### Freesurfer on Macaque

There are hardly any good tutorials or references on how one could generate a freesurfer surface using freesurfer. There are many problems to following the standard human analysis that simply does not work well for the macaque brain. Below is a work-in-progress tutorial on how to generate freesurfer surfaces. This tutorial requires FSL and it's associated tools, as well as a working installation of freesurfer. The easiest way of getting all this is to download the VirtualBox image of FreeSurfer from the MGH website and voila!  
  
Anyways, here goes the rough draft:  
  
1. You should have a high-contrast, low noise MPRAGE of your monkey's brain. We typically use 0.35 mm isotropic voxel resolution, and scan between 9 to 12 times (each scan runs for 15 minutes) to generate a good mean image.  
  
2. You should also aquire a T2 image while you acquire your MPRAGEs, as this will make skull extraction (a BIG deal with monkeys) much easier.  
  
3. You must get your images in the orientation that FSL likes (nifti files, with very particular dimension ordering). You can use fslswapdim function for this. If you are converting dicoms from the scanner to nifti's using the mri\_convert command (from the FreeSurfer distribution), make sure to pass the "--sphinx" argument to it. After this, run  
  
**fslswapdim inputvol.nii LR PA IS outputvol.nii**  
  
to correct the dimension directions as FSL likes it. Check with fsl\_view.  
  
4. If the images are properly aligned, you can now use the FSL Brain Extraction Tool (BET) to rip out the brain. Here, you can pass the T2 image for a much better skull stripping. Alternatively (haven't tried it, but in theory should work), you can generate a brain mask using the T2 by thresholding it, then filling the volume and cutting the brain out of the hi-res anatomical with this.  
  
5. Once you have a nice clean skull-stripped brain, you'll have to correct for the non-uniform intensity across the image. This can be achieved easily by FreeSurfer's implementation of the MNI's N3 correction tool. Apply this using "mri\_nu\_correct", as follows:  
  
**mri\_nu\_correct.mni --i skulStrippedBrain.nii --o skull\_stripped\_nu.nii --distance 24**  
  
The distance factor may need to be adjusted, depending on what type of coil you used, and how big your monkey is, etc. Increasing the distance factor makes the program look for lower-frequency modulations of the intensity, whereas smaller numbers (better for phased-array coils) look for higher spatial frequency modulations.  
  
6. You can then use the FSL FAST tool to segment your volume into white, gray, and csf. Output the white matter image for FreeSurfer, and leave the rest alone.  
  
7. Make a new subject directory in keeping with the FreeSurfer system by using mksubjdirs.  
  
8. Now comes the fun part: FreeSurfer wants 1mm isotropic voxels, but your images are 0.35 mm iso, so if you ask FreeSurfer to work with them, it will have to downsample them to 1mm. That's no fun, so we play a trick.  
  
8a. Start Matlab. Make sure to download the NIFTI toolbox from the NIFTI website. Using load\_nii, load the image you want to prep, like this:  
  
**nii = load\_nii('mynifti.nii');**  
  
Make sure the nifti file is not compress (not "niil.gz"). Then modify nii.hdr.pixeldim to reflect 1 mm voxel ( = [1 1 1 1 0 0 0], or just replace the 0.35 in the size vector by 1's).  
  
**nii.hdr.pixeldim = [1 1 1 1 0 0 0];**  
  
Now save the volume, keeping track of what you did:  
  
**save\_nii(nii, 'newNiftiName.nii');**  
  
8b. Finally, convert to MGZ format, and make sure to tell it to CONFORM:  
  
**mri\_convert -c invol\_fake1mm.nii outvol\_fake1mm.mgz**  
  
Now, do this for all your volumes. Then they'll be ready for FreeSurfer.  
  
9. Fill in your white matter surface:  
9a. load in tkmedit, like this:  
  
**tkmedit -f /directory/brain.mgz**  
  
9b. In tkmedit, make note of the VOXEL coordinates (bottom left of window, top row) for the corpus calosum and the pons.  
  
9c. Go back to the command prompt and exceute the following on the white matter image:  
  
**mri\_fill -CV 192 172 214 -PV 192 249 194 /subj/mri/wm/wm.mgz ../filled/filled.mgz**  
  
where CV and PV reflect the corpus callosum VOXEL coordinates, and PV that of the pons.  
  
9d. Check the results in tkmedit. Should be cute.  
  
10. Now, we follow the recon-all dev table, which uses mri\_pretess as follows:  
  
**mri\_pretess ../filled/filled.mgz 255 ../brain/nu.mgz ../filled-pretess255.mgz**  
  
Then,  
  
**mri\_tessellate ../filled-pretess255.mgz 255 ../lh.orig.nofix**  
  
Then,  
  
**mris\_extract\_main\_component ../lh.orig.nofix ../lh.orig.nofix**  
  
**mris\_smooth -nw ../lh.orig.nofix ../lh.smoothwm.nofix**  
  
**mris\_inflate -no-save-sulc ../lh.smoothwm.nofix ../lh.inflated.nofix**  
  
**mris\_sphere -q ../lh.inflated.nofix ../lh.qsphere.nofix**

And now, repeat this for the righ hemisphere (rh.orig)