

PC-ES (Point Cloud Electrode Selection) Software User Manual

Haley Richards, Sept '22



Section 1: Overview and Homepage

What you need:

- Point clouds of the EEG cap (.ply files)
- Reference data (optional)

Compatibility Requirements:

- Windows 10 OS
- Any hdEEG 256 Electrode cap

What it does and why:

Accurate localization of scalp electrodes is instrumental to mapping brain activity using high-density electroencephalography (hdEEG). Existing technologies for electrode localization can be costly and difficult to transport, which can restrict access to hdEEG monitoring. This software enables a novel and affordable electrode digitization technique by leveraging the 3D scanning feature in modern iPhones (and other 3D scanning devices). This interactive semi-automated MATLAB GUI intuitively allows the user to **visualize, select, and label all electrodes in a 256 EEG cap using point clouds alone.** To compare this method to other methods (photogrammetry, electromagnetic tracking, etc) there is an option to upload a set of reference data to compare to the results from PC-ES.

PC-ES was first designed to be compatible with 3D scanning features on modern iPhones using the Heges app. Since the Heges app can not take individual scans of the whole head, the app was originally designed to label and merge a variable number of partial scans of the head. **Figure 1.1** shows a high level diagram of the process. However, PC-ES is compatible with any scanning device that produces a .ply file, as well as a single and complete scan of the head.

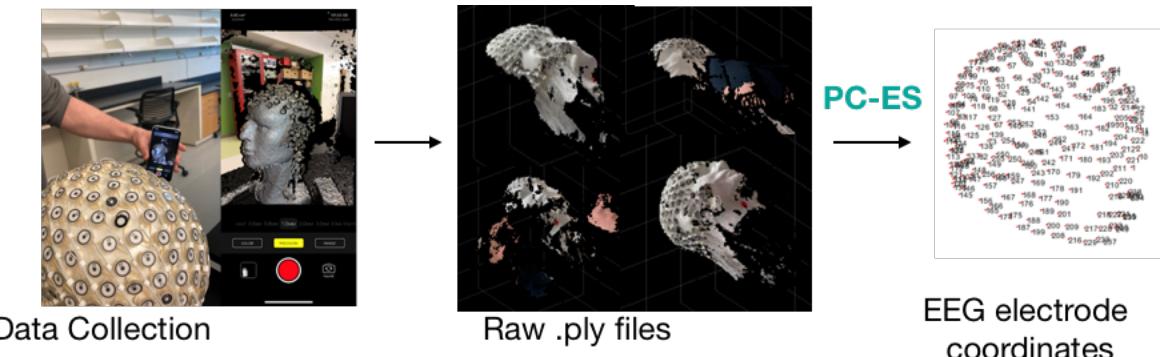


Figure 1.1 Schematic of EEG electrode localization using PC-ES and the Hege iPhone app

The processing approach is semi-automated, involving both user-driven and automatic processing steps. A flow chart of the image processing steps is shown in **Figure 1.2**.

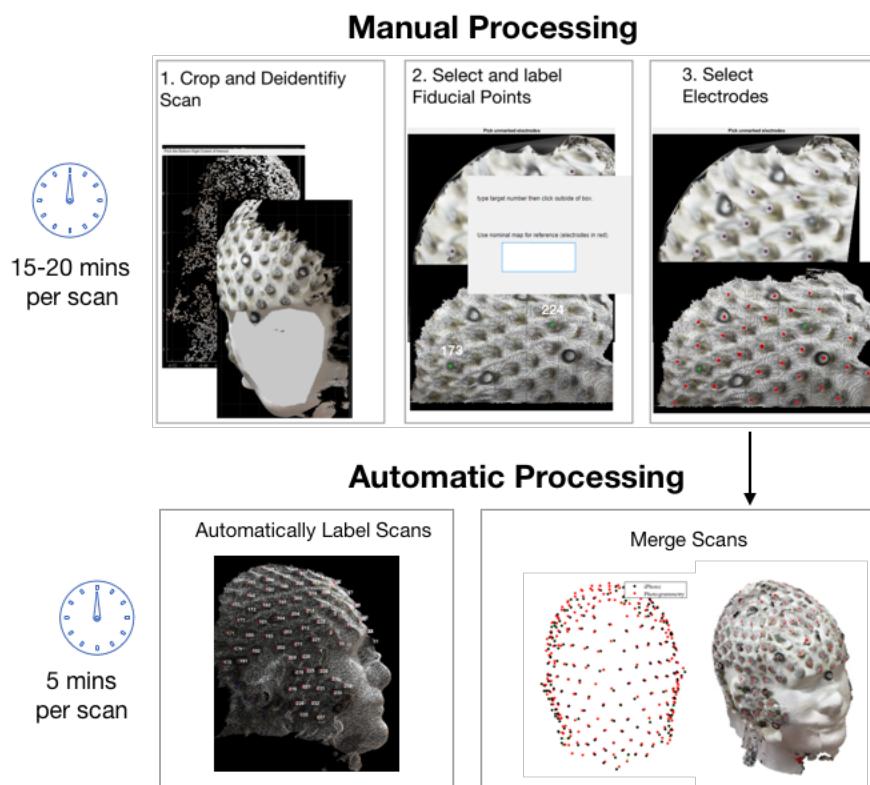


Figure 1.2 PC-ES Image processing workflow

Manual Processing

After uploading the scan, the user crops the scan for improved processing speed if needed and deidentifies the facial region for HIPAA compliance. The user then selects and manually

labels fiducial points (electrodes with known labels that are used as reference landmarks). These may be marked with selected colored stickers during data collection to ease in recognition.

Lastly, the user selects the remaining electrodes visible in the scan without assigning labels, concluding the manual processing steps. In the future, the manual processing steps can be automated through AI image classification algorithms.

Automatic Processing

After electrodes and fiducial points are marked, the program automatically labels the selected points, and uses them to sequentially merge the point clouds. This results in full a point cloud of the whole head in a single reference frame (**Figure 1.3 a)**, as well as a set of labeled coordinates (**Figure 1.3 b**). The program then identifies electrodes that the user has missed and interpolates them from the merged point cloud (**Figure 1.3 c**).

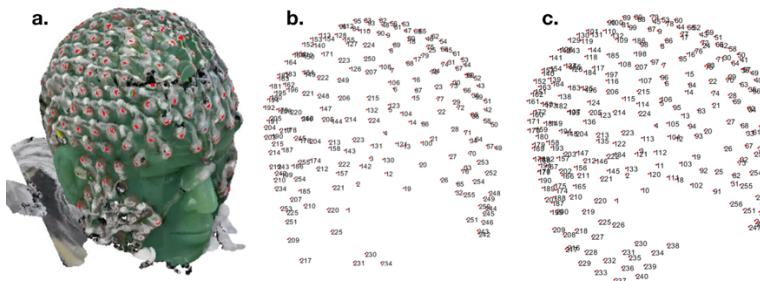
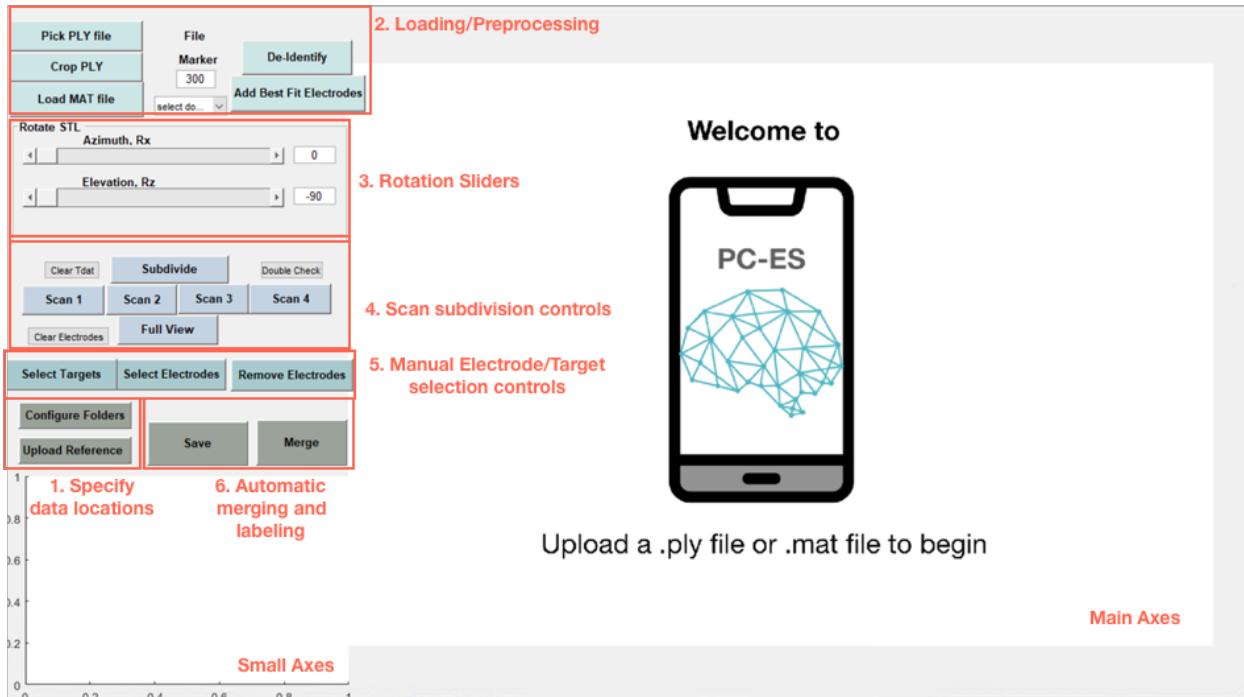


Figure 1.3 Example Results for a gel phantom: a. merged scan b. selected coordinates with labels c. all electrodes with labels

Figure 1.4 shows the PC-ES homepage with some key functions labeled roughly in process order. The rest of the guide describes these functions in detail.



1.4 PC-ES Homepage with key functions labeled

Section 2: Specify data to be used

Raw data

Run ‘PC-ES.m’. This will open the homepage. Click ‘configure folders’. The screen prompts the user to type the subject name, as shown in **Figure 2.1**.

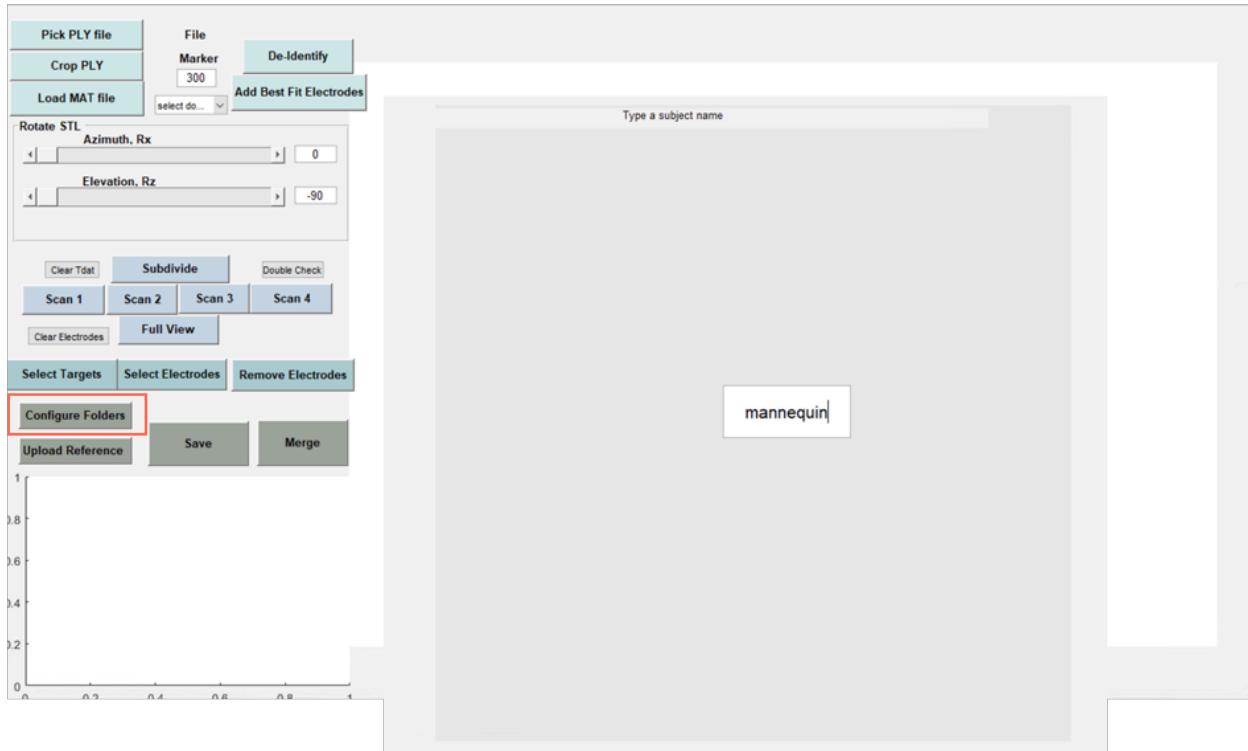


Figure 2.1 Entering the subject name

Then type the name of the subject into the text box, and click outside the box when finished. The screen then prompts to the user to select the directory where the raw .ply files are stored, shown in **Figure 2.2**. Navigate to and select the correct folder.

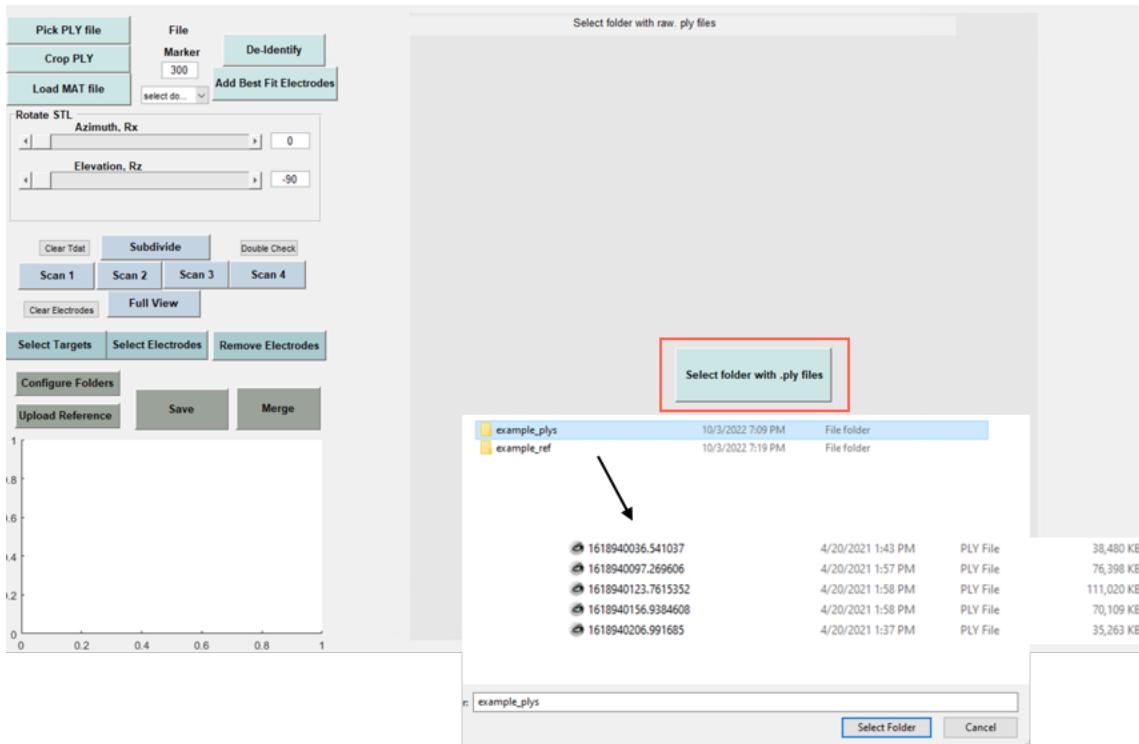


Figure 2.2 Selecting path to raw data

Reference Data

If you would like to compare other data to coordinates obtained using PC-ES, there is an option to upload a reference dataset through the ‘Upload Reference’ button. Either .mat or .sfp file types are accepted. The dataset should be a 256x3 array (# of electrodes, # of dimensions).

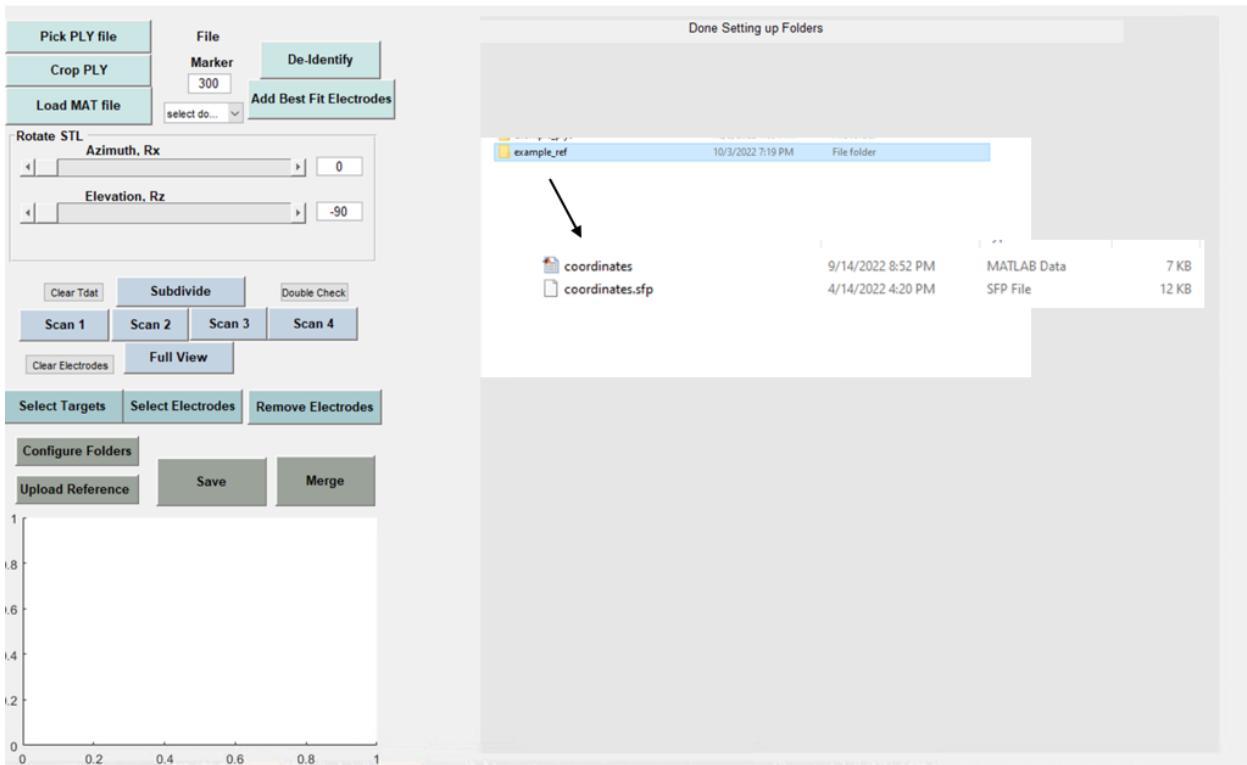


Figure 2.3 Uploading reference data

Folders

After the ‘Configure Folders’ task is carried out, a new folder called ‘dat’ appears in the working directory (if it was not there previously) and there is a folder in dat named ‘subject name’. In the dat/‘subject name’ folder, there are 4 folders: ‘subject name’_raw, ‘subject name’_cropped, ‘subject name’_elfound and ‘subject name’_saved. The ‘raw’ folder contains the raw .ply files specified by the user, the ‘cropped’ folder stores scans after they have been cropped but not labeled, the ‘elfound’ folder stores the processed scans and the ‘saved’ folder is empty and will store the outputs of the program. If the user has uploaded a reference dataset, there is an additional folder called ‘subject name’_pgdat, where the reference data is stored. Each of the files in the folder can be edited at any time without losing previous progress.

mannequin		
	10/3/2022 7:14 PM	File folder
└ mannequin_cropped	3/10/2022 11:20 PM	File folder
└ mannequin_elfound	10/2/2022 2:55 PM	File folder
└ mannequin_pgdat	12/1/2021 2:42 PM	File folder
└ mannequin_raw	3/10/2022 10:51 PM	File folder
└ mannequin_saved	10/3/2022 7:14 PM	File folder

Figure 2.4 Final folder set up

Section 3: Preprocessing

Cropping

Click ‘pick PLY File and navigate to the new subject ‘raw’ folder where the .ply files are stored as shown in **Figure 3.1**.

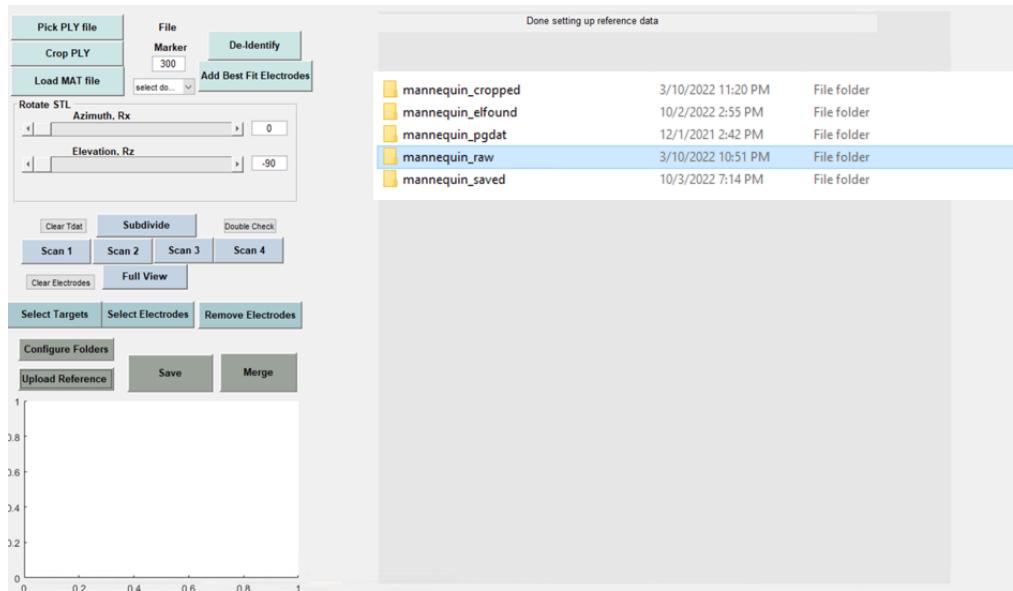


Figure 3.1: Uploading the raw point cloud

After the file has been uploaded, the message bar instructs the user: ‘Please Crop before Rotating./Translating. While cropping isn’t necessary, it is recommended because it can greatly speed up processing speed and improve the quality of the images used for electrode selection. Click the ‘Crop PLY’ button..The message bar instructs the user to ‘Pick the Top Left Extent of Interest’, and yellow cross hairs appear, shown in **Figure 3.2**. Once the top left extent of interest is clicked, the message bar instructs the user to ‘Click the bottom right extent of interest’ the same way. Once this is done the scan will switch views for another round of cropping with the same method.

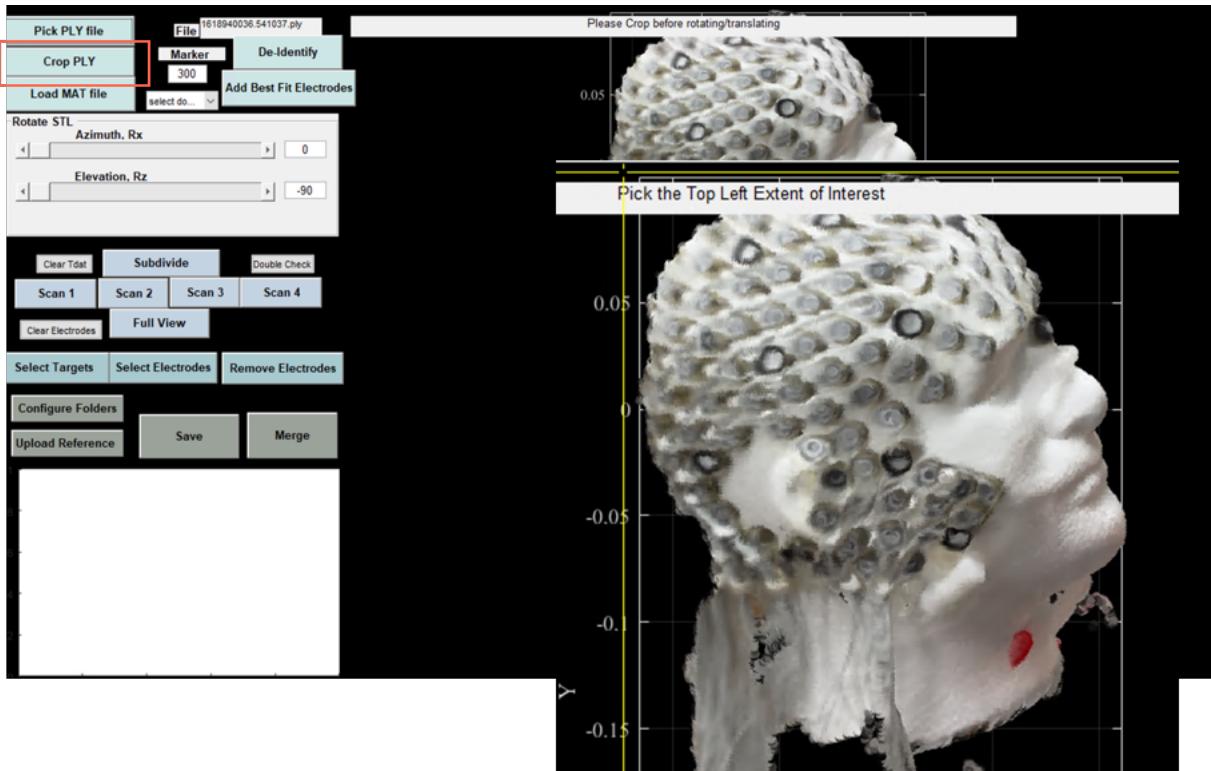


Figure 3.2 Cropping the raw point cloud

Scan Rotation/Deidentification

The next step in processing is to deidentify the scan, i.e. removing all of the identifying facial features for HIPAA compliance. This step and a variety of others are done through projecting the 3d point cloud into 2D to manually interact with an image instead of a 3D scan. In order to do that, the scan must be rotated so that the face is directly normal to the viewing angle, which is illustrated in **Figure 3.3**. Interactive rotation of the scans to optimize the viewing angle before projection steps is one of the essential features of PC-ES. Scan rotation is performed by adjusting the azimuth and elevation sliders that rotate the scan about its center point to an angle specified by the spherical coordinates.

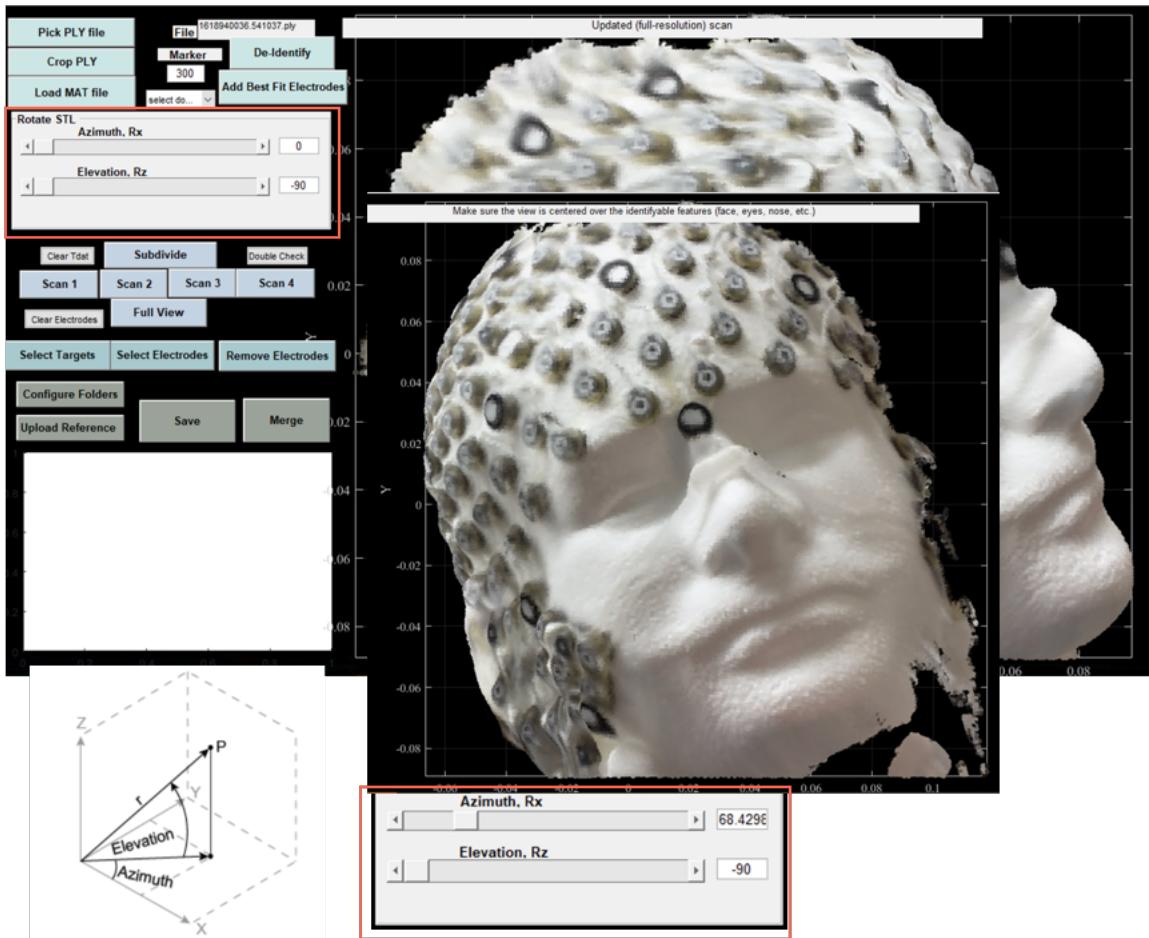


Figure 3. 3
Rotating the scan

To deidentify the scan click the ‘Deidentify’ Button. A window should pop up with a 2D projection of the point cloud and instructions to ‘Pick in a counter-clockwise direction the identifying region of the scan’ and the yellow crosshairs should appear. Once you are done clicking the circle, right click. The window should close and the main window should refresh with the clicked region now covered in grey, shown in **Figure 3.4**.

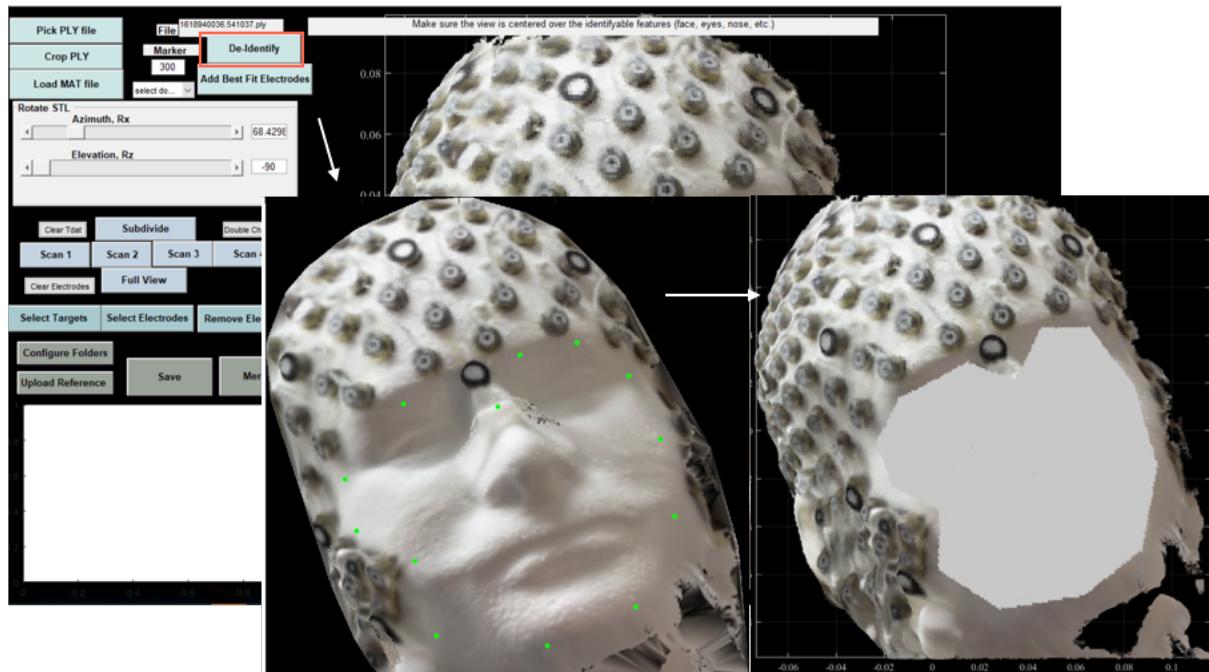
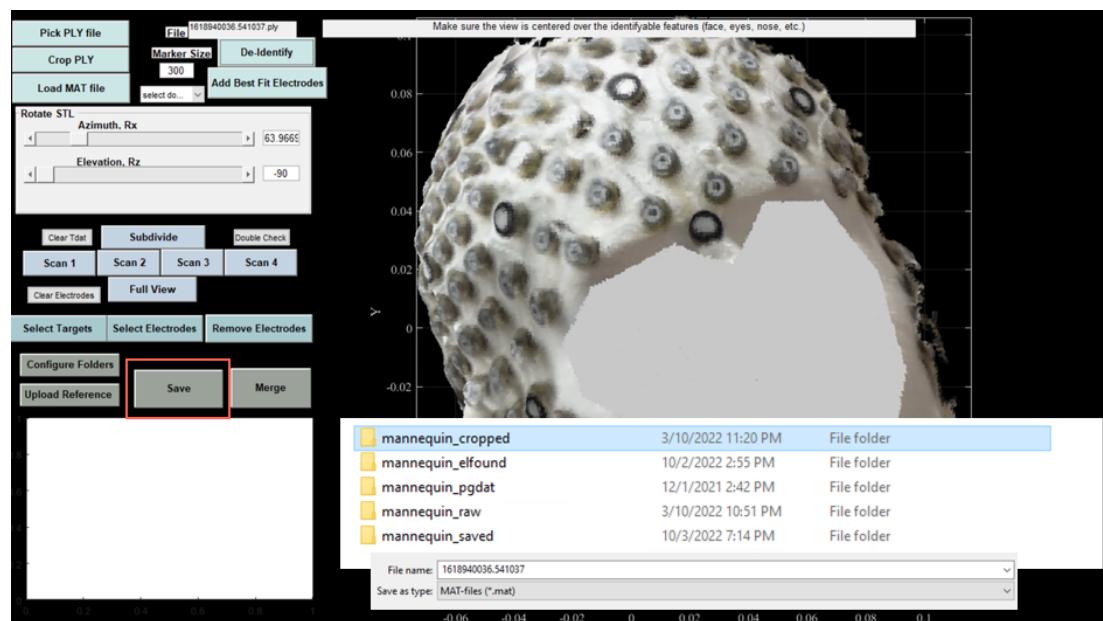


Figure 3.4 Deidentifying the scan

The MS (Marker Size) and downsample buttons allow the user to modify the resolution and marker size of the point cloud to optimize time and visualization. After a scan is cropped and deidentified, click the save button and navigate to the ‘cropped’ subject folder and save it as a .mat file with the same name as the previous .ply file (which should come up by default, but make sure to delete the .ply extension). See **Figure 3.5** for an example.



Section 4: Subdivision

Dividing the point cloud into smaller scans before processing can improve processing speed and the 3D image interpolation. Smaller scans can be rotated more quickly and provide a more zoomed-in window for electrode selection. The scans are subdivided using a kmeans clustering of the spherical coordinates of the whole scan into 4 distinct groups, shown in **Figure 4.1**

To subdivide the scans, click the subdivide button. The message bar notifies the user that the ‘scans are subdivided, choose scan to process. To select a scan, click on the scan number in the GUI. The message bar then shows what scan is currently in view.

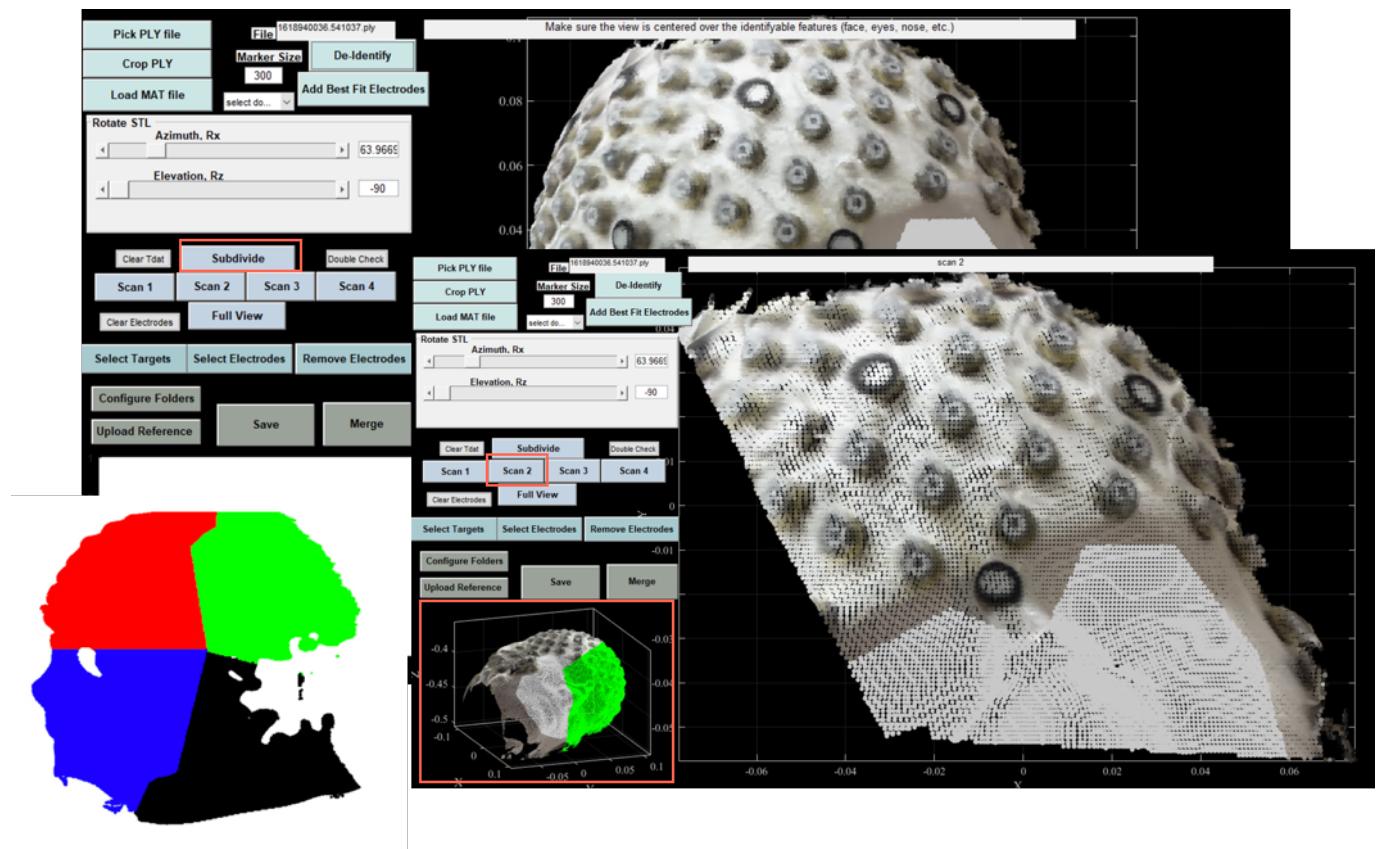


Figure 4.1 Subdividing the scan

One challenge with working with a smaller scan is that it is harder to know where on the head each one is located. To solve this problem, once the scans are divided and a scan is selected, the small axis shows the 3D point cloud of the head with the region of the current scan labeled in

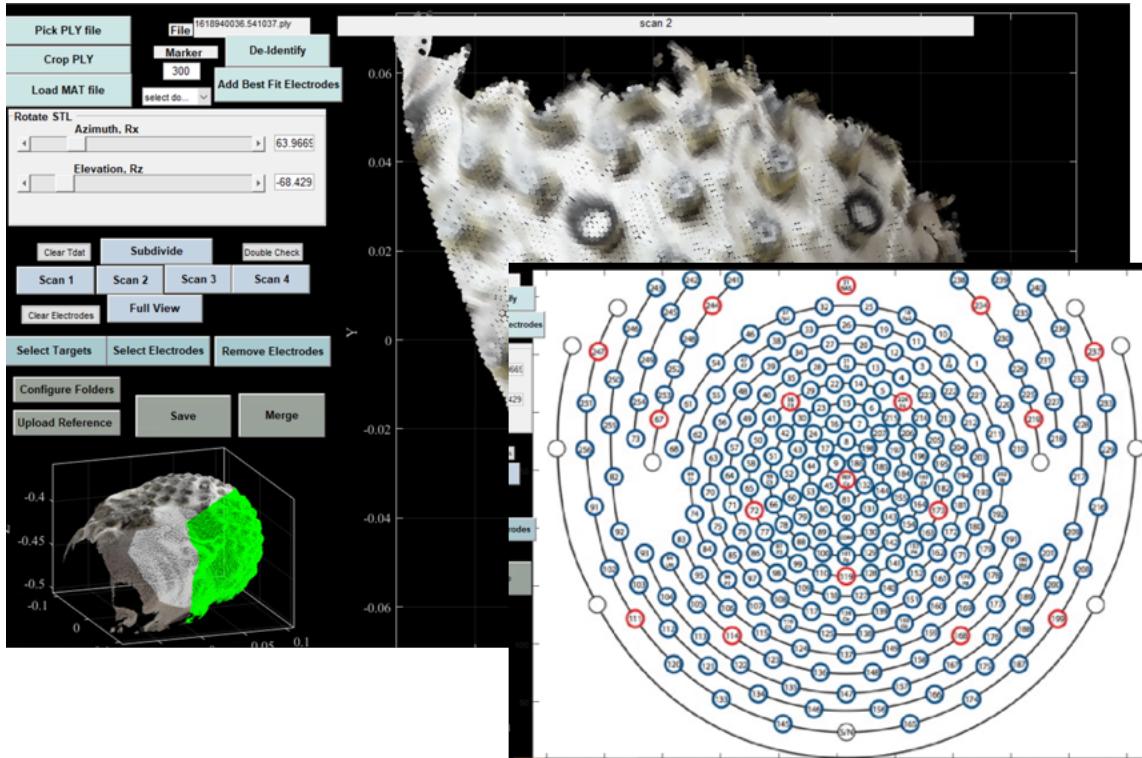
green. The small axis is manually rotatable. To return to the full point cloud, click ‘Full View’. All of the next steps are possible to do on the full point cloud as opposed to subscans, but at a higher computational cost.

Section 5: Manual Selection

Fiducial Electrodes

Labeling fiducial points accurately is instrumental to merging the scan accurately.

First rotate the scan so that many electrodes are normal to the viewer. Click on the ‘Select Targets’ button. A new window pops up with a prompt and cursor to select the fiducial points. The main axes shows a reference map (shown in **Figure 5.1**) to aid in matching electrodes in an image to numbers on the EEG cap. Any number of fiducial points can be selected at any point in time.



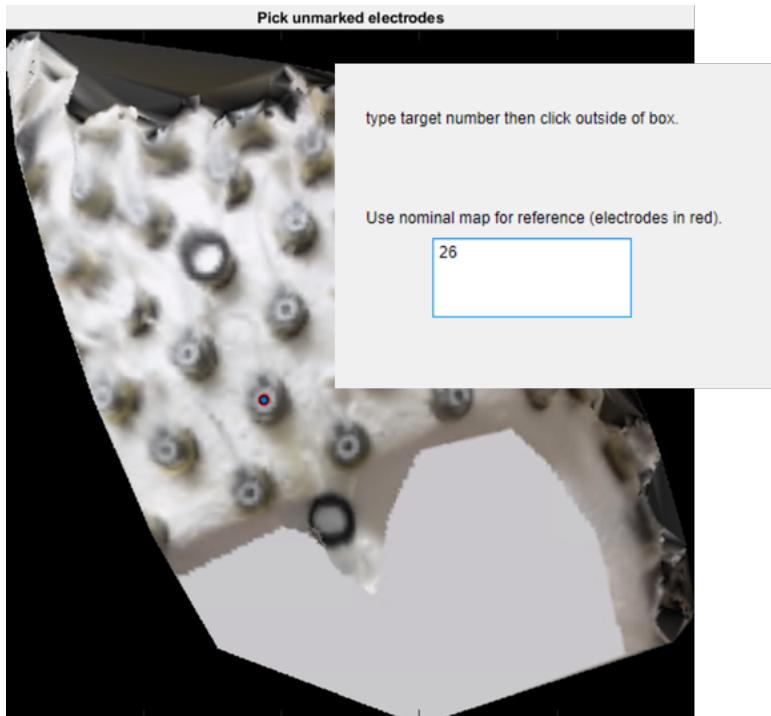


Figure 5.1 Labeling Fiducial Electrodes

All other Electrodes

After the fiducial points have been selected using the mouse, press the 'esc' key on the keyboard. A new window pops up prompting the user to enter a label for the selected points. After entering the number, click in the grey box but outside the white text box. If more than one fiducial point is entered for a given plane projection the intended labels for each point should be entered in the order that they were selected. After the fiducial points are labeled, they will be recorded on the scan in green, to avoid re-labeling. After fiducial points have been processed in one subscan, move on to the next until they are all completed. In the entirety of the scan, there should be at least 4 fiducial points entirely (though they need not be any in a given subscan).

After selecting and labeling fiducial points, click on all remaining electrodes in view. This is accomplished in a similar way to the fiducial points, with manual rotation of the 3d scan and plane projection of the normal facing view in a new window, shown in **Figure 5.2**. Unlike fiducial point selection, no label entry is needed. After the electrodes are labeled, they will show up in red.

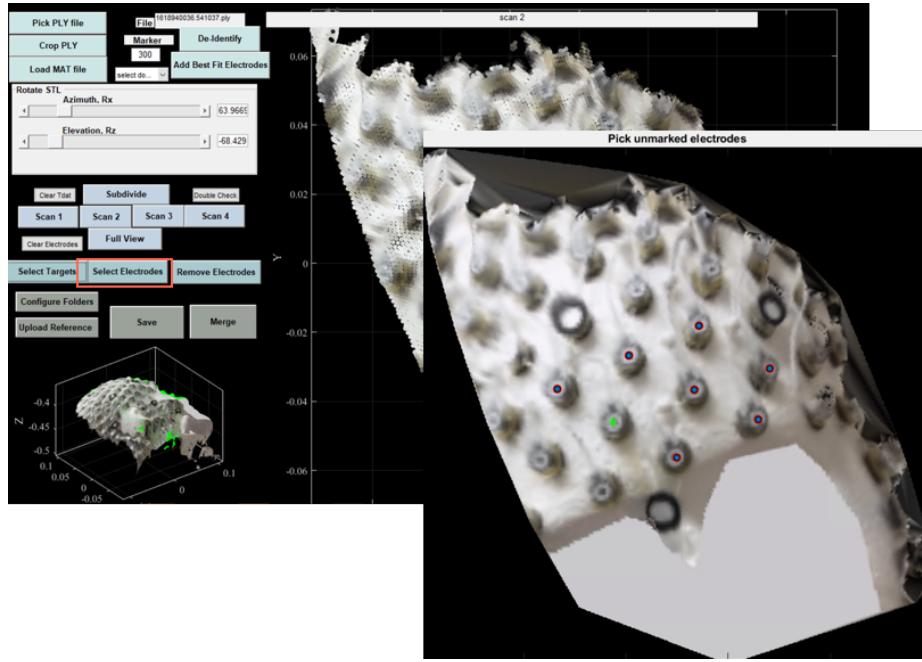


Figure 5.2 Selecting electrode locations

Electrode Removal and Troubleshooting

If one of the electrode locations is not correct and should be removed, rotate the scan to the plane normal to that point and click “remove electrodes”. A projection window opens with instructions to select the point. After selecting the point, press the right key. After the point has been removed, it turns black.

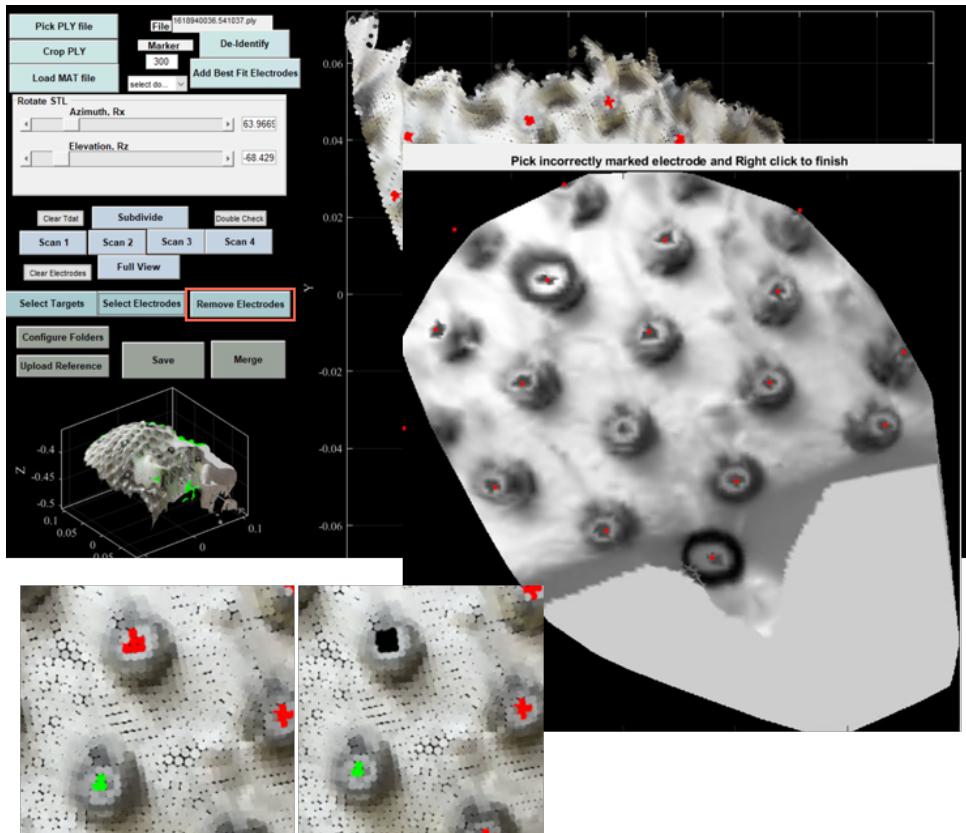


Figure 5.3 Removing single electrodes

To double check that no errors have been made in labeling, it is optional to click the ‘double check’ button. This plots the current scan with the fiducial markers in red and the electrodes in blue, shown in **Figure 5.4**. If the target points are not aligned well, it is possible to clear them through the ‘clear tdats’ button. Similarly to the ‘remove electrodes’ button, this turns the previously labeled electrodes black. If the scan needs to be reprocessed, it is possible to entirely start over with the ‘clear electrodes’ scan.

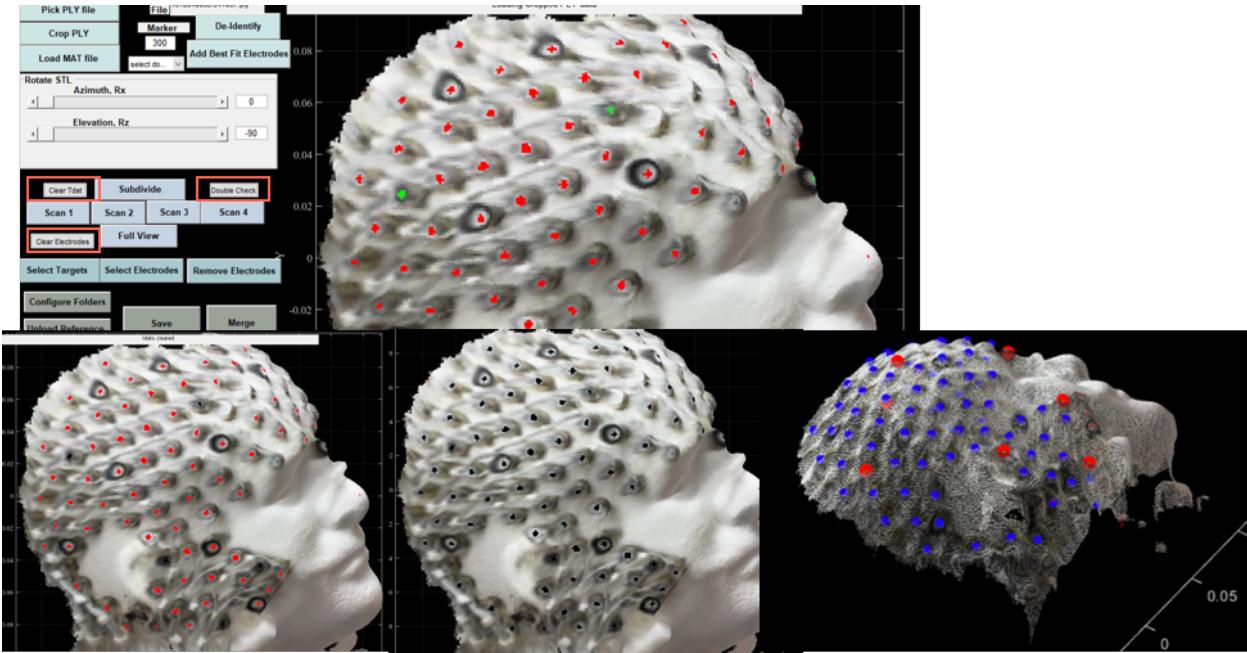


Figure 5.4 Troubleshooting

To save the processed scans, press the ‘save’ button and navigate to the ‘_elfound’ subject folder. Save the file with the same filename as the cropped scan. If processing another scan, close the app and re-run the code before opening another scan.

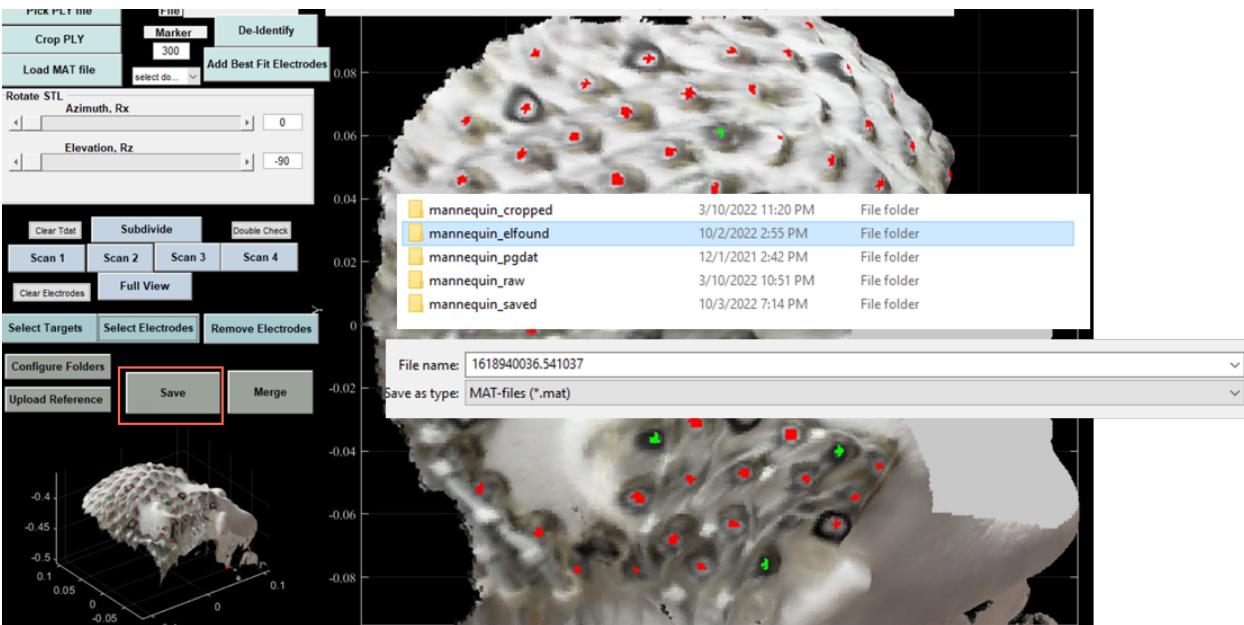


Figure 5.5 Saving processed scans

Section 6: Automatic labeling and merging

After all of the scans have been processed, click the ‘Merge’ button. The screen then prompts the user to re-enter the subject name and the thickness of the electrode cap used (in mm).

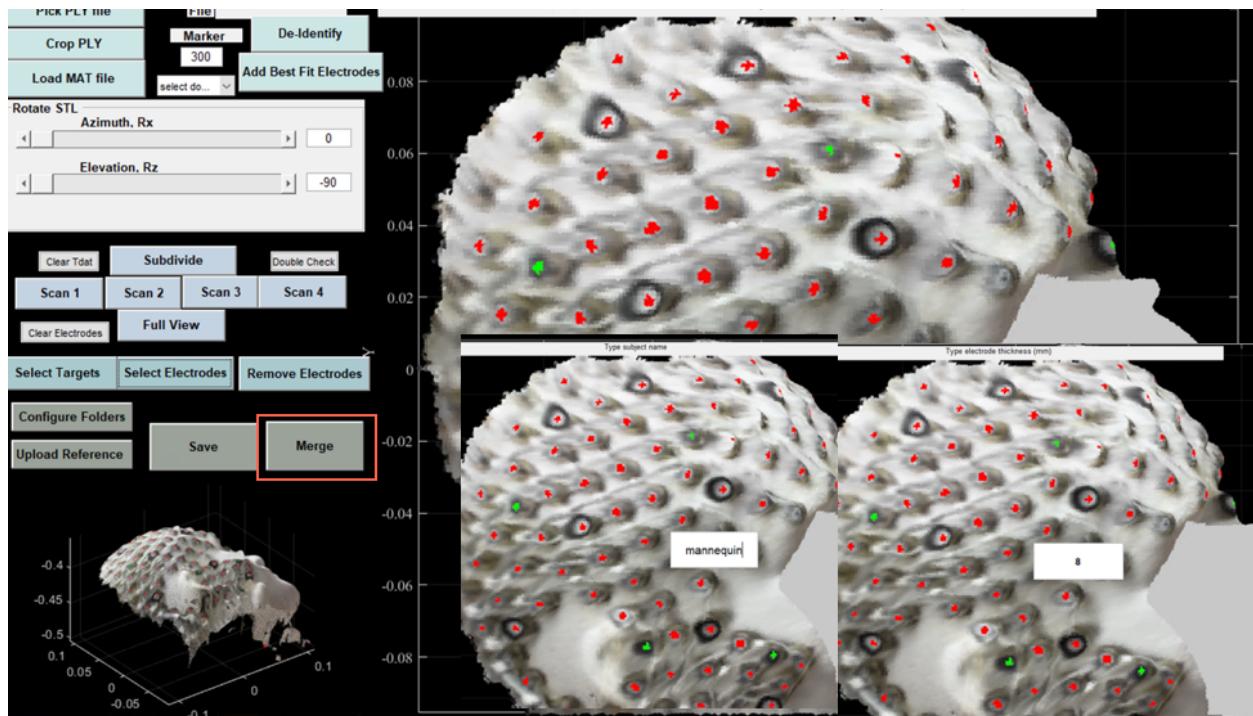


Figure 6.1 Merging scans

When the merging code has finished (approximately 15-30 min), the results are saved in the ‘saved’ subject folder. If no reference data has been uploaded, the program saves an image of the scan ‘subject name.png’ as well as a structure called merged_scan.mat. This structure includes the 256 coordinates (merged_scan.tdat), and the merged point cloud (merged_scan.colobj), shown in **Figure 6.2**.

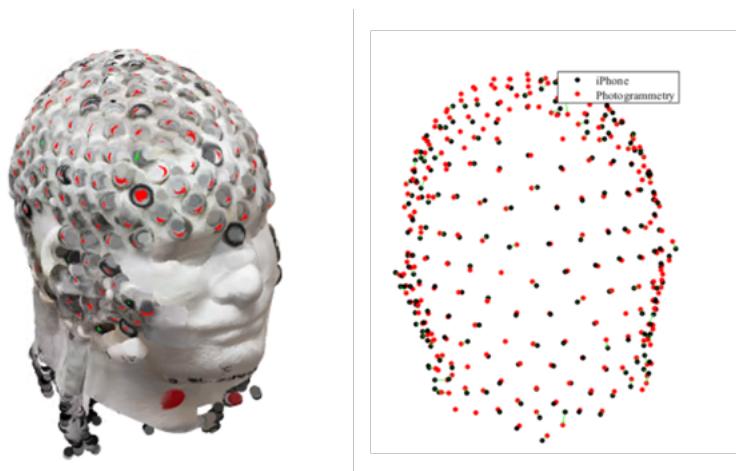


Figure 6.2 Merged scan and final coordinates

If the user has uploaded reference data as a point of comparison, then an additional variable is saved called `fullset_merging_data_<subject name>`. The structure includes the RMS error between the reference and the selected PCES coordinates in mm (`rms`), as well as the RMS error between the reference and the all 256 PCES coordinates in mm (`rms_fullset`).

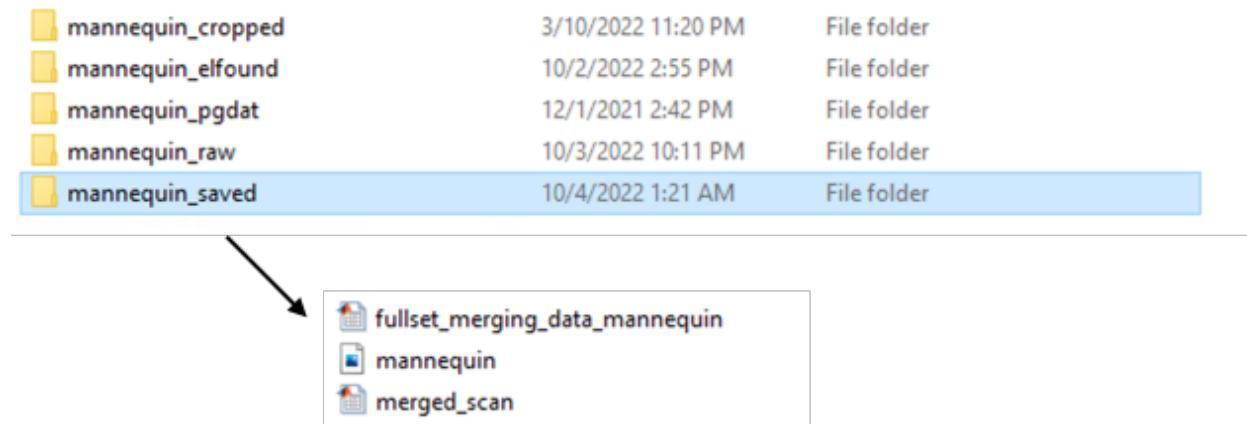


Figure 6.3 Data in the '_saved' folder