sEEG-Suite: An Interactive Pipeline for Semi-Automated Contact Localization and Anatomical Labeling with Brainstorm

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Summary

Stereoelectroencephalography (sEEG) is a critical tool for mapping epileptic networks in patients with drug-resistant epilepsy. Accurate localization and labeling of sEEG contacts are essential for identifying the seizure onset zone (SOZ) and ensuring optimal resective surgery. Traditional methods for localizing and labeling sEEG contacts rely on manual processing, which is prone to human error and variability. To address these challenges, we developed and integrated a semi-automatic sEEG contact localization and labeling pipeline within Brainstorm (Tadel et al., 2011), an open-source software platform for multimodal brain imaging analysis (Delaire et al., 2025; Medani et al., 2023; Nasiotis et al., 2019; Niso et al., 2019; Silva Castanheira et al., 2021; Tadel et al., 2019; Vakilna et al., 2025), widely adopted in the neuroscience community with over 50,000 registered users with an active online user forum. The software has been supported by the National Institute of Health (NIH) for over two decades. The pipeline presented in this paper performs: (1) import and apply rigid co-registration of post-implantation Computed Tomography (CT) or post-CT with pre-implantation Magnetic Resonance Imaging (pre-MRI), (2) post-CT image segmentation and semi-automatic detection of sEEG contacts using GARDEL (Medina Villalon et al., 2018), which has been integrated as a Brainstorm plugin, and (3) automatic anatomical labeling of contacts using standard and commonly used brain anatomy templates and atlases. Integrating this pipeline into Brainstorm brings the best of both worlds: GARDEL's automation and Brainstorm's multimodal data compatibility, and rich library of visualization and advanced analysis tools at both sensor and source level (Vakilna et al., 2025). This sEEG-Suite tool facilitates reproducible research, supports clinical workflows, and accelerates sEEG-based investigations of invasive brain recordings.

Tutorials and Documentation: Brainstorm offers a comprehensive collection of detailed tutorials that cover all major components of the platform, supporting users from basic data processing to advanced multimodal analyses. Within this ecosystem, the sEEG-suite is accompanied by its own dedicated tutorials, with each section of the suite linking to a corresponding resource. For convenience, the complete set of tutorials for stereo-electroencephalography (sEEG) analysis can be accessed here: sEEG-suite: Stereo-electroencephalography (sEEG) Analysis.

Figure 1 illustrates the complete end-to-end workflow for sEEG analysis in Brainstorm. The process begins with the acquisition of anatomical and implantation imaging, including both pre- and post-MRI and post-CT scans. The CT image is rigidly co-registered to the MRI to ensure alignment of anatomical and electrode information, after which skull stripping is applied to remove non-brain structures and CT artifacts. From the CT, an intensity thresholded isosurface is generated to identify candidate electrode contacts that will be used during the localization process. At this stage, Brainstorm offers two localization strategies: a manual interface that allows users to add/remove/merge/rename electrodes and add/remove contacts, and an automated localization procedure using GARDEL, which streamlines contact detection and reduces the need for extensive manual intervention. Once preliminary electrode positions are obtained, users can refine and correct them to generate a finalized set of electrode coordinates. These coordinates are then subjected to automated anatomical labeling, in which each contact is mapped to underlying cortical and subcortical structures based on atlas information derived from the MRI segmentation or provided from the different atlases available in Brainstorm. The localized and labeled electrode contacts can further be linked to the raw electrophysiological recordings, enabling Brainstorm to integrate anatomy with the corresponding time series data.
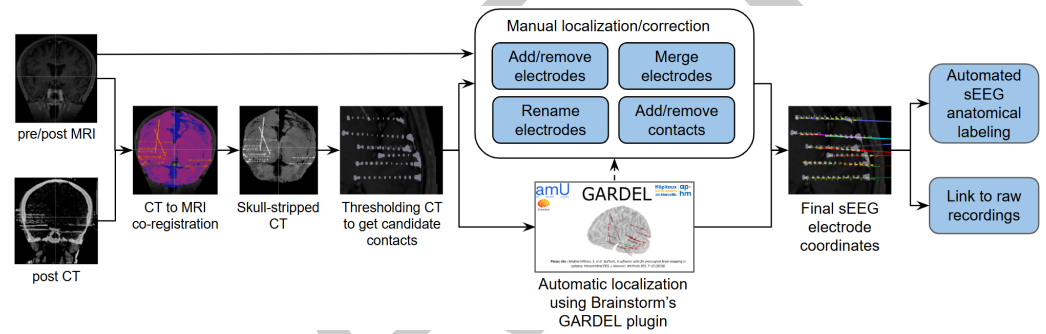
Figure 1: End-to-end flowchart for sEEG analysis in Brainstorm.

Anatomy and preprocessing: pre-MRI (Figure 2a) and post-CT (Figure 2b) scans are acquired for each subject. The post-CT volume is co-registered with the pre-MRI volume using the Statistical Parametric Mapping (SPM) or USC's CT2MRI (available as a Brainstorm plugin) (Figure 2c). The pre-MRI serves as an anatomically grounded reference for subsequent processing. Specifically, the pre-MRI is used to perform skull-stripping of the post-CT using tissue segmentation obtained either by BrainSuite (Shattuck & Leahy, 2002) or SPM (Friston et al., 1994) (using function mri_skullstrip.m), effectively removing extracranial tissues and eliminating artifacts associated with the sEEG electrode wire bundles (Figure 2d). The resulting artifact-free post-CT volume is then subjected to an automatic intensity thresholding to detect and extract metal artifacts which are potential candidates for electrode contact localization (Figure 2e). More details can be found in the tutorial: CT to MRI co-registration.

(a)   (b)   (c)   (d)   (e)

Figure 2: (a) pre-MRI; (b) post-CT; (c) post-CT co-registered to pre-MRI and skull-stripped using SPM (the colored image is the post-CT overlaid on the pre-MRI to show their proper alignment); (d) Skull-stripped post-CT by itself; (e) Isosurface generated from skull-stripped post-CT using intensity thresholding to capture metal artifacts as candidate contacts.

70 **Manual contact localization:** Prior to localizing the electrode contacts, knowledge of the
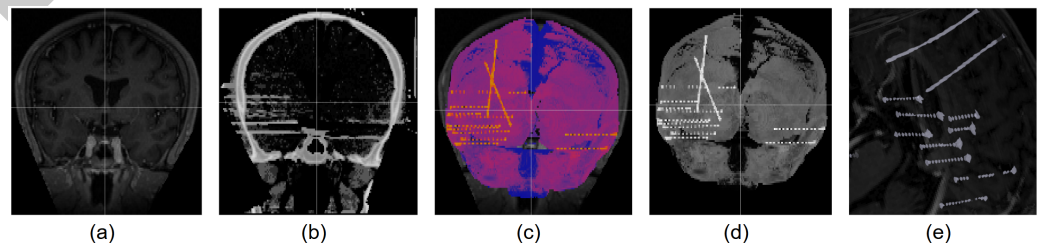71 implantation scheme is required in order to have the correct naming convention (used by the
72 center/neurosurgeons) for the various electrodes used. Brainstorm's iEEG graphical panel
73 allows creating an electrode implantation manually by first defining the electrode model and
74 constructor (through a list of predefined uniformly spaced electrode models from various
75 constructors, such as DIXI, PMT, etc, or users can choose to define and load their own model).
76 The user can then set the electrode tip and skull entry to render the electrode (Figure 3). This
77 process can be done in the 3D space (using the intensity thresholded mesh generated in the
78 previous section), in the 2D MRI viewer (using the intensity thresholded post-CT overlaid on
79 the pre-MRI), or only on post-MRI if the CT is not available. More details can be found in the
80 tutorial: SEEG contact localization and labeling.
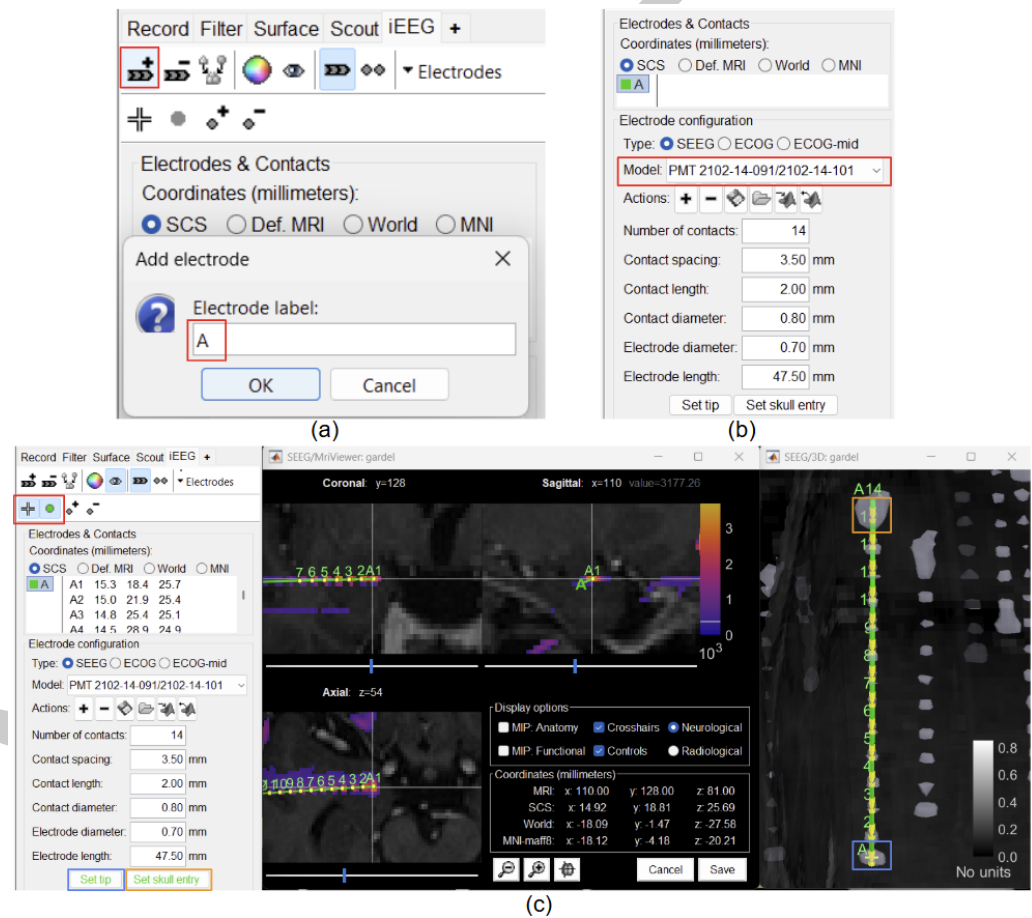
Figure 3: (a) Create an electrode and assign label to it (in red); (b) Define the electrode model (in red); (c) On the 3D figure (SEEG/3D: gardel), set the electrode tip (in blue) and skull entry (in orange) using the surface selection button (in red) to render the electrode both in 2D MRI viewer and 3D figure.

81 **Automatic contact localization:** With the click of a single button inside Brainstorm (Figure 4),
82 we have live, interactive visualization of the detection process, enabling users to observe contact
83 identification, grouping, and ordering in real time. The electrode names are automatically
84 assigned from **A**-**Z**, **AA**-**ZZ**, etc. in the order they are detected, which can be renamed
85 as desired during post-processing (Figure 5). On the button click, GARDEL uses the skull-
86 stripped post-CT volume along with the intensity threshold to identify high-density regions
87 corresponding to metallic artifacts that are considered as electrode contacts. These detected
88 points are grouped into individual leads, with contacts sorted along each electrode trajectory,
89 designating the deepest contact as the first in sequence. This integration reduces the need for

manual contact detection and electrode indexing, significantly streamlining the localization workflow. More details can be found in the tutorial: Automatic SEEG Contact Localization using GARDEL.
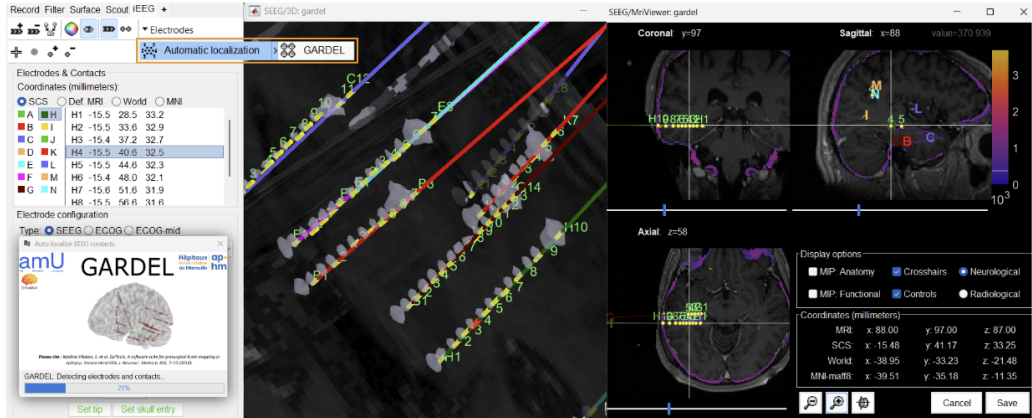

Figure 4: The Brainstorm interface displaying the automatically detected contacts, with the GARDEL button (in orange) that triggers the automatic detection.

Post-processing of the electrodes/contacts: All the necessary post-processing can be done using the Brainstorm interface interactively. If there is a wrongly detected electrode, we can delete and manually rectify it by creating it from scratch (as mentioned in the **Manual contact localization** section above) along with renaming them if needed (Figure 5). There could be cases where a single electrode may be detected as multiple in which case we need to merge them as one (Figure 6). We also allow fine-tuning at the contact level, where we can remove (Figure 7) or add (Figure 8) them. On doing any of the editing operations, it is also ensured that the ordering of the contacts is maintained with the deepest contact as first in the sequence. More details can be found in the tutorial section: Edit the contacts positions.
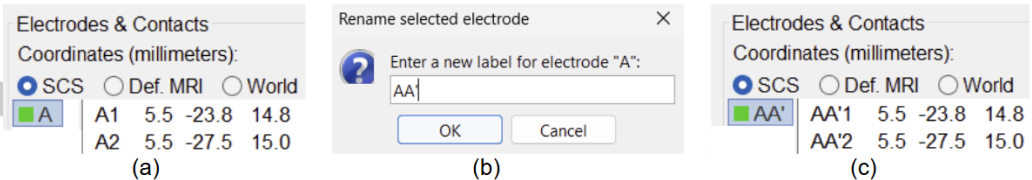

Figure 5: Renaming electrode (a) Electrode **A** before renaming; (b) Brainstorm interface to rename the electrode (double click on electrode **A** and change name to **AA'**); (c) Electrode **A** renamed to **AA'** (along with all the contacts).
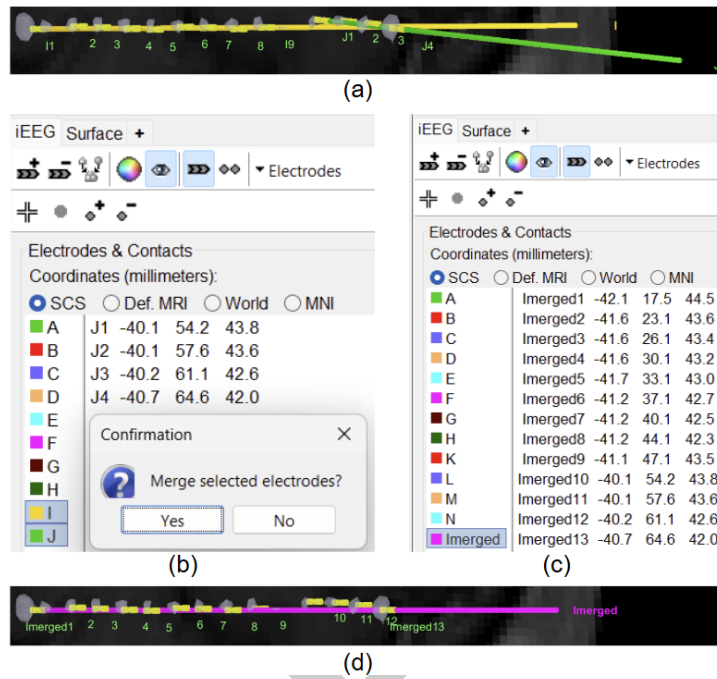
Figure 6: Merging electrodes using the Brainstorm iEEG panel; (a) Electrodes **I** and **J** are wrongly detected as separate electrodes; (b) Brainstorm interface showing option for merging them; (c) The merged electrode in iEEG panel (**I** and **J** get replaced by **Imerged**); (d) The rendered merged electrode.
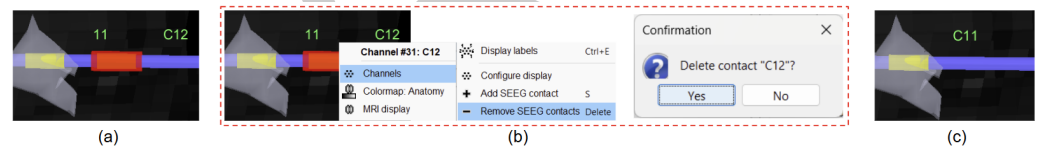
Figure 7: Removing a contact using 3D figure; (a) Wrongly detected contact (selected contact **C12** in red); (b) Brainstorm interface showing option for removing it (right click on the **C12** contact to get this menu); (c) Contact removed.
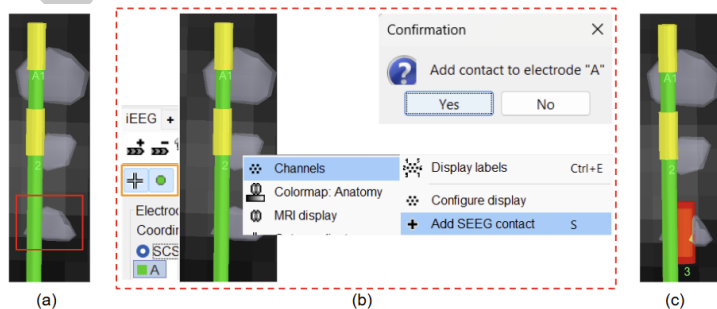
Figure 8: Adding a contact using 3D figure; (a) Missed detecting contact (3rd from top for electrode **A** in red); (b) Brainstorm interface showing option for adding it (turn on surface/centroid selection and select electrode **A** in iEEG panel, select the surface point and right click on it to get this menu); (c) Missing contact **A3** added.

Automated anatomical labeling: Brainstorm supports multiple standardized brain anatomy templates (ICBM152, Colin27, USCBrain, FsAverage, etc.) and brain atlases (AAL, Desikan-Killiany, Brainetome, Schaefer, etc.), all of which can be added from the interface as shown in

105 Figure 9(a-b). The spatial coordinates of contacts localized by the steps above are automatically
106 cross-referenced against these atlases, resulting in detailed anatomical labels (e.g., specific
107 cortical gyri, subcortical nuclei) as shown in Figure 9(c-d). This enriched labeling framework
108 provides a comprehensive anatomical context for each contact (the region of the brain the
109 contact belongs to), facilitating both clinical interpretation and research analyses. More details
110 can be found in the tutorial section on anatomical labeling. Work by (Taylor et al., 2021)
111 demonstrates a clinical validation study using this feature of Brainstorm.

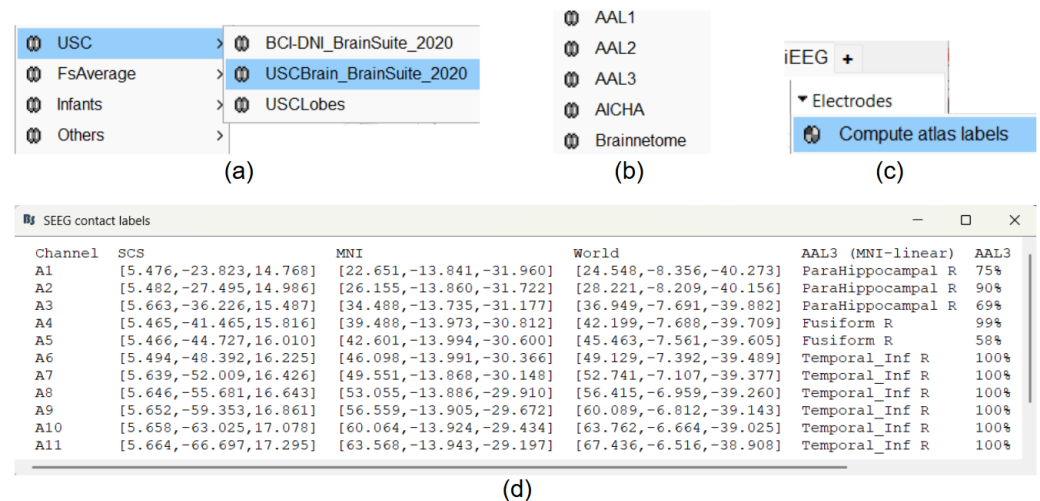**Figure 9:** (a) The different brain anatomy templates supported inside Brainstorm; (b) The different brain atlases supported inside Brainstorm; (c) Brainstorm interface to compute the anatomical labeling (in the iEEG panel select the electrode **A**, go to *Electrodes > Compute atlas labels*); (d) The computed anatomical labels for contacts in electrode **A** using the AAL3 atlas.

112 **Link to raw recordings:** Once the sEEG contacts have been localized, we can associate them
113 with the corresponding raw electrophysiological recordings. This link ensures that anatomical
114 localization can be directly tied to the recorded brain signals. To establish this connection, it is
115 essential that the contact names match exactly with the channel names in the raw recordings.
116 Any mismatch (such as differences in naming conventions, capitalization, or numbering)
117 will prevent Brainstorm from aligning the contacts with the appropriate channels. Detailed
118 instructions on how to perform this linking can be found in the tutorial section: Access the
119 recordings. Following these guidelines ensures that each localized contact is correctly mapped
120 to its electrophysiological data, allowing for reliable analysis and visualization. Once this step
121 is completed, users can proceed either with the sEEG data analysis within Brainstorm using its
122 rich and complete set of tools or export the final data into any of the supported formats for
123 analysis with other software.

Statement of need

125 Intracranial electrode localization, particularly for sEEG, is a foundational step in epilepsy
126 surgery planning and neuroscience research. At present, many researchers and clinicians
127 rely on manual workflows or a patchwork of separate tools for localization, which results
128 in time-consuming procedures, inter-operator variability, and fragmented pipelines. Manual
129 identification and labeling of electrode contacts can take several hours per subject, slowing
130 down the workflows, while subjective differences between operators introduce inconsistencies
131 in results. Moreover, existing practices often require multiple platforms, i.e., one for CT-MRI
132 co-registration, another for electrode detection, and another for anatomical labeling, and
133 another for data analysis, thereby adding unnecessary complexity and risk of errors in the final

134 results.

135 Integrating GARDEL with Brainstorm provides seamless, one-click deployment of intracranial
136 electrode localization directly within Brainstorm, eliminating the need for external scripts and
137 reducing manual intervention. This reduces localization time from hours to minutes (with some
138 minor post-processing), enabling researchers to efficiently scale analyses across larger patient
139 cohorts. The integration also enhances reproducibility by standardizing detection parameters,
140 minimizing manual intervention, and unifying the entire workflow of localization and labeling
141 with the advanced analysis of electrophysiological data into a single interactive environment.

142 While other tools, such as DEETO (Arnulfo et al., 2015), 3D Slicer's sEEG Assistant (Narizzano
143 et al., 2017), FASCILE (Ervin et al., 2021) and LeGUI (Davis et al., 2021) have demonstrated
144 dramatic speedups compared to manual localization, they do not provide an end-to-end
145 processing workflow from anatomical to functional analyses like Brainstorm that does.

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