

**Instructors: Takfarinas Medani, Yash Vakilna, Chinmay Chinara**

Once you have successfully installed and tested Brainstorm, proceed to download the data to be used in the workshop.

- Download the **raw data**:
  - <https://box.bic.mni.mcgill.ca/s/vJWC1ak9CW1M6YU>
- Unzip the downloaded raw data on your desktop: it will create a new folder named **workshopLAX\_raw**

**OUTLINE OF TOPICS COVERED IN THIS WORKSHOP****1. Introduction to Brainstorm Interface****2. EEG and MEG Analysis**

- Import anatomy
- Review Raw recordings
- Import events
- Frequency filters
- Artifact detection and correction
- Sensor level analysis
  - Import recordings
  - Review trials
  - Trial averages
- Source estimation
  - Forward model (aka Head model)
  - Noise covariance matrix
  - Computing inverse models
  - Atlases and Scouts

**3. SEEG Analysis**

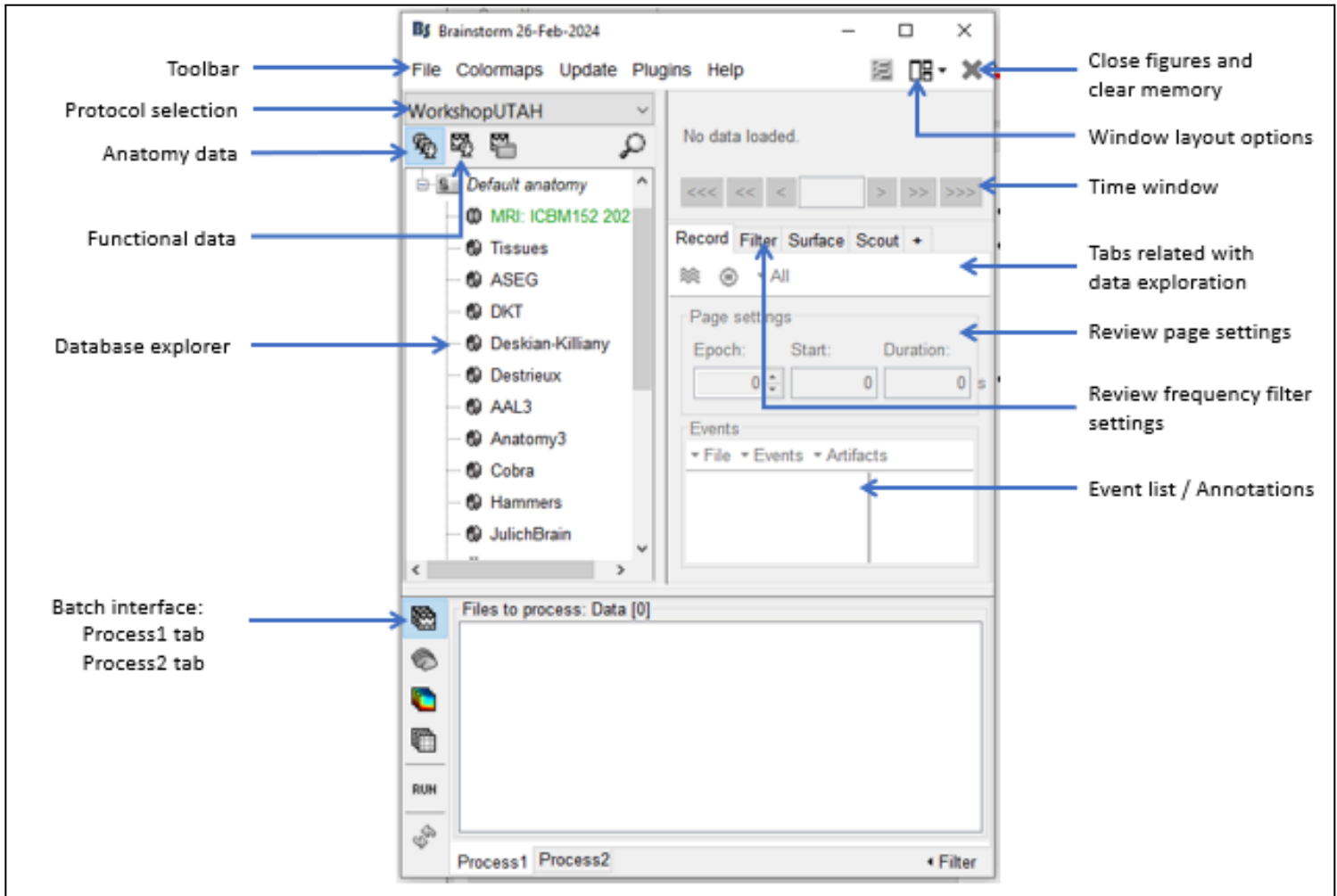
- Import anatomy
- Coregister and Normalize images to standard MNI space
- SEEG contact localization
- Review Raw recordings
- Modeling interictal spikes using Min-Norm Imaging
- Modeling ictal onset with Low Voltage Fast Activity (LVFA) using fingerprint analysis (Sensor Space)
- Appendix: How to run CAT12 segmentation from Brainstorm
- Appendix: Remove power line noise

**Preparing your dataset to be imported to Brainstorm**

- MRI DICOM files have to be converted to NIfTI format.
- EEG data can be imported to Brainstorm in native format or EDF file conversions.

## 1. Introduction to Brainstorm Interface

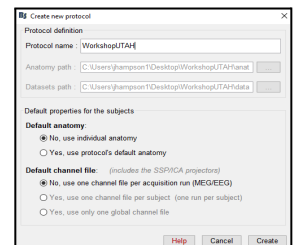
- CLOSE ALL YOUR APPLICATIONS, INCLUDING WEB BROWSERS
- Start Brainstorm: from Matlab or using the stand-alone application.



**\*\* red highlighted texts are processing steps we will be skipping during this workshop to save time**


## 2. EEG and MEG Analysis: Import Anatomy

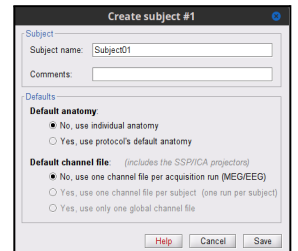
- Select File > New protocol: **WorkshopLAX**







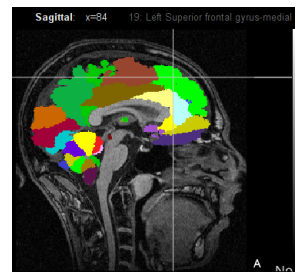
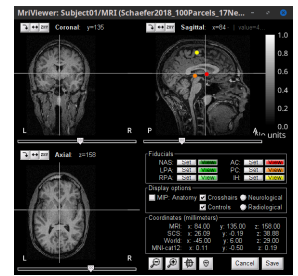
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
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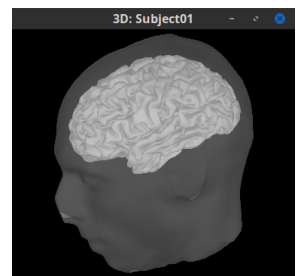
- o **No**, use individual anatomy
- o **No**, use one channel file per acquisition run (MEG/EEG)
- Introduction to database explorer (list of protocols, exploration modes...)
- Switch to anatomy view:  (1st button, on top of the database explorer)
- Right-click on protocol top node > New subject: **Subject01** (use Defaults)
- Right-click on the created subject > Import anatomy folder (**Do not select the (auto) option**)
  - o *Files of Type* **CAT12**
  - o Select the **anatomy** folder in **Desktop/workshop\_lax/**
  - o For *Number of vertices* set **15000**




- Once the MRI viewer opens
  - o Explain fiducial points and the coordinates (MRI, SCS, MNI)
  - o Set coordinates: , set fiducials: (MRI coords) **NAS [125, 230, 64] LPA [48, 141, 44] RPA [215, 140, 59]**
- Exploring MRI (  ): double-click or right-click > *Display* > *MRI Viewer*
  - o Exploring the volume (click, mouse wheel, sliders)
  - o Anatomical atlases, colormaps, colorbar, figure popup menu
- Exploring MRI (  ): right-click > *Display* > *3D orthogonal slices*
- Display cortex (  ): double-click or right-click > *Display*
  - o 3D figure: rotation, zoom
  - o Predefined views and keyboard shortcuts: left, right, top, etc
  - o Surface tab: smooth, sulci, edges
  - o Scouts tab: atlases and scouts

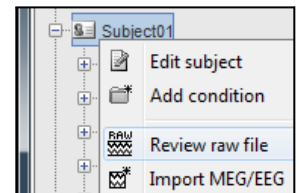


- Close all figures (  button at top-right): close all figures and empty the memory



### 3. EEG and MEG Analysis: Review Raw recordings

- Switch to functional view:  (2nd button, on top of the database explorer)
- Create **Link to raw file**: right-click on Subject01 >
  - o *Files of Type* **MEG/EEG: Yokogawa/KIT (\*.sqd; \*.con; \*.raw; \*.ave; \*.mrk)**



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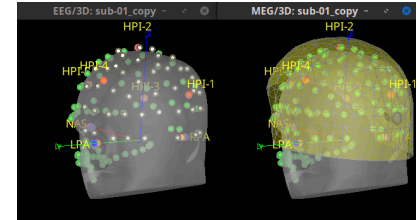
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- Select the file **SEF\_000-export.con** in the **data** folder in **Desktop/workshop\_lax/**
- Click on **Open**
- In the popup for **Refining registration**, click on **No**
- The sensor coregistration will show, close it for now

368 EEG060	EEG
367 EEG061	MISC
368 EEG062	EOG
369 EEG063	ECG
370 EEG064	MISC
371 EEG065	EEG

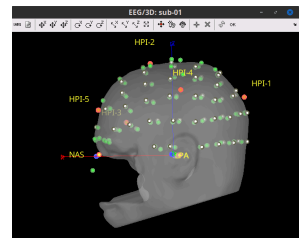
- Change the type of some channels, right-click on the channel file > *Edit channel file*:



- Channel **EO1** (208) and **EO2** (209): Change the type to **EOG**
- Channel **EKG+** (214): Change the type to **ECG**
- Channel **E** (231): Change the type to **Misc**
- Close the figure and accept to save the modifications

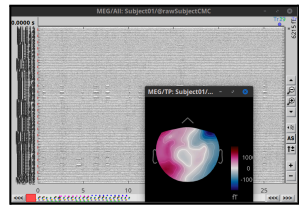


- Check sensor coregistration

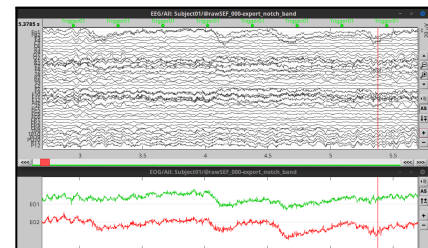
- ❖ right-click > *MRI registration* > *EEG:Check*  
Some electrodes are above or inside the head surface
- ❖ right-click > *MRI registration* > *EEG: Edit*
  - Select **Project electrodes on surface**
  - Click **OK** and save
- ❖ right-click > *MRI registration* > *MEG:Check*
- Close figures



- Review EEG signals:  right-click > *EEG* > *Display time series*
  - Display in columns (  ), display windows of 10s
  - Amplitude gain: buttons and shortcuts
  - Add a topography and set the window layout to weighted

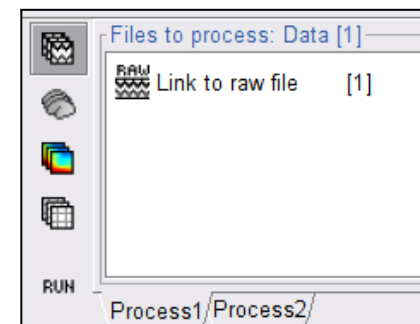
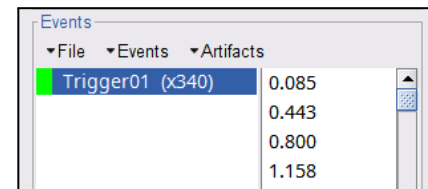


- Review MEG signals
- Review EOG signals
- Review EEG and EOG signals simultaneously
- Close all figures









## 4. EEG and MEG Analysis: Import events

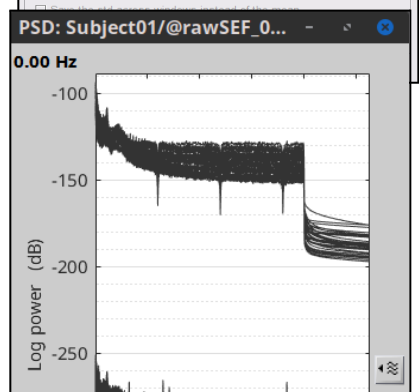
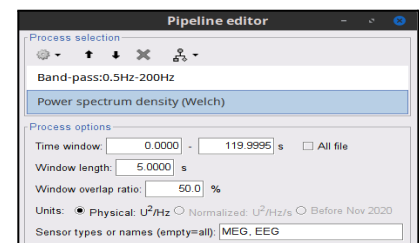
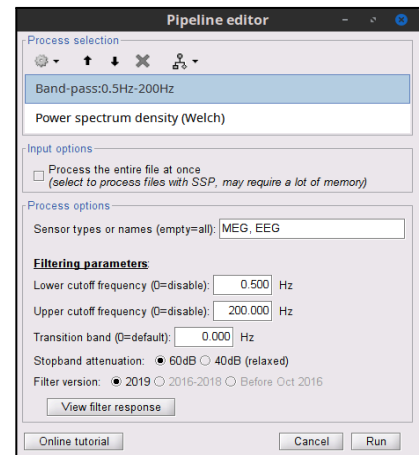
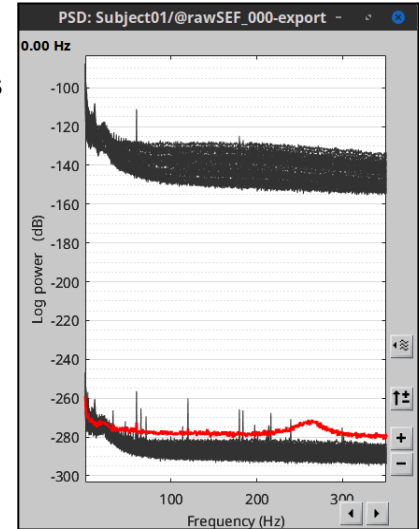
- Different ways of Importing events
- Right-click on Link to *raw file* > *TRIGGER* > *Display time series*
  - Display in columns. Notice that Trigger01 contains the information of the electric stimuli
- In the Record tab, menu *File* > *Read events from channel*
  - Event channel = **Trigger01**
  - Option = **TTL: detect peaks of 5V/12V on an analog channel**
  - Do **NOT** check the option **Accept zeros as trigger values**
- Close the figure with the timeseries to save modifications





## 5. EEG and MEG Analysis: Frequency filters

- Process section
  - Tabs **Process1**, **Process2**
  - File types:  recordings,  sources,  time-freq, and  matrices
- EEG and MEG: Filter power line artifact
  - Close all the figures
  - Drag-and-drop () raw file in *Process 1*, click [RUN]
  - Add the process: *Frequency, Power spectrum density (Welch)*
    - *Time window = All file, Window length = 5s, Overlap = 50%*
    - *Units = Physical*
    - *Sensor types = EEG, MEG*
  - Click on **Run**
- Open the new () PSD file
  - Two PSD groups, from top to bottom: **EEG** and **MEG** sensors
  - Peak around 11 Hz: alpha waves from the subject's brain
  - Peaks at 60Hz, 120Hz, 180Hz on EEG and MEG: Power lines (60Hz+harmonics)
  - Smaller peaks at 35Hz, 65Hz, 70Hz, 183Hz, 197Hz on MEG only: Unknown source
  - MEG sensor **LC11** appears to have a higher level of noise than all the other MEG sensors.  
Select the channel (it becomes red), right-click and *Mark selected as bad*  
This is often an indication of a bad channel, we can verify this by reviewing MEG signals
- Notch filter the raw file: Select: **Pre-process > Notch filter**
  - *Frequencies to remove (Hz) = 60, 120, 180 Hz*
  - *Sensor types = EEG, MEG*
  - Compute the PSD for the notch-filtered raw file, and open the new PSD file
- EEG and MEG: Bandpass filter
  - Drag-and-drop notch-filtered raw file in *Process*, click [RUN]
  - Add the process *Pre-process > Band-pass filter*
    - *Sensor types = EEG, MEG, Lower cutoff freq = 0.5 Hz, Upper cutoff freq = 200 Hz*
    - Click **View filter response** to see the filter properties
  - Select: **Frequency, Power spectrum density (Welch)**



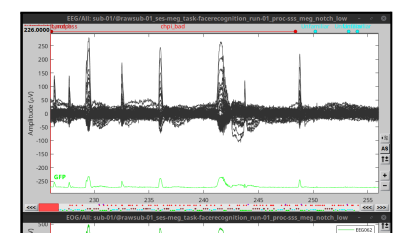
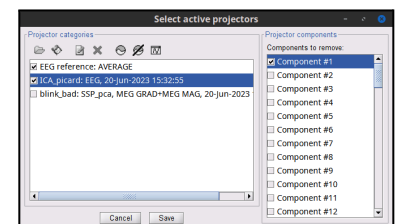
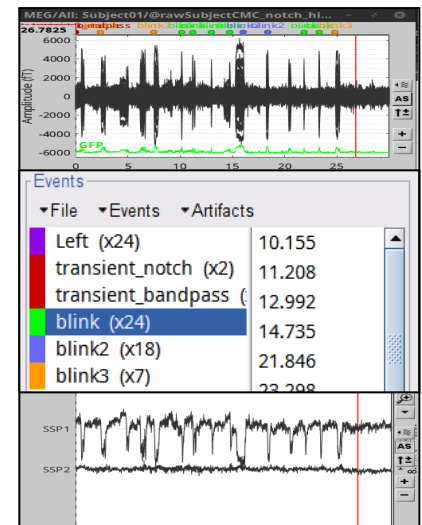
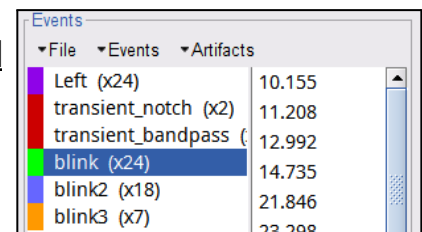
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- Add the process: *Frequency, Power spectrum density (Welch)*
- **Run** the pipeline
- EEG: re-reference to Average
  - Open the EEG timeseries for the bandpass filtered raw file (in folder **\_notch\_band**)
- Click on *Artifacts > Re-reference EEG* and use **AVERAGE** as EEG reference channel
- Delete intermediate files that won't be needed anymore:
  - Select folder **SEF\_000-export\_notch**
  - Press the Delete key (or right-click > *File > Delete*)



## 6. EEG and MEG Analysis: Eye-movement related artifacts and other artifacts

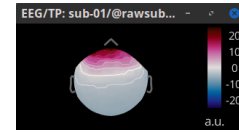
- Detect eye-movement events
  - Open the time series for EEG and EOG
  - In the Record tab, select *Artifacts > Detect eye blinks*, and use the parameters:
    - *Channel name = EO2, Time window = All file, Event name = blink*
  - Display MEG signals (along EOG) and see some blink occurrences
  - Merge all the **blink** event groups in a **blinks** group
- Detect heartbeat events
  - Open the time series for EEG and ECG
  - In the Record tab, select *Artifacts > Detect heartbeats*, and use the parameters:
    - *Channel name = EKG+, 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 blink artifacts from EEG with ICA
  - Open the time series for EEG
  - In the Record tab, select *Artifacts > ICA components*, and use the parameters:
    - *Time window = All file, Band-pass filter = [0, 0], Resample = 0*
    - *ICA algorithm = Picard, Number of ICA components = 0*
    - *Sort components based on correlation with = EOG, ECG*




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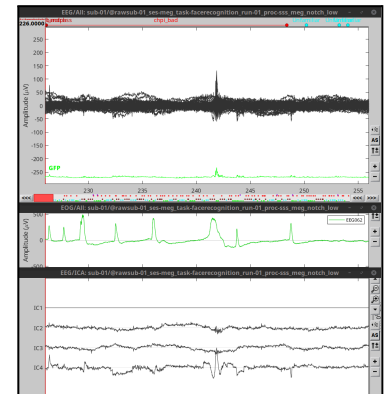
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- In the *Select active projectors* window, **uncheck** all ICA components, highlight the first eight and plot their time series (  ), and topologies (  )
- Open EEG and EOG time series and disable **auto scaling** ( **AS** ) in the 3 plots
- Check **Component #1** which is related to the ECG signal and impact of removing it from the EEG signal
- Check **Component #2** which seem related to the EOG signal and verify the impact of removing it from the EEG signal
- Click on **Save**, close all figures



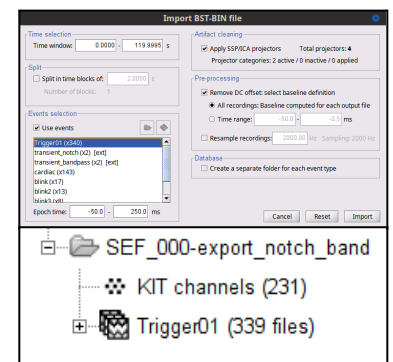
in the 3  
verify the


- Remove blink artifacts from MEG with SSP
  - Open the time series for MEG
  - In the Record tab, select *Artifacts > SSP: Eye blinks*, and use the parameters:
    - *Event name* = **blinks**, *Sensors* = **MEG**
  - In the *Select active projectors* window, **uncheck** all components, highlight the first two and plot them (  )
  - Open MEG (all) and EOG time series and disable **auto scaling** ( **AS** ) in the 3 plots
  - Check **Component #1** to verify the impact of removing it from the MEG signal
  - Click on **Save**, close all figures

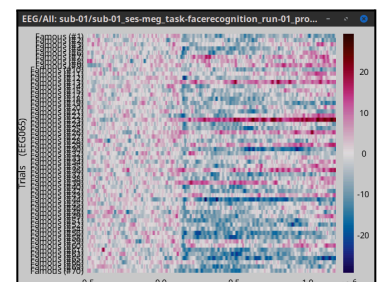


## 7. EEG and MEG Analysis: Import recordings

- Import in database
  - Right-click on the pre-processed file > *Import in database*, and use the parameters:
    - *Time window* = **0 - 119.9995 s**
    - Do **NOT** check **Split in time blocks**
    - Check **Use events** and select **Trigger01 (x340)**
    - *Epoch time* = **-50 to 250 ms**
    - Check **Apply SSP/ICA projectors**
    - Check **Remove DC offset**, select **All recordings**
  - Answer **Yes** to this question to discard the last epoch.
  - A new folder named **SEF\_000-export\_notch\_band** is created (no more **raw** indicator)





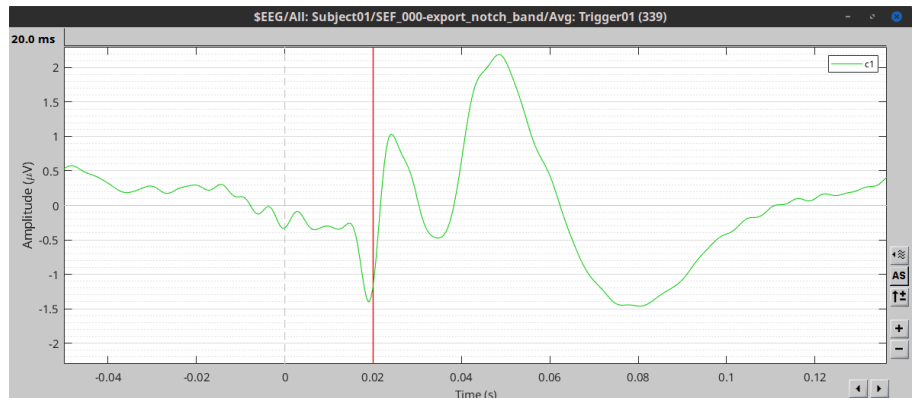
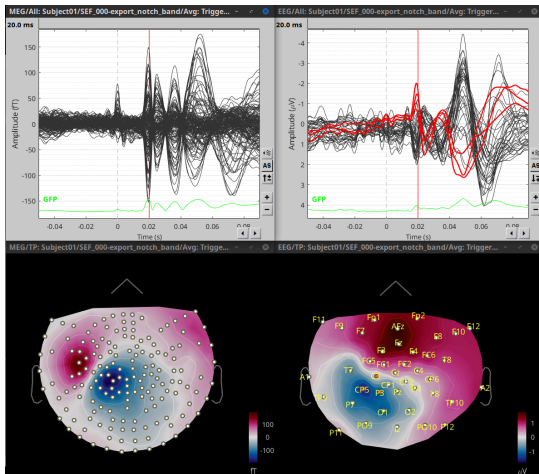
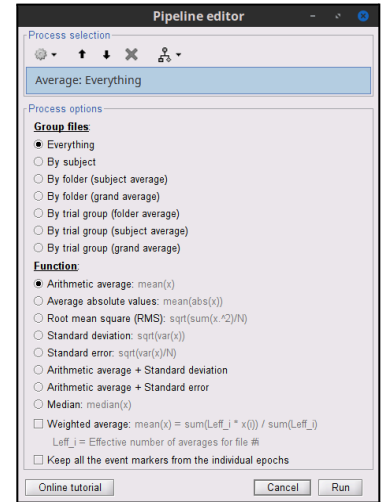
- Review trials
  - Trials groups (  ), contain same-name trials (often imported from with the same event)



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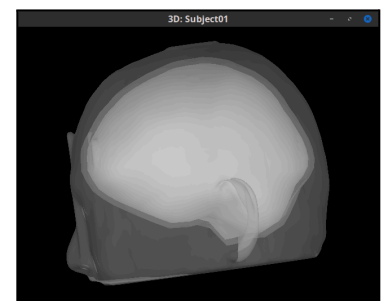
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- Trials containing an bad event (with **bad** in its name) are labeled as bad ( )
- Rastroplots: Right-click on trial group > *Display as image* > *EEG* select channel **CP5** in the Display Tab
- Average trials
  - Drag and drop all the trial groups in Process1
  - Run process *Average* > *Average files*:
    - *Group files* = **Everything**, *Function* = **Arithmetic average**
- Check different plots for the average somatosensory evoked potential (SEP) in **EEG** signals, and the somatosensory evoked fields (SEF) in **MEG** signals. Plot both topographies
- Create a sensor cluster
  - Open the *Cluster* tab by clicking on the plus sign (+) at the right of *Record* tab <sup>NEW</sup> <sub>IND</sub>
  - Click on  to create a new cluster by indicating the sensor names, use **C3, CP5 and P3**
  - Plot the cluster time series with on the plot button (  )
- Observe Components N20, P25, N33 and P45 visible over left somatosensory cortex in EEG and their respective fields in MEG
- Close all figures. Do not save the created cluster
- 




## Forward model (aka Head model)

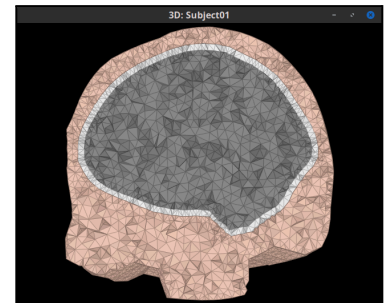
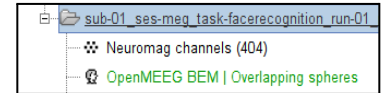
- Computing boundary element (BEM) layers
  - Go to the anatomy view
  - Right-click on **Subject01** folder > *MRI segmentation* > *Generate BEM surfaces*
    - Select **Brainstorm**



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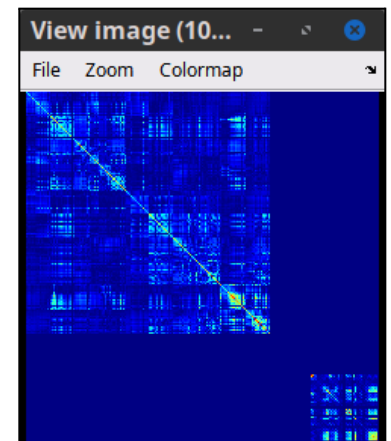
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- Number of vertices: *Scalp* = **1082**, *Outer skull* = **642** and *Inner skull* = **642**
  - Thickness of layers, Skull (mm) **4**
  - **Note:** This number of vertices is selected to avoid long computations during the workshop. Otherwise, values of **1922 vertices** can be used.
- Right-click on the default cortex (in green) > *Force inside skull*
- The **fix** cortex is now selected as default
- Compute the head model for EEG and MEG
  - Go back to the functional data view
  - Right-click on the channel file (  ) in the imported data folder > *Compute head model*
    - *Source space* = **Cortex surface**
    - *Forward model* = **MEG: Overlapping spheres** and **EEG: OpenMEEG BEM**
    - Click on **OK**
      - Use default BEM layers and conductivities
      - Use default OpenMEEG options
    - The process may take up to 5 min
- Demo: the forward model can be computed also using the FEM method
  - Computation of FEM meshes from BEM surfaces. They can be computed from volumes
- Forward model can be computed with the DUNEuro plugin





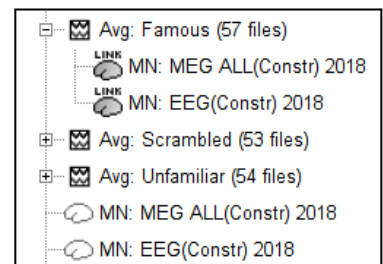
## 9. EEG and MEG Analysis: Noise covariance matrix

- Compute noise covariance for EEG and MEG from pre-stimulus baselines
  - Select the trial group, right-click > *Noise covariance* > *Compute from recordings*:
    - *Baseline* = **[-50, 0] ms**, *Sensors* = **EEG and MEG**
  - Select **Block by block**





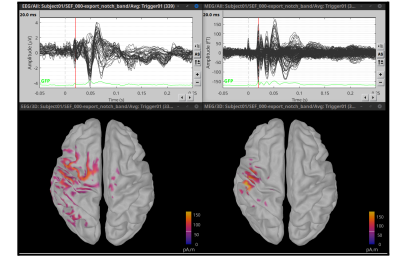
## 10. EEG and MEG Analysis: Computing inverse models

- Compute inverse model (EEG)
  - Right-click on the head model (  ) > *Compute sources*, use these parameters:
    - Select **Minimum norm imaging**, Select **Current density map**
    - Select **Constrained: Normal to the cortex**
    - *Sensors* = **EEG**
- Compute inverse model (MEG)
  - Right-click on the head model (  ) > *Compute sources*, use these parameters:
    - Select **Minimum norm imaging**, Select **Current density map**





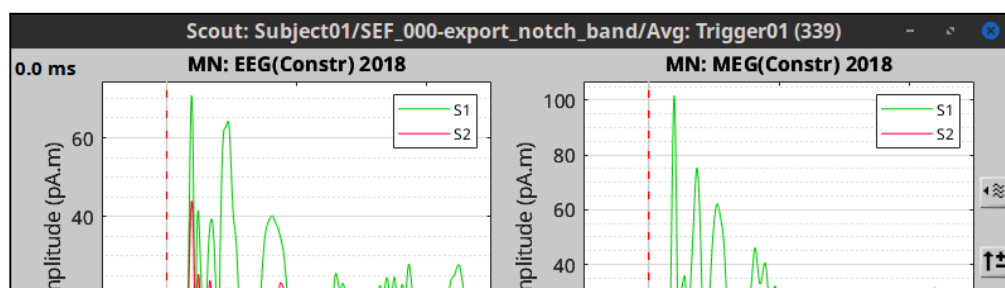
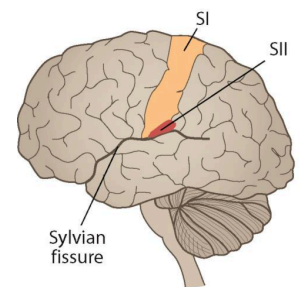
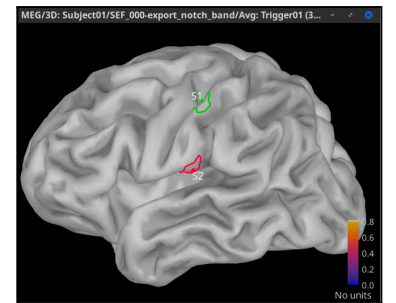


- Select **Constrained: Normal to the cortex**
- **Sensors = MEG**
- Explanation on the inversion kernel (  ) and link (  ) files in the database
- Explore the estimated average **Avg: Trigger (339)** at 20ms
  - Display EEG and MEG **time series** (butterfly mode)
  - Display the **sources** derived from EEG and from MEG data
  - Set the colormap to local maximum (maximum in that time slice)
    - Right-click on the colorbar > Colormap: sources > Maximum Local
  - Set time to **100 ms**
  - Set **Smooth = 30%** and **Amplitude** threshold to **40%** (both in Surface tab)
- Explore other times, and the evolution of the brain activity



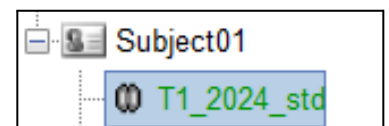
## 11. EEG and MEG Analysis: Atlases and Scouts

- Display the **sources** derived from EEG and MEG data
  - In the Scout tab, use the dropbox to select different Atlases
  - Operations with Atlases and Scouts
- Create Scouts
  - Open the sources (from MEG) for the average, left view
  - Select the **User Scouts** atlas
  - Create scout **S1** (primary somatosensory cortex) on the left hemisphere
    - Go to Time **20 ms**, Amplitude threshold **60%** Smooth = **30%**
    - Scout tab: Click on *Select point* (  ), then point on activity in the post central gyrus
    - Grow Scout to 20 vertices
    - Rename to S1 (double-click on the scout in the list)
    - Review trace: Absolute values
- Create a second scout **S2** (secondary somatosensory cortex) on the left hemisphere
  - Go to Time **50 ms**, Amplitude threshold **20%** Smooth = **30%**
  - Scout tab: Click on *Select point* (  ), then point on activity in the bottom part of the post central gyrus, which is the anatomical location of S2.
- Review S1 and S2 traces together in absolute values. For sources from EEG and MEG



## 12. SEEG Analysis: Import Anatomy

- **Import T1 pre-implantation: (5 mins)**
  - Right-click on **Subject01** > **Import MRI**
  - Select format: **MRI: NifTI**
  - Select file: **T1\_2024\_std.nii.gz**
  - Introduction to the MRI viewer: Click, mouse wheel, color bar, popup
  - In the MRI Viewer, click on **Compute MNI normalization** and select

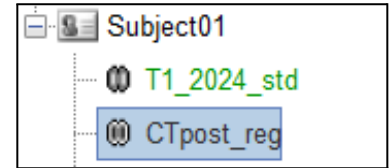


# Workshop Los Angeles

December 2024

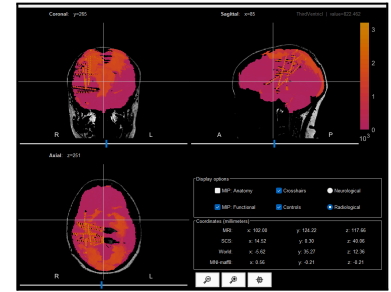
the **maff8** algorithm. This sets default positions for the fiducials Coordinate systems: MRI, SCS, World, MNI and also does MNI normalization

- Click **Save**
- **Import post-implant CT: (10 mins)**
  - Prerequisites: **BrainSuite** , **ct2mrireg plugin**
  - Right-click on the **Subject01** > **Import CT**
  - Select format: **MRI: Nifti**
  - Select file: **CTpost\_std.nii.gz** (pre registered **CTpost\_reg.nii.gz**)



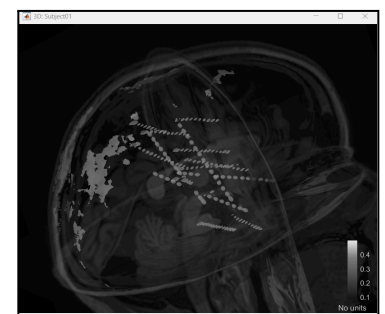
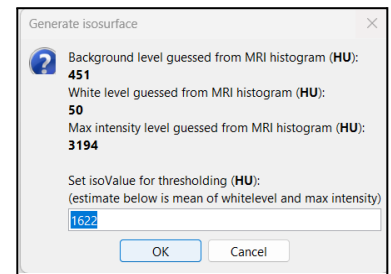
### 13. SEEG Analysis: Coregister and Normalize images to standard MNI space

- **Select coregister using CT2MRI and select Yes both to reslice volume and clean CT volume.** (Select **Ignore** and select **No** for reslice volume as the CT is already co-registered.)
- The MRI viewer opens automatically, showing the post-implantation CT volume as a colored layer on top of the previous volume. Use this display to validate that the co-registration of the two volumes is correct (all the parts of the head must align well).

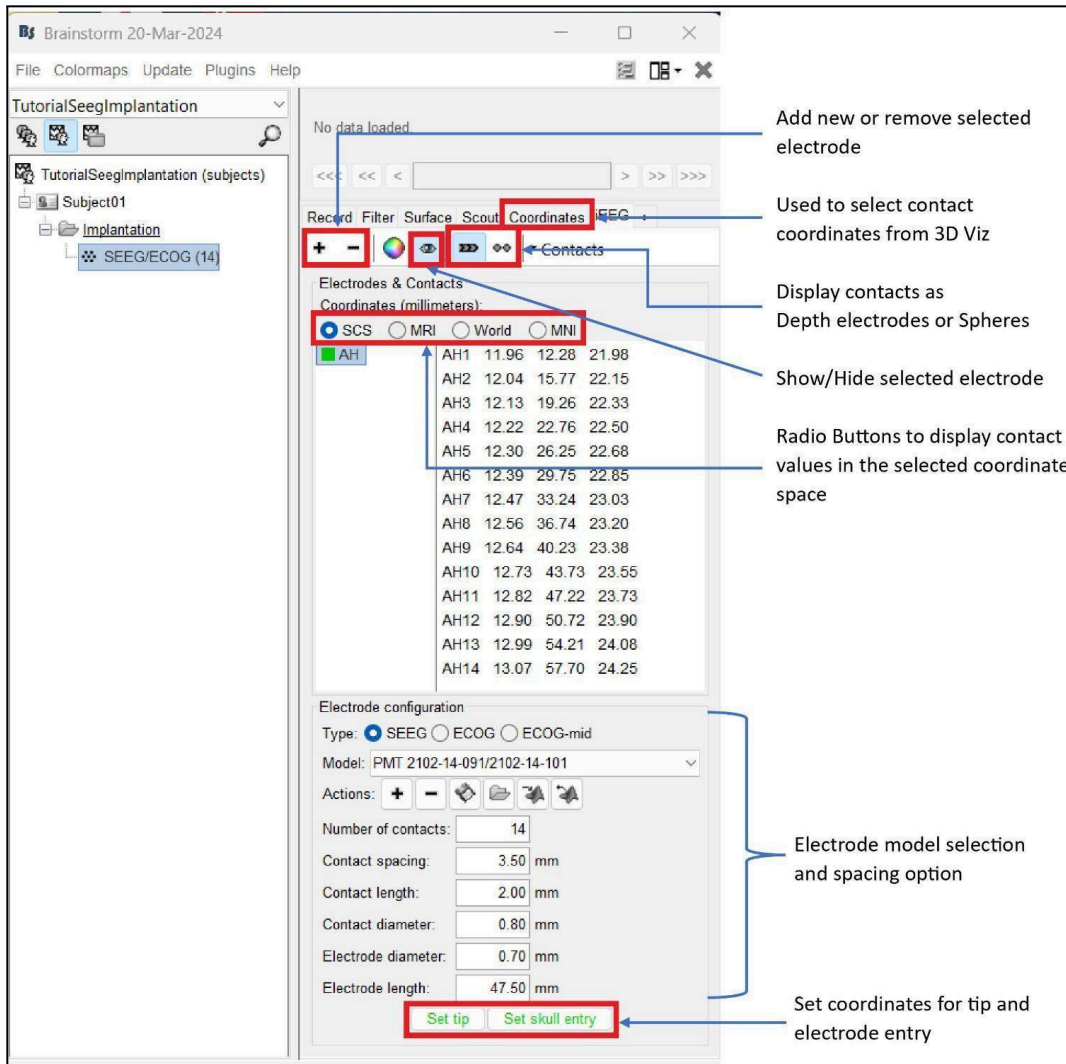


- **Generate isoSurface (2 mins)**

- This creates a thresholded mesh from the CT to separate the contacts from the rest. This aids the user towards localization of the electrodes and its contacts more accurately.
- Right click on **CTpost\_reg**> **CT segmentation** > **Generate threshold mesh from CT**
- Set the isoValue for thresholding, the estimation is from the mean of white level and max intensity of the CT. You can leave it as default, select **OK**
- An isosurface is generated showing the contact as blobs overlaid on the 3D MRI slices. The **Thresh** slider under **Surface options** can be used to fine tune and regenerate mesh with different isoValues.



### 14. SEEG Analysis: Contact localization

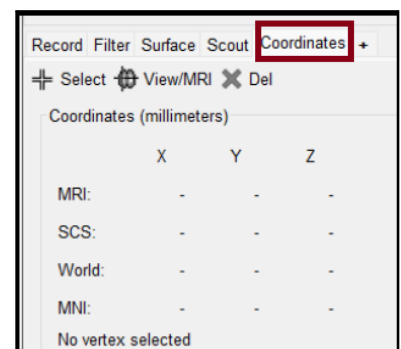


The screenshot shows the Brainstorm software interface with several key components highlighted and annotated:

- Panel Management:** A '+' icon is used to add new or remove selected electrodes.
- Coordinate Selection:** The 'Coordinates' panel tab is used to select contact coordinates from 3D visualization.
- Display Options:** A 'Contacts' icon is used to display contacts as depth electrodes or spheres.
- Coordinate System:** Radio buttons allow switching between coordinate systems: SCS (Selected), MRI, World, and MNI.
- Electrode List:** A table displays 14 electrodes (AH1-AH14) with their X, Y, and Z coordinates in millimeters.
- Electrode Configuration:** A section for setting electrode parameters:
  - Type:  SEEG,  ECOG,  ECOG-mid
  - Model: PMT 2102-14-091/2102-14-101
  - Number of contacts: 14
  - Contact spacing: 3.50 mm
  - Contact length: 2.00 mm
  - Contact diameter: 0.80 mm
  - Electrode diameter: 0.70 mm
  - Electrode length: 47.50 mm
- Coordinate Setting:** 'Set tip' and 'Set skull entry' buttons are used to set coordinates for the electrode tip and skull entry point.

## • Manual contact labeling (30 mins)

- Right click on **CTpost\_reg** and choose **SEEG/ECOG implantation**. This takes you to the functional tab and **Subject01 > Implantation > SEEG/ECOG (0)** channel gets created. The MRI Viewer (CT overlaid MRI) and 3D Viz (isoSurface+3D MRI Slices) load up as well along with the **Panel iEEG**.
- Click the **+** icon from the list of panel tabs and choose **Add: Coordinates**. This adds the **Panel Coordinates** which will be used to select points from the 3D Viz.
- On **Panel iEEG** Click on the **+** (**Add new electrode**). This opens up the **Add electrode** window. Enter anything under the **Electrode label** based on your convention. For this e.g., enter **AH** and press **OK**.
- Select **SEEG**, and choose the electrode model (**PMT**



The 'Add electrode' dialog box shows the 'Coordinates' panel selected. It includes a table for coordinate selection:

	X	Y	Z
MRI:	-	-	-
SCS:	-	-	-
World:	-	-	-
MNI:	-	-	-

Buttons for 'Select', 'View/MRI', and 'Del' are visible. The status at the bottom indicates 'No vertex selected'.

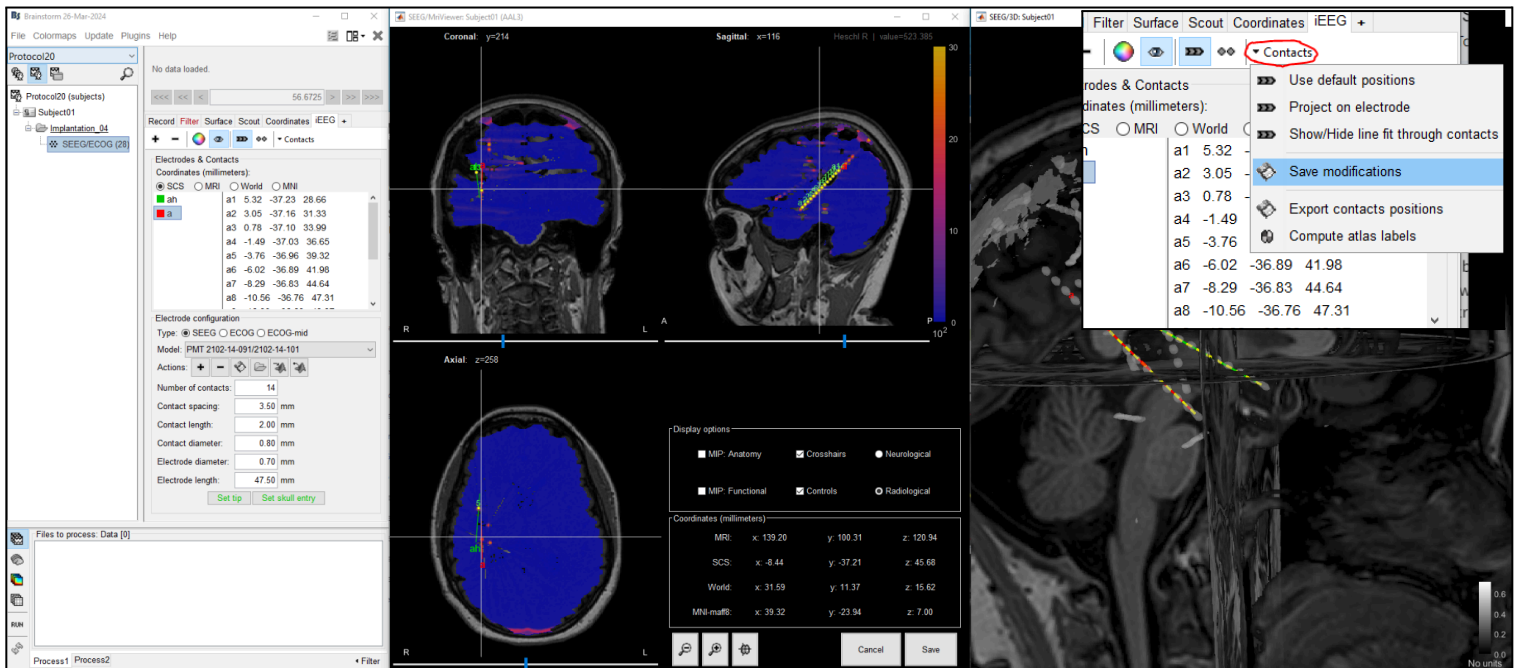
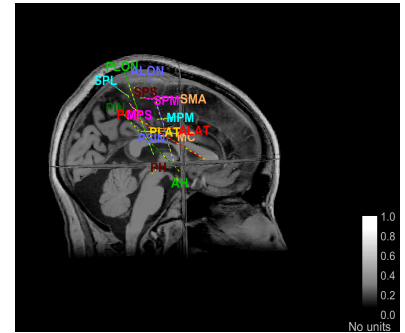
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**2102-14-091/2102-14-101** which is a 14 contact electrode.

- Switch to the **Coordinates** panel, click **Select** and choose the deepest contact from the isosurface in 3Dviz. This should plot a yellow crosshair marker point on the contact blob and also update the crosshair in the MRI Viewer.

**Note:** You can play around with the **Thresh** slider under **Surface** tab to get better visibility of the contacts as required

- Switch back to the iEEG panel and click **Set tip** and the button turns green, indicating that the tip has been set. This point in 3D is at the centroid of the blob, which gives a more accurate location of the contact.
- Go back to the **Coordinates** tab and repeat the steps above for the skull entry
- Now click **Set skull entry** and the button turns green indicating that the entry point has been set. The MRI Viewer gets updated with the electrode.



- Click on **Save** in the MRI Viewer. This saves the new channel file and updates the number of channels in the database explorer. Click **Yes** for any other **Save** windows that pop up.
- Double-click the **Implantation > SEEG/ECOG** channel in the Functional tab to get an updated 3D Viz and MRI Viewer with all the electrodes.
- Repeat these steps for each SEEG electrode except the last step of saving.
- For saving all the further electrodes, click on **Contacts > Save Modifications** to update the



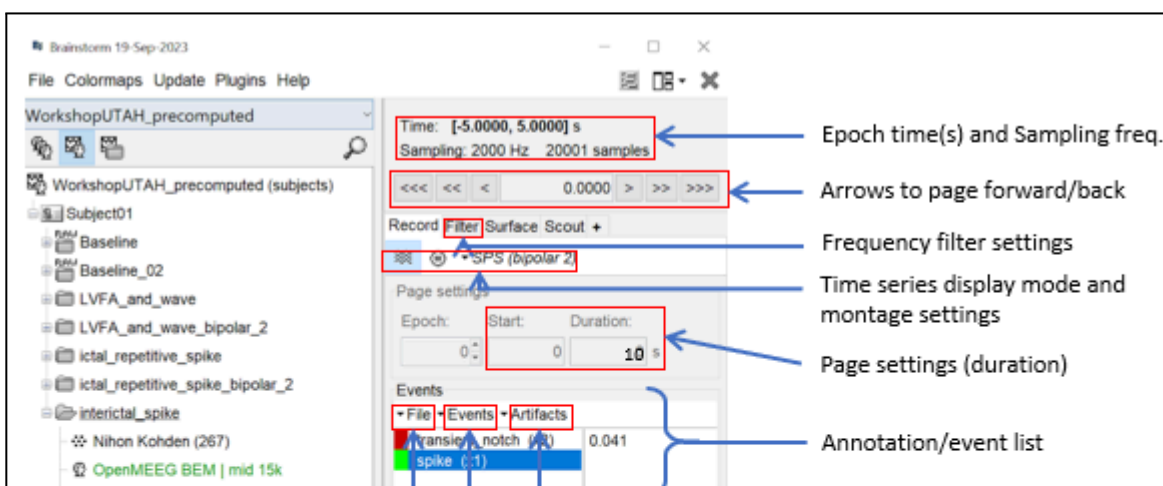
channel information and that saves the changes to the database.

- **Anatomical labeling (5 mins)**

- Switch to the anatomy view.
- Right-click on **Subject01 > Add MNI parcellation > AAL3**. Repeat with parcellation: **Hammers83, Hammers95**.
- Close all the figures. Switch back to the Functional view.
- Right-click on the channel file > **iEEG atlas labels**
- Create **Subject01.tsv** and click **OK**. **Select all the available options: coordinates in various coordinate systems, volume parcellations, surface parcellations.**
- The output is a table, one row per sensor contact in the channel file, for each sensor: coordinate location in the parcellation atlas and probability of the label .

Channel	MNI	AAL3 (MNI-linear)	AAL3 (MNI-linear)_prob	Hammers95 (MNI-linear)	Hammers95 (MNI-linear)_prob
ah1	[39.877,11.669,-5.910]	Insula R	82%	insula_ant_inf_c R	88%
ah2	[40.176,8.912,-3.437]	Insula R	66%	G_insula_mid R	69%
ah3	[40.475,6.155,-0.964]	Insula R	62%	G_insula_post R	62%
ah4	[40.773,3.398,1.509]	Insula R	96%	G_insula_post R	92%
ah5	[41.072,0.641,3.982]	Insula R	89%	G_insula_post R	98%
ah6	[41.371,-2.116,6.456]	Insula R	89%	G_insula_post R	80%
ah7	[41.670,-4.873,8.929]	Rolandic_Oper R	64%	G_insula_post R	60%
ah8	[41.968,-7.630,11.402]	Rolandic_Oper R	52%	PL_postce_G R	86%
ah9	[42.267,-10.387,13.875]	Rolandic_Oper R	59%	PL_postce_G R	94%
ah10	[42.566,-13.144,16.348]	Rolandic_Oper R	88%	PL_postce_G R	98%
ah11	[42.864,-15.901,18.822]	Rolandic_Oper R	100%	PL_postce_G R	100%
ah12	[43.163,-18.658,21.295]	Rolandic_Oper R	82%	PL_postce_G R	97%
ah13	[43.462,-21.415,23.768]	N/A	N/A	PL_supramarginal_gyrus R	99%
ah14	[43.761,-24.172,26.241]	N/A	N/A	PL_supramarginal_gyrus R	100%

## 15. SEEG Analysis: Review Raw recordings (15 mins)




Annotations for the screenshot:



- Epoch time(s) and Sampling freq.
- Arrows to page forward/back
- Frequency filter settings
- Time series display mode and montage settings
- Page settings (duration)
- Annotation/event list

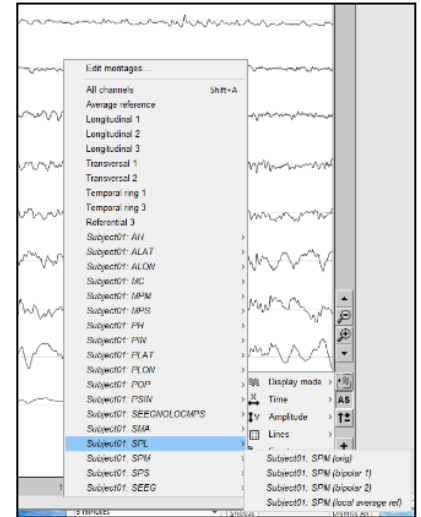
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December 2024

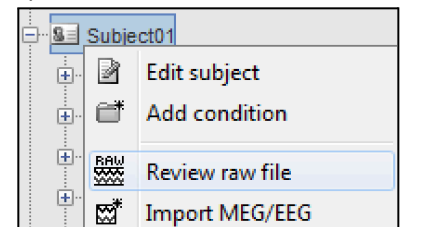
- In the functional view:  (2nd button, on top of the database explorer)
- Create Link to raw file: right-click on **Subject01 > Review raw file**
- Files of Type **EEG: EDF/EDF+**
  - Select the file **Baseline.edf** in the data folder
  - Click on **Open**

- Review SEEG: Right-click on **Link to raw file > SEEG > Display time series**

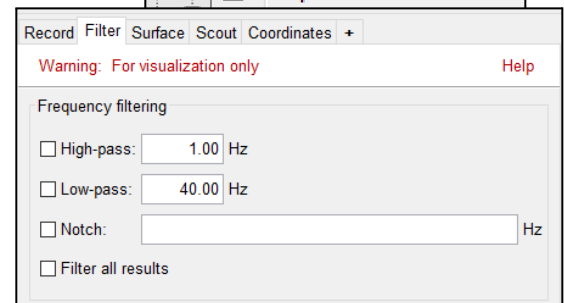
- Display in columns: Button  in the Record tab > **Display mode > Column**
  - **Amplitude**: Buttons and shortcuts, Display menu
  - **Time**: Display windows of 15 seconds, Scroll with F3, Auto-Scale button
- Select bad channels + right click > **Channels > Mark selected as bad** (if needed)
- Montages: click **Display configuration**  > **Montage > Subject01: SEEG > Subject01 SEEG: (bipolar 2)**
  - Select the montage for the dataset (Average, Referential, Transversal or longitudinal)
  - For the SEEG dataset, select **bipolar 2** montage for continuous chain.



- Filter settings for review are set under the **Filter** tab in the panel
  - this is only for visualization
  - Select the checkbox to turn ON the high or low frequency filter.

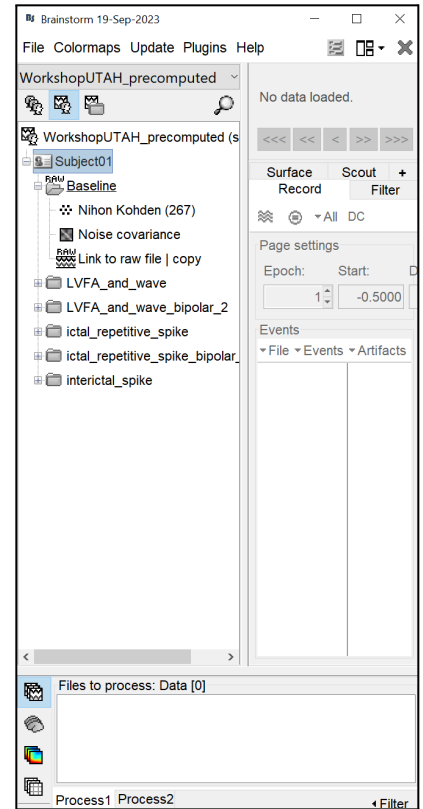


- Add annotations:
  - Got to record view > **Events > Add Group > Event A**
  - Select 2 peaks and press **E**
  - Got to record view > **Events > Add Group > Extended**
  - Drag across the window
  - Press **E**
  - Save annotation: **File > Save modifications**



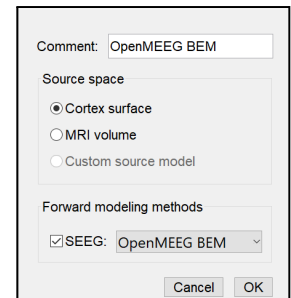
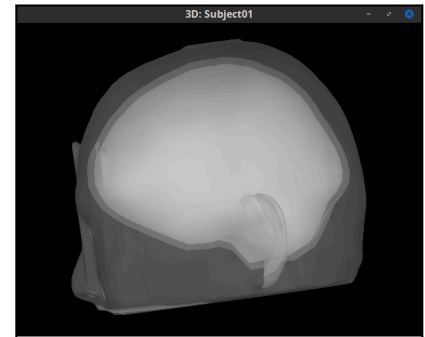
### 16. SEEG Analysis: Import precomputed Brainstorm protocol (5 mins)

- Prerequisite: Download from the zip file from url: <https://box.bic.mni.mcgill.ca/s/Yqjt3scilijtHMqF>
- Open Brainstorm
- Click **File > Load Protocol > Load from zip file**
- Click on **...**, and point to the downloaded zipped file: **WorkshopUTAH\_precomputed.zip**
- Protocol called **WorkshopUTAH\_precomputed** should appear

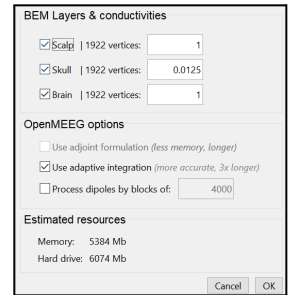


### 17. SEEG Analysis: Modeling interictal spikes using Min-Norm Imaging (Yash Vakilna)

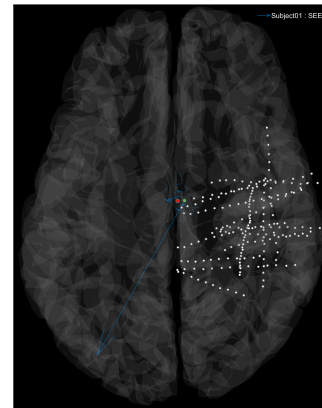
- **Compute Forward Model (aka Head Model) (10 mins)**
  - Computing boundary element (BEM) layers
    - Prerequisite: **OpenMEEG** plugin
    - Go to the anatomy view
    - Right-click on **Subject01** folder > **MRI segmentation > Generate BEM surfaces**
      - Select Brainstorm
      - Number of vertices: Scalp = **1922**, Outer skull = **1922** and Inner skull = **1922**
      - Thickness of layers, Skull (mm)= **4**
      - **DON'T CLICK [OK]**
    - Double-click on **mid\_15002V** to make it as the default cortex (in green). If already green, no need to double-click.
  - Compute the head model for SEEG



- Go back to the functional data view, navigate to the **interictal\_spike** folder and expand it
- Right-click on the **Nihon Kohden channel file** ( 📄 ) > **Compute head model**
  - Source space = **Cortex surface**, Forward model = **SEEG: OpenMEEG BEM**, click **OK**
  - Use default BEM layers and conductivities.
  - Use default OpenMEEG options.
  - **DON'T CLICK [OK]**
- Copy the head model files to the other folders
  - Right-click on the head-model file ( 📄 **OpenMEEG BEM | mid 15k**) > **Copy to other folders**

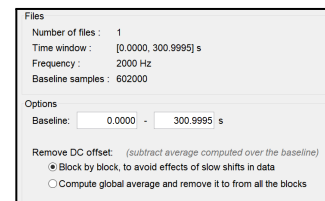






- View Leadfield vectors
  - Right-click on head-model file ( 📄 ) > **View SEEG leadfield vectors**
  - Select reference=**MC2**, click **OK**
  - Make sure scouts are unselected
    - Go to the Scout tab, and make sure **ALL** and **SEL** are unselected
    - Go back to the **Surface** tab
  - Select Transparency = **90**, and **Press Shift+Up arrow** till the arrows are visible
  - Press **E** to show the electrode
  - Press **Up/down** to change the Reference electrode, **right/left** to change the Target
  - Press **X** to close all figures

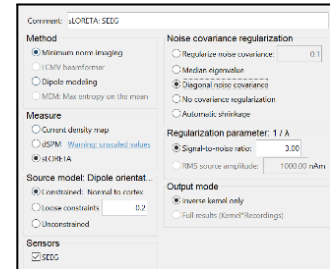


## ● Compute Noise Covariance Matrix (for SEEG) (15 mins)





- Explain Process section
  - Tabs Process1, Process2
  - File types: 📄 recordings, 📄 sources, 📄 time-freq, and 📄 matrices
- Switch to **Baseline folder**
- Compute **Link to raw file | copy** ( 📄 ) for sEEG from Baseline recording
  - Select the trial group, right-click > **Noise covariance** > **Compute from recordings**:
    - Baseline = **[0, 301] s**
    - Select **Block by block**
    - **DON'T CLICK [OK]**

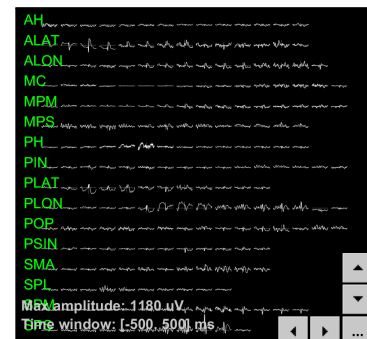
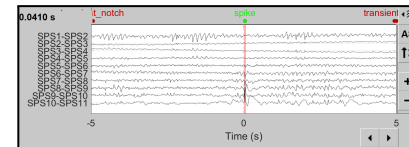


- Copy the Noise Covariance (  ) across other folder
  - Right-click noise covariance file > **Copy to other folders**
- Compute Inverse Model (5 mins)
  - Switch to the interictal\_spike folder,
  - Right-click on the head model (  ) > **Compute sources**, use these parameters:
    - Click on **Show Details**
    - Select **Minimum norm imaging**, Select Measure: **sLORETA**
    - Select **Constrained: Normal to Cortex**
    - Select Noise covariance regularization: **Diagonal noise covariance**
    - Sensors = **SEEG**
    - **DON'T CLICK [OK]**
  - Explanation of the **inversion kernel** (  ) and **link** (  ) files in the database



- Display sensor time series (5 mins)


- Display time series
  - Right-click on **Recording** (  **Spike (#1) ...** ) > **SEEG** > **Display time series**
  - On the right side of the figure, Select (  ) > **Montage** > **Subject01: SPS** > **Subject01: SPS (bipolar 2)**
  - Select the first peak of **SPS10-SPS11 (Time 0.041s)**
- Display 2D Layout of the spike
  - Right-click on **Recording** (  ) > **SEEG** > **2D Layout**
  - Click  on the corner and select **[-500, 500]**

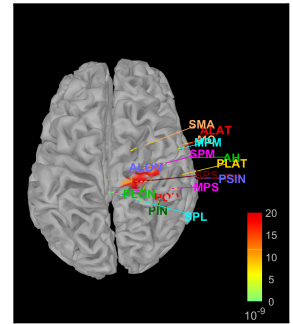





- **View Inverse Modeling results (10 mins)**

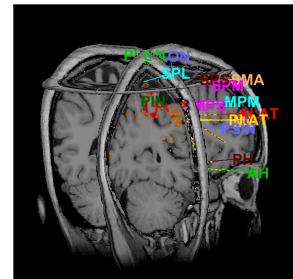
- Display on Cortex

- Right-click on link (  sLORETA ...) > **Cortical activations > Display on cortex**
    - Show sensors:
      - **Ctrl+L** – SEEG contacts, **Ctrl+E** – for sensors
    - Show colormap Bar: Right Click on **Colorbar > Colormap: Sources > Permanent menu**
      - Select **Maximum: Custom [0, 2]**
      - **Contrast: -18, Brightness: 99**
      - Switch to Surface tab, Select **Amplitude: 56%**




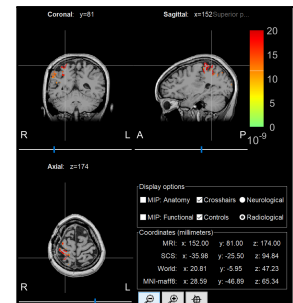
- Display on 3D MRI Viewer

- Right Click on link (  ) > **Cortical activations > Display on MRI (3D)**
    - Right Click and drag to select Axial, Coronal, and Sagittal slices
    - Press **M** to go to voxel with Maximum Intensity




- Display on MRI viewer

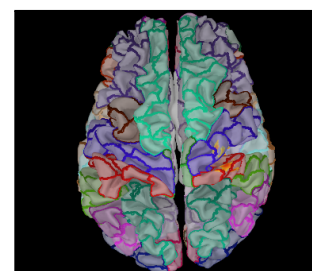
- Right Click on link (  ) > **Cortical activations > Display on MRI (MRI Viewer)**
    - Right Click on **Colorbar > Electrodes > SEEG contacts**
    - Show colormap Bar: Right Click on **Colorbar > Colormap : Sources > Permanent menu**
    - Explain Radiological and Neurological view
    - Explain MIP function and MIP anatomical



- **Atlases and Scouts (5 mins)**

- Display sources on the Cortical surface

- Right-click on link (  ) > **Cortical activations > Display on cortex**
    - In the **Scout** tab, use the dropbox to select different Atlases
    - Display **Desikan-Killiany** and **Destrieux**
    - Subdivided Desikan-Killiany
      - **Atlas > Subdivide atlas > Area > Area of the sub-regions (cm<sup>2</sup>): 5**
      - **DON'T CLICK [OK]**

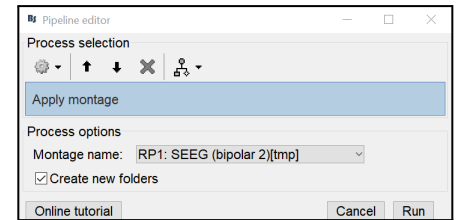
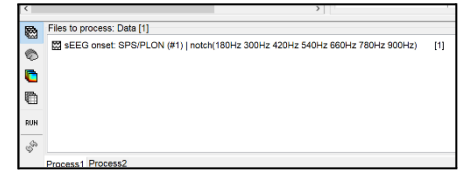


- Press **×** to close all figures

## 18. SEEG Analysis: Modeling ictal onset with Low Voltage Fast Activity (LVFA) using fingerprint analysis (Sensor Space) (Yash Vakilna)

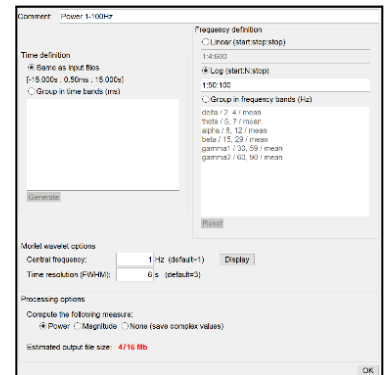
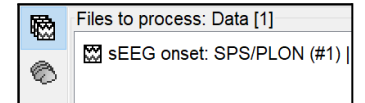
### • Compute Bipolar Montage (5 mins)

- Navigate and expand **LVFA\_and\_wave** folder
- Press **X** to close all figures
- Drag-and-drop (📁) recording file in **Process 1**, click **[RUN]**
- Add the process: **Standardize>Apply Montage**
  - Montage name: **Subject01: SEEG (bipolar 2)[tmp]**
  - Select **Create new folders**
  - **DON'T CLICK [RUN]**
- A new folder with **bipolar\_2** suffix will appear



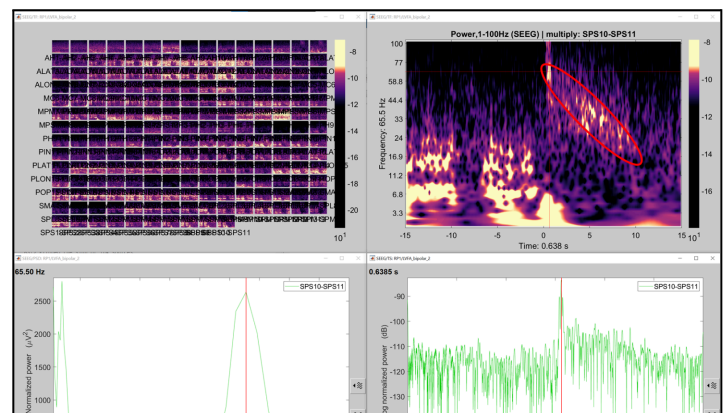
### • Compute Time-Frequency decomposition (5 mins)

- Navigate and expand **LVFA\_and\_wave\_bipolar\_2** folder
- Delete any previous recordings in the Process 1 tab below
- Drag-and-drop (📁) recording file in **Process 1**, click **[RUN]**
- Add the process: **Frequency>Time-Frequency (Morlet wavelets)**
  - Sensor type: **SEEG**
  - Select **Spectral flattening: Multiply output power values by frequency**
  - Click **Edit ...**
    - Frequency definition: **Log (start:N:stop), 1:25:100**
    - Central Frequency: **1 Hz**, Time resolution (FWHM): **6s**
    - Click **[OK]**
    - **DON'T CLICK [RUN]**



### • View Time-frequency maps (10 mins)

- Expand (📁 sEEG onset ...) recording file, right-click on **Power (🌈)**, and select **All channels**
- Click on **Smooth display, Log(Power)**
- Click on **SPS8-SPS9**
- Right-click on **Colorbar>Colormap: Timefreq >Permanent menu**
- Set Turn-off **[Absolute Value]**(if on), **Maximum: Local, Contrast: 49, Brightness: -65**
- Demonstrate Left-click and Drag on colorbar to select appropriate Brightness and Contrast



**Workshop Los Angeles****December 2024**

- Right-click on the colored time-frequency plot > **Power Spectrum, Time Series**
- Click to **×** close all figures

## SEEG Analysis: Appendix

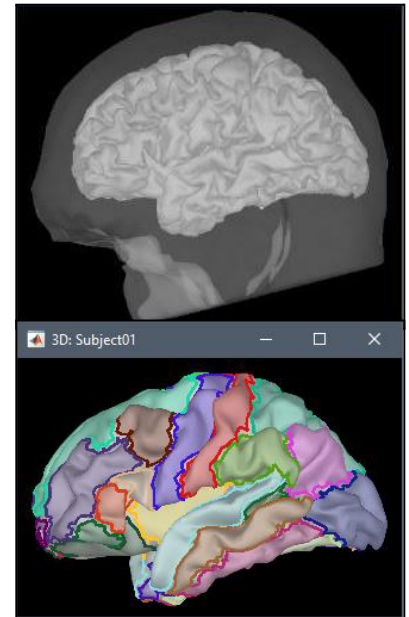
### How to run CAT12 segmentation from Brainstorm

- Display cortex:
- Close figure, double-click on **cortex\_15002V** (low-resolution pial surface)
- 3D figure: **Rotation, zoom, predefined views**
- Surface tab: **Smooth slider, sulci, edges**
- Scout tab: **Parcellations of the surface vertices**
- Volume parcellations: **AAL3, Hammers, tissues**
- Adjust transparency, change the atlas, non-linear MNI transformation
- Add MNI parcellation: **Schaefer2018\_100\_7net**


Import T1 post-implantation:

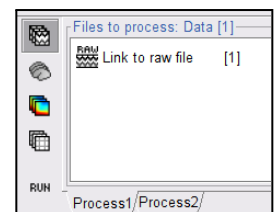
- Right-click on **Subject01 > Import MRI**
- Select file: **/xxx/xxxx/xxxxx.nii.gz**
- Apply transformation: **YES**
- How to register: **IGNORE** (volumes are already co-registered with SPM)
- Reslice the volume: **YES** (so we can overlay them)
- Surface tab: Adjust threshold with slider **Data options: Amplitude**

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



### Remove power line noise.

- Compute Periodogram
  - Close all the figures
  - Drag-and-drop (  ) raw file in **Process 1**, click **[RUN]**
  - Add the process: Frequency, Power spectrum density (Welch)
  - Time window = **All file**, Window length = **\_ s**, Overlap = **50%**
  - Units = **Physical**
  - Sensor types = **SEEG**
  - Click on **Run**
- Review Periodogram
  - Peaks at 60Hz, 120Hz, 180Hz on EEG and MEG: Power lines (60Hz+harmonics)





# Workshop Los Angeles

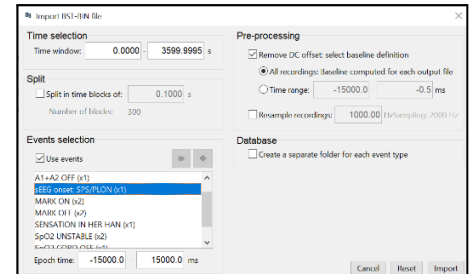
December 2024

- Process Notch filter
  - Select: **Pre-process > Notch filter**
  - Frequencies to remove (Hz) = **180, 300, 420, 540, 660, 780, 900Hz**
  - Sensor types = **SEEG**

- **Import recordings**

- Import in database
  - Right-click on the pre-processed file > Import in database, and use the parameters:

- Time window = **0 - 119.9995 s**
- Do NOT check Split in time blocks
- Check **Use events** and select **sEEG onset**
- Epoch time = **-15000 to 15000 ms**
- Check Remove DC offset, select **All recordings**



- A new folder named **\_** is created (no more **raw** indicator)