

FreeSurfer subcortical segmentation Quality Check instructions

ENIGMA-OCD Working Group
December, 2014

FreeSurfer is a set of tools for analysis and visualization of cortical and subcortical brain imaging data. FreeSurfer has a highly automated processing stream that is very accurate. However, sometimes the automatic reconstructions contain small errors. Before submitting data based on the FreeSurfer reconstruction to any subsequent analyses, it is important to verify that the FreeSurfer reconstructions are free from errors and excluded if necessary.

In the automatic subcortical segmentation, each voxel in the normalized brain volume is assigned one of about 40 labels, determined by location and intensity. Among others, these labels include:

Cerebral White Matter	<u>Thalamus</u>	Vessel
Cerebral Cortex	<u>Caudate</u>	Lesion
Lateral Ventricle	<u>Putamen</u>	Third Ventricle
Inferior Lateral Ventricle	<u>Pallidum</u>	Fourth Ventricle
Cerebellum	<u>Hippocampus</u>	Brain Stem
White Matter	<u>Amygdala</u>	Cerebrospinal Fluid
Cerebellum Cortex	<u>Accumbens</u>	

In the first ENIGMA OCD instruction file, we created a LandRvolumes.csv file, which contains a table with volumes (in mm³) of the ventricles, thalamus, caudate, putamen, pallidum, hippocampus, amygdala, accumbens, and intracranial volume (ICV) for each subject.

The quality of segmentation of these subcortical brain regions needs to be assessed. Step 6 'Perform outlier detection' of the instructions already visualized the subjects that were identified as outliers. However, a bad segmentation does not automatically lead to an outlier. Thus, we need to evaluate the segmentation of the other structures per subject as well.

To judge the segmentation of each structure per subject in FSLview can be very time consuming. Therefore, we created the webpages of the QC output in step 8 'Perform quality check on the webpage'. The idea of these webpages is to verify the segmentation in a quick and easy manner. So do not stare for hours at each pixel.

If you have no experience in neuroanatomy, it is useful to hold a brain atlas next to you. Of course do hold in mind that each brain is different and structures may therefore deviate.

We may assume FS does an accurate job with the segmentations. If one voxel is missing in a structure or is crossing the border of a structure we may be lenient.

A few examples of bad segmentations cover:

- the shape of the structure is not delineated properly (figure 1)
- part of the segmentation of one structure overlaps with that of another adjacent structure (figure 2)
- part of the structure is left out (figure 3)

Another sign of poor segmentation may be asymmetrical delineation. However, note that if a subject has skewed head position in the scanner, the structures may appear asymmetric while they are in fact not.

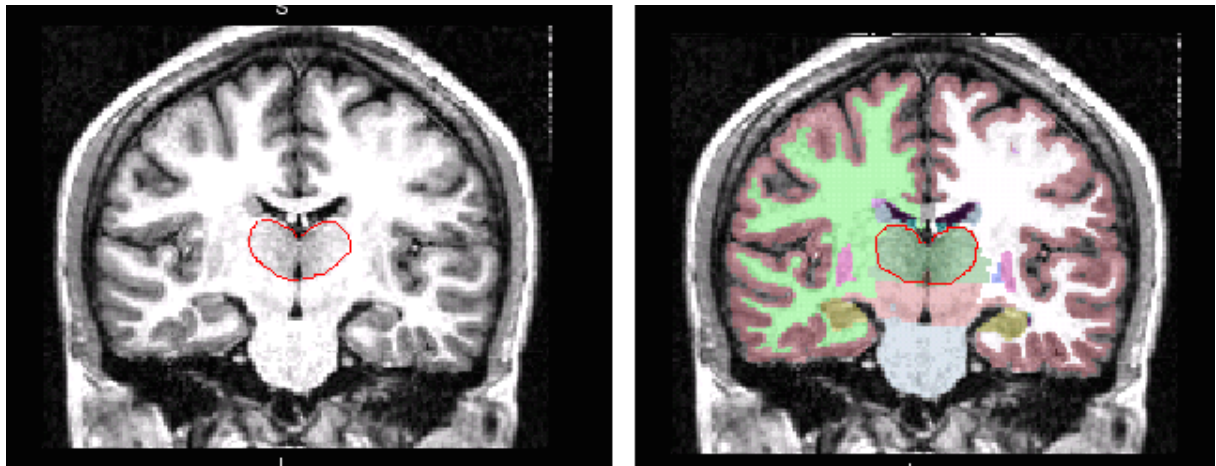


Figure 1: the shape of the thalamus is not delineated properly. The dark green color exceeds the thalamus boundaries

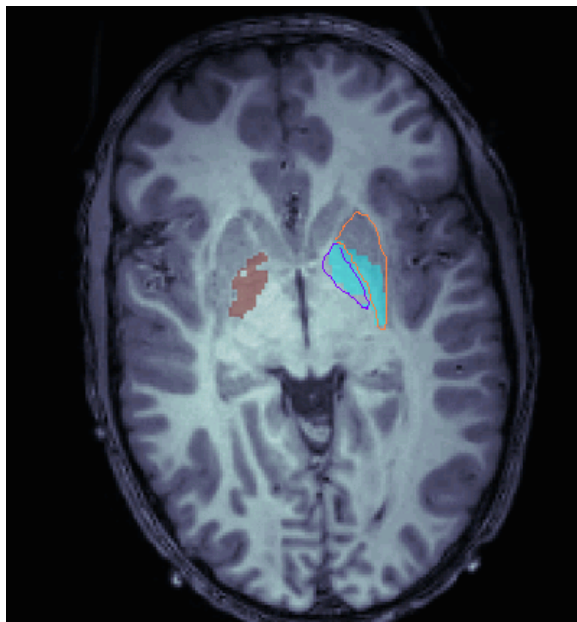


Figure 2: the left pallidum (delineated with purple) overlaps with the putamen (delineated with orange)

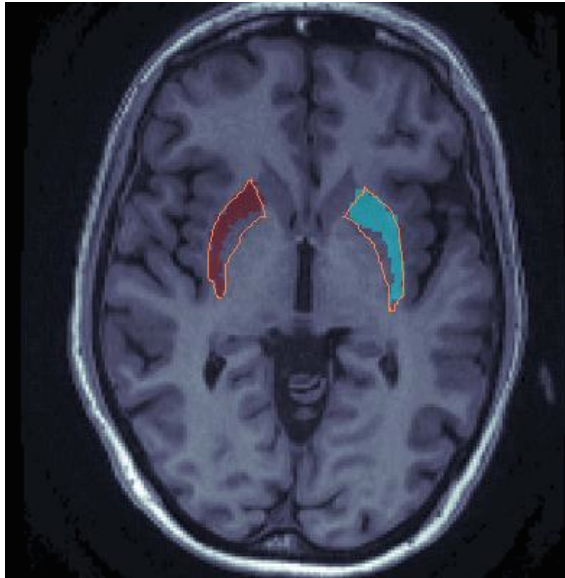


Figure 3: part of the putamen is left out

So far, we have observed poor quality of the putamen and pallidum segmentations. Therefore, we ask you to pay extra attention to these structures. Especially the putamen is an important structure in OCD. Thus, it is important to look critically at the segmentation of this structure. Nevertheless, it is difficult to determine and describe which segmentations are 'good enough'. Hence, a few examples of poor segmentations and 'relatively good' segmentations follow beneath.

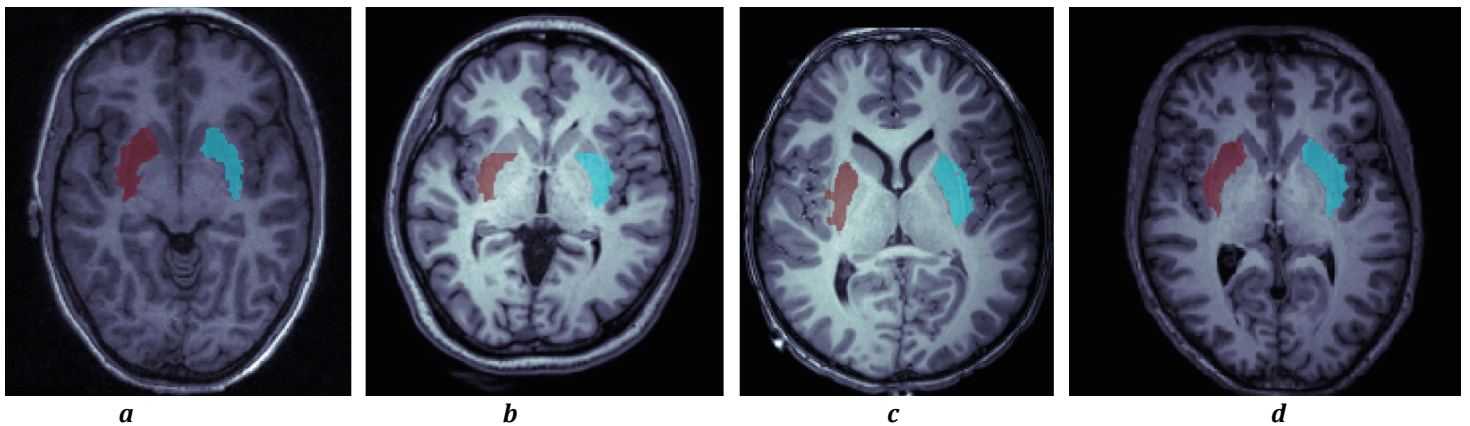


Figure 4: Poor segmentations *a* messy shape, *b* part of the putamen is left out, *c* overlap with the right (red) pallidum, *d* exceeding outer boundaries of the putamen (the claustrum is included)

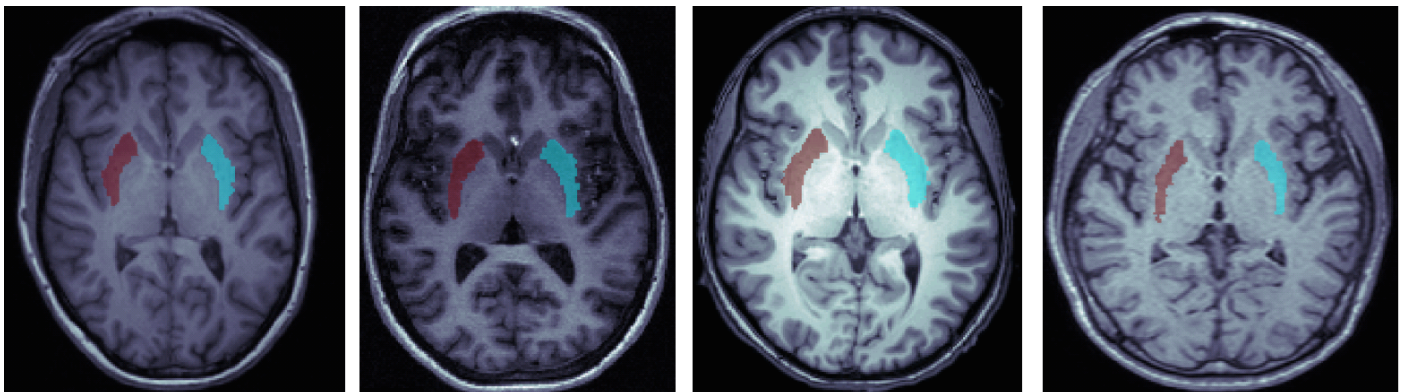


Figure 5: Relatively good segmentations

Sometimes the quality of the original T1 scan is very poor (i.e. too low contrast) leading to the fact that we cannot see the boundaries of the subcortical structures and we cannot judge whether the segmentation is correct. In this case, depending on the quality of the original T1 scan either one or more structures or the entire subject should be excluded.

When you notice the quality of a segmentation is poor on the webpage, always verify this in FSLview. Instead of a 2D representation, we now get a 3D representation, which contributes to an improved judgment of the segmentation.

Also in case of doubt, opening the image in FSLview may be very helpful. Whereas sometimes holes in a structure on the webpage may look like poor segmentation, evaluating adjacent slices in FSLview may show that it is actually the transition of two structures and the segmentation is actually correct.

Another advantage of FSLview is that you can adjust the color intensity of the segmented structures. If you lighten the color, you can verify whether the subcortical segmentation follows the intensity boundaries of the original T1 scan.

To open the segmentation of a subject in FSLview, go to the mri subfolder in the output folder of a specific subject

`subjxxx/mri`

and type:

```
mri_convert --out_orientation RAS --in_type mgz --out_type nii T1.mgz T1.nii ;  
mri_convert --out_orientation RAS --in_type mgz --out_type nii aseg.mgz aseg.nii ;  
fslview T1.nii aseg.nii -t 0.2 -l "MGH-Subcortical";
```

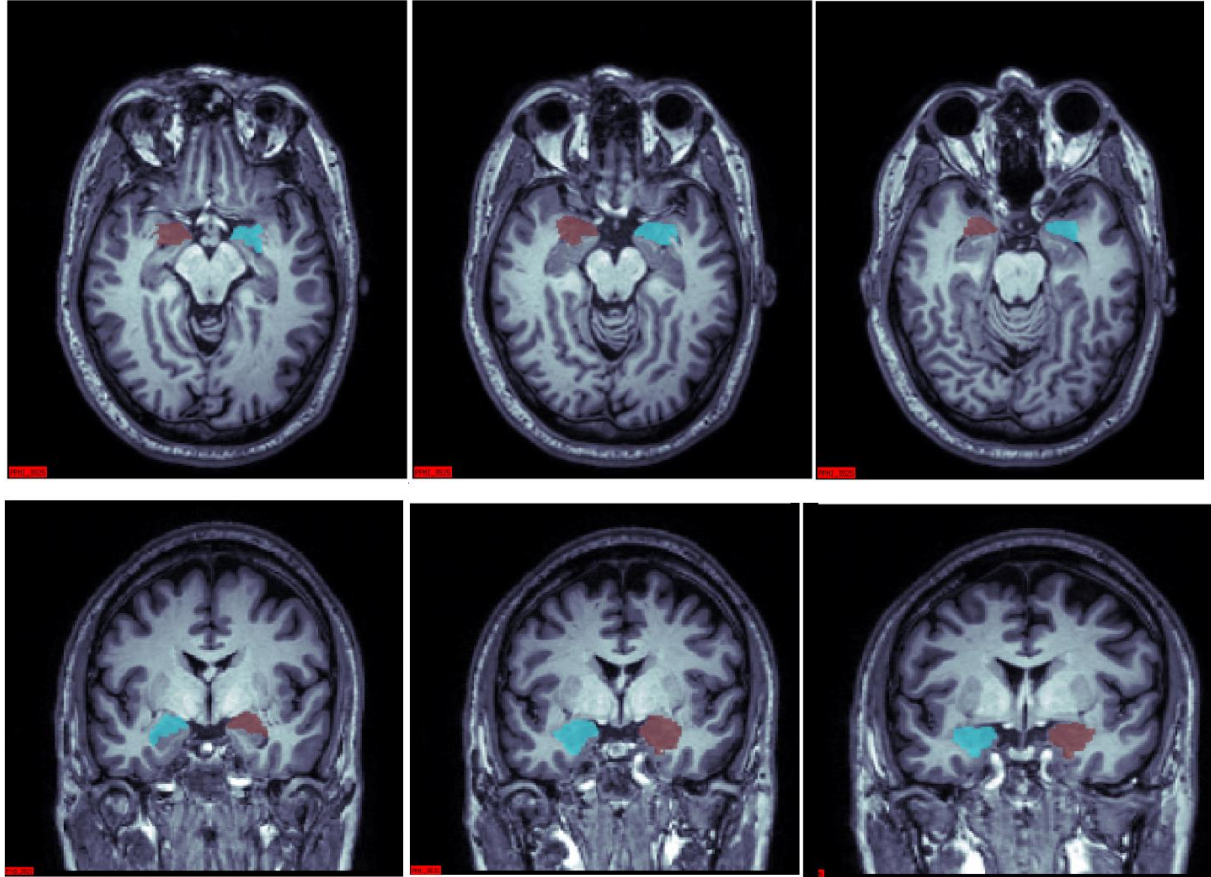
Based on the histogram plots, outlier detection and the quality check on the webpage, you may have identified some poor segmentations. You can try to re-run “recon-all” on the subjects showing poor segmentations.

If this does not help, you have to exclude these volumes from LandRvolumes.csv by marking them with an “x” and re-run the ENIGMA_plots.R on your updated LandRvolumes.csv. Send us the histograms and SummaryStats.txt once you are finished.

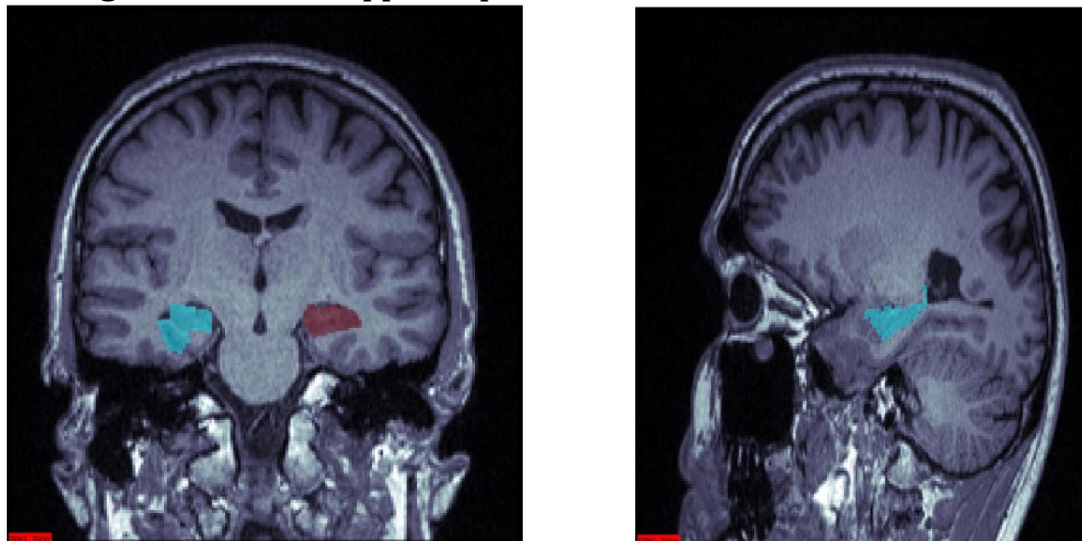
Additional examples bad segmentations

(Added March 2017, Janna Marie Bas-Hoogendam & Nynke Groenewold; examples from ENIGMA-OCD wg)

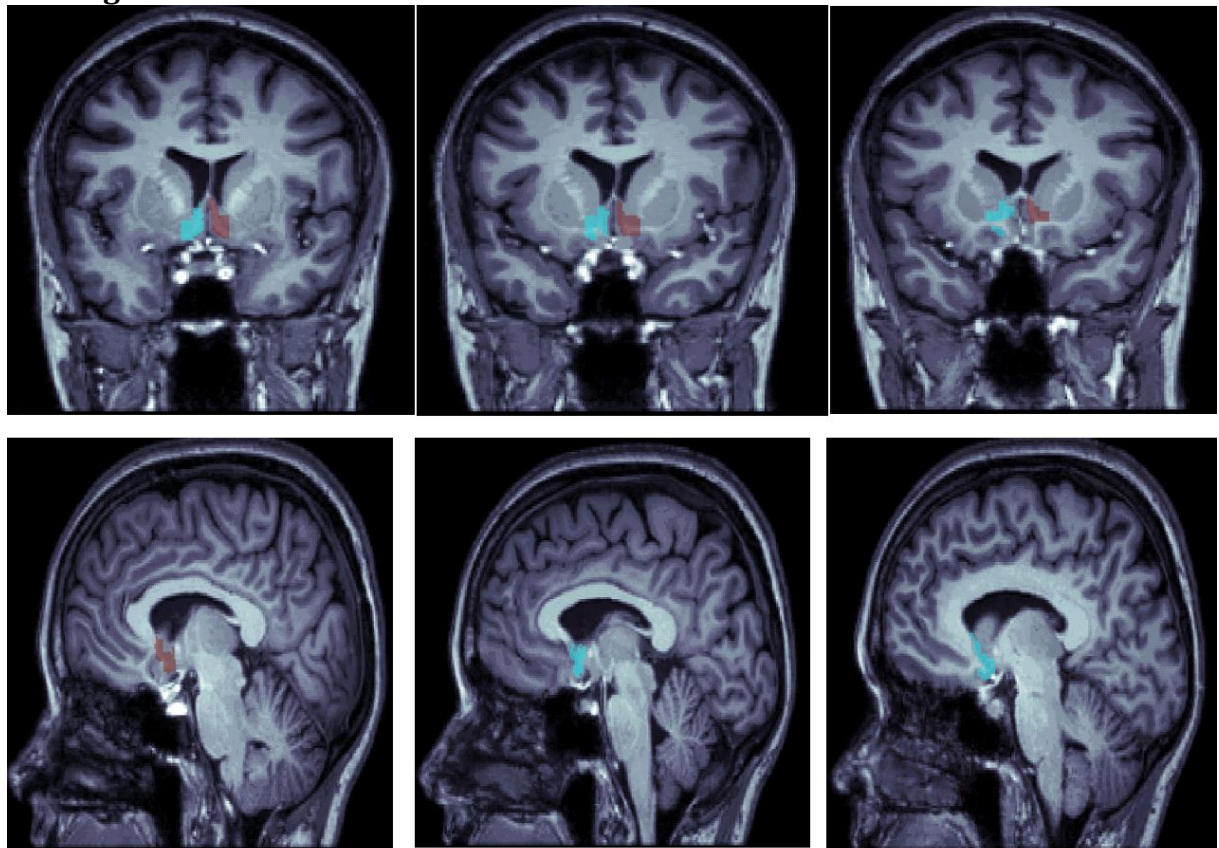
Bad segmentation amygdala - overestimation



Bad segmentation left hippocampus



Bad segmentation left Nacc –overestimation



Bad segmentation right caudate

