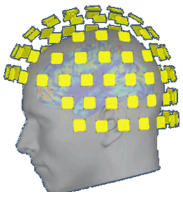
BRAINSTORM TUTORIAL

Takfarinas Medani, Anne-Sophie Dubarry &
Maximilien Chaumon

Brainstorm
http://neuroimage.usc.edu/brainstorm



USC University of Southern California

McGill UNIVERSITY

UTHealth Houston

OUTLINE OF TOPICS COVERED IN THIS WORKSHOP

1. Brainstorm download and installation

Brainstorm is available in an open-source MATLAB application (MATLAB license required) and a standalone Java executable (free). Both are available for download in the same package. Please follow the instructions on this page for a complete installation and configuration:
https://neuroimage.usc.edu/brainstorm/Installation
To make sure that Brainstorm is correctly installed on your computer and ready for the workshop

- **Start Brainstorm:**
  - With Matlab: Go to the installation folder and type ***brainstorm*** in the Matlab terminal
  - Without Matlab:
    - Windows: **Double-click** on **brainstorm3.bat**
    - MacOS: **Double-click** on **brainstorm3.command** and wait for instructions
    - Linux: From a terminal, **run**:

```
cd brainstorm3/bin/R2023a/
./brainstorm3.command
```

Check this link for more details: https://neuroimage.usc.edu/brainstorm/Installation#Start_Brainstorm

- ⚠ **Having any issues with Brainstorm:** Please follow the instructions on this page:

  https://neuroimage.usc.edu/brainstorm/WorkshopGeneralInstall

2. Workshop datasets

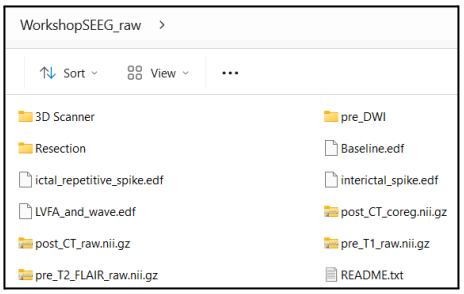
Once you have successfully installed and tested Brainstorm, proceed to download the data to be used in the workshop. We will provide you with the raw data and the precomputed Brainstorm protocol. You can either follow this walkthrough to reproduce these steps from the raw data or directly load the precomputed results to explore the outcomes and additional features. Since some sections involve lengthy computations, we recommend loading the precomputed protocol during the workshop. You can consistently reproduce these computations on your own afterward.

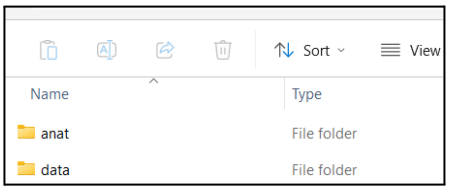
📜 *If not yet done, please download the data from the following links:*

- **WorkshopSEEG_raw**: https://tinyurl.com/5a8yeca4
- **WorkshopSEEG_precomputed**: https://tinyurl.com/5n6hb6yz

Extract all the folders above to your desktop.

In this workshop session, we will work on a SEEG dataset recorded at the *Epilepsy Monitoring Unit* at *UTHealth Houston*. The data is distributed as **raw** and **pre-processed Brainstorm protocol** data.





- **raw** data is located in the file **WorkshopSEEG_raw.zip,** which contains raw anatomical scans and SEEG recordings (in EDF format).
  - The anatomical scans include
    - One raw pre-implantation T1 and T2 MRI
    - One raw post-implantation CT scan
    - One post-implantation CT coregistered to the T1, resliced and skull-stripped using SPM

- One raw diffusion-weighted MRI (DWI)

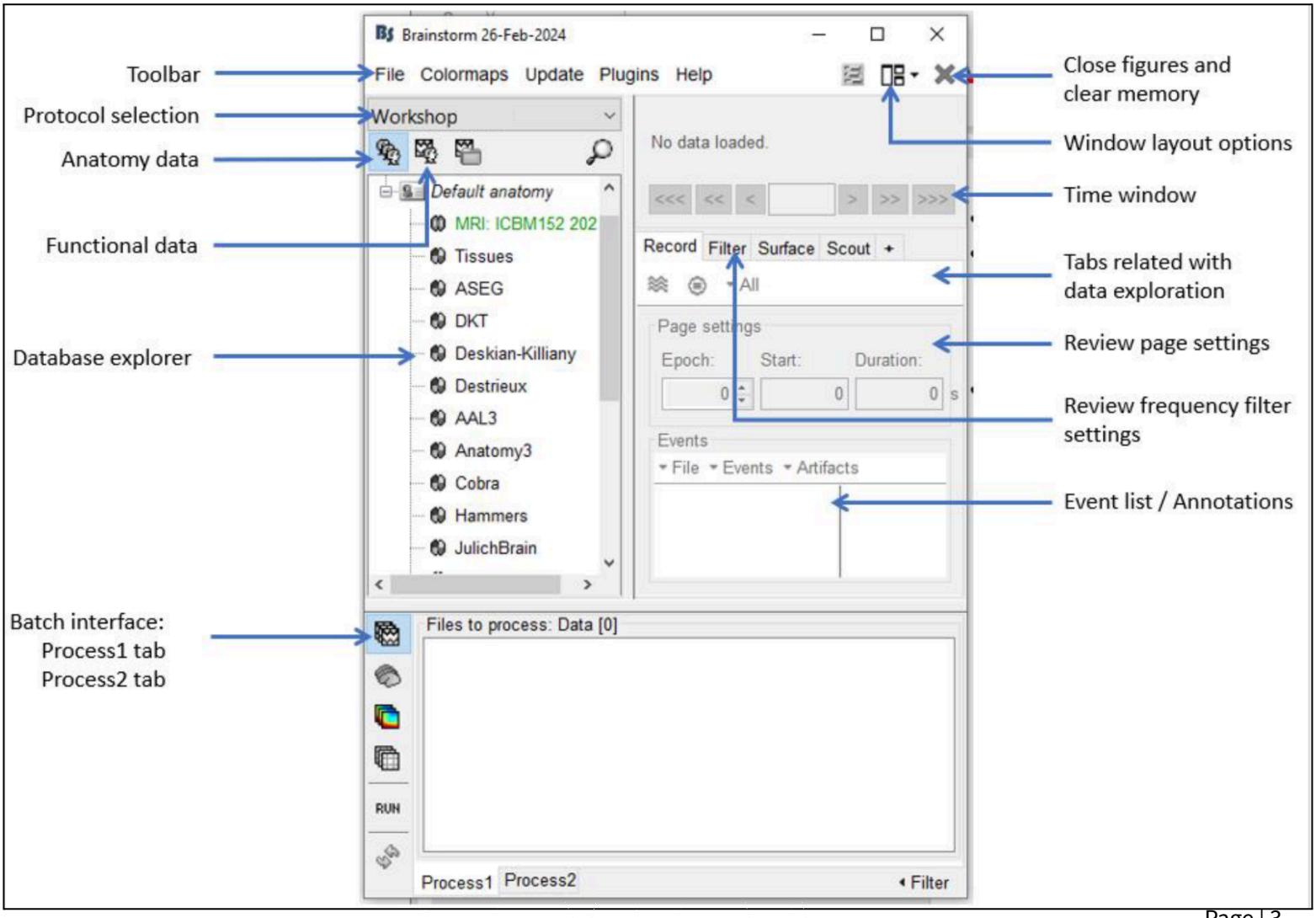
■ The raw SEEG recordings correspond to the following:

- One file containing baseline recordings: *"Baseline.edf"*
- Two files containing seizure onset:
  a. Seizure onset with Low-voltage-fast-activity: *"LVFA_and_wave.edf"*
  b. Seizure with Ictal repetitive spiking: *"ictal_repetitive_spike.edf"*
- One file with interictal spike: *"interictal_spike.edf"*

o **WorkshopSEEG_precomputed.zip** contains the pre-processed Brainstorm protocol folder.

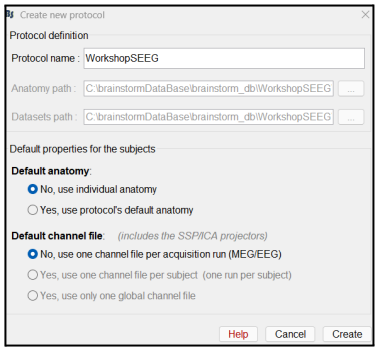
3. Introduction to Brainstorm Interface

- CLOSE ALL YOUR APPLICATIONS, INCLUDING WEB BROWSERS
- Start Brainstorm: from MATLAB or using the stand-alone application.
  - Please refer to this page for more instructions: https://neuroimage.usc.edu/brainstorm/Installation#Start_Brainstorm



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

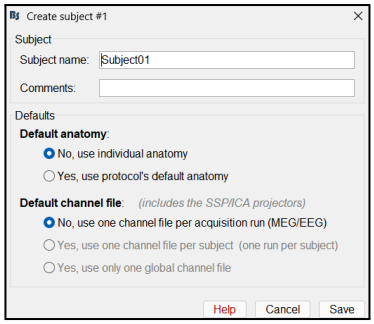
4. Create a new Brainstorm Protocol & Subject



- **Select > File > New protocol > WorkshopSEEG**
    - **No**, use individual anatomy
    - **No**, use one channel file per acquisition run (MEG/EEG)
- **Create a New subject**

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

- Right-click on protocol top node > New subject: **Subject01** (use Defaults)

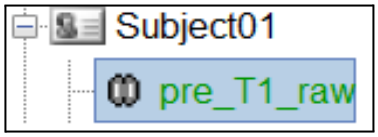


You can find more details here:

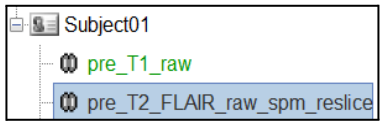
https://neuroimage.usc.edu/brainstorm/Tutorials/CreateProtocol

5. Import & explore anatomical data in Brainstorm

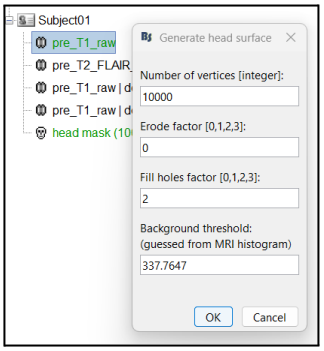
- **Import T1 pre-implantation: (5 mins)**
    - Right-click on **Subject01 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
    - Select file: **/Desktop/WorkshopSEEG_raw/pre_T1_raw.nii.gz**
    - **Introduction to the MRI viewer: Click, mouse wheel, color bar, popup**
    - In the MRI Viewer, click on **Compute MNI normalization** and select the **maff8** algorithm. *This sets default positions for the fiducials Coordinate systems*: MRI, SCS, World, and MNI, and also does MNI normalization. This process can take ~**1 minute**.
    - Click **Save & Close**



- **Import and coregistration of T2 pre-implantation: (3 mins)**
    - Right-click on **Subject01 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
    - Select file: **/Desktop/WorkshopSEEG_raw/pre_T2_FLAIR_raw.nii.gz**
- Brainstorm asks about registering the new T2 with the reference T1 image:
    - MRI Orientation: **Yes**
    - Select the option: **SPM** [if not installed, Brainstorm will download and install SPM as plugin]
    - Reslice the volume: **Yes**
- This process will take a **few minutes**, just be patient, and once completed, close the MRI viewer. A new node will appear in the database. It contains the T2 MRI co-registered with the T1 MRI.



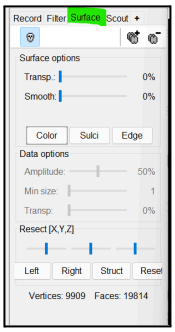
- **Explore the Brainstorm MRI viewer (5min)**
  - Explain fiducial points and the coordinates (MRI, SCS, MNI)
  - Set coordinates: , set fiducials, (MRI coords)
- Exploring MRI ( ): double-click or right-click > Display > MRI Viewer
  - Exploring the volume (click, mouse wheel, sliders)
  - Anatomical atlases, colormaps, colorbar, figure popup menu
- Exploring MRI ( ): right-click > Display > 3D orthogonal slices
- Close all figures (button at top-right): close all figures and empty the memory.

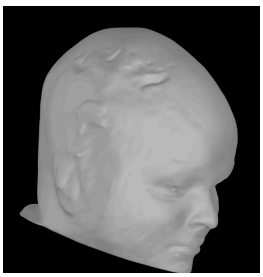


- **Generate head surface from the MRI: (5 mins)**

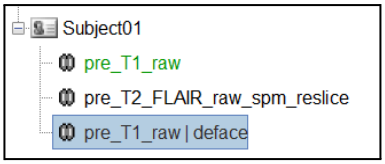
Once the fiducials are set, Brainstorm can generate a head surface from the MRI.

- Right-click on **pre_T1_raw> MRI Segmentation > Generate head surface**
  keep the default values and click OK, this process will take ~2min.
- A new node will appear on the database , double click to open this new surface or right-click **> Display**
  - 3D figure: rotation, zoom, Surface Tab
  - Predefined views and keyboard shortcuts: left, right, top, etc
  - Surface tab: smooth, sulci, edges
  - Scouts tab: atlases and scouts



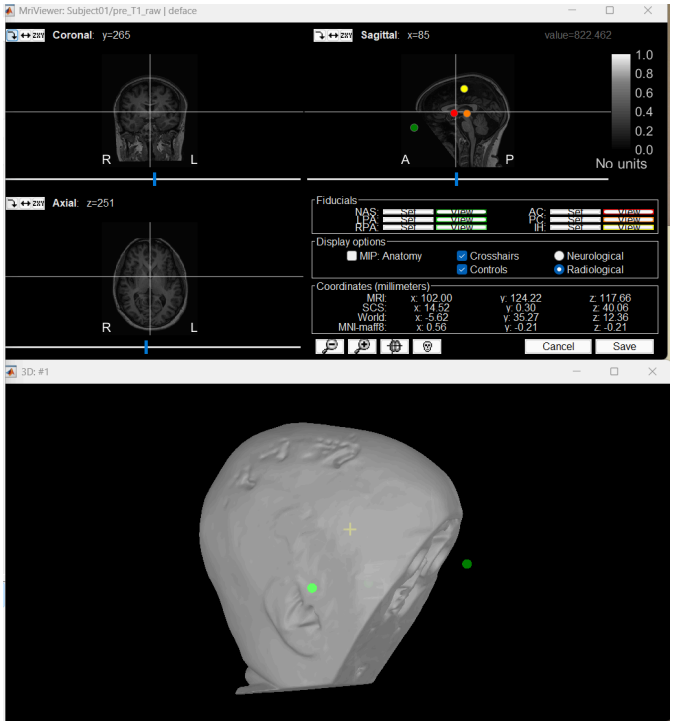


- **Optional: Defacing MRI data (anonymize the subject): (3 mins)**
  - Right-click on **pre_T1_raw > Deface Volume**
  - A new MRI volume will appear in the database



This option uses SPM and cuts the volume below a predefined cutting plan.

📜*If you have the BrainSuite package installed, Brainstorm offer a second option for the defacing. It uses a predefined mask to anonymize the MRI without cutting off the front of the head (**see the figure on the right**). This can be performed from the **Process** tab > **Import > Import Anatomy > Deface MRI Volumes**.*



6. MRI Segmentation in Brainstorm

📜 *In this section, we explain how to perform MRI segmentation and the supported tools/files within Brainstorm.*

⚠ DO NOT RUN THE MRI SEGMENTATION DURING THE WORKSHOP ⚠

We will provide you with the precomputed files in the following sections.

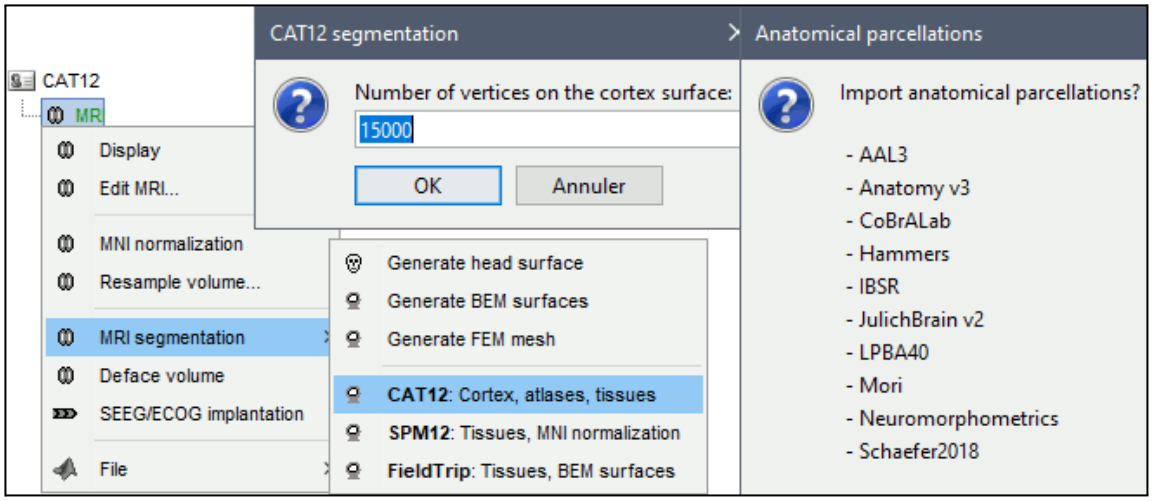
For estimating the brain sources of the Ephys signals, the subject's anatomy must include at least three files: a T1-weighted MRI volume, the envelope of the cortex, and the surface of the head. Brainstorm cannot extract the cortex envelope from the MRI, you have to run this operation with an external program of your choice. The results of the MRI segmentation obtained with the following programs can be automatically imported: FreeSurfer, BrainSuite, BainVISA, CAT12, and CIVET.

CAT12 is the only application fully interfaced with Brainstorm, and available for download as a Brainstorm plugin. FreeSurfer is widely regarded as a reference in this domain; therefore, we will provide a precomputed FreeSurfer segmentation for this workshop. However, we can also use CAT for this analysis.

- **MRI Segmentation with CAT12**

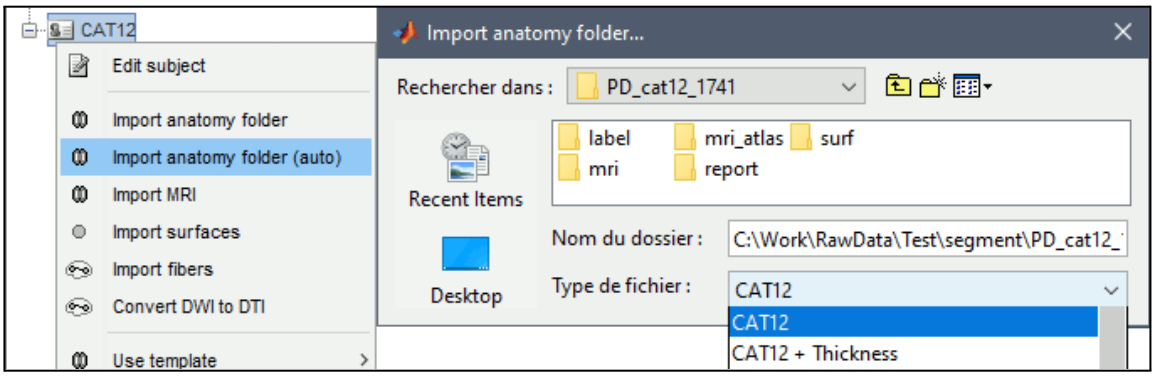
CAT12 is an SPM12 toolbox, it can efficiently replace FreeSurfer to generate the cortical surface from any T1 MRI. It runs on any OS in about 1 hour. It is fully interfaced with Brainstorm as a plugin. CAT12 requires the prior installation of SPM12. Both are MATLAB-based programs that can be installed automatically as Brainstorm plugins.

- **How to Run CAT from Brainstorm:**
  - Switch to the anatomy side of the database explorer .
  - Right-click on the **MRI > MRI segmentation > CAT12**.
  - Two options can be selected interactively:
    The number of final vertices in the cortex surfaces and the computation of additional volume parcellations.



- **How to Import CAT Segmentation to Brainstorm:**

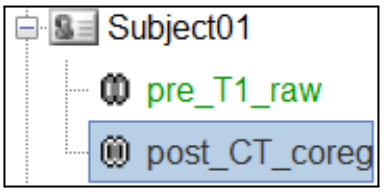
If you need to import an existing CAT segmentation, follow the following procedure.



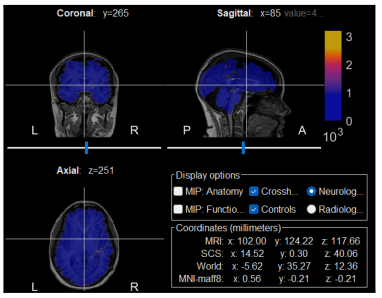
- Right-click on the **Subject > Import anatomy folder**.
- A figure is automatically shown at the end of the process to visually check that the low-resolution cortex and head surfaces were generated correctly and imported. You can find more details in this tutorial: https://neuroimage.usc.edu/brainstorm/Tutorials/SegCAT12

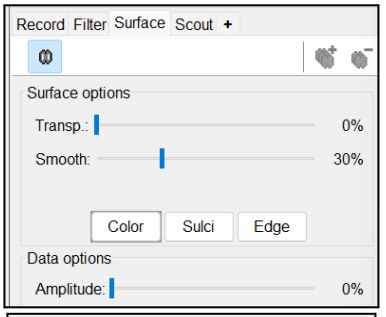
7. SEEG contact localization

📜 *In this section, we will just demonstrate **only one electrode**. The full localizations will be explored later in the precomputed protocol, where all the 267 contacts of the 16 electrodes are marked by a clinician using Brainstorm.*

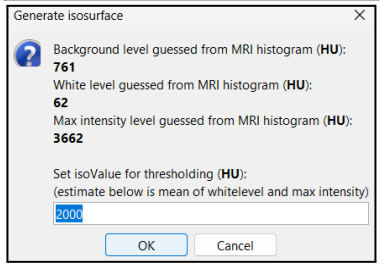


- **Import post-implant CT and coregister to pre-implant MRI: (10 mins)**
  - Prerequisites: **SPM plugin [already installed]**
  - Right-click on the **Subject01 > Import CT**
  - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
  - Select file: **Desktop/WorkshopSEEG_raw/post_CT_coreg.nii.gz**
  - Select **Ignore** and choose **No** for reslice volume and **Skip** for skull stripping as the provided **CT is already pre-processed with these steps**)
  - The MRI viewer opens automatically, showing the post-implant 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).
  - **Surface** tab **> Data options > Amplitude**, set the slider to **0%** to see the whole overlay.

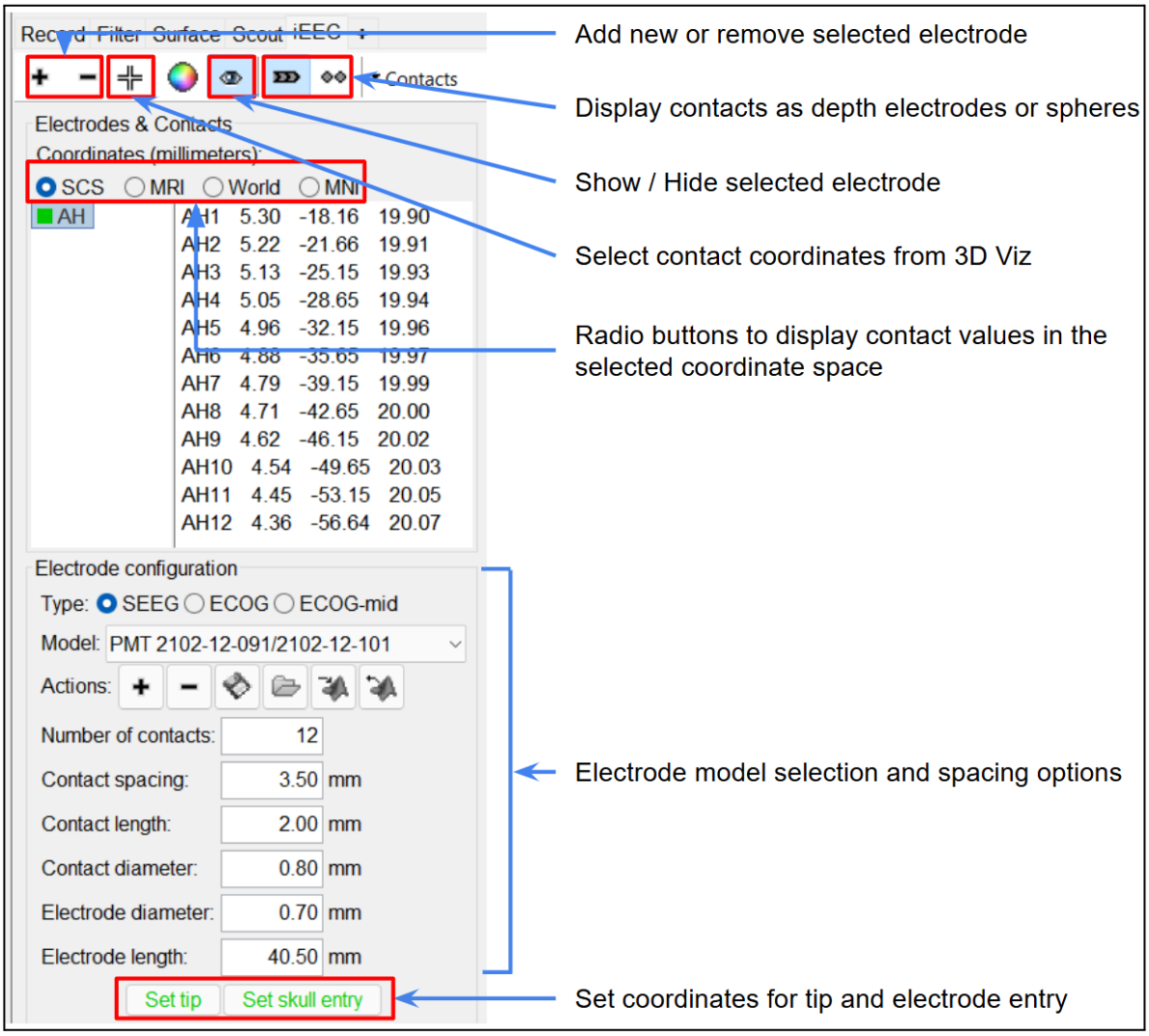




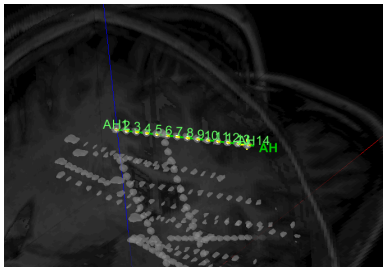
- **Generate isoSurface (2 mins)**
  - This creates a thresholded mesh from the CT to separate the contacts from the rest. This aids the user in the localization of the electrodes and their contacts more accurately.
  - Right-click on **post_CT_coreg > CT segmentation > Generate threshold mesh from CT**
  - Set the isoValue for thresholding; the estimation is based on the mean white level and max intensity of the CT. Set the value to 2050 Hounsfield Unit (HU). Select **OK.**
  - An isosurface is generated, showing the contact as blobs are overlayed on the 3D MRI slices. **Surface** tab **> Thresh** slider can be used to fine-tune and regenerate mesh with different isoValues till you get a clear view of the contacts with minimal artifacts.



- **Overview of the Panel iEEG**



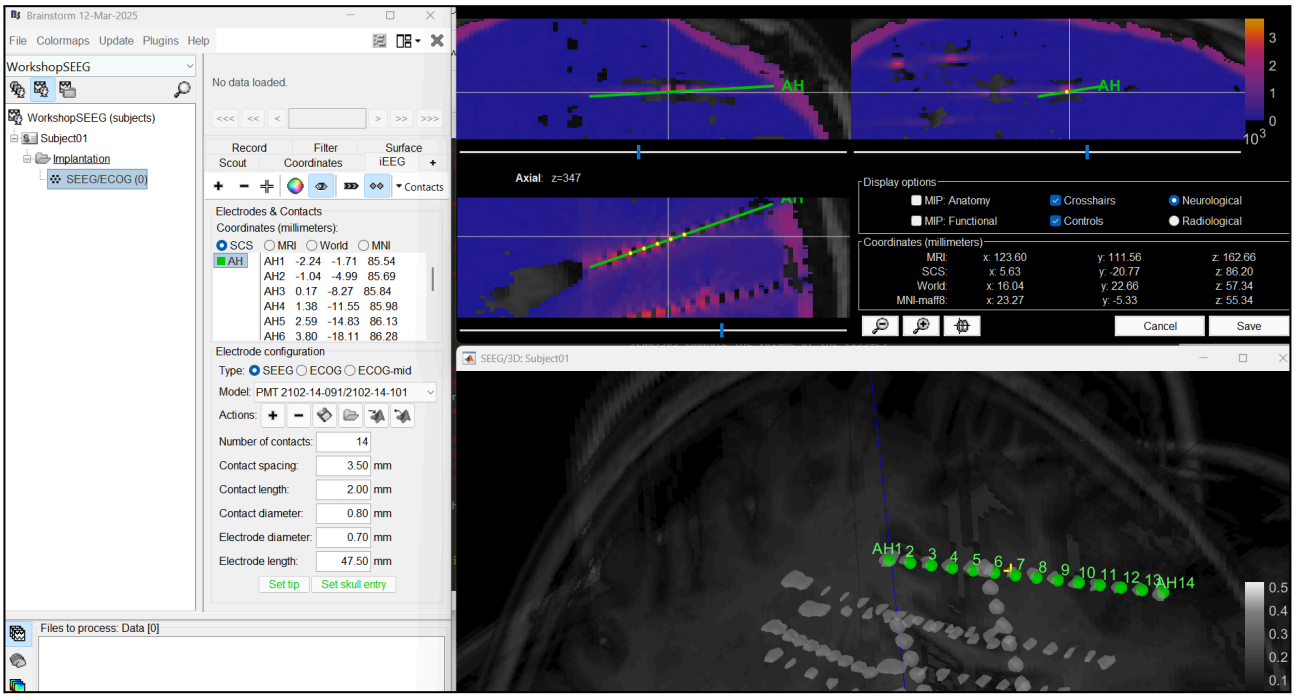
- **Manual contact labeling (10 mins)**
  - Right-click on **Subject01 > SEEG/ECOG implantation**. Choose **MRI+CT+IsoSurf**. This takes you to the functional tab and **Subject01 > Implantation > SEEG/ECOG (0)** channel gets created. The MRI Viewer (CT overlayed MRI) and 3D Viz (isoSurface+3D MRI Slices) load up as well, along with the **Panel iEEG**.
  - On **Panel iEEG,** Click on the **+ (Add new electrode)**. This opens up the **Add electrode** window. Under the **Electrode label,** enter **AH** and press **OK** (you can use any name based on your convention).
  - Select **SEEG**, and choose the electrode model (**PMT 2102-12-091/2102-14-101**), which is a 12 contact electrode.
  - On **Panel iEEG**, click the ( ) button (shortcut: Ctrl+P) to activate coordinate selection in 3D 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.

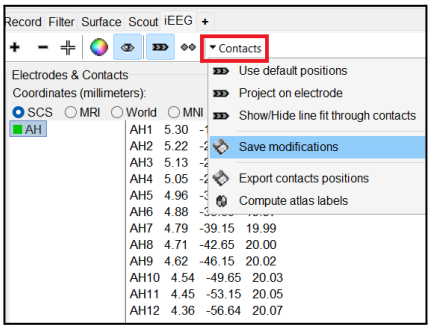
📜 *You can play around with the **Thresh** slider under the **Surface** tab to get better visibility of the contacts in 3D with minimal artifacts.*

- 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.

- With coordinate selection active, repeat the steps above and choose a contact closer to the skull 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.
- Right-click on **Subject01** and choose **SEEG/ECOG implantation** 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.
- To save all the further electrodes, click on **Contacts > Save Modifications** to update the channel information and also save the changes to the database.
- For more details, please refer to the Brainstorm tutorial:



https://neuroimage.usc.edu/brainstorm/Tutorials/IeegContactLocalization

- **Anatomical labeling (5 mins)**
  - Switch to the Anatomy view.
  - Right-click on **Subject01 > Add MNI parcellation > AAL3**.
  - 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 default options on all the steps: coordinates in various coordinate systems, volume parcellations, and 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.

SEEG contact labels

Channel	SCS	MNI	World	AAL3 (MNI-linear)	AAL3 (MNI-linear)_prob
AH1	[5.305,-18.157,19.895]	[19.135,-11.912,-24.224]	[12.360,27.284,-8.751]	ParaHippocampal R	88%
AH2	[5.219,-21.656,19.911]	[22.739,-12.052,-24.203]	[15.857,27.143,-8.802]	ParaHippocampal R	84%
AH3	[5.134,-25.155,19.926]	[26.343,-12.191,-24.182]	[19.353,27.002,-8.854]	ParaHippocampal R	55%
AH4	[5.048,-28.653,19.942]	[29.947,-12.331,-24.161]	[22.850,26.861,-8.905]	Hippocampus R	81%
AH5	[4.963,-32.152,19.957]	[33.551,-12.471,-24.139]	[26.347,26.720,-8.956]	Hippocampus R	100%
AH6	[4.877,-35.651,19.972]	[37.156,-12.610,-24.118]	[29.844,26.579,-9.007]	Hippocampus R	98%
AH7	[4.792,-39.150,19.988]	[40.760,-12.750,-24.097]	[33.341,26.438,-9.058]	Hippocampus R	75%
AH8	[4.706,-42.649,20.003]	[44.364,-12.890,-24.076]	[36.837,26.297,-9.109]	Fusiform R	23%
AH9	[4.621,-46.148,20.019]	[47.968,-13.030,-24.054]	[40.334,26.156,-9.160]	Temporal_Inf R	6%
AH10	[4.535,-49.647,20.034]	[51.572,-13.169,-24.033]	[43.831,26.015,-9.211]	Temporal_Mid R	29%
AH11	[4.450,-53.146,20.050]	[55.176,-13.309,-24.012]	[47.328,25.874,-9.262]	Temporal_Mid R	70%
AH12	[4.364,-56.645,20.065]	[58.781,-13.449,-23.991]	[50.825,25.733,-9.313]	Temporal_Mid R	87%

  - For more details, please refer to the Brainstorm tutorial: https://neuroimage.usc.edu/brainstorm/Tutorials/Epileptogenicity#Anatomical_labelling

Optional: Automatic SEEG contact localization and labeling (Brainstorm+GARDEL)

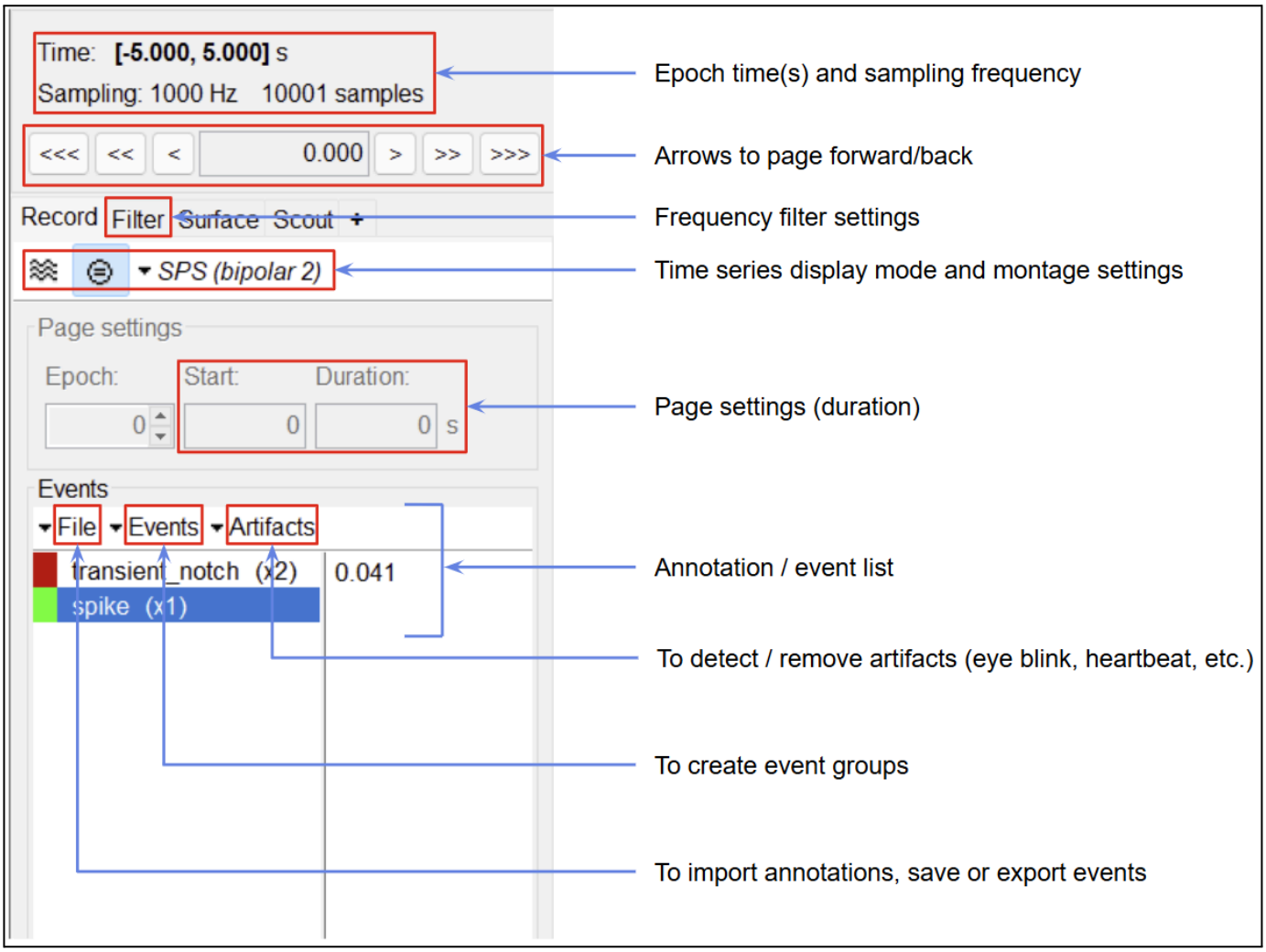
Brainstorm also provides access to tools for automatic sEEG contact localization. However, this software version is not yet available for public use. For more details, you can refer to the following resources:

- Abstract: https://www.researchgate.net/publication/386140762
- Demo video: https://www.youtube.com/watch?v=ixyH4DqNU6E
- Tutorial: https://neuroimage.usc.edu/brainstorm/Tutorials/IeegContactLocalization
- GitHub: https://github.com/brainstorm-tools/brainstorm3

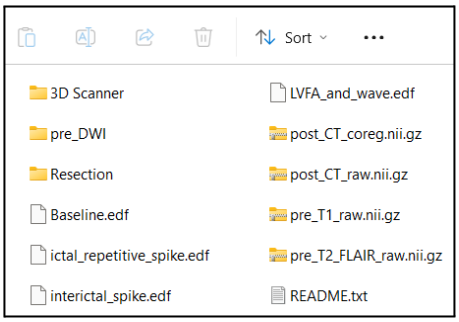
The version is expected to be released next month.

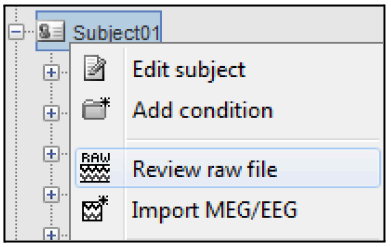
8. Review RAW recordings

- **Overview and exploring the functional tab interface [Record and Filter]**

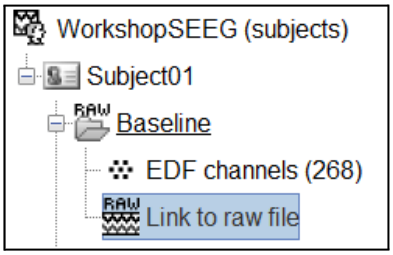


- **The raw SEEG recordings correspond to the following:**
  - One file containing baseline recordings: *"Baseline.edf"*
    - *300s "Normal" brain activity [marked by **epileptologist**]*
  - Two files containing seizure onset:
    - Seizure onset with Low-voltage-fast-activity: *"LVFA_and_wave.edf" [30 seconds of data]*
    - Seizure with Ictal repetitive spiking: *"ictal_repetitive_spike.edf" [30 seconds of data]*
  - One file with interictal spike:
    - *"interictal_spike.edf" [10 seconds of data around a marked spike]*





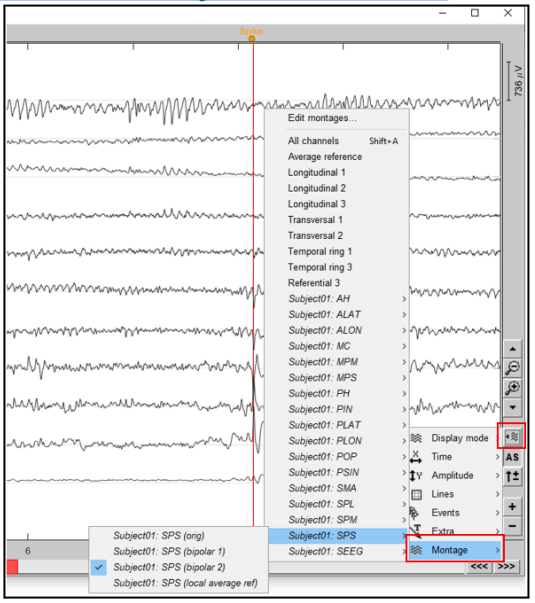
- In the functional view:  (2nd button, on top of the database explorer)
  - Create Link to raw file: right-click on **Subject01 > Review raw file**
  - Files of Type **EEG: EDF/EDF+**
    - Select the file **WorkshopSEEG_raw/Baseline.edf**
    - Click on **Open**
- Review SEEG: Right-click on the **Link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

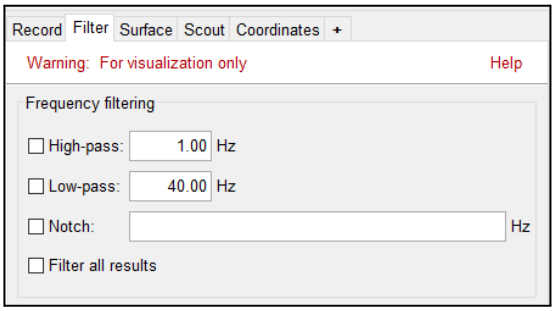


  - Display in columns: Button  in the Record tab **> Display mode > Column**
    - **Amplitude**: Buttons and shortcuts, Display menu
    - **Time**: Display windows of 15 seconds, Scroll with
      - Next Page: F3 /Previous Page: Shift+F3
      - Use (Auto-Scale) button to scale amplitude while changing the page
    - **Shortcuts**: See the tooltips in the time panel for important keyboard shortcuts

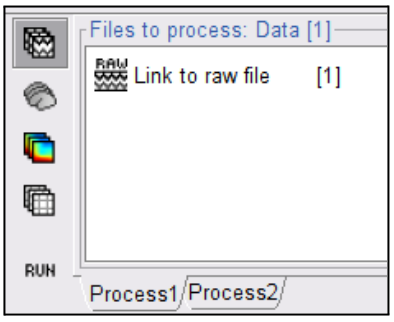
📜 visit this link for complete keyboard shortcuts:
https://neuroimage.usc.edu/brainstorm/Tutorials/ReviewRaw#Mouse_and_keyboard_shortcuts

  - Select bad channels + right click **> Channels > Mark selected as bad** (if needed)
  - Montage Selection: 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** montages for the continuous chain.
  - Filter settings for review are set under the **Filter** tab panel
    - ⚠ This is only for visualization ⚠
    - Select the checkbox to turn ON the high or low-frequency filter, and set any value.
  - Add annotations on the recording:
    - 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, select peaks , Press **E**
    - Save annotation: **File** > **Save modifications**



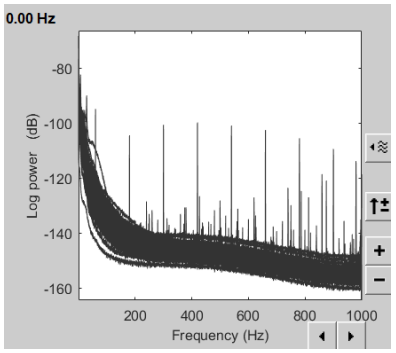


9. Preprocessing

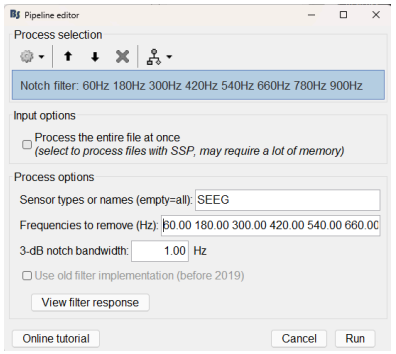


Remove power line noise.

- Compute Periodogram/Power spectrum density (PSD)
  - Close all the figures
  - Drag-and-drop (RAW) raw file in **Process 1, click [RUN]**
  - Add the process ( ): Frequency, Power spectrum density (Welch)
  - Time window = **All file**, Window length = **5 s**, Overlap = **50%**
  - Units = **Physical**
  - Sensor types = **SEEG**
  - Click **Edit…** and select **MATLAB's FFT defaults** and click **OK**
  - Click on **Run**



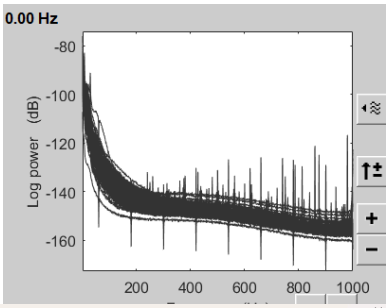
- Review Periodogram
  - Peaks at 60Hz, 120Hz, 180Hz on SEEG: Power lines (60Hz+harmonics)
- Process Notch filter
  - Select: **Pre-process > Notch filter**
  - Sensor types = **SEEG**
  - Frequencies to remove (Hz) = **60, 180, 300, 420, 540, 660, 780, 900Hz**
  - **Click on View filter response**

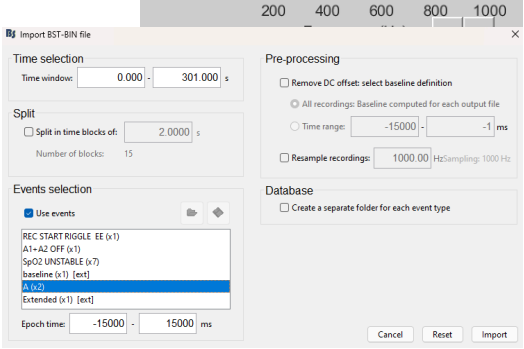


- Review Periodogram
  - Troughs at 60Hz, 120Hz, 180Hz on: Power lines (60Hz+harmonics)

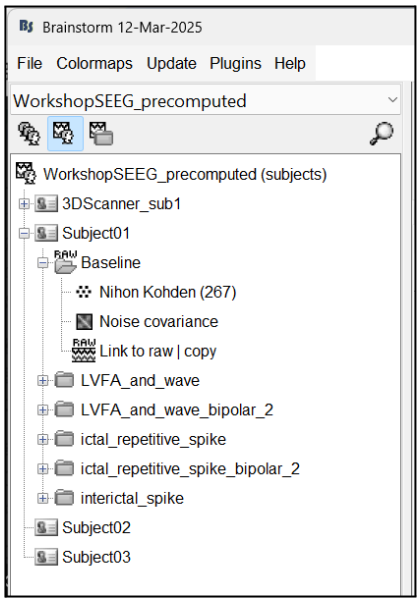
Import recordings

- Import in database
  - Right-click on the pre-processed file > Import in database, and use the parameters:
- Time window = **0 - 300.9995 s**
- Do NOT check Split in time blocks
- Check **Use events** and select **A**
- Epoch time = **-2000 to 2000 ms**
- Check Remove DC offset, select **All recordings**
  - A new folder named **A** is created (no more **raw** indicator)





10. Import precomputed Brainstorm protocol



📜 *Prerequisite: If not yet done, please download the precomputed data from the following link:* https://tinyurl.com/5n6hb6yz

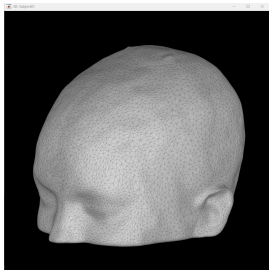
- Open Brainstorm
- Click **File > Load Protocol > Load from the zip file**
- Click on ..., and point to the downloaded zipped file: **WorkshopSEEG_precomputed.zip**
- A protocol called **WorkshopSEEG_precomputed** should appear.
- ⚠ If you double-click on the (RAW) **Link to raw** and you get a warning message about a missing file, click **Pick File…** you need just to link to the correct EDF file: **/Desktop/WorkshopSEEG_raw/Baseline.EDF**

11. 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 sEEG: the Boundary Element Method (BEM) and the Finite Element Method (FEM). However, only the BEM method is used in the subsequent sections. For more detailed documentation, please refer to the following link: https://neuroimage.usc.edu/brainstorm/Tutorials/HeadModel

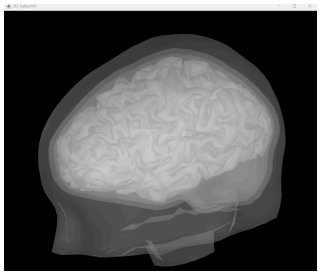
- **Generate BEM head surfaces from the MRI:**

The BEM surfaces will be used for multiple purposes, including the display of head models, the computation of the forward solution using the BEM method, and the visualization of results.



- Switch to anatomy view: (1st button, on top of the database explorer)
- Right-click on **Subject01**

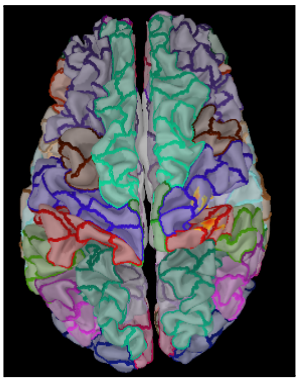
  > MRI segmentation > Generate head surfaces( )> OK
  - This will generate a surface file named *"head mask"* estimated from the T1 MRI.



- Right-click on Subject01 **> 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**
  - Click OK [This process will take ~2min]

- This will generate three surfaces (head, outer skull and inner skull) estimated from the*"head mask"* and the "*cortex*" obtained from the segmentation. The BEM surfaces will be used for the BEM forward computation.

- **Set the default cortex to be used as the source space**
  Double-click on **mid_15002V** to make it as the default cortex (in green), or *right-click> set surface type> Cortex*. If it's already green, there is no need to double-click. This will make sure to use this surface as the source space for the forward computation.

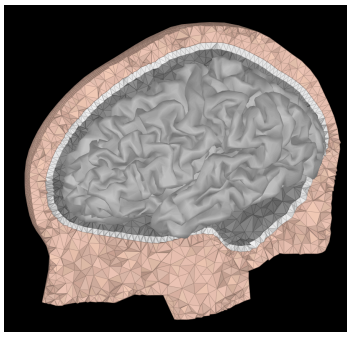


- Display cortex ( ) and the other surfaces:
  - Double-click or right-click **> Display**
  - 3D figure: rotation, zoom, transparency
  - Predefined views and keyboard shortcuts: left, right, top, etc
  - Surface tab: smooth, sulci, edges
- Close all figures (button at top-right)

- **Atlases and Scouts (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**
      - **Click on** ALL
  - Subdivided Desikan-Killiany
    - **Atlas > Subdivide atlas> Area >**
      - **Area of the sub-regions (cm^2): 5**
    - **DON'T CLICK [OK]**

Optional: Generate FEM head model (geometry):

The FEM head model relies on the volume mesh (with tetrahedron) that can be either generated from the nested BEM surfaces (simplified FEM mesh) or from the MRI data, where a more realistic head model can be generated.



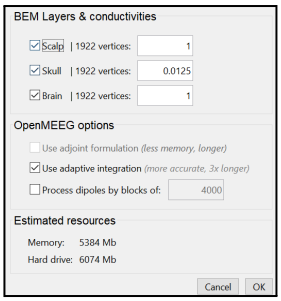
- **Generate FEM from BEM surfaces:**
  - Press and hold "Ctrl" then select with the mouse the BEM surfaces
  - Right Click on the selected surfaces **> Generate FEM Mesh > Iso2mesh > MergeMesh > Keep default values > OK**
    - The **Iso2Mesh** plugin will be installed automatically > **Agree**

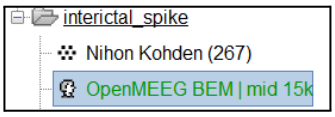
📜 *Read more about FEM mesh here: https://neuroimage.usc.edu/brainstorm/Tutorials/FemMesh. It is also possible to process the diffusion MRI (DWI) and generate conductivity tensors for the white matter.*

12. Modeling interictal spikes using Min-Norm Imaging

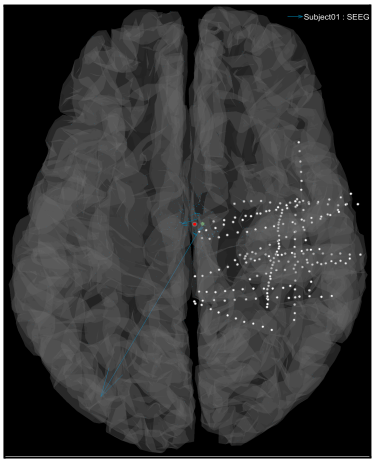
⚠ PLEASE DO NOT RUN ANY COMPUTATION IN THE FOLLOWING SECTIONS DURING THE WORKSHOP ⚠
Most of the following steps require significant computation time.
We will provide you with the precomputed files [output of the computation].

- **Compute Forward Model (aka Head Model) (10 mins)**
  - Compute the head model for SEEG using the OpenMEEG
    - Prerequisite: **OpenMEEG** plugin
    - 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 modeling methods = **SEEG: OpenMEEG BEM**, click **OK**
      - Use default BEM layers and conductivities.
      - Use default OpenMEEG options.
        DON'T CLICK [OK]
      - Once completed, a new node 🧠 will appear on the database





    - Copy the head model files to the other folders.
      - Right-click on the head-model file (🧠 **OpenMEEG BEM | mid 15k**)**> Copy to other folders.** 📜 *Since the other folders contain data collected from the same subject using the same set of electrodes, we do not need to re-compute the head model.*
  - View Leadfield vectors
    - Right-click on head-model file (🧠) **> View SEEG lead field vectors**
    - Select reference=**MC2**, click **OK**
    - Click on the figure and press **E** to display the electrodes
    - 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 the Shift+Up arrow** till the arrows are visible.
    - Press **Up/down** to change the Reference electrode, **right/left** to change the Target
    - Press ✖ to close all figures

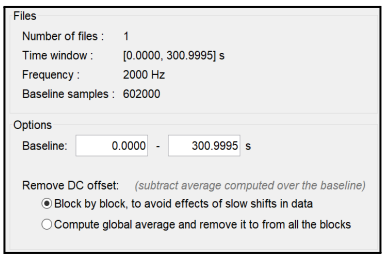


Optional: FEM Method with Duneuro

The forward model can also be computed using the FEM method

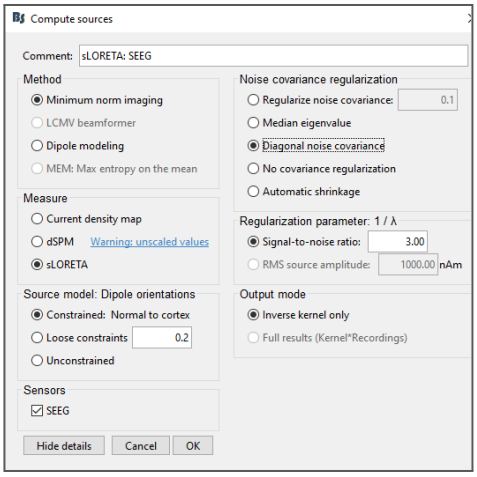
- The forward model can be calculated with the DUNEuro plugin

- **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**

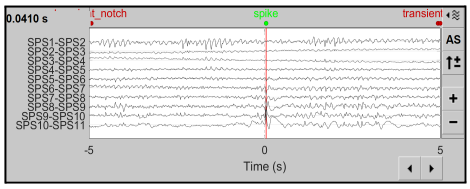


  - Compute **Link to raw file | copy** ( ) for sEEG from Baseline recording
    - Select the trial group, right-click **> Noise covariance > Compute from recordings**:
      - Baseline = **[0, 301] s**
      - Select **Block by block**
      - **DON'T CLICK [OK]**
      - Copy the Noise Covariance ( ) to all the other folder
        - Right-click noise covariance file > **Copy to other folders**

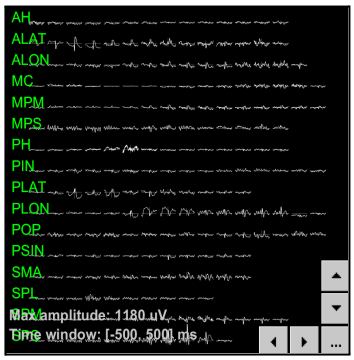
- **Compute Inverse Model [Estimate the brain activity from the sEEG recordings](5 mins)**
  - Switch to the **interictal_spike folder,**
  - Right-click on the head model ( ) **> Compute sources**, use these parameters:
    - Click on **Show Details**
    - Select **Minimum norm imaging**,
    - Select Measure: **sLORETA** [there are different methods]
    - 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



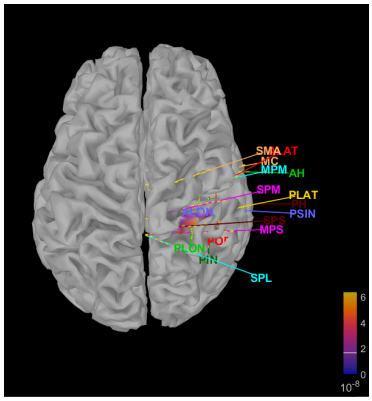
- **Display sensor time series (5 mins)**
  - Display time series
    - Right-click on **Recording** (**Spike (#1) …**)**> SEEG> Display time series**
    - On the right side of the figure,
    - Select ( ) **> Montage > Subject01: SPS >Subject01: SPS (bipolar 2)**
    - Select the first peak of **SPS10-SPS11 (Time 0.041s)**



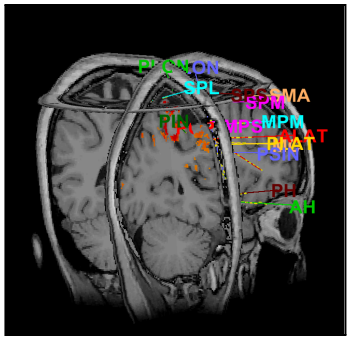
  - Display the 2D Layout of the spike
    - Right-click on **Recording** ( )**> SEEG> 2D Layout**
    - Click ... on the corner and select **[-500, 500]**

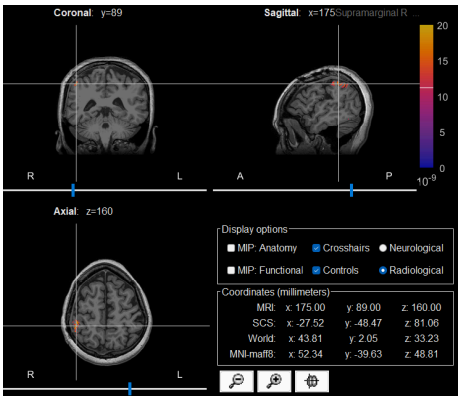


- **View Inverse Modeling results (10 mins)**
  - Display on Cortex
    - Right-click on link (**sLORETA …**) **> Cortical activations > Display on cortex**
    - Show sensors:
      - **Ctrl+L** – SEEG contacts, **Ctrl+E** – for sensors
    - Show colormap Bar: Right Click on **Colorbar > Colormap: Sources > Permanent menu**
      - Select **Maximum: Global**
      - **Contrast: -0, Brightness: 0**
      - Switch to Surface tab, Select **Amplitude: 26%** and **Min size: 13**



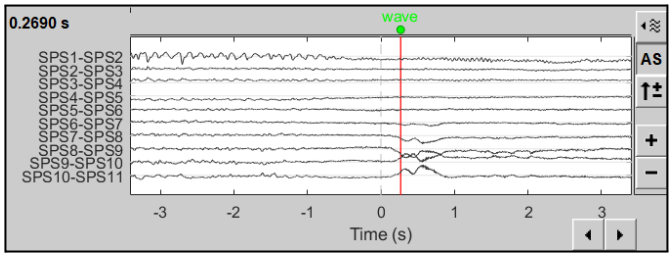
  - Display on 3D MRI Viewer
    - Right Click on link ( ) **> Cortical activations > Display on MRI 3D**
    - Show sensors:
      - **Ctrl+L** – SEEG contacts,
    - Right Click and drag to select Axial, Coronal, and Sagittal slices
    - Press **M** to go to voxel with Maximum Intensity
  - Display 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**
    - Set Amplitude: **56%,** and press **M** to select the voxel with maximum intensity
    - Explain the Radiological and Neurological view
    - Explain MIP function and MIP anatomical





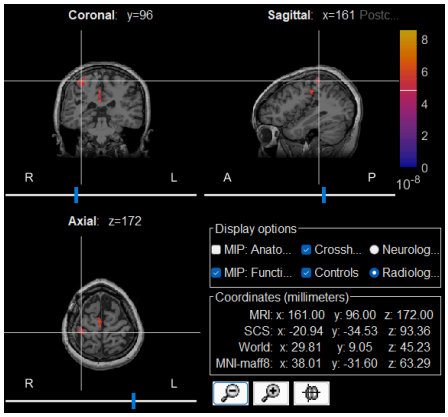
13. Modeling ictal wave using Min-Norm Imaging

In this section same computation steps are performed as in the previous section.



Compute Inverse Model

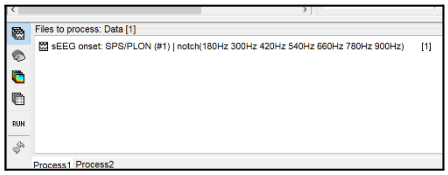
- Navigate and expand **LVFA_and_wave**
- **Display sensor time series (5 mins)**
- **View inverse modeling results (2 mins)**
- Display on MRI viewer
  - Switch to Radiological
  - Right Click on **Colorbar>Electrodes>SEEG contacts**
  - Show colormap Bar: Right Click on **Colorbar > Colormap: Sources > Permanent menu**
  - Set **Threshold=60%. Min size: 13**
  - Set **Maximum: Local**



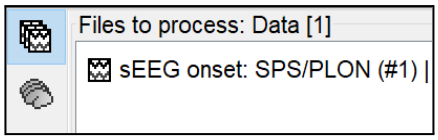
14. Modeling ictal onset with LVFA using fingerprint analysis (Sensor Space)

LVFA: Low Voltage Fast Activity

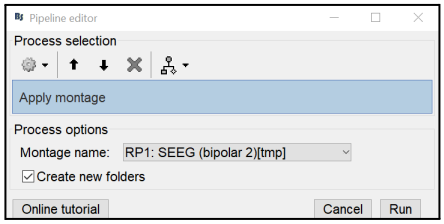
Compute Bipolar Montage (5 mins)



- Navigate and expand the **LVFA_and_wave** folder
- Press ✖ 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

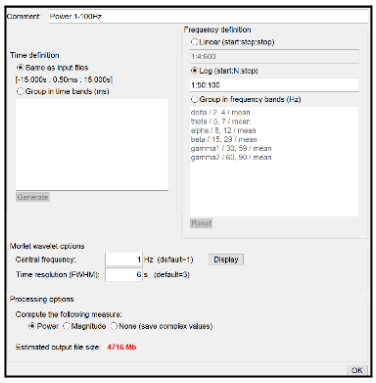


Compute Time-Frequency decomposition (5 mins)



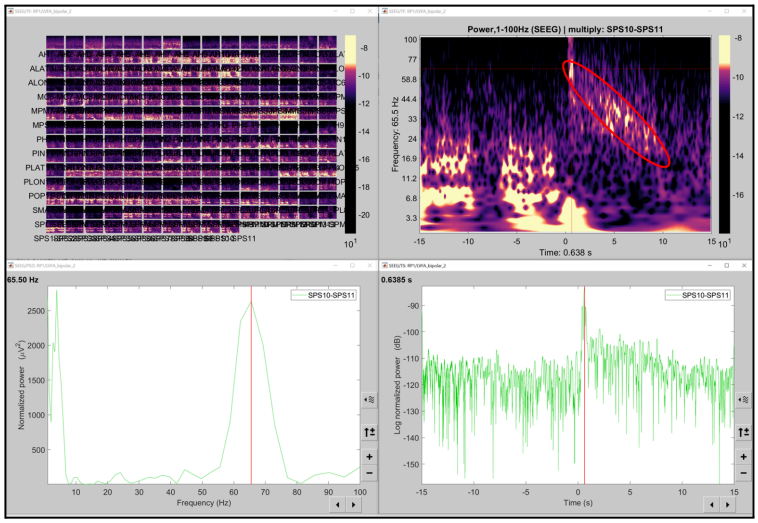
- Navigate and expand **LVFA_and_wave_bipolar_2** folder
- Delete any previous recordings in the Process 1 tab below
- Drag-and-drop (🔲) recording file in **Process 1, click [RUN]**
- Add the process: **Frequency>Time-Frequency (Morlet wavelets)**
  - Sensor type: **SEEG**
  - Select **Spectral flattening: Multiply output power values by frequency**
    [📜 Normalizing/enhancing the detection of oscillatory components across frequencies]
  - Click **Edit …** to view and edit the parameters of the TF Morlet wavelets

- 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)**
  - Give an overview off all the channels involved in the EZ patterns [Pre-Ictal Spikes, Chirp -Narrow band of fast activity–, Suppression of slow pre-ictal frequencies]
- Click on **SPS8-SPS9**
  - Check also **PIN7-PIN8**
- 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 the color bar to select the appropriate Brightness and Contrast
- Right-click on the colored time-frequency plot > **Power Spectrum, Time Series**
- Click to close all figures



📜 *The sensor-level analysis identifies all electrodes that record epileptic activity with the associated fingerprint pattern. However, since this pattern can appear across multiple channels, accurately mapping it to its corresponding cortical region can be challenging. Therefore, analyzing it in source space may provide additional insights, allowing to examine the fingerprint at the level of cortical patches (rather than at the channel level).*

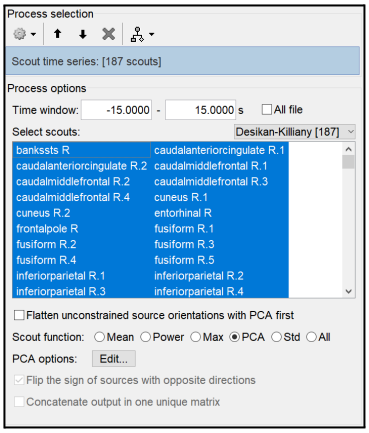
In the two previous sections, the analysis relies on two key concepts: Minimum Norm (MinNorm) imaging for source reconstruction and time-frequency (TF) analysis in sensor space.

In the next section, we will evaluate the fingerprint analysis in the source space.

15. Modeling ictal onset with LVFA using fingerprint analysis (Source Space)

Change folder

- Switch to folder **LVFA_and_wave**



Compute Source model

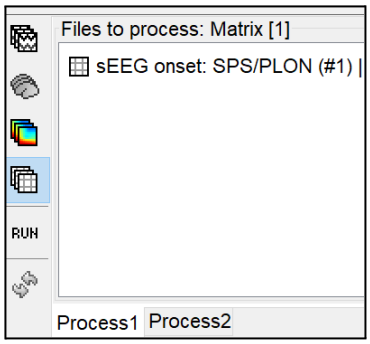
- Same as in previous sections [all the steps are already completed]

Extract Scout time series

- Drag-and-drop link (LINK) in **Process 1, click [RUN]**
- Add the process: **Extract>Scout time series**
  - Select **Desikan-Killiany [187]**
  - Select Scout function: **PCA**
  - **DON'T CLICK [RUN]**

Compute Time-Frequency decomposition

- Drag-and-drop ( ) matrix file in **Process 1, click [RUN]**
- The rest of the steps are the same as in previous sections

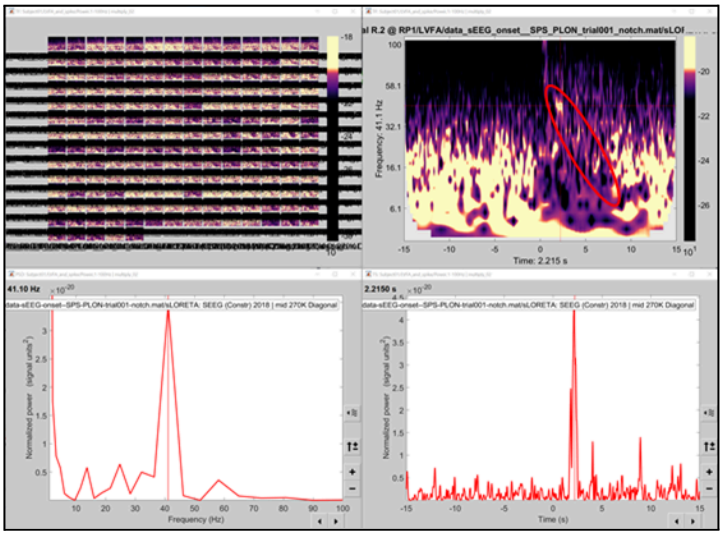


Display on Cortex

- Right-click on link (LINK) **> Cortical activations > Display on cortex**
- Select the **Scout** tab
  - Select Desikan-Killiany [187] atlas, click SEL
  - Select Scout: **postcentral R.2**

View Time-frequency maps

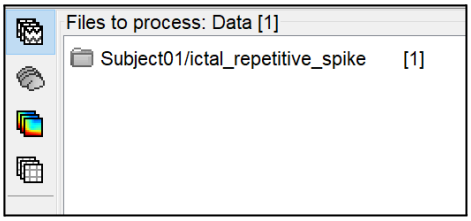
- Expand (sEEG onset …) recording file, right-click on Power ( ), and select **All channels**
- Click on **Smooth display, Log(Power)**
- Click on **postcentral R.2**
- Right-click on **Colorbar>Colormap: Timefreq >Permanent menu**
- Set **Maximum: Local, Contrast: 52, Brightness: -63**
- Right-click on the colored time-frequency plot > **Power Spectrum, Time Series**
- Click to close all figures



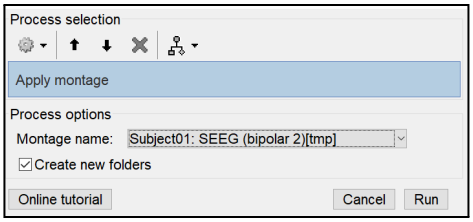
Demonstrate Left-click and Drag on the color bar to select the appropriate Brightness and Contrast
https://neuroimage.usc.edu/brainstorm/Tutorials/Colormaps

16. OPTIONAL: Modeling ictal onset with repetitive spiking (Sensor and Source Space)

Compute Bipolar Montage

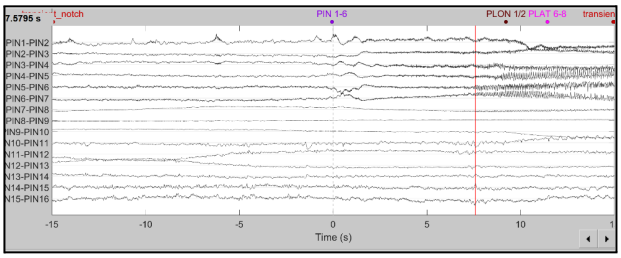


- Navigate and expand **ictal_repetitive_spike** folder
- Close all the figures
- Drag-and-drop ( ) recording file in **Process 1, click [RUN]**
- Add the process: **Standardize>Apply Montage**
  - Montage name: **Subject01 SEEG (bipolar 2)[tmp]**
  - Create a new folder
- **DON'T CLICK [RUN]**
- A new folder with **bipolar_2** suffix will appear



Display time-series

- Navigate to the folder with **bipolar_2** suffix
- Right-click on Recording, **SEEG>Display time-series**
- Change Montage to **PIN > PIN (orig)**

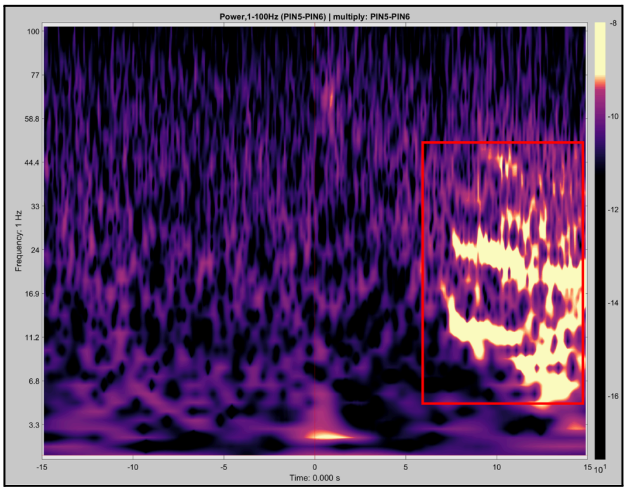


Compute Time-Frequency decomposition

- Same as in previous sections, only for the sensor **PIN5-PIN6**

View Time-frequency maps

- Expand (sEEG onset …) recording file, RrRight click on **Power**( ) , and select **One channels**
- Click on **Log(Power)**
- Click on **PIN5-PIN6**
- Right-click on colorbar**>Colormap: Timefreq >Permanent menu**
- Set **Maximum: Custom** [-18.5, -8], **Contrast**: 23, **Brightness**: -60



Computing inverse models

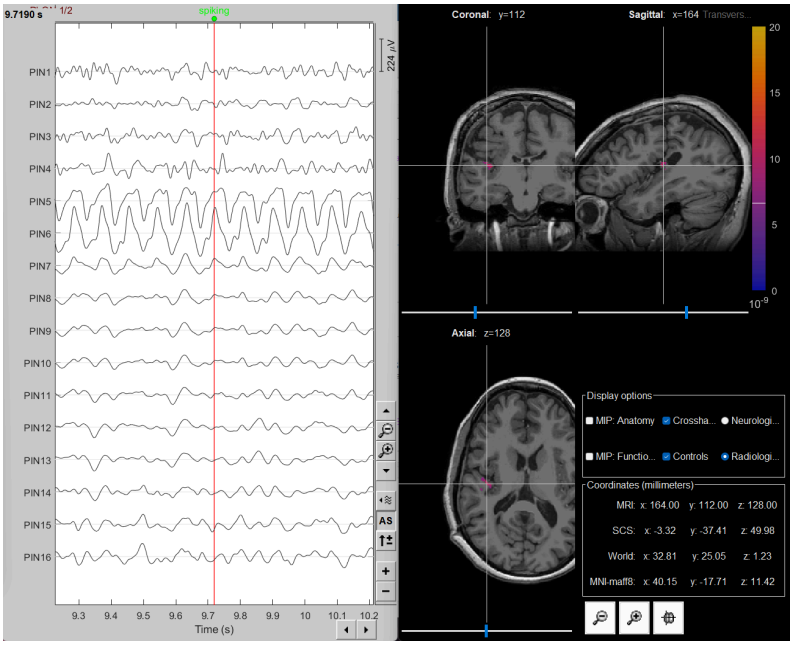
- Change back to the **ictal_repetitive_spike** folder
- Same as in previous sections

View inverse modeling results

- Display time-series
  - Right-click on Recording, **SEEG>Display time-series**
  - Change **Montage** to **PIN(orig)**
  - Set Frequency filter
    - High-pass: **5 Hz**

- Low-pass: **55 Hz**

- Display sources 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: Source** > **Permanent Menu**
  - Maximum: **[0, 2]**
  - Click on the **Surface tab,** set Amplitude: **33%**
  - Explain **MIP's functional** and **MIP anatomical**



17. OPTIONAL: Post-surgical anatomical data processing and resection delineation

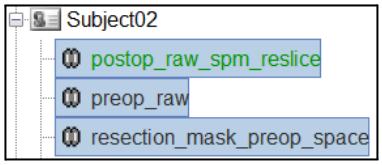
BrainSuite's module auto resection labeling can coregister pre- and post- surgery MRI's of subjects that underwent surgical resection. The module coregisters pre- and post- surgery MRI images and identifies resection as a volumetric mask. This volumetric mask can be imported as a MRI parcellation (aka MRI atlas) in the subject space and then used to generate volume scouts in the source space. The method takes into account linear and nonlinear deformations occurring due to the resection surgery. The resection mask is identified in both pre-op MRI and post-op MRI coordinates. **The resection mask in pre-surgery MRI space could be useful for identifying SEEG electrodes within the resection** or **to identify anatomy that has been resected. The resection mask in post-surgery MRI space could be useful as a registration mask**.

Please refer to the github page and Brainstorm documentation for more details on the process.

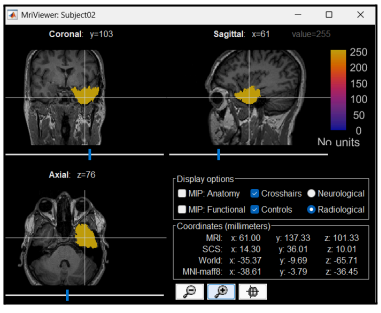
In the section below, we will just be importing a BrainSuite precomputed resection mask into Brainstorm and visualize it.

📜 *Precomputed sample for the steps below is also available in **WorkshopSEEG_precomputed.zip***

- **Method-1: Resection mask identification in pre-surgery MRI space**
  - New subject: **Subject02**
  - **Import T1 pre-surgery MRI**
    - Right-click on **Subject02 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
    - Select file: **/Desktop/WorkshopSEEG_raw/Resection/preop_raw.nii.gz**
    - In the MRI Viewer, click on **compute MNI normalization** and select the **maff8** algorithm.
    - Click **Save & Close**



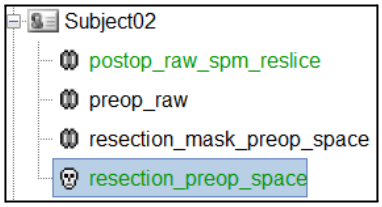
  - **Import T1 post-surgery MRI**
    - Right-click on **Subject02 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
    - Select file: **/Desktop/WorkshopSEEG_raw/Resection/postop_raw.nii.gz**
  - Brainstorm asks about registering the new T1 with the reference T1 image
    - Select the option: **SPM** [if not installed, Brainstorm will download and install SPM as plugin]
    - Reslice the volume: **Yes**

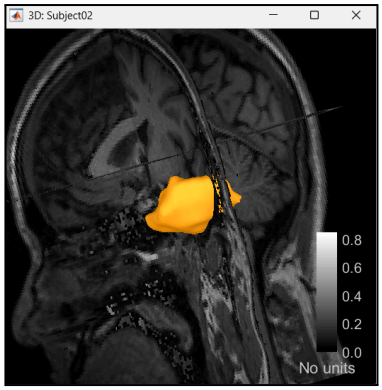


  - **Import processed resection mask in pre-surgery MRI space**
    - Right-click on **Subject02 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**

- Select file: **/Desktop/WorkshopSEEG_raw/Resection/resection_mask_preop_space.nii.gz**
- Select **Ignore** for coregistration and **No** for reslicing
  - Coregistration cannot be performed on the resection mask
  - The resection is already in the pre-surgery MRI space
- Display resection on the post-surgery MRI
  - Right-click on **postop_raw_spm_reslice > Set as default MRI**
  - Right-click on **resection_mask_preop_space > Display > Display on default MRI**

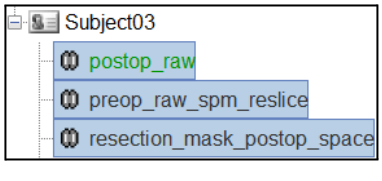
- **Optional (for visualization): Create a 3d volume for the resection mask**
  - Right-click on **resection_mask_preop_space > MRI segmentation > Generate head surface**
    - Number of vertices: **10000**
    - Erode factor: **0**
    - Fill holes: **0**
  - Click **OK**.
  - Rename the generated surface **head mask** to **resection_preop_space**.
  - Display resection volume on the post-surgery MRI
    - Double-click **resection_preop_space** to open the volume in the 3D viewer
    - **Surface** tab **> Color** button (choose something that is not gray for better visualization of the resection)
    - **Surface** tab **> Add a surface > Anatomy**

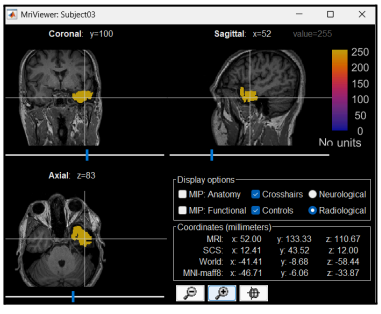




📜 *Precomputed sample for the steps below is also available in **WorkshopSEEG_precomputed.zip***

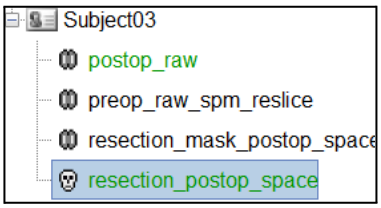
- **<u>Method-2: Resection mask identification in post-surgery MRI space</u>**
  - New subject: **Subject03**
  - **Import T1 post-surgery MRI**
    - Right-click on **Subject03 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
    - Select file: **/Desktop/WorkshopSEEG_raw/Resection/postop_raw.nii.gz**
    - In the MRI Viewer, click on **compute MNI normalization** and select the **maff8** algorithm.
    - Click **Save & Close**
  - **Import T1 pre-surgery MRI**
    - Right-click on **Subject03 > Import MRI**
    - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**

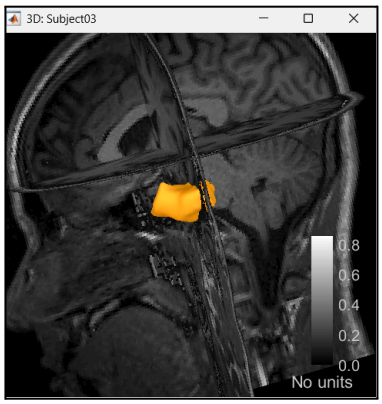




- Select file: **/Desktop/WorkshopSEEG_raw/Resection/preop_raw.nii.gz**

- Brainstorm asks about registering the new T1 with the reference T1 image
  - Select the option: **SPM** [if not installed, Brainstorm will download and install SPM as plugin]
  - Reslice the volume: **Yes**
- **Import processed resection mask in post-surgery MRI space**
  - Right-click on **Subject03 > Import MRI**
  - Select format: **MRI: NIfTI (*.nii, *.nii.gz)**
  - Select file: **/Desktop/WorkshopSEEG_raw/Resection/resection_mask_postop_space.nii.gz**
  - Select **Ignore** for coregistration and **No** for reslicing(the resection is already in the pre-surgery MRI space)
  - Display resection on the post-surgery MRI: Right-click on **resection_mask_postop_space > Display > Display on default MRI**
- **Optional (for visualization): Create a 3d volume for the resection mask**
  - Right-click on **resection_mask_postop_space > MRI segmentation > Generate head surface**
    - Number of vertices: **10000**
    - Erode factor: **0**
    - Fill holes: **0**
  - Click **OK**.
  - Rename the generated surface **head mask** to **resection_postop_space**.
  - Display resection volume on the post-surgery MRI
    - Double-click **resection_postop_space** to open the volume in the 3D viewer
    - **Surface** tab **> Color** button (choose something that is not gray for better visualization of the resection)
    - **Surface** tab **> Add a surface > Anatomy**





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