

Instructions for Localizing Electrodes on 3D Brain Image

(on lab computer)

For set up patient files, only do Localizing Electrodes on the CT Image:

Connecting to the Server (if you do not see a connection already)

Go to *Files* and on the left tab there should be “+ Other Locations.”

Go to ncs1 and you will be asked for the Username and Password. The ncs1 window should pop up.

Coregistration of the CT and MRI (T1) images

Open a Terminal window.

If not in the environment already, enter the Anaconda environment *registration_env*. If you are in it you should see (base) [ksr@ss001](#): before each line.

Changing the config and setting up directors of patient data (for your files):

Go to */home/ksr/Desktop/contact_localization*, and there should be folder *raw* and *freesurfer_output*.

In *raw* there should be folders called *efriXX*. (may change for other patient files). Within each patient folder is a *premri* and a *postcti* folder with dicoms (.dcm) image files. If this is not set up, you should take files from the server. For EFRI patients, these are in *Public/EFRI/0raw/SUBJECTXX/EFRIXX-pre-MRI-T1* and *EFRIXX-post-CT* and put in folders with these names under *raw/efrixx/premri* and *post cti*

Go to */home/ksr/Downloads/neuroimg_pipeline/pipeline/config*. Open the *local_config.yaml*.

Change directories at top to location of *raw* and *freesurfer_output* folders. At the bottom list all patients (e.g. 'efri06', 'efri07'). Do in python formatting. Mind spacing, commas, etc.

Running the Image Coregistration:

Go to */home/ksr/Downloads/neuroimg_pipeline/pipeline/reconstruction*

Run

```
snakemake -n # dry run
snakemake # real run
```

Outputs in *freesurfer_output* should include CT.nii and T1.nii, which are needed for manual electrode localization. If ran successfully a text file called *efriXX_recon_success.txt* should be made, and if run again with the config file unchanged, these patients will not be run. This is likely not run well if there are ~30 dicom files for CT or fMRI.

If it gets stuff, look for the patient responsible in the error. Remove their name from the config list and run again.

*This step parcellates the brain into smaller atlas locations. Also, it produces the CT.nii and T1.nii files needed for localizing the electrodes on the CT image.

Running the Image Reconstruction:

Go to */home/ksr/Downloads/neuroimg_pipeline/pipeline/reconstruction*, and run the snakemake functions above again.

*This step find the best coefficients from the affine transform used to relate the CT and the MRI images. This is important for mapping onto a 3D brain.

Localizing Electrodes on the CT Image:

Open */home/ksr/Downloads/neuroimg_pipeline/pipeline/contact_localization/matlab/run_localization_fieldtrip_v3.m*

If settings are not correct, change pathway to SPM12 and fieldtrip packages, and change directories to the locations for *freesurfer_output* and *raw* shown above. This should already be set.

You must change subjID to the current subject. You should change your_intials to your initials (e.g. CRS). The rest of the information should change to this correct subject.

Press Run. A window will pull up with a 3D image of a brain, and you will be prompted about whether to change the coordinates. Enter 'n'.

A new window with three view of the 3D brain and the CT with bright electrodes will appear.

Use the 3D images to click the electrodes (white squares), while simultaneously looking at the brain maps. For EFRI patients these are in *home/colocalization/EFRI_PPT*. If the map indicates you are looking at shank A. The inner most electrode should be A1. Click twice on A1 on the drop down when your cursor is in the correct position. (You can zoom in to make sure you are most centered.) The A1 should turn black on the list, and a red cross-hairs should appear. Do this for all electrodes on the list. Then, close the window when you are done. Files will automatically save.

(Potentially, there will be Check points to make sure the brain is scaling correctly. These will be ref_eyes, ref_back, ref_top. We will, ask you to click these too to see how well the brains align.).

Source of the pipeline is (https://github.com/adam2392/neuroimg_pipeline) Pipeline Installation Instructions

Written by Cynthia Steinhardt (CRS), last edited by CRS 6/26