COREGISTRATION

Note: all commands mentioned in this document will be of the form:

```
mri_convert filename orig.mgz
```

where the words in green mean that you need to substitute the appropriate parameters.

Part I: Create the surfaces

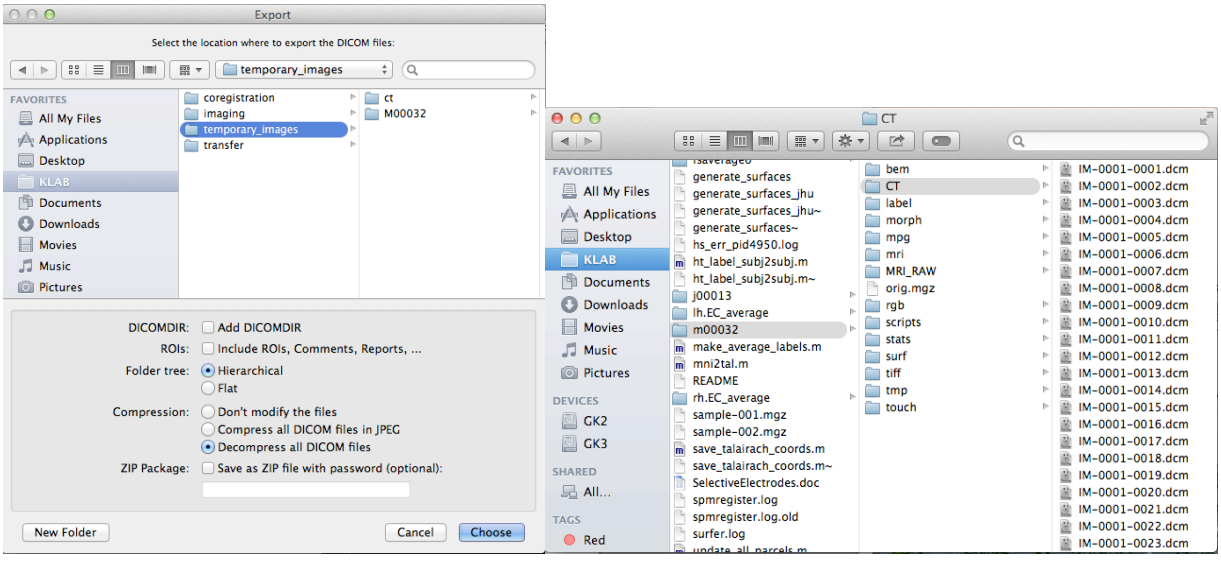
1. Create the subdirectory structure by entering (from the `/KLAB/coregistration/folder`):

```
mksubjdirs subject
```

2. Copy raw CAT and MRI data

Inside the `subject` directory create the subdirectories CT and MRI_RAW. Insert the CD containing the CAT and MRI images and open Osirix.

Choose the appropriate CT and go to `File->Export->Export to DICOM files(s)` and export the files to the folder `/KLAB/temporary_images/.` Be sure to check 'Decompress all DICOM files' and 'Flat folder tree. Then, copy the exported DICOM files to the `/KLAB/registration/subject/CT` folder. Do the same for the MRI.



4. From now on, all commands should be entered from within the /KLAB/coregistration/subject/ folder.

Convert the CT DICOM files to a .NII file using the following command:

```
mri_convert filename CT.nii
```

where filename is the name of the first file in the CT directory. For example,

```
mri_convert CT/IM-0001-0001.dcm CT.nii
```

5. Display the surface using:

```
tkmedit -f CT.nii
```

It is good when electrodes are visible.

6. Use the same command to convert the MR file to .MGZ file.

```
mri_convert filename orig.mgz
```

where filename is the name of the first file in the MRI directory. For example,

```
mri_convert MRI_RAW/IM-0001-0001.dcm orig.mgz
```

If the T1 image was correctly identified, somewhere in the output of mri_convert there should be a line of the form:
Protocol: t1***
Synonyms (or at least approximate synonyms) for T1 are “RAGE”, “MPR”, or “MPRAGE”. Basically, you want an MRI scan that doesn’t have any clutter outside the head (sometimes they will put notes or letters in), that shows a good separation between white matter and grey matter, and that doesn’t have bright artifacts.

Note: if this returns an error, try running with the flag “-it dicom”. (e.g.)

```
mri_convert -it dicom MRI_RAW/IM-0001-0001.dcm orig.mgz
```

7. Copy the MRI surface to mri/orig/001.mgz

```
cp orig.mgz mri/orig/001.mgz
```

8. Calculate the Talairach transform from the MRI image by using:

```
recon-all -s subject -autorecon1
```

This should take about 30 min.

If the subject's brain had no prior surgeries and is shaped “normally”, this is probably fine, but it's wise to verify that the Talairach transform makes sense by running

```
tkregister2 --mgz --s subject --fstal
```

and making sure that the two volumes (hit the compare button to toggle between them) are about the same shape. If not, or if autorecon1 fails, or if you suspect it might be bad because the subject's brain was unusually shaped or was missing tissue, follow instructions at

https://surfer.nmr.mgh.harvard.edu/fswiki/FsTutorial/Talairach_freeview

instead of running autorecon2 and autorecon3.

Next run:

```
recon-all -s subject -all
```

This should take about 12-24h. At the end of this the pial surface should be ready for coregistration.

Part II: Align CAT and MRI surfaces and localize the electrodes

9. `spmregister` makes an automated "best-guess" coregistration attempt. It works as follows:

```
spmregister --mov movable_vol --s subject --reg transf_matr
```

The `movable_vol` is the CT file, which is being adjusted to match the MRI scan of the specified subject (assuming your freesurfer directories are properly set up). The output, a transformation matrix, is saved to `transf_matr`. For example:

```
spmregister --mov CT.nii --s m00029 --reg spmregister.dat
```

10. After running this, you'll want to tweak things by hand, using the command given in the last line returned by spmregister (using tkregister2):

```
tkregister2 --mov CT.nii --surf orig --reg spmregister.dat
```

Adjust the movable volume (the CT image) by translating, rotating, and scaling in three dimensions. You want the CT image to line up as closely as possible with the MR image. Perfect alignment won't be possible, since the CT image was taken after surgery while the MR image was taken before surgery, but for the rest of the head make sure the pial surface is within the skull and that corresponding bones match up in both images. When you are happy with the alignment, hit **Save** (this will save the transfer matrix file). Keep in mind while performing the alignment that in T1 bones look black while in the CAT scan bones look white.

11. Next you need to apply the transformation to create a new .nii file for the CT volume, using `mri_vol2vol`. This function is called in the following way:

```
mri_vol2vol --targ mri_file --mov movable_vol --reg transf_matr
--o transformed_vol
```

This function does not take advantage of the subject directories and conventions set up with freesurfer, so you need to provide the full path to the structural MRI file you're using. The movable volume is, again, the CT file. You also input the transformation matrix generated by `spmregister` and tweaked by `tkregister2`. --o specifies a new .nii file that will hold the transformed CT image. For example:

```
mri_vol2vol --targ mri/T1.mgz --mov CT.nii --reg spmregister.dat
--o CT_to_T1.nii
```

12. Finally, you must locate and label the electrodes in the coregistered volumes. Load the MR image with **Freeview**.

From the File menu, select Load Volume … and load your final CT*.nii file (e.g. CT_to_T1_final.nii).

From the File menu, load one of the pial surface files (e.g. lh.pial) as the main surface. If you wish to have surfaces for both hemispheres, you can load the other surface file (rh.pial). Switch the surface colors to gray by changing the Curvature to Off.

You are now ready to locate all the electrodes. You should be able to find edges and corners of grids and strips in the CT image and match them to the corresponding edges and corners in the map from the hospital. Turning on the Show intensity projection map, under the Volume tab for the CT volume, can help in orienting yourself. Additionally you can build a 3D view of the electrodes in the Volume tab by:

(1) Checking Show as isosurface in 3D view
(2) Checking Extract all regions
(3) Adjusting the Low/High threshold to get the best rendering of the electrodes. The high threshold should generally be maximized, and the low threshold ~200 points below that.

For each electrode on the map, do the following:

(1) Find the electrode in the CT image.
(2) Click on its center to place the cursor on it.
(3) Verify from all three views that the cursor is on the electrode.
(4) If the cursor is not on the pial surface, move it out or in (relative to the brain) until it is on the pial surface. Note that some views will be much more appropriate than others for this - if your viewpoint is normal to the pial surface, it will be impossible, whereas if your view gives you a perpendicular cross-section of the cortex it will be easy. If this is a depth electrode, you can skip this step.
(5) Verify from all three views that the cursor is on the pial surface as close as possible to the electrode.
(6) **Important**: Verify from the 3D view that you are marking the correct electrode number.
(7) In the excel sheet, note the Name, Channel, Hemisphere (lh or rh) of the electrode. Also, copy the Volume Index and the Surface index information from the **cursor** information in freeview:

Cursor		
RAS	-37.48, 79.08, 38.81	
TkReg RAS (…	-34.09, 58.86, 40.16	
CT_to_T1	2442.64	[162, 88, 187]
rh.pial	SurfaceRAS	[-34.09, 58.86, 40.16]
	Vertex	N/A
lh.pial	SurfaceRAS	[-34.09, 58.86, 40.16]
	Vertex	133534 [-34.87, 58.86, 39.56]

(8) Add additional notes in the comments section. If this is a depth electrode, copy the Volume Index information and the SurfaceRAS information. Put Depth instead of Vertex.
(9) Here is what the excel sheet should look like:

	A	B	C	D	E	F	G
1		Patient:	j00030				
2							
3	**Name**	**Channel**	**Hemisphere**		**Volume Index**		**Surface Index**
4	LLT-1	1	rh	3210	[124, 113, 79]	Vertex	20194 [4.43, -49.48, 16.09]
5	LLT-2	2	rh	3864.73	[125, 107, 85]	Vertex	22740 [3.50, -42.54, 21.21]
6	LLT-3	3	rh	4056.62	[127, 98, 92]	Vertex	31356 [0.98, -35.44, 29.26]
7	LLT-4	4	rh	4094.35	[127, 93, 102]	Vertex	43456 [1.29, -25.87, 35.11]
8	ASD-1	5	rh	2571.48	[109, 90, 85]	Depth	[19.00, -43.00, 38.00]
9	ASD-2	6	rh	2858.72	[108, 90, 88]	Depth	[20.00, -40.00, 38.00]
10	ASD-3	7	rh	3151.89	[109, 96, 93]	Depth	[19.00, -35.00, 32.00]

Important additional notes

- For depth electrodes, the numbering starts from distal-proximal (e.g. the farthest from the surface electrode is LHD-1, and the closest to the surface is LHD-8).
- For interhemispheric electrodes, there is a platinum marker that helps you with the orientation. Typically interhemispherics also come with a diagram marking the electrode orderings.

13. After you are done, open **MATLAB**, go to the /KLAB/coregistration/scripts/ folder, and run the following command:

```
labels = convertXLStoLabels('subject','filename');
```

For example, convertXLStoLabels('m00105','m00105.xls'). This program should finish without any errors.

14. Important: double check that the correct number of labels were made in the **all, right**, or **left** folders and that the number of labels in the **all.label, all_surf.label, left.label, left_surf.label, right.label, right_surf.label** files are correct!

Part III: Display the labels on the brain surface

15. To view the electrodes, we use a separate program called Slicer 3D. To load the electrodes, run the following command from the Terminal in the /KLAB/coregistration/ folder:

```
./slicer_display.sh subject filename
```

For the filename, enter the filename used in convertXLStoLabels but without the .xls. For example, if you had the XLS file j00030.xls, type:

```
./slicer_display.sh j00030 j00030
```

Part IV: Quality Control

16. Check the following quality control points:
    1. Electrodes are on the surface, and not buried in the sulcus.
    2. Electrodes are spaced properly, following a grid/strip/depth geometry.
    3. Electrode numberings are correct. Check each grid/strip/depth individually against the clinician's electrode maps.
    4. Electrodes are not double-labeled.
    5. The electrode locations are correct.

17. Fix any mislabeled/missing electrodes and repeat steps 13-16 until everything is correct.