer figures, more complicated to process



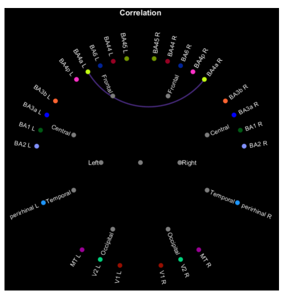
Optional: Display the scouts time series for all ROIs, compare LCMV with dSPM

Optional: Dipole scanning / Volume source models

- Right-click on channel file > Compute head model
  - MRI volume, MEG: Overlapping sph, Regular grid, brain, 5mm
  - Right-click on head model > Compute sources > Dipole modeling
  - Demo: Display dipole maps (not a distributed source model)



- Select the dipoles map in Process1
  Run process Sources > Dipole scanning: [50,300]ms
  - View dipoles
  - Demo: Dipole fitting with FieldTrip ft_dipolefitting (70-100ms, MEG MAG)



16:45-17:00 Connectivity Analysis at source level

- Select all the **Famous Average** trials in Process1/**[sources]**
  Run process: Connectivity> Correlation NxN >
  - 100-500ms, user scouts, Brodman

Right-click on the connectivity node> Display as Graph or >as Image

Many other measures are available; here we illustrate just the correlation.

📜 Read more: https://neuroimage.usc.edu/brainstorm/Tutorials/ConnectivityLfp

If time allows, explain how to generate the scripts and download the data for the next session.

DAY3: Thursday, Oct 30

AM Session: Get and report results with confidence I – Univariate approach

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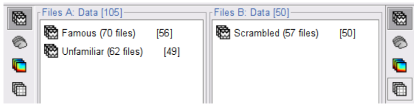
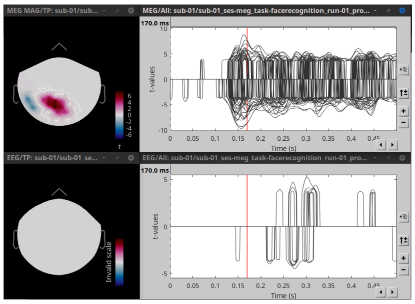
Within-subject analysis

10:15-11:00 Statistical testing





- **Parametric t-test on sensors**

  In Process2 tab:

  FilesA=**Famous** and **Unfamiliar** trials, FilesB=**Scrambled** **(all trials, not the average)**

  Run process: *Test > Parametric test: Independent [different var]*

  Time window = **[0 - 500] ms**

  Test statistic = **Student's t-test (equal variance)**

  Select **Two-tailed**

  Right-click > MEG (all) > Display time series + Press CTRL+T for 2D topo

  Right-click > EEG > Display time series + Press CTRL+T for 2D topo

  In **Stat** tab: set alpha threshold to **0.01**, **FDR** correction,

  Check **Signals**, **Time**

Around 170 ms, several sensors show a strong deflection (|t| > 5–10), indicating a significant difference between conditions (*familiar vs. scrambled*). The topography reveals a large positive cluster over the occipito-temporal region, suggesting higher amplitudes for faces, consistent with the **face-selective M170 component.**

Note: The *parametric t-test* assumes a normal distribution of the data.

Advantages: Analytic, fast, and simple to compute; very efficient when assumptions are met.

Limitations: Sensitive to violations of normality; not ideal for small sample sizes or EEG/MEG data with non-Gaussian noise.

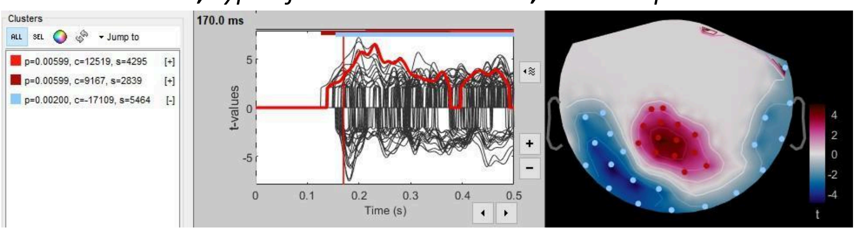
- **Cluster-based statistics (MEG sensors) [non-parametric/cluster correction]**

  Run process: *Test > FieldTrip: ft_timelockstatistics*

  Sensor type = **MEG MAG,** *Time window* = **[0,300] ms**

  Number of randomizations = **1000 ,** *Test* = **Independent t-test**

  Select **two-tailed,** *Type of correction* = **cluster,** *Cluster alpha* = **0.05**



- [**Optional: Perform cluster-based statistics for EEG sensors**]()
- **Permutation t-test (on sources)**

  In Process2 tab: FilesA=**Famous** and **Unfamiliar** trials, FilesB=**Scrambled**

  Select "Process sources (🧠)" on both sides

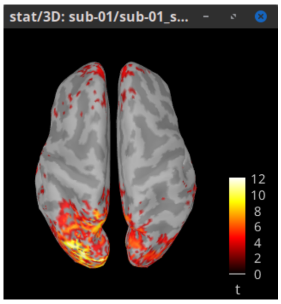
  Use the Filter to select sources from **MEG**

  Run process: *Test > Permutation test: Independent*

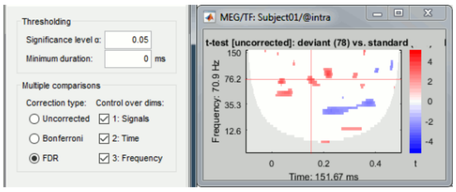
  Time window = **[140,170] ms**

Select the **Average selected time window**
Test statistic = **Student t-test (equal variance)**
Select **two-tailed**
Number of randomizations = **1000**

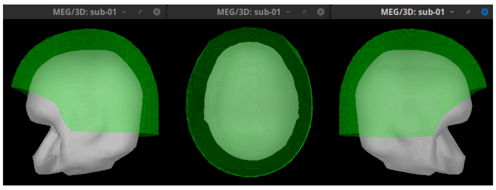
Open the statistics results
Right-click figure > *Colormap: Stat2 > Absolute values*
Right-click figure > *Colormap: Stat2 > Colormap > Sequential > Hot2*



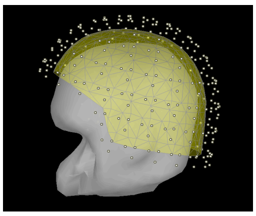
- **Optional: Nonparametric test on time-frequency maps**
  To run a test on time-frequency maps, all trial-wise decompositions (here, **Famous, Scrambled, Unfamiliar**) must be available, which can be time-consuming. To simplify, here we do the TF computation for just a single channel, **EEG065**.
  We computed the TF map for each of the **Famous** trails above. Do the same for **Scrambled, Unfamiliar**.
  Drag-drop them into Process1. Run process *Frequency > Time-frequency (Morlet wavelets)*.
  Sensor type: **EEG065**.
  Click Edit…
  Measure=*Magnitude*: It is more standard to test the square root of power (amplitude).
  Select *Save individual…* to save the individual TF maps. Click OK. Click Run.
  Do not normalize the TF maps for a test within a single subject (only for group studies)
  In Process2, FilesA=**Famous** and **Unfamiliar** trials, FilesB=**Scrambled**
  Select [Process time-freq]
  Run process: Test > Permutation test: Independent, 1000 randomizations, no correction



Subject average (within subject across runs/sessions):
In the following steps, we will conduct a within-subject analysis across different conditions. We will use a precomputed Brainstorm protocol for sub-01, which includes three runs.
In the Brainstorm window, click on **File > Load protocol > Load from zip file** and select the precomputed protocol **<PracticalMEEG_sub-01_3-runs.zip>** from the material folder.

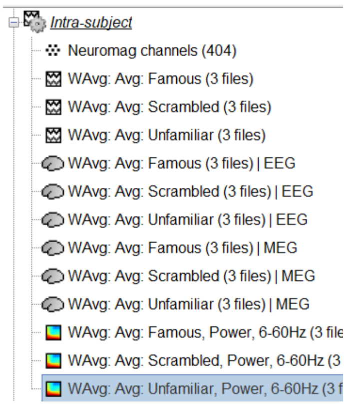


- **Coregistration of the acquisition runs**
  For this subject, all the runs have been registered to a common head position with MaxFilter. To verify this, select all the channel files within a single subject, right-click, and then select **Display sensors > Vectorview306 helmet**.
  The surfaces representing the MEG helmet are perfectly overlapping for all the runs.



📝 Why is it necessary to check alignment for MEG sensors but not for EEG?

- **Sensor EEG/MEG**
  Drag-drop all the time series **Avg** files (3 per run) from the three folders to Process 1 [total of 9 files]
  Run process: *Average > Average files:*
  Group files = **By trial group (subject average)**
  Function = **Arithmetic average**
  Check the **Weighted average**
  (weighted: different runs with different # of epochs)
  Run



- **Sources EEG**
  Drag-drop all the folders to Process 1 [select source], add filter EEG
  Run process: *Average > Average files:*
  Group files = **By trial group (subject average)**
  Function = **Arithmetic average**
  Check the **Weighted average**
  Add the process: *File > Add tag*

Tag to add = **EEG**, Select **Add to file name**

Run pipeline

- **Optional: Average MEG Sources**

  Repeat the same process as with EEG, changing the selected files and the added tag to MEG

- **Optional: Average Time-frequency maps**

  Keep all the selected subjects in Process 1. Select button **[Process time-freq]**.

  Perform the weighted average of the time-frequency files in (a total of 9 files/3 per run)

  Select the option **Match signals between files using their names**

Now we have all the subject averages across the sessions: MEG/EEG, sources, and time-frequency.

Faces vs Scrambled

To analyze the face vs. non-face, we will create recordings, **faces:** average response (**Famous + Unfamiliar**)

In Process 2, drag-drop the subject recordings average for **Famous** in Files A, and the subject recordings average for **Unfamiliar in** Files B

Add the process *Other > Average A&B* and select **Weighted average**

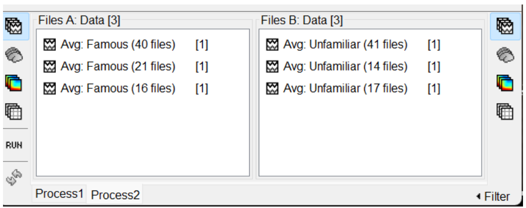
Add the process *File > Set name* with *New name* = **WAvg: Avg: Faces**

Run process: *Average > Average files:*

Group files = **By trial group (subject average)**

Function = **Arithmetic average**

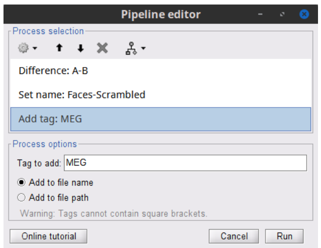
Check the **Weighted average**, then click Run



- **Optional: Repeat for sources (from EEG and MEG)**, do not forget to add their respective tags (Avg: Faces | EEG and Avg: Faces | MEG)
- **Optional: The Same process can also be performed for the TF maps**

  A new file named **WAvg: Avg: Faces** will be added to all the folders, including the intra-subject

  Explore the different results in time and space.



Difference between Faces & Scrambled

- **For EEG/MEG recordings:**

  In Process 2, drag-drop the subject **recordings** average for **Faces** in Files A, and the subject recordings average for **Scrambled** Files B [*from the intra-subject folder*]

  Add the process *Difference > Differences: A-B*

  Add the process *File > Set name* with *New name* = **Faces-Scrambled**

  Explore the time series and topography of the differences

- **For EEG sources:**

  In Process 2, drag-drop the subject **sources** average (obtained with EEG) for **Faces** in Files A, and the subject **sources** average for **Scrambled** Files B

  Add the process *Difference > Differences: A-B*, uncheck **Use absolute values**

  Add the process *File > Set name* with *New name* = **Faces-Scrambled**

  Add the process: *File > Add tag*, *Tag to add* = **EEG**, Select **Add to file name**

- **Optional: For sources from MEG:**

  Repeat the same steps as with sources from the EEG/add tags MEG

📝 Around which time do the differences become significantly different from the baseline values?

Optional: Difference between Famous & Unfamiliar

During computation time: discuss and explain interactions with:

- FieldTrip: Structure conversions, direct calls
- MNE-Python: Python objects and call Python function (though Matlab >= 2015b)

  Check here: https://neuroimage.usc.edu/brainstorm/MnePython

  Review the example files within the folder brainstorm/python/

  https://www.mathworks.com/help/matlab/matlab_external/install-the-matlab-engine-for-python.html

- EEGLAB: Functions embedded in the Brainstorm distribution (runica.m)
- SPM: Export to .nii or .gii files (online tutorial)

📜 **Read more here: Export to SPM:**
An alternative to running the statistical tests in Brainstorm is to export all the data and compute the tests using an external program (such as R, MATLAB, or SPM).
Multiple menus exist to export files to external file formats (right-click on a file > File > Export to file).
Two tutorials explain how to export data specifically to SPM:

- Export source maps to SPM8 (volume)
- Export source maps to SPM12 (surface)

📜 **Read more about statistics in Brainstorm:** https://neuroimage.usc.edu/brainstorm/Tutorials/Statistics

If time allows, explain how to generate the scripts and download the data for the next session.
How to write your own process: https://neuroimage.usc.edu/brainstorm/Tutorials/TutUserProcess
Scripting: https://neuroimage.usc.edu/brainstorm/Tutorials/Scripting#Loop_over_subjects

DAY4: Friday, Oct 31
AM Session: Get and report results with confidence II – Multivariate approach

10:15-12:00 Group level analysis

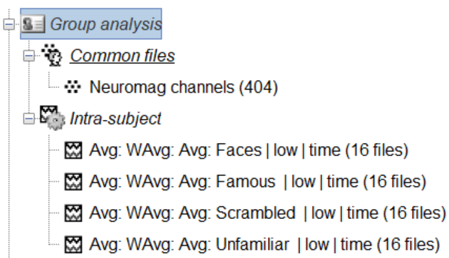
Subject Grand averages:
In this session, we will use a precomputed Brainstorm protocol for 16 subjects with 6 sessions. We will conduct group-level analysis across the different conditions.
In the Brainstorm window, click on **File > Load protocol > Load from zip file** and select the precomputed protocol **<PracticalMEEGGroup_pruned.zip>** from the provided material folder. Once completed, you should see the 16 subjects listed in the Anatomy and Functional tabs.

Summary of the analysis:

- Subject and grand averages for each condition (Famous, Unfamiliar, Scrambled).
- Normalization of these averages (Z-score for the sources, or ERS/D for the time-frequency maps).
- Projection of the sources results on a template and spatial smoothing of the source maps.
- Contrast between faces (famous+unfamiliar) and non-faces (scrambled): difference of averages and significance test.
- Contrast between famous faces and unfamiliar faces: differences in averages and significance tests.
- Sensors of interest: EEG070 (or EEG060 or EEG065 if EEG070 is marked as bad)

The methodology we will follow for computing averages and other statistics is described in the tutorial "Workflows".
Note: This session demonstrates how to run the analysis using the interface (Brainstorm GUI), but for large datasets, manual processing is inefficient and error-prone. Users are encouraged to script group analyses instead, first prototyping the analysis pipeline for a few subjects using the interactive interface, then generating the corresponding MATLAB script, and finally running it on all subjects for reproducibility. Script creation is detailed in the online Scripting tutorial.

Subject averages: Filter and normalize
Before comparing the averages across subjects, we will low-pass filter the signals below 32Hz (to smooth possible latency differences between subjects) and normalize the source & TF values with respect to a baseline.



- **EEG/MEG Sensor**
  In Process 1, select all the Intra-subject folders from all subjects, and then select **[Process recordings]**.

For a faster selection, you can use the "Functional data (sorted by conditions)" view. [64 files]
Select process **Pre-process > Band-pass filter**: 0Hz-32Hz, MEG, EEG, 60dB, 2019, Overwrite.
Add process **Extract > Extract time**: Time window=**[-200,900]ms, overwrite**
Selecting a smaller time window eliminates most of the possible edge effects caused by the filter.
Add process **Average > Average files**: **By trial group (grand average)**
Arithmetic average, not weighted. Click Run.

A new item labeled "Group Analysis" will appear in the database explorer that has the same structure as a subject. It contains the average of the 16 files from all 16 subjects for each condition.
- For the "**Group analysis/Inter-subject**" folder: the variable refers to the subjects (average of 16files or subjects)
- For the "**sub-XX/intra-subject**" folder: the variable refers to the runs [sessions] (average of 6 files or sessions)

📝 It is ok to compare EEG sensor subject averages, but it is not the case for MEG sensor subject averages. Why?

Note that averaging MEG recordings across subjects is not accurate; however, it can be used to obtain a general idea of the group effects (for more information).

- **MEG Sources**

  In Process 1, select all the Intra-subject folders from all subjects, and then select **[Process sources]**
  16 files available, the provided data contains only the MEG [face-scramble]
  Select process **Pre-process > Band-pass filter**: 0Hz-32Hz, 60dB, MEG, Overwrite
  Add process **Extract > Extract time**: Time window=**[-200,900]ms**
  Add process **Standardize > Baseline normalization**: Baseline=[-200,-5]ms, Z-score, Overwrite.
  Click Run.
  Three tags are added to the files: " low(32Hz) | time (-202ms,900ms) | zscore"
- **Optional: Time frequency**
  - In Process 1, select all the Intra-subject folders from all subjects, and then select **[Process time-freq]**.
  - Run process **Standardize > Baseline normalization**: Baseline=[-200,-5]ms, ERS/ERD, Overwrite
    One tag is added at the end of the comments of the averaged time-frequency maps.

Sensor Difference: Faces - Scrambled:

- **Differences of averages**

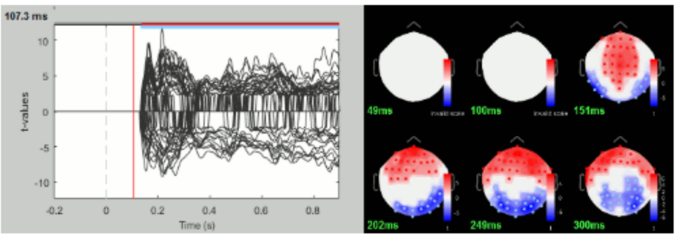
We could compute the contrasts directly from the grand averages, but we will do it from the subject averages because the same file selection will be used for the statistics (next step).
In Process2: FilesA = all the Faces subject averages (from the Intra-subject folders).
In Process2: FilesB = all the Scrambled subject averages (from the Intra-subject folders).
Run process: **Test > Difference of means**: Arithmetic average, Not weighted. Click Run.

- **Significance testing**

In Process2: Keep the same file selection.
Run process: **Test > Parametric test: Paired**: All file, All sensors, No average, two-tailed.
Rename the file: **Faces - Scrambled: Parametric t-test**. Display with **α=0.05, FDR-corrected**.

We can run other tests in a similar way, with almost identical results.
Process: **Test > Permutation test: Paired**: All file, All sensors, Paired t-test, 1000 randomizations. Display with **α=0.05, FDR-corrected**.
Process: **Test > FieldTrip: ft_timelockstatistics**: All file, EEG, Paired t-test, 1000 randomizations, correction=cluster, cluster alpha=0.05.

Note: The cluster-based statistics must be executed on one type of sensor at a time (EEG, MEG, MAG, or MEG GRAD), because it tries to identify spatio-temporal clusters that **group** adjacent sensors.



Bonus: Histograms checking the distribution of the data:

In Process1: all the Faces subject averages (from the Intra-subject folders).

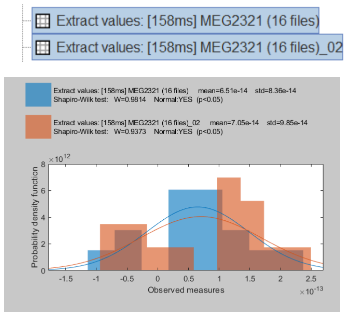
Run process **Extract > Extract values**:

Options: Time=**[160,160]ms**, Sensor="**MEG2321**", Concatenate **time** (dimension 2)

Do the same for the Scrambled

To display the distribution of the values in these two files:

select them simultaneously, right-click > **File > View histograms**.



Exercice: Famous - Unfamiliar

- **Differences of averages**

  In Process2: FilesA = all the Famous subject averages (from the Intra-subject folders).

  In Process2: FilesB = all the Unfamiliar subject averages (from the Intra-subject folders).

  Run process: **Test > Difference of means**: Arithmetic average, Not weighted.

  Rename the file: **Famous - Unfamiliar**.

- **Significance testing**

  In Process2: Keep the same file selection.

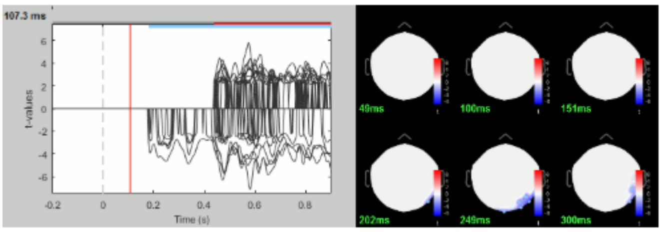
  Run process: **Test > Parametric test: Paired**: All file, All sensors, No average, two-tailed.

  Rename the file: **Faces - Scrambled: Parametric t-test**. Display with **α=0.05, FDR-corrected**.

  In Process2: Keep the same file selection.

  Run process: **Test > Parametric test: Paired**: All file, All sensors, No average, two-tailed.

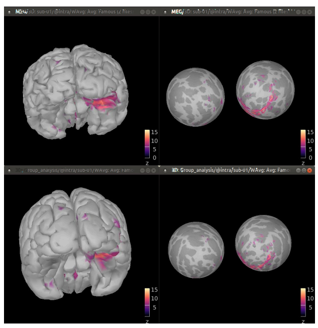
  Rename the file: **Faces - Scrambled: Parametric t-test**. Display with **α=0.05, FDR-corrected**.



Group analysis: Sources (only MEG: Faces-Scrambled; online tutorial includes all data)

Project sources on template

The sources were estimated on the individual anatomy of each subject; the resulting cortical source maps cannot be averaged directly. We first need to re-interpolate all the individual results on a common template (the ICBM152 brain, available in the "default anatomy" folder of the protocol). We also need to extract the absolute values for these source maps: the sign of the minimum norm maps are relative to the orientation of the current with respect to the surface normal, which can vary between subjects.



- In Process1, select all the **Intra-subject** folders from all the subjects, select **[Process sources]**.

  For a faster selection, you can use the view "Functional data (sorted by conditions)".
- Select process **Pre-process > Absolute values**, Overwrite.
- Add process **Sources > Project on default anatomy**, select **Cortex surface.** Click Run.

Check the coregistration process

- In subject **sub-01** folder **Intra-subject** sources)

Right-click on it > *Cortical activations > Display on cortex*
Right-click on it > *Cortical activations > Display on spheres*

- In subject **Group analysis** folder **Intra-subject** sources
  Right-click on it > *Cortical activations > Display on cortex*
  Right-click on it > *Cortical activations > Display on spheres*
- Set the **back** view, tilted towards the front, and use the same view for all plots

Reduce the surface smoothness in both cortices to appreciate that they are different

Spatial smoothing

The source maps estimated with constrained orientations can show very focal activity: two adjacent vertices may have very different normals, and therefore very different current values. When averaging multiple subjects, the peaks of activity may not align very well across subjects. Smoothing spatially the source maps may help obtain better **group** results.

- In Process 1, select all the source maps in Group Analysis.
- Run process **Sources > Spatial smoothing**: use absolute, FWHM 3mm, fixed FWHM, overwrite

MEG: mean (|Faces-Scrambled|)

- In Process1, select all the source files in **Group**_analysis/Faces-Scrambled|MEG
- Run process **Average > Average files**: By folder (grand average), Arithmetic Average, Not weighted
- Click Run

Regions of interest: OFA (Occipital Face Area), FFA (Fusiform Face Area), V1

MEG: Chi2-test |Faces-Scrambled|=0

- In Process1, select all the source files in **Group**_analysis/Faces-Scrambled|MEG
- Run process **Test > Parametric test against zero**: All file, One-sample Chi2-test two-tailed
- Screen capture: α=0.05 FDR-corrected

📝 What is the area where the **Faces** shows a higher activation than **Scrambled**?

Read more: [MEG visual tutorial: Group analysis]

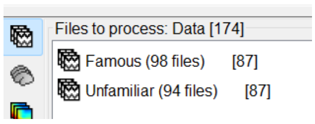
Bonus: Decoding with cross-validation

In this session, we will demonstrate how to perform MEG/EEG decoding within Brainstorm, a type of multivariate pattern analysis (MVPA), using support vector machines (SVMs). SVM decoding requires the LibSVM library (website). Brainstorm will install it automatically as a plugin when needed. On Linux and MacOS, you may have to explicitly recompile the library:

- In the MATLAB command window, execute "which svmtrain". If it returns an error message ('svmtrain' not found), you need to compile the library manually.
- Locate the MATLAB sub-folder in the libsvm installation folder:
  $HOME/.brainstorm/plugins/libsvm/libsvm-master/matlab
- In MATLAB, navigate to this folder and execute the "make.m" function.
- If it doesn't work, please refer to the instructions in the README file located in the same folder.
- You need a C compiler to be available on your computer. Mac users can use XCode.

Cross-validation is a model validation technique used to assess how the results of our decoding analysis generalize to an independent dataset. Here we will use the trials from the sub-01; please switch to your previous protocol with one subject.

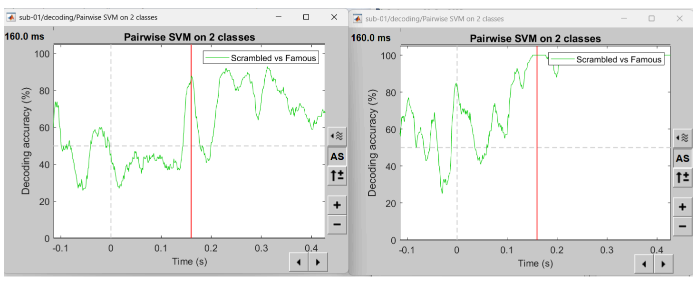
We require individual trials to perform this analysis. Switch to any protocol where you have the individual trials. For example, the "**PracticalMEEG**" protocol



- Scrambled and Famous trials to the Process1 tab
- Select process "Decoding > SVM decoding"

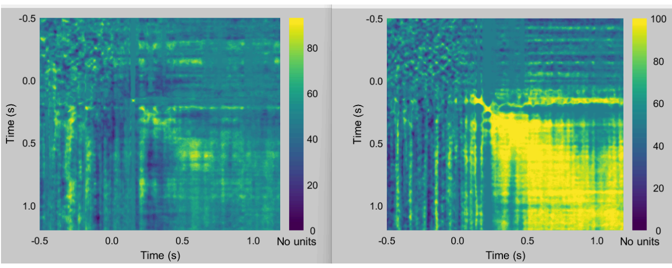
Sensor **EEG**, Low pass **32**Hz, N permutations **50,** N folds **5,** Decoding pairwise**, Run**

- Repeat the same steps for MEG



Intuitively, you might have expected to use the Process2 tab to decode famous vs. scrambled. However, the decoding process is also designed to handle pairwise decoding of multiple classes (not just two classes) for computational efficiency, allowing more than two categories to be entered in the Process1 tab.

The process will take some time. The results are then saved in a file within the **decoding** folder. The resulting matrix represents the decoding accuracy over time. The left plot shows EEG decoding accuracy, and the right plot shows MEG results for distinguishing between *scrambled* and *famous* faces. Both curves illustrate how effectively the classifier distinguishes between the two conditions over time. MEG generally shows a sharper and higher decoding peak than EEG, which is more affected by volume conduction and artifacts. Decoding accuracy increases around **150–250 ms**, suggesting that the neural representations of faces and scrambled images differ most during this time window. To explore this further, one could focus the analysis on this specific period.



Temporal generalization:
Repeat the above process, but select 'Temporal Generalization'.
The process will take more time (~10 minutes per modality). The results are then saved in a file in the 'decoding' folder.

Both EEG and MEG decoding revealed discrimination between famous and scrambled faces starting around 150 ms. MEG showed stronger and more sustained accuracy (150–600 ms), indicating a stable neural representation of face category information. EEG decoding was weaker and more transient (180–300 ms), reflecting rapid changes in scalp patterns and lower spatial specificity due to volume conduction.

Read more here: https://neuroimage.usc.edu/brainstorm/Tutorials/Decoding

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