

GRIDlab

PROTOCOL: CORTICAL RECONSTRUCTION

HOW TO RUN CORTICAL RECONSTRUCTIONS (RECONS)

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1 RUNNING RECONS PROTOCOL

One of the first things to do when we get a subject is to reconstruct a rough 3D model of where the implanted electrodes are on their brain using MR (pre-op) and CT (post-op) images. This takes some time so please start this as soon as you have all the resources necessary.

1.1 THE PURPOSE

Why perform recon?

1.2 BACKGROUND

Talairach coordinates and stuff

Dicom files (.dcm) are file types commonly used in medical settings. In our case, the dicom files contain information for slices (cross-sections) of the brain obtained during scans (MRI and CT). Expect usually a little over a hundred dicom files for MRI and also a little over a hundred dicom files for CT per subject.

More info about .nii here <http://nifti.nimh.nih.gov/nifti-1>

1.3 PROCESS OVERVIEW

The MATLAB function **ReconstructCorticalSurface** consolidates the MRI dicom files (.dcm), which contain slice information, and generates a header file that contains all of that information, which is then converted to an image file. FreeSurfer then pushes these to appserver.cs.washington.edu to reconstruct images with folds. This reconstruction takes about 4-12 hours to run on appserver (one of the machines in the lab). This MATLAB function also processes the CT dicom files and outputs a header file, which is then used to generate electrode positions for the CT scan in BiImage Suite.

Once the MR reconstruction is finished and electrode positions generated in BiImage Suite, the CT data are then aligned to the MR surface reconstruction using the MATLAB script once more.

2 INITIAL SETUP

You only need to do initial setup once on the machine you plan to use.

1. Create a new folder where you usually keep your MATLAB code to contain all the code necessary for running recons
 - a. For ease of writing this tutorial, I have named my folder **RECONS**
2. Pull the most up-to-date recon code from the GRIDlab GitHub repository
<https://github.com/uwgridlab/CodeBase>

3. Once you pull all the files, edit `runBeforeRecon.m` to match the file path on your machine (see below)

```
setenv('matlab_devel_dir','C:\Users\Nile\MATLAB\StartingCodeRepo');
```

Note that the path must be adjusted to where you have your **StartingCodeRepo folder*

4. Download and install the latest stable version of Yale University's [BioImage Suite software](#) (which was version 3.01 as of September 14, 2015).
5. Download and install [MRICron](#), which includes a DICOM to NIfTI converter (dcm2nii). Make sure you select for the correct operating system.

3 RUNNING RECONS

Recons can be ran as soon as the MR and CT files are available on Krang. **IMPORTANT:** Only have one person/machine perform recons at a time!

3.1 FILE CONVERSION

1. Copy the subject's folder from Krang into your RECONS folder
 - a. For example, if the subject's ID is abc123, by the end of this step, you should have **RECONS\abc123** where the **abc123** folder contains **ct**, **images**, **mri**, and **surf** folders
2. In the subject folder (now on your machine), open the **mri\rawdicom** folder and make sure there are several DCM files, all of which should be at least 100 KB in size
3. Repeat step 2 for the **ct\rawdicom** folder (note, the DCM files will be larger here, maybe around 500 KB)
4. Create a new folder called **mri\old_rawdicom** and move all the files from **mri\rawdicom** to this new folder. The folder **mri\rawdicom** should now be empty.
5. Open dcm2nii (part of the program MRICron), make sure the Output Format is set to SPM8 (3D NiftI nii) and drag and drop the **mri\old_rawdicom** folder into the window. This will generate two to three nii files in the **mri\old_rawdicom** folder. Move the first nii file produced by dcm2nii into the **mri\rawdicom** folder. Delete the other nii file(s) which will most likely start with "o" or "c".
6. Repeat steps 4 and 5 for the ct folder. This concludes the use of dcm2nii. Now let's return to MATLAB.

3.2 MATLAB PORTION

7. In MATLAB, make sure the **RECONS** folder (and all subfolders) are added to path
8. Run **runBeforeRecon.m**
9. In the command window, enter

```
ReconstructCorticalSurface('abc123','C:\Users\nilew\MATLAB\RECONS')
```

**Replace abc123 with the actual subject ID and make sure to use your correct path*

10. If this is the first time you're running recons on your current machine, you may have to go through some configuration steps (skip this step if you aren't prompted)

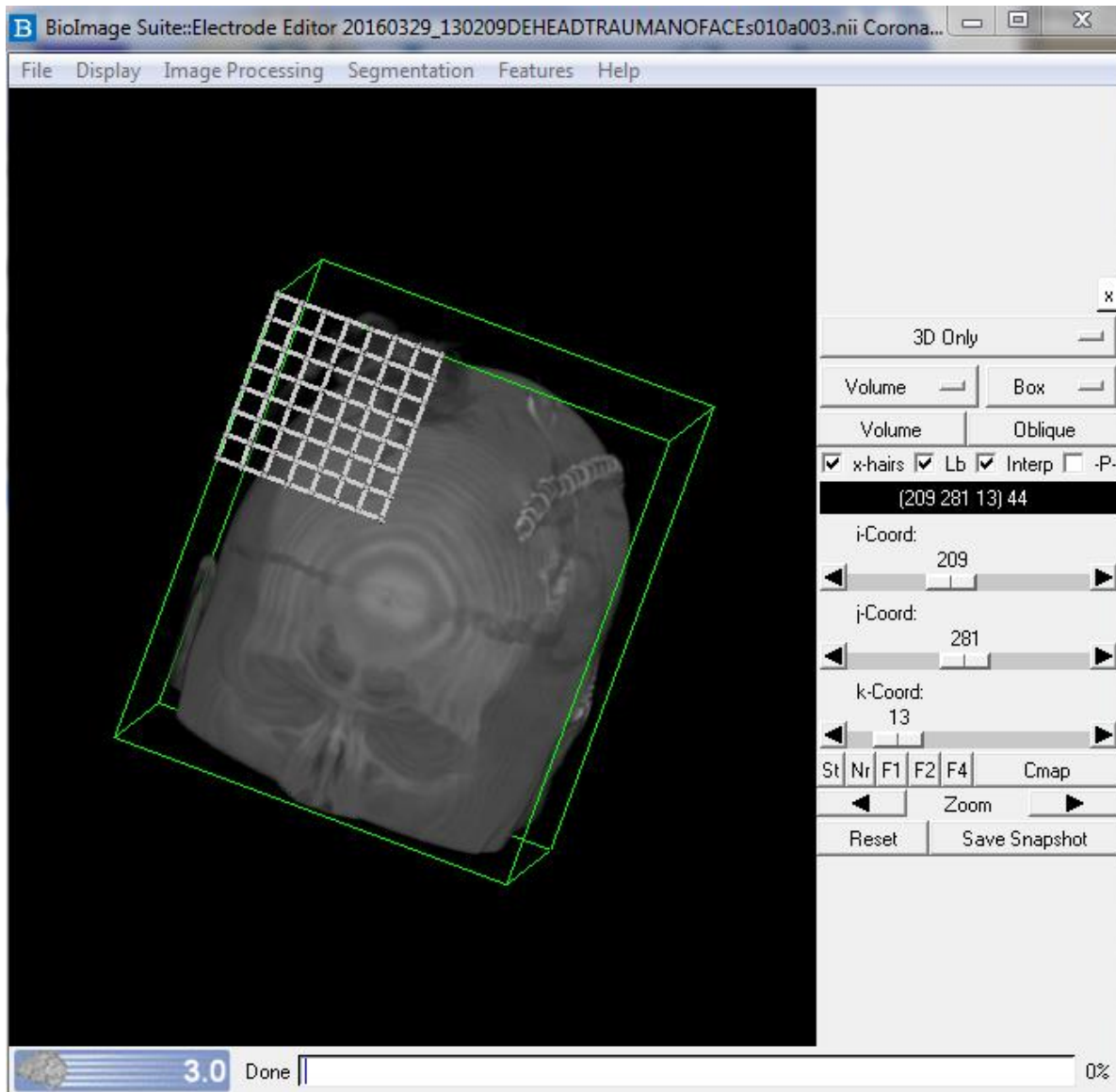
- a. Server URL is **appserver.cs.washington.edu**
 - b. Login name for linux server is **[REDACTED]**
 - c. Remote directory for freesurfer installation is **/warehouse/freesurfer**
 - d. Use GPU accelerated CUDA binaries for Freesurfer? **Yes**
11. The function will begin processing the MRI dicom files and push the converted header and image files to appserver, which will take 4-12 hours (on appserver, not on your local machine). The function will also process the CT dicoms and output the header files **abc123_ct.hdr**, **abc123_ct_reoriented**, and **rabc123_ct_reoriented.hdr**.
12. In the meantime, go on to section 3.3 to generate the grids.

3.3 BIOIMAGE SUITE PORTION

Program controls

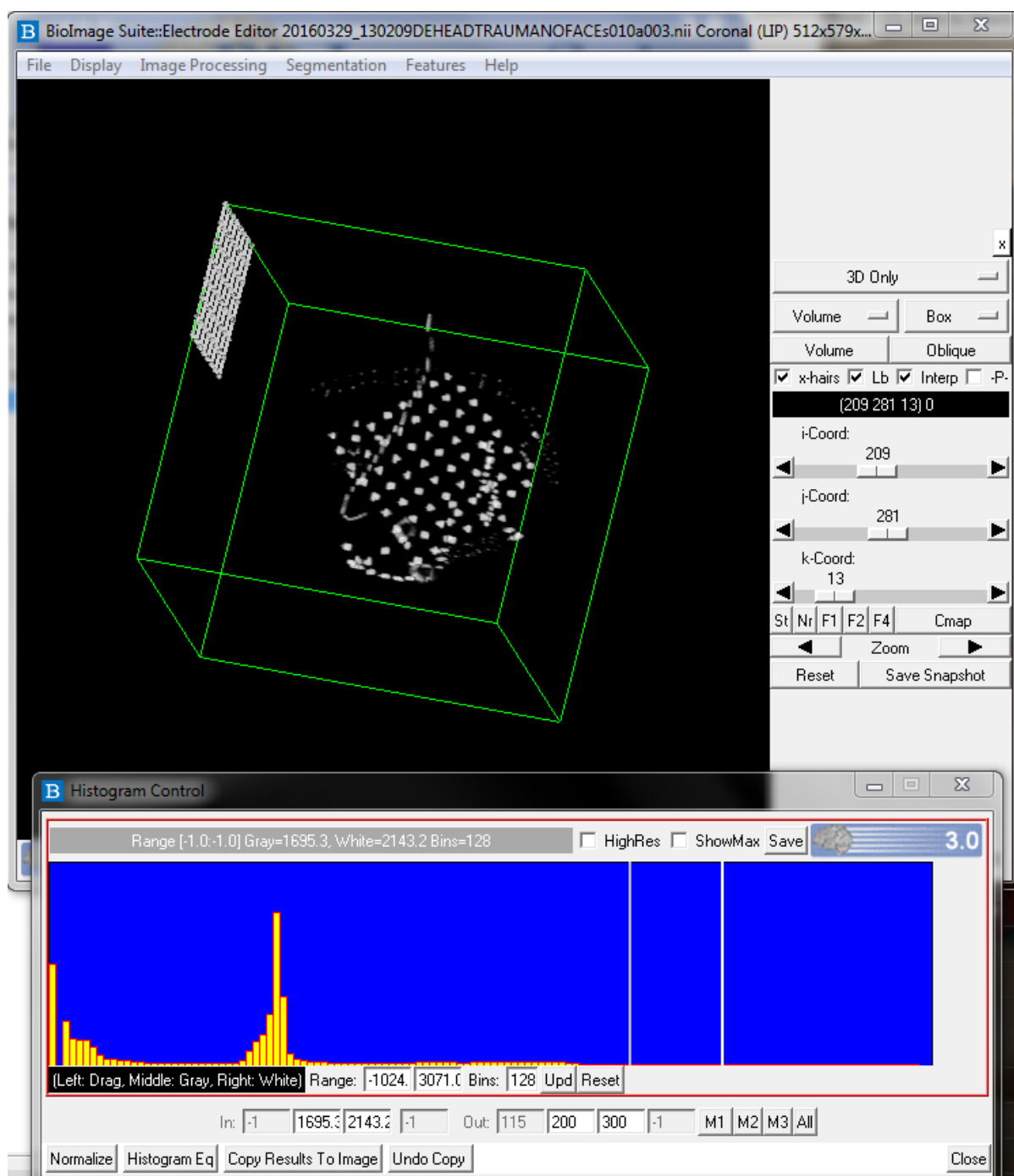
Electrode Editor Window	
Pan	Right Click + Drag
Rotate	Left Click + Drag
Zoom	Middle Click + Drag
Place Electrode	Shift + Click
Histogram Control	
Move White Bar	Right Click
Move Gray Bar	Middle Click

13. Open the BioImage Suite menu, select **“Editors”** in the left-side navigation menu, and select **“Electrode Editor”**.
14. Two additional windows will pop up, the “Electrode Control autosave” window and “BioImage Suite::Electrode Editor” window. Click on the latter and go to **File > Load**. Load **rabc123_ct_reoriented.hdr** in the CT folder.
- a. Note that there is an ‘r’ at the front of the header file. The ‘r’ indicates that this file has the MR registered to CT.
 - b. This is ultimately what you are using to generated bistrodes
15. In the same window, adjust the settings on the right side to match the following:
 3-D slice mode → 3D only
 3-slice → Volume
16. Click the “Volume” button to bring up the “Volume Control” window. Make sure the “Show Volume” box is checked and Texture2D is changed to Texture3D.
17. Your window should now look something like this (see image below).



We want to isolate the electrodes from the rest of the scan. We will do this by adjusting what densities we would like to look at.

18. Go to Image **Processing > Histogram Control**. This will bring up the Histogram Control window, showing the distribution of densities in the CT scan. The electrodes are denser than bone and tissue (which we do not want to see) so let's select for only high densities to display. Do this **by moving the white bar** (maximum density) in the histogram over to the right side and by **moving the gray bar** (median density) closer to the white bar, but to the left of it (as seen in the image below). **Click the "Histogram Eq" button** to apply changes. Now look at the main window. If there is still a fair amount of bone visible and the electrodes are not easy to see, then adjust the white and gray bar until you are satisfied. There may be some residual splotches here and there but the point of this step is to make it so YOU can clearly see where the electrodes are.

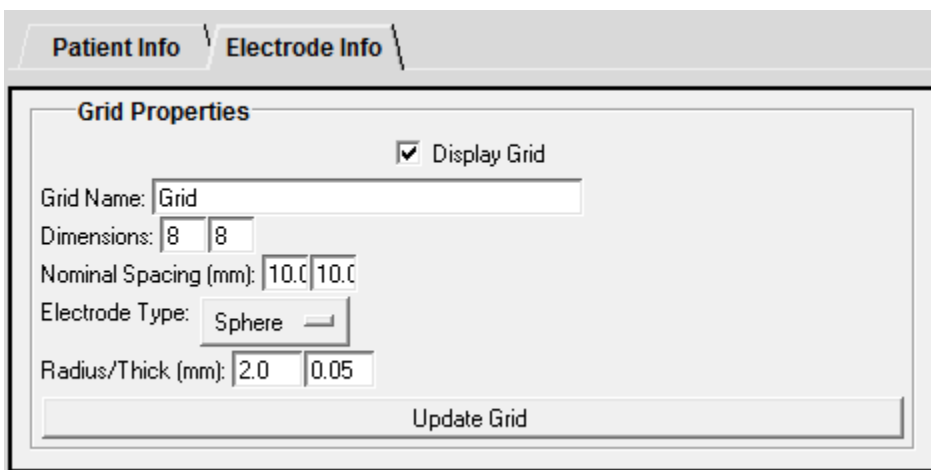


The electrodes are now easy to see in the scan. The following steps are for assigning these now visible electrodes to a 3D grid (or strip, etc).

19. Go to the “Electrode Control autosave” window. In the “Patient Info” tab, type in the subject ID for “Description”. In the “Comment” text box, list the areas covered by the electrodes (such as LMT LAT LPT LO SD ID). *If this just resets to the default text, don’t worry about it. We would like to have*

descriptions but Biolmage Suite might have a habit of not saving this.

20. In the same tab, there should be a “1. Grid” under “Grid Information”. If not, click “Add New Grid” to create a blank grid. With this grid selected, click on the “Electrode Info” tab.
21. In “Grid Properties”, make sure the dimensions and grid name (such as grid, LPT, LAT, etc.) are correct.



22. Select **Edit > Full Edit Mode**. Now check the “**Button Pick**” box in “Editing” (right side of the window).

Let’s start electrode assignment.

23. **Click the bottom left cell** in “Electrode Arrangement”. This corresponds to electrode 1. In Biolmage Suite, the bottom left cell is 1, the cell above it is 2, above that is 3 ... and the cell to the right of cell 1 is cell 9 etc.
24. Now **shift + click** the electrode in the scan that you believe is channel 1. If you are not sure where electrode 1 is on the grid, refer to any images of the electrodes. The wires come out from the bottom of the grid so electrode 1 will generally be along the edge opposite to where the wires exit. Electrode 2 will always be physically located left or right relative to electrode 1 (not above or below it). Refer to the sample images below for reference.

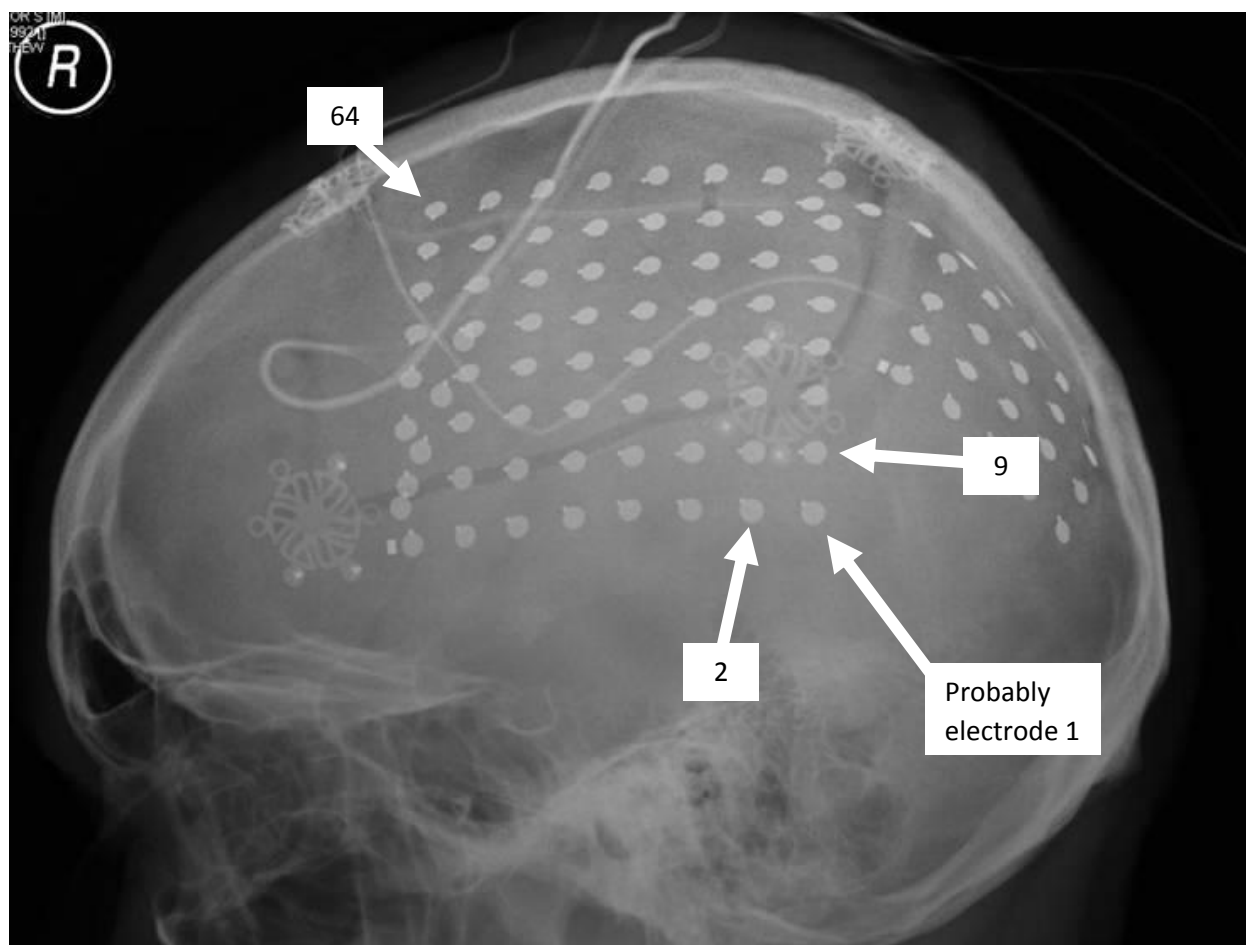
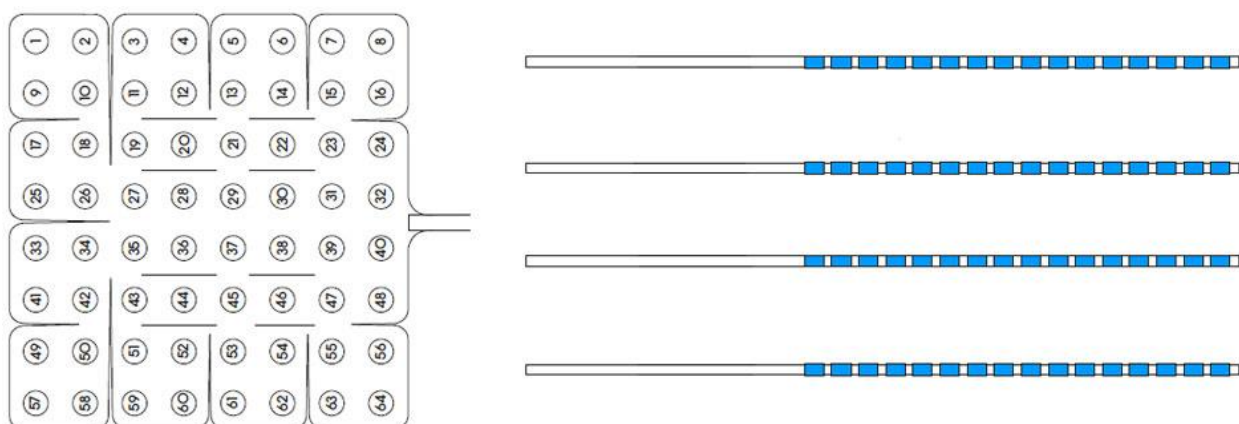
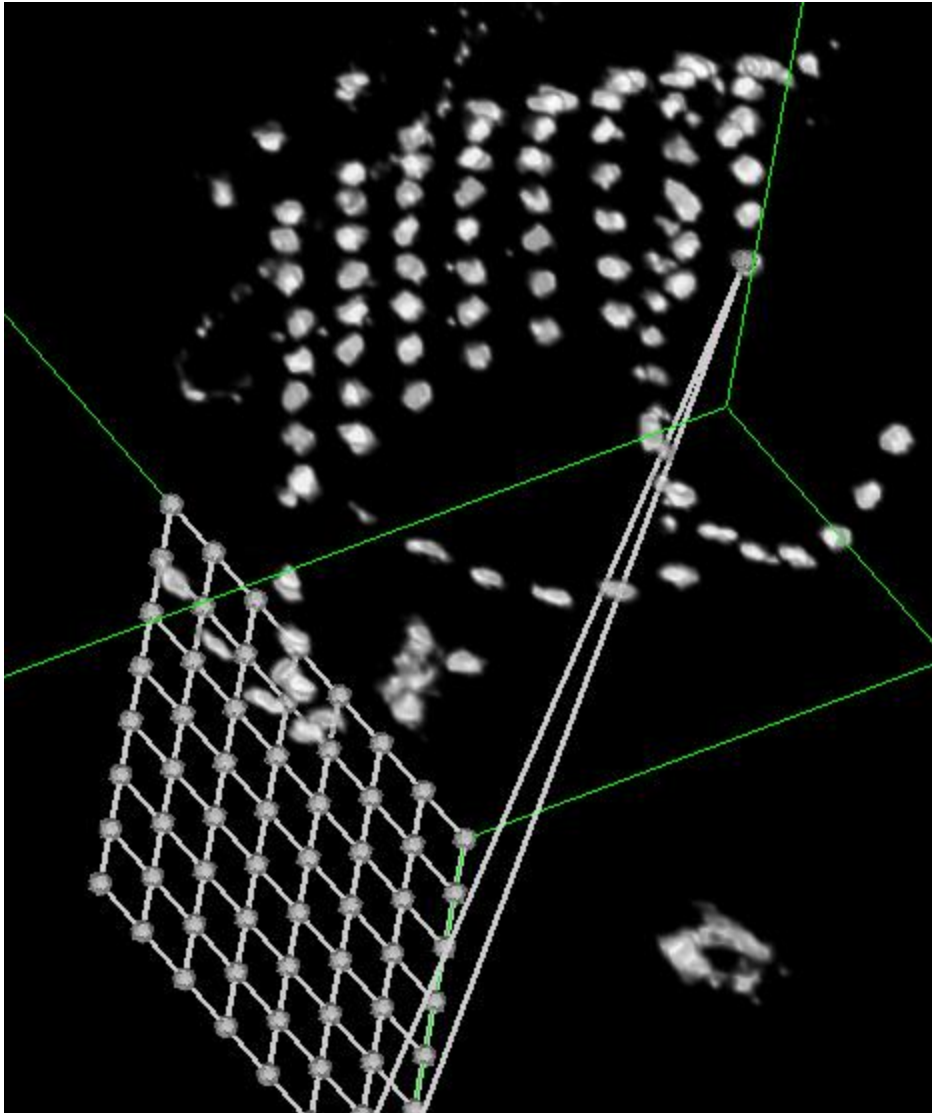


Image taken from <http://www.stlouischildrens.org/our-services/epilepsy-center/surgical-procedures/subdural-electrode-recording> (probably should've just used an image from a previous subject of ours but whatever...)

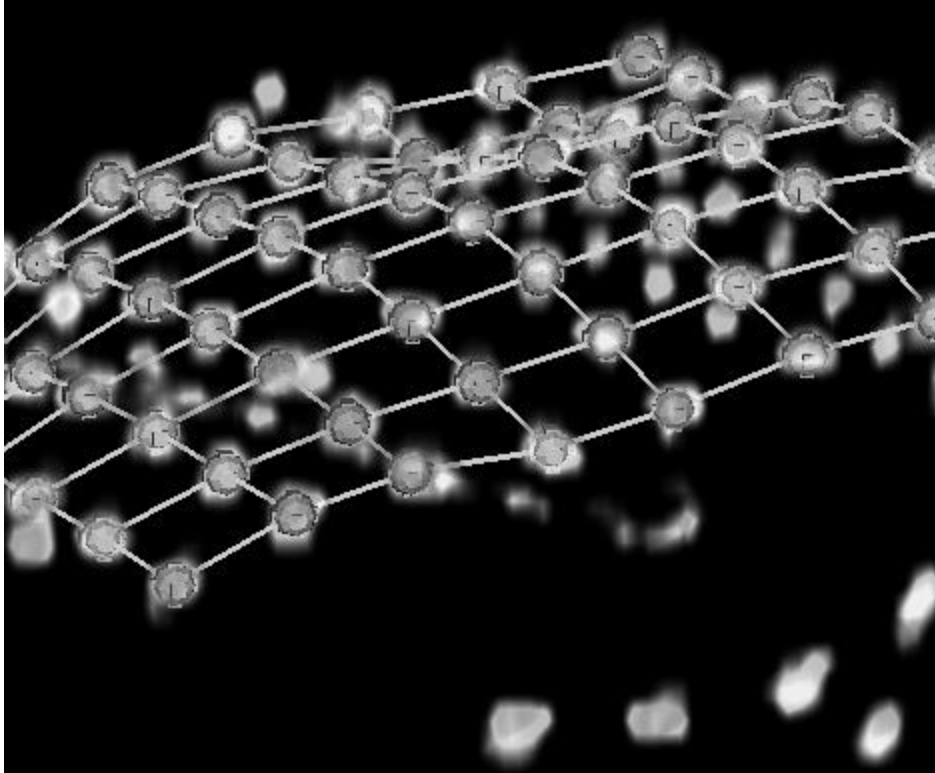


When zoomed out, your scan should look something like the image below now. It may look a little strange now but it will look more like a grid once you continue assigning.



25. Go back to the “Electrode Arrangement” window and click cell 2 (the cell directly above the bottom left one).
26. Go back to the scan view and **shift + click** what you believe to be electrode 2.
27. Continue this pattern. When you reach the top cell in the arrangement grid and assign the electrode there, go onto the next column to the right and start from the bottom and work your way up.

When you are done, the grid should look something like the image below. Note that all the assigned electrodes seem to fit along the surface of the brain (as they should) and there are no electrodes randomly deep in the brain or way above. If you do see any out of place electrodes, you may have accidentally assigned (shift + click) the electrode to a random blotch in the scan. Fix this by simply repeating the assignment for the electrode (click in “Electrode Arrangement” and shift + click in the main window). Rotate and zoom as much as needed to make sure you select the correct spot. If it’s still difficult to select the correct electrode, select a smaller VOI size in Volume Trace (default 10). Changing VOI size may be useful when selecting for smaller depth electrodes.



28. Repeat steps 23 - 27 for any other set of electrodes present (such as strips and depth electrodes). Remember to make sure the Dimensions in the Grid Properties are set correctly before you start assigning electrodes (for example, 1 x 6 for a 1 x 6 strip).
29. After you have assigned every electrode (grids and strips), in the “Electrode Control autosave” window, go to **File > Export > Export Values as Text**. Navigate to the subject’s recon folder, create a new sub-folder called **other**, enter that folder, and save the file as **bis_trodes.txt** (case-sensitive).
30. **Do not** close BioImage Suite yet. Keep the program open as you run the last steps in MATLAB so you can check which strips or depth electrodes are associated with grid_2, grid_3, etc.

3.4 BACK TO MATLAB

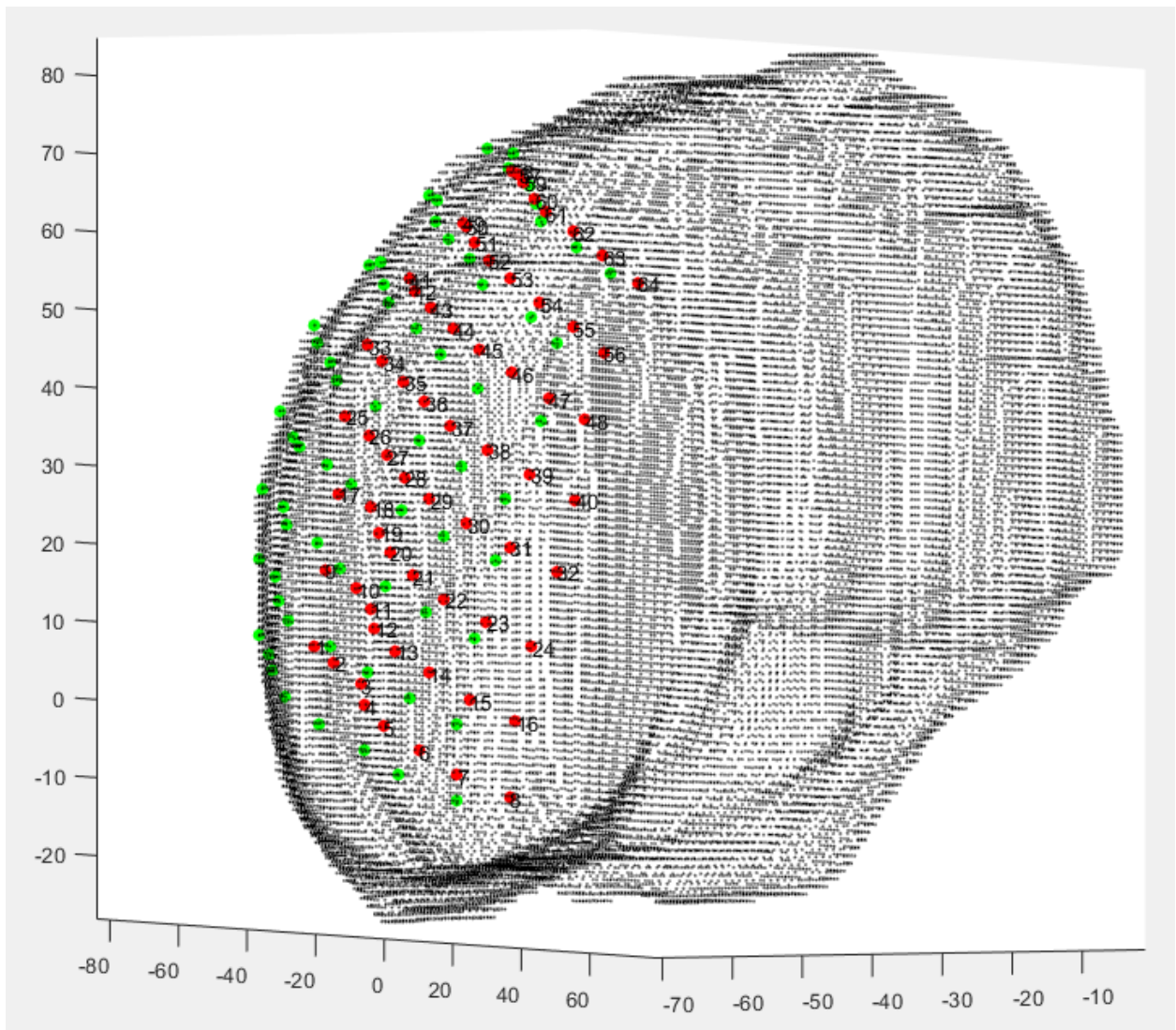
31. After 4-12 hours have passed since you ran `ReconstructCorticalSurface`, rerun the script **runBeforeRecon.m**
32. And then rerun the following line. Please replace abc123 with the subject ID and replace the example path with your correct path.

```
ReconstructCorticalSurface('abc123','C:\Users\nilew\MATLAB\RECONS')
```

The function should detect `bis_trodes.txt` in the **other** folder and know that you have executed this function before.

The function will then prompt you for information about the electrodes. It will prompt you in the order of “grids” you created in BioImage Suite. This means that you should be asked about the actual grid first, and then about any strips or depth electrodes you created afterwards.

33. Enter **l** or **r** to indicate which hemisphere the grid is placed and type **1**, **2**, or **3** to indicate what type of grid this is. A new figure window will pop up as a result.
34. Select the **Rotate 3D tool** in the window and rotate the image to see if the electrodes are where you expect them to be. The green dots are the projected positions (which should be on the surface) and the red dots are the original positions (which may be a little inside the brain... see image below).

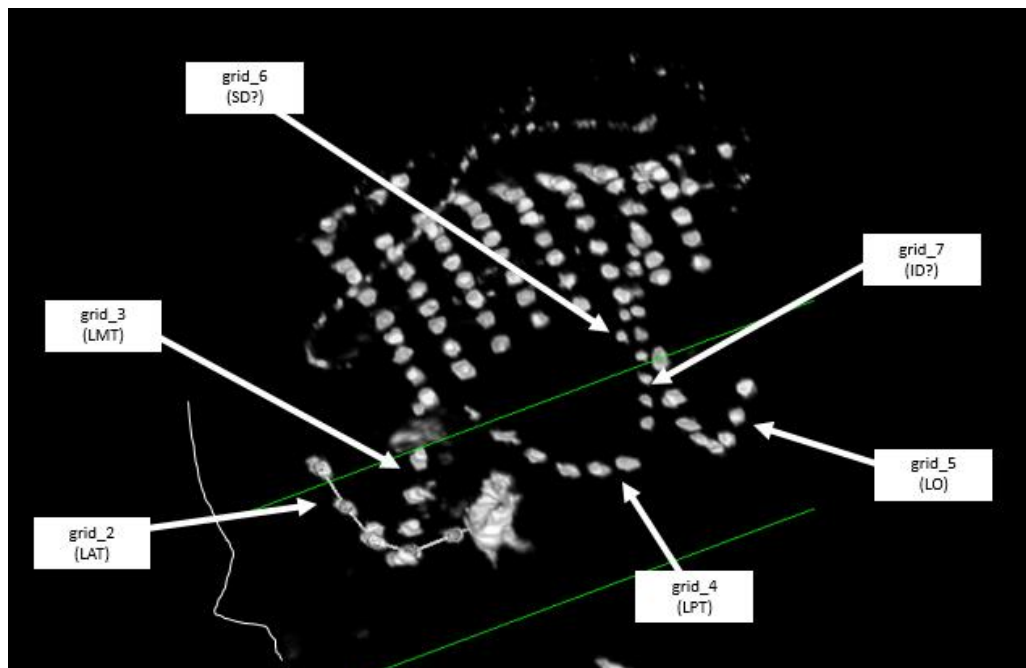


35. Enter **1** to accept the projected positions (green) or **2** to accept the original positions (red). Generally you can just type '1' and be done with the grid but feel free to use the other options as necessary.
36. You will then be prompted for the next "grid". This will be a strip or depth electrode, if you have any.
37. Continue the process until you have gone through all the grids. Feel free to go back to BiImage Suite to double check which grid is which. Note that no figure will pop up for the depth electrodes.
38. Once you are done, the MATLAB command window output should say "Completely finished reconstructions! All surfaces have been generated!" You should now have **bis_trodes.mat** and **trodes.mat** in your subject folder.

3.5 RENAME GRIDS

Because BiImage Suite may not have saved grid names, we need to make sure that the grid names in `trodes.mat` are understandable. **If they are saved correctly, you do not need to go through this section.**

39. In your MATLAB command window, type `clear all` to remove all variables in your workspace.
40. Load `trodes.mat`. Your workspace will now have all the variables stored in `trodes.mat`.
41. Refer to BiImage Suite to remember which grid (i.e. `grid_2`, `grid_3`, etc.) corresponds to which strip. See the figure below as an example.



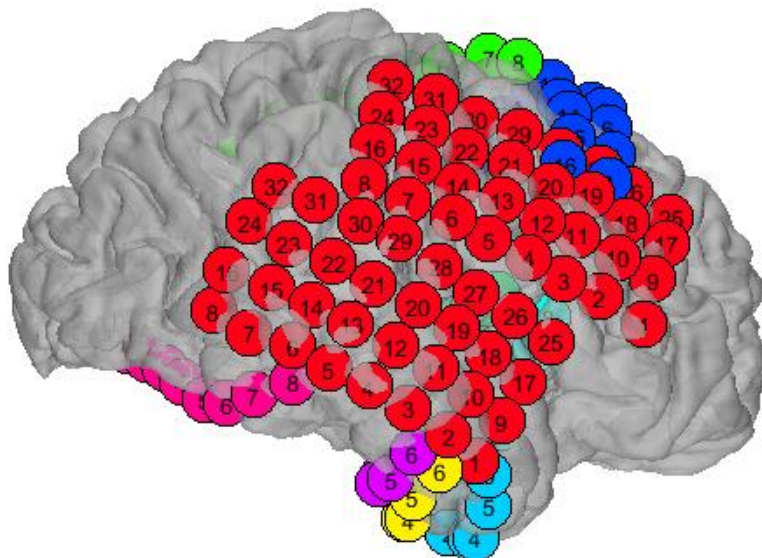
42. In MATLAB, rename each variable that does not have a meaningful name. For example, for the subject above, I renamed grid_2 to LAT, grid_3 to LMT, etc.
43. Also, do not forget to change the grid names in TrodeNames. Do this by manually renaming in the Command Window with `TrodeNames{n} = 'grid name'`. For example, for the subject above, I entered the following

```
>> TrodeNames{2}='LAT';
>> TrodeNames{3}='LMT';
>> TrodeNames{4}='LPT';
>> TrodeNames{5}='LO';
>> TrodeNames{6}='SD';
>> TrodeNames{7}='ID';
```
44. Now that everything is renamed, save your current Workspace as `trodes.mat` (overwrite).

3.6 GENERATING STILL IMAGES

Reconstructions are now done and all you have to do is generate some images to upload to Krang.

45. When you pulled the code from the gitlab repository, you also pulled a folder called 'plot'. In that folder, open `plotRecon.m`
46. Save a copy of `plotRecon.m` into your subject's folder and make all changes to that copy.
47. As commented in `plotRecon.m`, you must edit the subject ID, hemisphere, weight, montage, and label variables to match your current subject. Please refer to the comments in the code.
48. After making adjustments and running the script, you should get a figure like the one below (note, this is for a different subject than the one I've been using throughout this document so the placement and number of strips do not match).
49. In the figure window, go to **File > Save As** and save the figure as a **PNG** (portable network graphic) file in the subject's **images** folder (if this does not exist yet for some reason, create a subdirectory called **images**). Name the file appropriately (such as `recon_lat.png`).



3.7 GENERATE ROTATING ANIMATED GIF

Another useful visualization of these recons is a rotated animated gif. This is especially useful when there are depth electrodes.

50. Open the script **plotRotatingGIF.m** and edit all the information as necessary (see code comments).
51. Run the script.
52. Now you should have a GIF output to your main subject folder. Go ahead and move this to the images folder.

3.8 SHARE THE FILES

Now that everything is generated, it's time to upload things back onto Krang.

53. Open up FileZilla (or any FTP software), login to Krang, navigate to the subject folder (`/m-gridlab/gridlab/subjects/abc123`) and drag-and-drop **trodes.mat** and the **“other” folder** into the subject directory.
54. Then drag-and-drop the images you generated into the “images” sub-directory (order of uploading does not matter).
55. You are now officially done!

4 TROUBLESHOOTING

There are many things that can go wrong when running recons (as is the case for many other things in life). Below are some issues that have been run into before. They are not listed in any particular order.

4.1 CANNOT START 'BEGINFREESURFER'

If you get an error like the one below, there may be an issue with the DCM files.

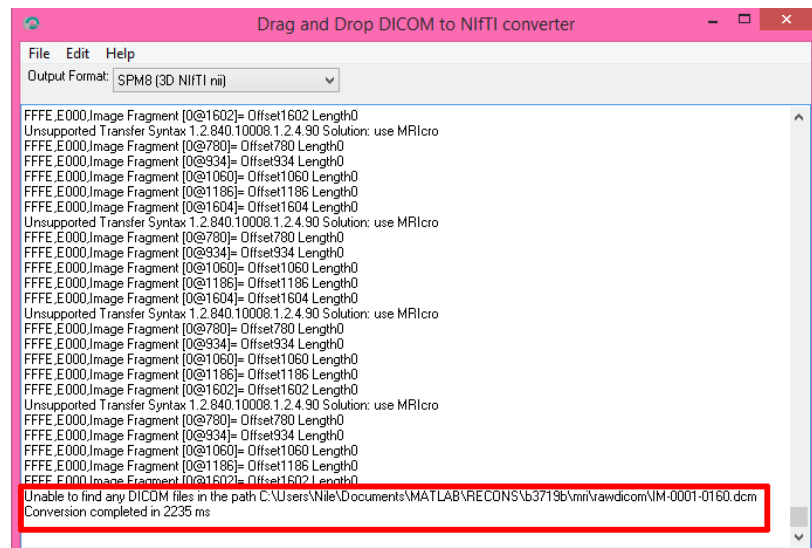
```
EDU>> runMeFirst
EDU>> ReconstructCorticalSurface('b3719b', 'C:\Users\Nile\Documents\MATLAB\RECONS')
Current patient data path: C:\Users\Nile\Documents\MATLAB\RECONS\
** Processing MRI
Dicom file
Reading dicom header
Concatenating dicom files
Rename file
Error using movefile
All arguments must be one-dimensional
strings.

Error in
ReconstructCorticalSurface>BeginFreesurfer
(line 608)
    movefile(dicomOut.files{1},[getenv('recon_patientCode')
    '_mri.img']);

Error in ReconstructCorticalSurface (line
41)
    BeginFreesurfer(baseDir, mriDir,
    ctDir, surfDir);
```

We ran into this issue in early September 2015 when Kurt had to pull the scans from Osirix due to unfortunate work circumstances (radiology upgraded their Microsoft desktop client).

From this error message (and looking at the code a little), it looked like there was something going on with the conversion from DCM into SPM friendly format, so we tried to convert the DCM files with the conversion software dcm2nii. When using this software, we saw that the software could not find the dicom files although they were clearly present (paths were correct and everything). We are assuming this is some issue with the metadata in the dicom files.



SOLUTION: Don't use dicoms pulled from Osirix. If you only have those, wait until Kurt can pull the files normally again.

4.2 SIMILAR TO ISSUE 4.1

If you run into a MATLAB error like that shown in Section 4.1 (troubleshooting) but it seems that the metadata is fine for the dicom files (via checking with dcm2nii), then follow the steps below.

Take all dcm files from the `mri\rawdicom` folder and move them into a separate folder called `mri\old_rawdicom`. Then use the `dcm2nii` program to convert the dicoms into NIfTI (drag and drop the `old_rawdicom` folder into the program and this will generate three .nii files... make sure `dcm2nii` is set to have the output format SPM8). Take the first nii produced by `dcm2nii` and move that file into `mri\rawdicom`. Delete the two remaining nii files in `old_rawdicom`. Repeat this process for the files in the `ct` folder as well.



Then rerun `ReconstructCorticalSurface` in MATLAB like normal. You should not get an error and instead just have to wait a little while the code sets up the freesurfer workspace.

If nothing happens and MATLAB says that the freesurfer workspace is being setup for more than like a few minutes, cancel the operation by hitting `ctrl+c` in MATLAB and rerun

`ReconstructCorticalSurface`. This trouble was encountered and resolved March 31, 2016.

If you accidentally forgot to do this ct dicoms and you get freesurfer started on the mri files, then you'll get an error similar to what was shown before so you'll have to perform the following steps to get the CT files in too.

Open up `ReconstructCorticalSurface` and put a break in at line 47 which should say `freesurferComplete = ~isempty(file);` and rerun `ReconstructCorticalSurface`. The function will now stop there. Instead of continuing, go down to the section in the code called "Align CT to MRI" which should be around line 718. Highlight the entire section and hit ctrl + enter to run this section. Now everything should be running just fine.

The following is an example of when things are going right.

```
>> ReconstructCorticalSurface('78283a','C:\Users\nilew\MATLAB\RECONS')
Current patient data path: C:\Users\nilew\MATLAB\RECONS\
Querying if freesurfer has completed...
Recon complete!
Zipping results...
mri_convert mri/lh.dpial.ribbon.mgz out/lh.dpial.ribbon.nii.gz
$Id: mri_convert.c,v 1.179.2.2 2011/05/16 20:53:47 greve Exp $
reading from mri/lh.dpial.ribbon.mgz...
TR=0.00, TE=0.00, TI=0.00, flip angle=0.00
i_ras = (-1, 0, 4.84288e-08)
j_ras = (1.35973e-07, 0, -1)
k_ras = (0, 1, 0)
writing to out/lh.dpial.ribbon.nii.gz...

mri_convert mri/rh.dpial.ribbon.mgz out/rh.dpial.ribbon.nii.gz
$Id: mri_convert.c,v 1.179.2.2 2011/05/16 20:53:47 greve Exp $
reading from mri/rh.dpial.ribbon.mgz...
TR=0.00, TE=0.00, TI=0.00, flip angle=0.00
i_ras = (-1, 0, 4.84288e-08)
j_ras = (1.35973e-07, 0, -1)
k_ras = (0, 1, 0)
writing to out/rh.dpial.ribbon.nii.gz...

Retrieving cortical ribbon plots...

lh.dpial.ribbon.nii.gz      | 32 kB | 32.0 kB/s | ETA: 00:01:01 | 1%
lh.dpial.ribbon.nii.gz      | 2006 kB | 2006.1 kB/s | ETA: 00:00:00 | 100%

rh.dpial.ribbon.nii.gz      | 32 kB | 32.0 kB/s | ETA: 00:01:02 | 1%
rh.dpial.ribbon.nii.gz      | 2033 kB | 2033.6 kB/s | ETA: 00:00:00 | 100%

Unzipping...
Freesurfer reconstruction complete!

**NOTE**
Please generate the electrode positions using BioImage Suite and export
fx >>
```

4.3 ISSUE RERUNNING RECONSTRUCTCORTICALSURFACE IN SECTION 3.4

If you get the following error, then you might need to make the following minor adjustment.

```
K>> ReconstructCorticalSurface('78283a','C:\Users\nilew\MATLAB\RECONS')
Current patient data path: C:\Users\nilew\MATLAB\RECONS\
Error using save
Cannot create 'bis_trodes.mat' because '78283a'
does not exist.

Error in BioImageToMatlab (line 64)
eval(cmd);

Error in
ReconstructCorticalSurface>ProjectElectrodes (line
93)
    BioImageToMatlab(getenv('recon_patientCode'));

Error in ReconstructCorticalSurface (line 85)
    ProjectElectrodes(baseDir);
```

This error is caused by the function `BioImageToMatlab` trying to save `trodes.mat` into a directory that doesn't exist. It might be trying to save in `RECONS\abc123\abc123` instead of just in `RECONS\abc123`.

To fix this, open the function `BioImageToMatlab` for editing (should be located in `RECONS\StartingCodeRepo\Visualization\Recon`).

Scroll down to around line 56 where it says

```
cmd = ['save ' fullfile(myGetenv('subject_dir'), subjid, 'bis_trodes.mat') '
AllTrodes TrodeNames '];
```

Then either replace this line (create a new line after) with the following line of code.

```
cmd = ['save ' 'bis_trodes.mat' ' AllTrodes TrodeNames '];
```

Save the function and then rerun the following line with the correct subject ID and path.

```
ReconstructCorticalSurface('abc123','C:\Users\nilew\MATLAB\RECONS')
```

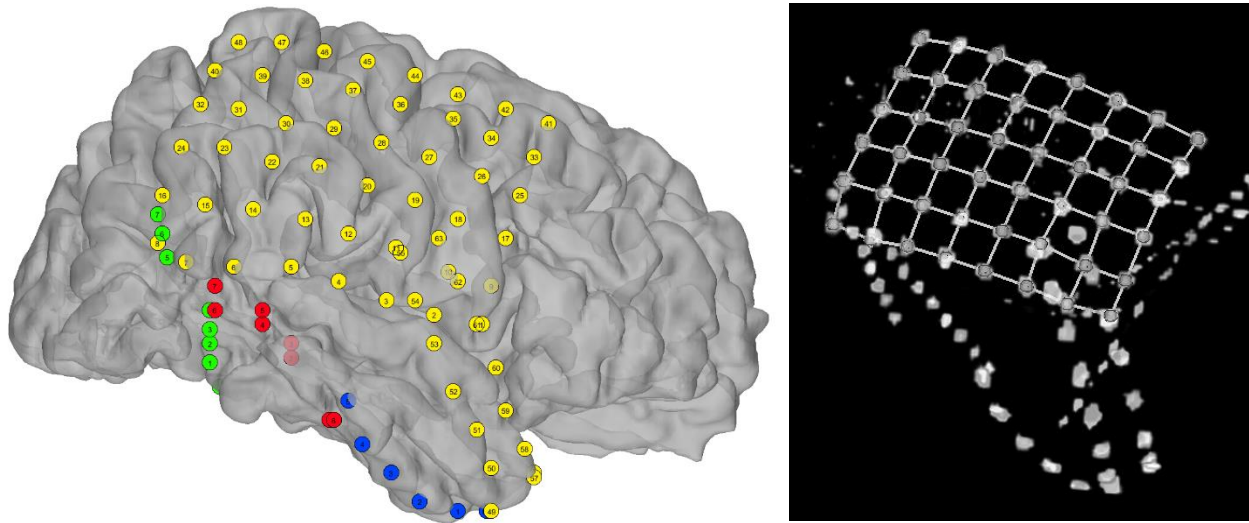
4.4 FORCE QUIT A RECON MID-RUN

If you want to cancel a recon while MR files are being reconstructed by appserver using freesurfer, perform the following steps. You may want to do this if you accidentally used the wrong ct or mri files, mistyped the subject ID, etc.

1. Access appserver by doing one of the following
 - a. Remote into **[REDACTED]**@appserver.cs.washington.edu (password is the same as when you inputted stuff the first time for recons on your machine)
 - b. Going over to appserver in CSE290 and logging in to appserver (scroll lock + scroll lock + 1 + enter) (password is the same for when you inputted stuff the first time for recons) and open up a new terminal
2. Type in **ps ux | grep freesurfer**
3. Take note of all the PID numbers (the first four digit numbers to appear on most lines)
4. Kill the processes associated with **recon-all** first and then kill the component pieces by using the following
 - a. Type **kill PIDnumber** for each PID (except for the grep PID, which will most likely be the last line outputted by **ps ux | grep freesurfer**)
 - b. For example,
kill 5593
kill 5594
 - c. Check that the processes are actually killed by typing **ps ux | grep freesurfer** again
 - d. If the processes aren't really dead, try stronger kill commands in the following order
 - i. **kill -15 PIDnumber** (SIGTERM, the softest kill, this is what we did when we just did kill by itself)
 - ii. **kill -2 PIDnumber** (SIGINT, same as ctrl + C)
 - iii. **kill -9 PIDnumber** (hard kill)
5. Once these processes are killed, navigate to the parent directory of the subject folder
cd /warehouse/freesurfer/subjects
6. Check what subject folders are present by typing **ls**
7. Once you confirm that the subject's folder is there, delete it by typing **rm -rf subjID**
 - a. For example, **rm -rf abc123**
8. Now if you type **ls** again, you should see that the subject's folder has now been deleted
9. Now you're free to rerun recons for this subject from MATLAB on your own computer

4.5 ELECTRODES CLUMPING WHEN PROJECTED ONTO THE RECONSTRUCTED SURFACE

Sometimes after projecting the CT electrode coordinates (in your `bis_trodes.txt` file) onto the reconstructed surface (the last step in `ReconstructCorticalSurface`), the electrodes may look strangely positioned. For example, in this subject (b3179b), the red and green strips are oddly clumped and not straight like how they looked in the CT.



This issue is brought about by `ReconstructCorticalSurface` trying to project the electrode positions onto the surface, which dips and folds in a way that doesn't work well with the provided coordinates this time.

To fix this problem, manually displace the electrodes and use these displaced coordinate values instead of the projected positions.

1. In your file explorer, navigate to your `subjectFolder/other` and make a copy of `bis_trodes.txt`. You should now have two files with identical content called `bis_trodes.txt` and `bis_trodes_ORIGINAL.txt`.
2. Open `bis_trodes.txt` with an editor such as NotePad++ (not just regular notepad, as this is known to occasionally introduce issues with tabs or spacing).
3. Manually change the x-values (first column of numbers) for the strips that are projecting strangely. You want to change these values so that the electrodes would be placed above the surface of the brain. Do this by offsetting the x-values by a negative value such as -10. See the image below.

bis_trodes_ORIGINAL.txt

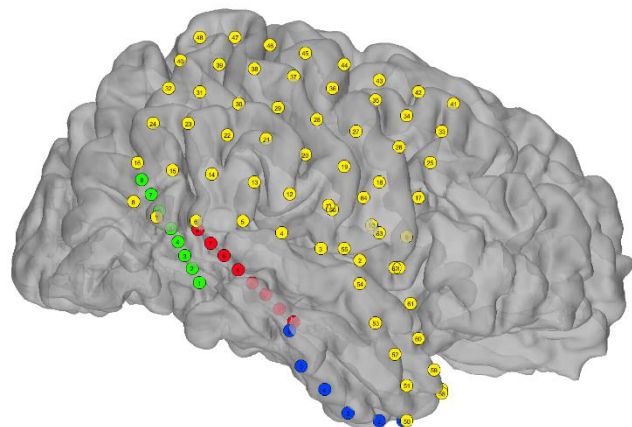
73	RAD	RAD8	84	115.111	166.5	0.000
74	RAD	RAD7	83.0833	118.625	163.208	0.000
75	RAD	RAD6	82.2083	121.75	159.75	0.000
76	RAD	RAD5	81.44	125.48	156.2	0.000
77	RAD	RAD4	81	128.81	152.571	0.000
78	RAD	RAD3	80.2917	131.792	149.083	0.000
79	RAD	RAD2	79.95	135.55	145.6	0.000
80	RAD	RAD1	79.12	138.76	142	0.000
81	RPD	RPD8	83.5	102.357	180.857	0.000
82	RPD	RPD7	84.6	106.2	178.5	0.000
83	RPD	RPD6	86.2	110.5	176.4	0.000
84	RPD	RPD5	87.6667	114.889	173.444	0.000
85	RPD	RPD4	91.0455	118.273	171.591	0.000
86	RPD	RPD3	94.2727	121.818	169.864	0.000
87	RPD	RPD2	97.4783	125.043	167.957	0.000
88	RPD	RPD1	100.368	128.737	166.105	0.000
89						

bis_trodes.txt (subtracted 10 from x coordinate values)

73	RAD	RAD8	74	115.111	166.5	0.000
74	RAD	RAD7	73.0833	118.625	163.208	0.000
75	RAD	RAD6	72.2083	121.75	159.75	0.000
76	RAD	RAD5	71.44	125.48	156.2	0.000
77	RAD	RAD4	71	128.81	152.571	0.000
78	RAD	RAD3	70.2917	131.792	149.083	0.000
79	RAD	RAD2	69.95	135.55	145.6	0.000
80	RAD	RAD1	69.12	138.76	142	0.000
81	RPD	RPD8	73.5	102.357	180.857	0.000
82	RPD	RPD7	74.6	106.2	178.5	0.000
83	RPD	RPD6	76.2	110.5	176.4	0.000
84	RPD	RPD5	77.6667	114.889	173.444	0.000
85	RPD	RPD4	81.0455	118.273	171.591	0.000
86	RPD	RPD3	84.2727	121.818	169.864	0.000
87	RPD	RPD2	87.4783	125.043	167.957	0.000
88	RPD	RPD1	90.368	128.737	166.105	0.000
89						

4. Save bis_trodes.txt
5. Create a new text file that makes it obvious that the bis_trodes.txt file (and therefore trodes.mat produced later on) have been manually edited. For example, a text file called “RAD and RPD MANUALLY DISPLACED – readme”, which then has a description inside such as “all x-values offset by -10”.
6. Open MATLAB and add all necessary things to path / set environment as you would when running ReconstructCorticalSurface during the final step. If you still have bis_trodes.mat and trodes.mat from the last time you ran recons on this subject (with the oddly placed electrodes), delete those two files in order to be able to rerun ReconstructCorticalSurface.
7. Run (use the actual subject ID and path)
`ReconstructCorticalSurface('abc123', 'C:\Users\nilew\MATLAB\RECONS')`
8. Go through and project positions of electrodes for grids and strips that display as expected. Once you get to the troublesome strips, use “2. Original Positions” instead of “1. Projected positions”.
9. Once you are done, you will now have a new trodes.mat file where the x-values for the affected grids are displaced. Use this trodes.mat file to produce the recon images.

Now you should have something like this, which looks much closer to what we expected.



4.6 APPLYING A TRANSFORMATION MATRIX TO TRODES COORDINATES

In the rare case you *do* need to apply a transform matrix to the electrode positions (trodes.mat), you will need to apply the transform to the variables that make up bis_trodes.mat before it is saved and used to make trodes.mat.

When would this even be necessary? If the CT coordinates are strange and need manual adjusting (like with subject 6d865b), you may be given a transform matrix to work with. Note that for subject 6d865b, we had to use a different transform matrix than what was provided. If I remember correctly, I believe we got the matrix by comparing the affine parameters of the MR and CT images using mricron.

For information on the format of transform matrices, web search 'affine transformation matrix' to find resources such as <https://www.cs.utexas.edu/users/fussell/courses/cs384g/lectures/lecture07-Affine.pdf> (not sure if that will still be active when you are reading this, but just as an example).

Follow the below steps to apply a transformation matrix to the CT electrode positions.

1. Generate bis_trodes.txt as you normally would
2. Put a breakpoint in the function BioImageToMatlab at the line that saves bis_trodes.mat (should be around line 55, function in StartingCodeRepo/Visualization/Recon)
3. Run ReconstructCorticalSurface
4. In Debug Mode, run the following code either in a script or directly in the Command Window (make sure to adjust the matrix to fit your transformation matrix)

```
for name = {'ATD', 'Grid', 'PPD', 'PTD', 'Ref', 'ST', 'AllTrodes'}
    eval([name{1} ' = ' name{1} ' * [1 0 0;0 0 -1;0 1 0];' ]);
    eval([name{1} ' = ' name{1} ' - repmat([64 0 0], length(' name{1} '), 1);' ]);
end
```

Note that the matrix in the code above is the same as what is shown to the right. This matrix flips the Y and Z axes and shifts the X coordinate values by 64 units.

$$\begin{bmatrix} 1 & 0 & 0 & -64 \\ 0 & 0 & -1 & 0 \\ 0 & 1 & 0 & 0 \end{bmatrix}$$

5. Hit Continue to continue running the code and complete co-registration as you normally would to generate trodes.mat
6. Plot the electrodes on the reconstructed surface as you normally would to make sure the coordinates in trodes.mat make sense
7. You should be done!

4.7 RESTARTING AN ENTIRE RECON

Go into appserver and delete the subject's folder from the freesurfer directory (see the end of section 4.4 for more detail).

Bam.

4.8 INDEX EXCEEDS MATRIX DIMENSIONS, ISSUE WITH BIS_TRODES.TXT

If you get the following error when running `ReconstructCorticalSurface` after generating `bis_trodes.txt`, then keep on reading.

```
Index exceeds matrix dimensions.
```

```
Error in BioImageToMatlab (line 15)
```

```
trodeIdx =  
str2double(c{2}{1}(length(trodeName)+1:end));
```

```
Error in ReconstructCorticalSurface>ProjectElectrodes  
(line 93)
```

```
BioImageToMatlab(getenv('recon_patientCode'));
```

```
Error in ReconstructCorticalSurface (line 85)
```

```
ProjectElectrodes(baseDir);
```

Sometimes, BioImage Suite (on Windows at least) will insert strange spacing when exporting values as text into `bis_trodes.txt`. This is an issue where the txt file is being saved as a Windows file (improperly) instead of in UNIX format.

If you open `bis_trodes.txt` with Notepad, everything will look normal. However, if you open up `bis_trodes.txt` in another program such as Notepad++, you'll see the really strange spacing that is actually present (strange on the left of the screenshot, normal on the right).

1	#					1	#					
2	#Electrode	positionx	positiony	positionz		2	#Electrode	positionx	positiony	positionz		
3	Grid					3	Grid1	Grid18	68.0345	101.69	165.793	0.000
4						4	Grid1	Grid116	67.6897	92.6207	161.69	0.000
5						5	Grid1	Grid124	68.8846	83.5385	157.269	0.000
6						6	Grid1	Grid132	70.72	74.96	152.68	0.000
7						7	Grid1	Grid17	64.4286	106.157	143.464	0.000
8	Grid					8	Grid1	Grid115	64.8846	96.6923	152.692	0.000
9						9	Grid1	Grid123	66.6522	87.7391	148.522	0.000
10						10	Grid1	Grid131	69.7918	143.556	0.000	
11						11	Grid1	Grid16	63.1	110.3	148.5	0.000
12						12	Grid1	Grid114	63.579	101.158	143.895	0.000
13	8	130.587	134.522	182.978	0.000	13	Grid1	Grid122	66.92125	139.708	0.000	
14	Grid					14	Grid1	Grid130	69.9583	84.0833	135.083	0.000
15						15	Grid1	Grid15	61.7778	114.815	139.444	0.000
16						16	Grid1	Grid113	62.9231	105.923	135.269	0.000
17						17	Grid1	Grid121	65.8148	97.130.63	0.000	
18						18	Grid1	Grid129	70.88.9583	126.333	0.000	
19	Grid					19	Grid1	Grid14	61.119.167	130.625	0.000	
20						20	Grid1	Grid112	63.8333	110.708	126	0.000
21						21	Grid1	Grid120	67.0417	102.083	121.958	0.000
22						22	Grid1	Grid128	70.9167	93.8333	117.375	0.000
23						23	Grid1	Grid13	63.8519	124.333	122.778	0.000
24	16	135.49	136.367	174.857	0.000	24	Grid1	Grid111	66.8438	115.781	118.188	0.000
25	Grid					25	Grid1	Grid119	69.2692	107.192	113.423	0.000
26						26	Grid1	Grid127	72.5417	98.9167	109.125	0.000
27						27	Grid1	Grid12	68.1379	129.655	115	0.000
28						28	Grid1	Grid110	70.2143	121.143	110.464	0.000
29						29	Grid1	Grid118	71.9429	112.486	105.629	0.000
30	Grid					30	Grid1	Grid126	74.6667	103.958	100.333	0.000
31						31	Grid1	Grid11	71.6667	134.917	107.833	0.000
32						32	Grid1	Grid19	73.7407	126.63	102.222	0.000
33						33	Grid1	Grid117	75.2414	117.828	97.5172	0.000
34						34	Grid1	Grid125	77.4583	109.292	92.3333	0.000
35	24	136.688	136.167	165.208	0.000	35	Grid2	Grid28	71.77.2	134.65	0.000	
36	Grid					36	Grid2	Grid216	76.7778	69.5556	132.278	0.000
37						37	Grid2	Grid224	82.3636	61.4546	129.591	0.000
38						38	Grid2	Grid232	86.8696	52.8696	126.957	0.000
39						39	Grid2	Grid27	72.125	81	125.188	0.000
40						40	Grid2	Grid215	78.3333	73.4445	122.944	0.000
41	Grid					41	Grid2	Grid223	83.4348	64.6957	120.87	0.000
42						42	Grid2	Grid231	88.4211	56.5263	117.895	0.000
43						43	Grid2	Grid26	74.8	85.25	116.55	0.000
44						44	Grid2	Grid214	79.5238	77.0476	113.571	0.000
45						45	Grid2	Grid222	84.4762	68.7619	110.952	0.000
46	32	135.583	135.417	155.854	0.000	46	Grid2	Grid230	89.6522	60.1304	108.304	0.000

While you can just manually delete all the strange spacing to get something more normal (like what we see on the right), this is time consuming and inefficient, especially if you realize you made a mistake and need to reselect electrodes in Biolmage Suite.

To fix the weird spacing in one fell swoop, use one of the following methods.

Method 1. GVIM

1. If you do not have vim, download gVim from <http://www.vim.org/download.php>
2. Open bis_trodes.txt with gVim (either by opening gVim and loading the file, or by right-clicking the file in file explorer and selecting “Edit with vim”)

When you open the file, you should see a lot of ^M characters (which is not what we want to see in a healthy bis_trodes.txt file). We will be getting rid of these characters.

```

bis_trodes.txt (C:\Users\nilew\MATLAB\RECONS) - GVIM
File Edit Tools Syntax Buffers Window Help
#Electrode      positionx      positiony      positionz
Grid^M^M^M^M^M      Grid^M^M^M^M^M8 130.587 134.522 182.978 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M16      135.49 136.367 174.857 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M24      136.688 136.167 165.208 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M32      135.583 135.417 155.854 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M40      134.02 134.745 146.098 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M48      134.061 134.02 136.551 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M7 126.898 143.469 182.592 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M15      131.756 145.089 174.022 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M23      134.159 145.523 164.864 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M31      135.02 144.88 155.18 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M39      135.057 144.377 145.434 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M47      135.038 143.654 136.192 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M6 122.592 152.245 181.775 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M14      127.163 153.465 173.046 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M22      130.255 154.298 164.085 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M30      132      154.021 154.542 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M38      133.13 153.826 145.13 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M46      133.959 153.224 135.306 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M5 119.696 161.391 181.478 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M13      123.592 162.347 172.653 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M21      126.125 162.771 163.208 0.000
Grid^M^M^M^M^M      Grid^M^M^M^M^M29      128.235 162.863 153.765 0.000
<ers\nilew\MATLAB\RECONS\bis_trodes.txt" 78L, 4027C      1,1      Top
  
```

3. In the editor, hit the escape key to make sure you are not in insert mode, and then type the following line and hit enter

```
:%s/\r//g
```

What this line does is replace all instances of `\r` (which is shown as `^M`) with nothing. The general structure of the command is `%s/(find)/(replace)/(optional extra commands)`, where `:` indicates the start of a command, `%` indicates apply to the whole document, `s` means substitute, `/` denotes separation of arguments, and `g` makes sure this command applies to all instances within a line and not just the first instance.

For more information about `\r`, see this ASCII chart (important part put as a screenshot to the right), <http://www.bluesock.org/~willg/dev/ascii.html>

```
end of line sequences
Windows end of line sequence: \r\n
Unix end of line sequence: \n
Mac end of line sequence: \r
```

4. Save the document and exit by using the following command (again, making sure you are not in insert mode)

`:wq` ← This command writes the file (`w`) and quits the program (`q`).

5. You should now be able to run `ReconstructCorticalSurface` without any issues now

Method 2. Git Bash

1. If you do not have Git Bash, get Git here <https://git-scm.com/downloads>
2. In your file explorer, navigate to the folder containing `bis_trodes.txt`, right-click somewhere in there that is not on any specific file or folder, and select “Git Bash” to open a terminal
3. Once the terminal is open, type in the following command

```
dos2unix bis_trodes.txt
```

```

MINGW32/C:/Users/nilew/MATLAB/RECONS
Welcome to Git (version 1.9.5-preview20150319)
Run 'git help git' to display the help index.
Run 'git help <command>' to display help for specific commands.

nilew@OMELETTE /C:/Users/nilew/MATLAB/RECONS
$ ls
0a80cf  6d865b were the recons from hell.txt  bis_trodes.txt
0b5a2e  78283a                                others
362645  96498c                                recons by nilew.xlsx
3f2113  Miah                                  runMeFirst.m
50f366  acabb1                                testing.txt
6d865b  b3719b

nilew@OMELETTE /C:/Users/nilew/MATLAB/RECONS
$ dos2unix testing.txt
dos2unix: converting file testing.txt to UNIX format ...

nilew@OMELETTE /C:/Users/nilew/MATLAB/RECONS
$

```

Do not pay attention to my path here. You will need to do this where `bis_trodes.txt` should be, inside `subjID/other`

This command converts `bis_trodes.txt` from DOS format to UNIX format. This will get rid of all the ^M characters you can see visually in Method 1.

4. You should now be able to run `ReconstructCorticalSurface` without any issues now

4.9 FREESURFER STILL RUNNING! UNABLE TO OPEN CONNECTION: HOST DOES NOT EXIST

If you get something like the below error, there may be an issue with Appserver's network connection.

```
>> ReconstructCorticalSurface('ba6cb1', 'C:\Users\nilew\MATLAB\RECONS')
Current patient data path: C:\Users\nilew\MATLAB\RECONS\
Querying if freesurfer has completed...
Freesurfer still running!
Most recent freesurfer message:
---
Unable to open connection:
Host does not exist
---
Freesurfer is running. Run this script again in a while to check if has completed
```

When this happened to me, I went over to Appserver to check the output file in the subject's folder (/warehouse/freesurfer/subjects/ba6cb1) and saw that it actually completed successfully earlier in the day. The issue was connecting from MATLAB to Appserver. I noticed that the wired internet connection for Appserver was not working, so I switched to wireless (which worked when I opened up an internet browser), but did not fix this issue.

I kept trying and eventually after a few hours, things seemed to magically work.

^^ turns out that the Ethernet was just unplugged... Everything was good after that

4.10 WHITE MATTER VOXELS

When running recons on young children, you may run into the following error.

```
>> ReconstructCorticalSurface('e32dc1', 'C:\Users\nilew\MATLAB\RECONS')
Current patient data path: C:\Users\nilew\MATLAB\RECONS\
Querying if freesurfer has completed...
Freesurfer still running!
Most recent freesurfer message:
---
If white-matter contains few if any voxels of value 110,
try adding wm control-points to nu.mgz, and re-run recon-all.

Linux appserver 2.6.38-8-generic #42-Ubuntu SMP Mon Apr 11 03:31:24 UTC 2011 x86_64 x86_64 x86_64 GNU/Linux

recon-all -s e32dc1 exited with ERRORS at Fri Dec 9 13:14:35 PST 2016

For more details, see the log file /warehouse/freesurfer/subjects/e32dc1/scripts/recon-all.log
To report a problem, see http://surfer.nmr.mgh.harvard.edu/fswiki/BugReporting
```

To get past this issue, open the function `ReconstructCorticalSurface.m` and scroll down to the section checking if freesurfer was started but not completed (around line 51). There should be a nested if-statement as follows.

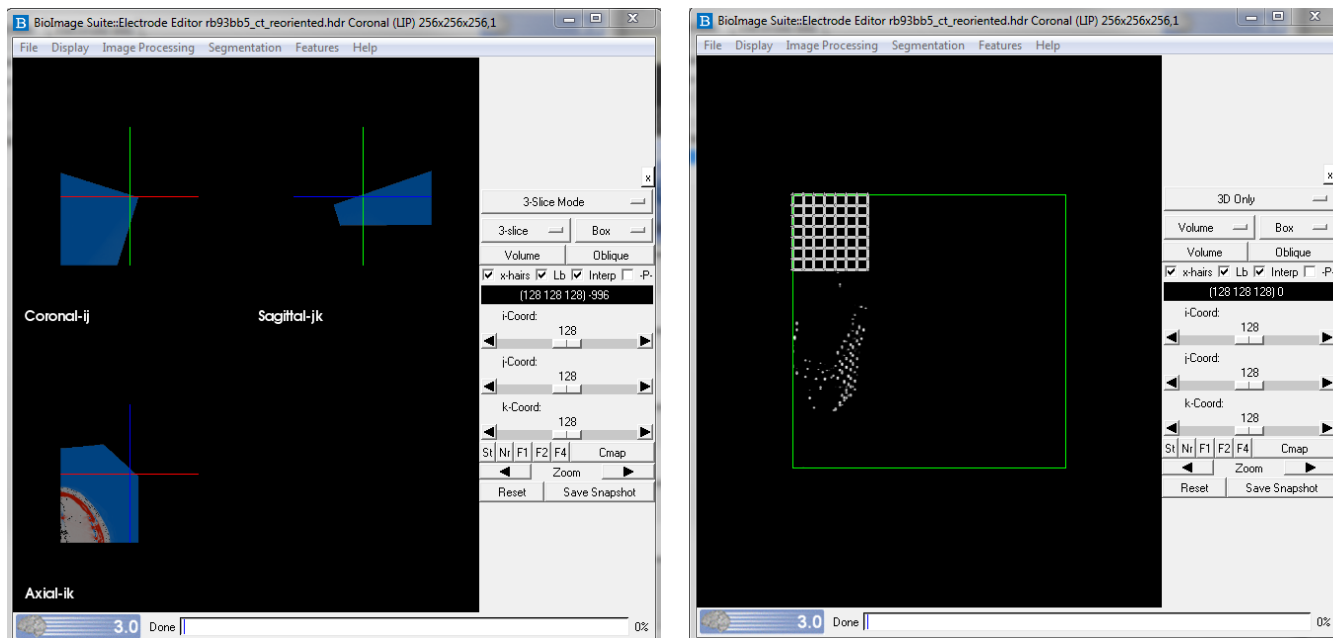
```
%If freesurfer was started but not completed, check to see if it's
%still going
    if freesurferStarted == 1 && freesurferCompleted == 0
        freesurferCompleted = PollFreesurferComplete(); %set this to 1 if you run
        into a white matter voxel error
        if freesurferCompleted == 1
            GetFreesurferResults(mriDir);
            fprintf('Freesurfer reconstruction complete!\n');
        end
    end
```

In the above code excerpt, change the second line so that `freesurferComplete = 1` instead of `= PollFreesurferComplete()`. You can actually do this to expedite the recon process in general, since we do not need all the processes after the pial surfaces are complete. By doing this the first time in this one case, we discovered that most of the lengthy processes in freesurfer are not vital to what we need. In fact, we can stop freesurfer once the pial surfaces are generated (I think... double check this last point).

Now rerun `ReconstructCorticalSurface('subjectID', 'pathHere')` and the recon should continue.

4.11 OFFSET AND TRUNCATED CT IN BIOLIMAGE SUITE

Sometimes, more likely with Children's subjects than with Harborview ones, you might run into an issue where the CT file we use in BioImage Suite (rSubjectID_ct_reoriented) is offset and truncated. The case seen below is for subject b93bb5, where we received the mri and ct .nii files directly from Children's.



We tried using the other CT files (subjectID_ct_reoriented and subjectID_ct), but BioImage Suite would crash whenever we tried to do Histogram EQ, making it impossible to select electrodes.

After James did a ton of work to figure out what was going on, it turns out the issue was with the coordinate axis of the MRI and not with the CT. His guess is that someone at Children's must have offset the center coordinate of the anatomical from the locator scan. As a result, the MRI x-axis origin was over 100 mm offset to the right, which truncated the aligned CT. So, James recentered the MRI .nii file using AFNI 3drefit, to then rerun the recons using this .nii for the MRI rather than the one originally provided.

How to recenter the .nii

1. Upload mri/subjID_orig.nii to datadrive in gridlab001
2. Open a terminal to gridlab001 and navigate to datadrive
3. Check the coordinates using the following function
 - a. `3dinfo subjID_orig.nii`
 - b. Notice how the provided coordinate range is not centered around zero (for R-to-L extent, A-to-P extent, and for I-to-S extent)
4. Then run the following function
 - a. `3drefit -xorigin cen -yorigin cen -zorigin cen subjID_orig.nii`
5. Then rerun 3dinfo to see this reentered
6. Now pull this re-centered .nii file into your local recon folder and rerun the recons
 - a. Note, if you did these steps before starting the recon process, just start as normal using this file

- b. If you started the process already and found out things are off-center and cutoff through opening BiImage Suite, you will need to terminate the running recon and clear this subject's directory before rerunning with the centered .nii

4.12 POLLING FOR ORIG.MGZ LOOP

When starting a recon, if you get the following, where it repeats “trying again in 3s...” for like over a minute, check to see if appserver is actually turned on in [REDACTED].

```
Starting reconstruction job...
```

```
Polling for orig.mgz...  
  trying again in 3s...  
  trying again in 3s...  
  trying again in 3s...  
  trying again in 3s...  
  trying again in 3s...  
  trying again in 3s...
```

This issue should be fixed once you turn the machine on so that you can access it for recons.