Manual quality control procedure for structural T1 scans

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Background information

Tissue classification and anatomical labeling was performed on the basis of the T1- weighted MR image using the well- validated and well-documented FreeSurfer v5.3.0 software (http://surfer.nmr.mgh.harvard.edu/). FreeSurfer can run on Mac, Windows and Linux platforms. For the quality assessment described in this manual the Gui **TKmedit** was used to visually inspect all FreeSurfer-processed scans (the end product of the pre-processing FreeSurfer pipeline). For more background information and tutorials on these processing steps in FreeSurfer, visit their website https://surfer.nmr.mgh.harvard.edu/

In this manual, our approach to control the quality of FreeSurfer-processed T1 anatomical scans is explained. First, during the data collection we visually inspected each T1 scan, and repeated the scan when the quality was not sufficient (i.e. affected by motion, see also Backhausen et al., 2016). After data collection, we processed the data as described in the Method section of the manuscript, resulting in FreeSurfer-processed scans for each time point for each participant. These FreeSurfer-processed scans were controlled for quality.

Determining whether a participant's Free-surfer processed scan is of sufficient quality for further analyses is susceptible to both inter-rater and intra-rater variability, and the methods used differ across studies and sites. With this manual we aim to provide more objective guidelines for the quality check of T1 scans. Therefore a step-by-step approach of the process is provided, as well as examples of MRI scans that we consider of sufficient and non-sufficient quality.

1. Set up the environment for quality control procedure

Prior to this step, the scans for each time point for each participant have been pre-processed in FreeSurfer (http://freesurfer.net/fswiki/FreeSurferAnalysisPipelineOverview). Given that we worked with longitudinal data, we have used the longitudinal pipeline (http://freesurfer.net/fswiki/LongitudinalProcessing).

1.1 Start FreeSurfer and tkmedit

To start quality control procedure for a specific scan from a participant, open FreeSurfer:

```
module load freesurfer/5.3.0
```

Set up path for your subject directory:

```
export SUBJECTS_DIR=/[subjects folder]/
```

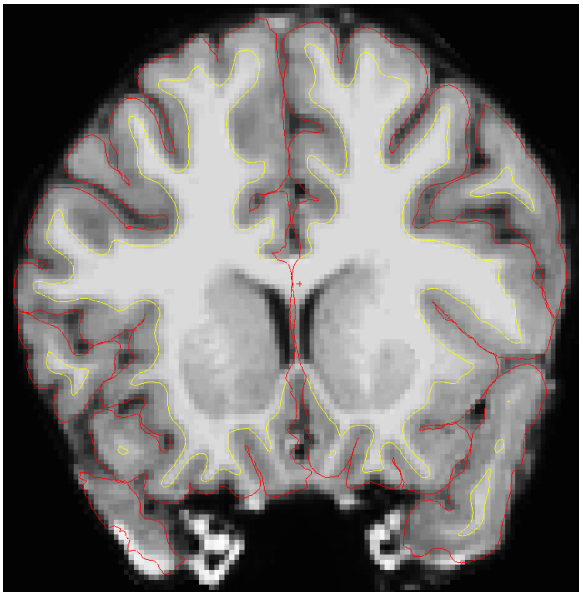
After this set-up, the following steps should be repeated for each individual participant. First, open the brainmask of the processed T1 image, open the original T1 scan as auxiliary images and overlay the reconstructed pial and gm/wm boarder surfaces:

```
tkmedit $CorrectDir brainmask.mgz -aux T1.mgz -surface lh.white -aux-surface rh.white
```

It is possible to create a simple script to automate this process and only enter the participant number. Now an image of the parcellated brain is opened in tkmedit, a tool by FreeSurfer (https://surfer.nmr.mgh.harvard.edu/fswiki/TkMeditGuide). Two surfaces are displayed, in red the pial surface (i.e. the boundary between gray matter of the brain and the cerebrospinal fluid that surrounds the brain) and in yellow the division between white matter (WM) and gray matter (GM) in the brain. As a result, your image should appear as follows (see Figure 1). The original

T1 scan (including skull) is opened as auxiliary file, meaning that it is not visible immediately but can be opened from the tkmedit gui (button 4, see Figure 2).

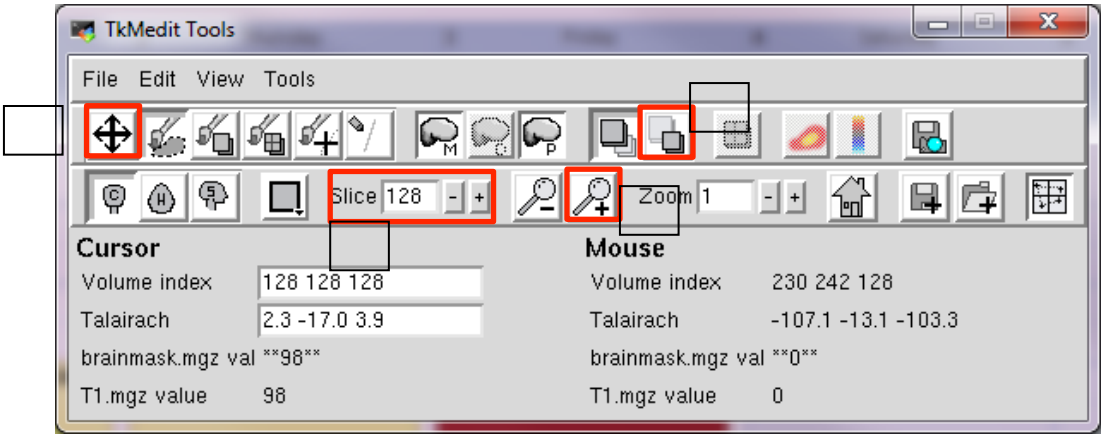
Figure 1. Example of parcellated scan opened in tkmedit, with visual plotted pial surface (red) and WM/GM division (yellow).



1.2 Set-up tkmedit window

We perform the quality control from the anterior to the posterior regions of the brain. The scan will automatically open at slice 128, so to start your quality control procedure in the anterior region of the brain, type "215" in box 1 (see Figure 2). Then use the "+" and "-" buttons to scroll through the brain and find the most anterior slice of the brain. It is also possible to scroll through the brain using the arrow keys on the computer keyboard. To ensure comparability between subjects, enlarge the tkmedit window to always approximately the same size, and zoom in on the brain (if necessary) in order to perform a more detailed quality control (button in tkmedit interface shown in Figure 2.2). Finally, activate the cursor so you can move the image around to inspect relevant parts (button in tkmedit interface shown in Figure 2.3).

Figure 1 Example of tkmedit interface, with highlighted areas indicating slice selector (1), zoom in button (2), cursor activation button (3) and auxiliary file activation button (4).



2. Perform quality control procedure

2.1 General information quality control procedure

After setting up the environment for the quality control procedure, each T1 scan has to be screened carefully. To assess the quality of the scan, we used four criteria:

1) Is the reconstructed image affected by movement?
2) Are the temporal poles missing in the reconstruction of pial surface (red line) and gray matter/white matter division (yellow line)?
3) Is dura/skull included in the reconstruction of pial surface (red line)?
4) Are parts of the brain missing in the reconstruction of pial surface (red line) and gray matter/white matter division (yellow line) (other than temporal poles)?

Each criterion was scored with zero if errors are absent (i.e. answered with no). Each criterion was scored with one (i.e. answered with yes) if errors are visible. We only scored with 'one' if the criterion was met on at least 3 consecutive slices of the scan. The reason for this was that sometimes a brain area appears to be missing, but this is due to the structure of the brain: it is possible that a specific slice is positioned between two gyri of the brain, and therefore that area of the brain appears to be missing. However, on the next slice the brain area should be visible again. Therefore, each criterion had to be met on several consecutive slices.

Each criterion was assessed for the left and right hemisphere separately. Therefore, to perform the quality control procedure for each scan per participant, we inspected each hemisphere twice (e.g. first scrolling back and forth through the left hemisphere, then repeating the procedure for the right hemisphere). Together, these criteria (more detailed information provided below) lead to a final evaluation of the scan, expressed in a numerical rating of overall quality (1-4: excellent (1), good (2), etc).

2.2 Keeping track of your findings

To keep track of our findings for each participant, we used a datafile (see attached template). In this file each line contains information on an individual participant. A short overview of the different columns is provided below:

Column A (*Subject*): the unique subject number

Column B (*Final Score*) the final rating for an individual scan

Columns C-M: Space to score the various criteria (LH = left hemisphere, RH = right hemisphere)

Column N (*Notes)*: Space for additional comments

For an example see Figure 3.

Figure 3. Example of quality control datafile, with individual lines with information for each participant.

Subject	Final_Score	Excessive_movement	Temp_pole_miss_LH	Temp_pole_miss_RH	Dura_LH	Dura_RH	Missing_Anterior_LH	Missing_Anterior_RH	Missing_Superior_Medial_LH	Missing_Superior_Medial_RH	Missing_Posterior_LH	Missing_Posterior_RH	Notes
Subject001	1	0	0	0	0	0	0	0	0	0	0	0	
Subject002	1	0	1	1	0	0	1	1	1	1	0	0	Minor parts anterior and temporal lobe missing

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2.3 Criteria for quality control: **step-by-step**

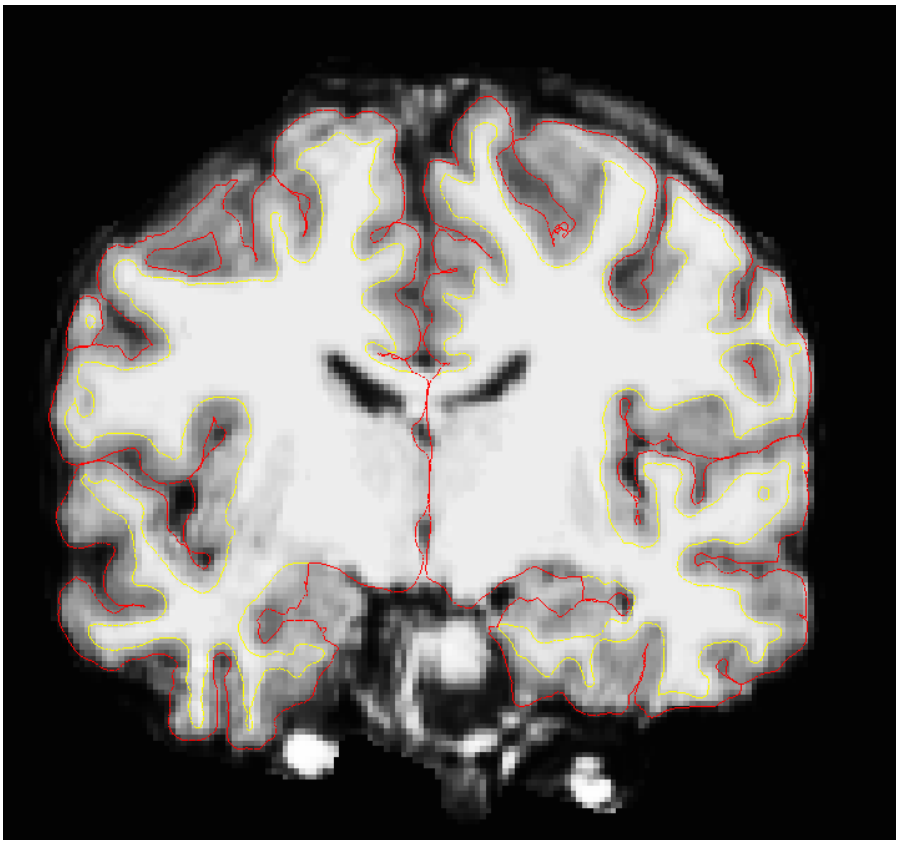
Below we provide step-by-step details of the different criteria.

Criterion 1: Is the reconstructed image affected by movement?

(0=NO, 1=YES)

If participants have moved too much in the scanner (Backhausen et al., 2016), this can sometimes be visible as rings in the cortex (like growth rings on a tree; see Figure 4 for an example). Even though reconstruction has been completed, it was very difficult to evaluate whether this resulted in sufficient reconstruction as grey and white matter can hardly be distinguished. This scan was therefore be scored as 1 in *Excessive movement,* (column C) as it was affected by movement.

Figure 4. Example of a FreeSurfer processed image affected by movement.

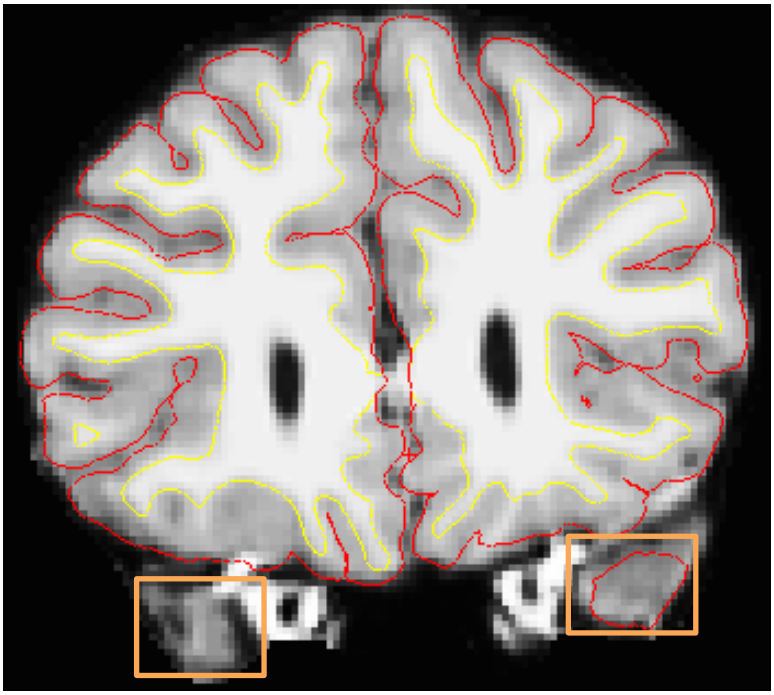


Criterion 2: Are the temporal poles missing in the reconstruction of pial surface (red line) and gray matter/white matter division (yellow line)?

(0=NO, 1=YES)

When you inspect the scan from the anterior (prefrontal) to posterior areas (occipital), the temporal poles (i.e. the extending part of the temporal lobe) becomes visible. The pial surface should be fitted around the entire brain, including temporal poles. For an example of temporal poles missing in the reconstruction, see Figure 5. The pial surface of the temporal pole should be constructed from the first visible point of the temporal pole. Although in Figure 5 the left temporal pole is clearly visible, the pial surface had not been reconstructed (highlighted by left square), so *Temp Pole Miss LH* (column D) was scored as 1 if this was the case for three consecutive slices. The right temporal pole was visible and has been reconstructed (highlighted by right square). Note that there were also small parts of the right temporal pole missing, but this was not the case for three consecutive slices, so *Temp Pole Miss RH* (column E) was scored as 0.

Figure 5. Example of temporal pole missing in reconstruction.

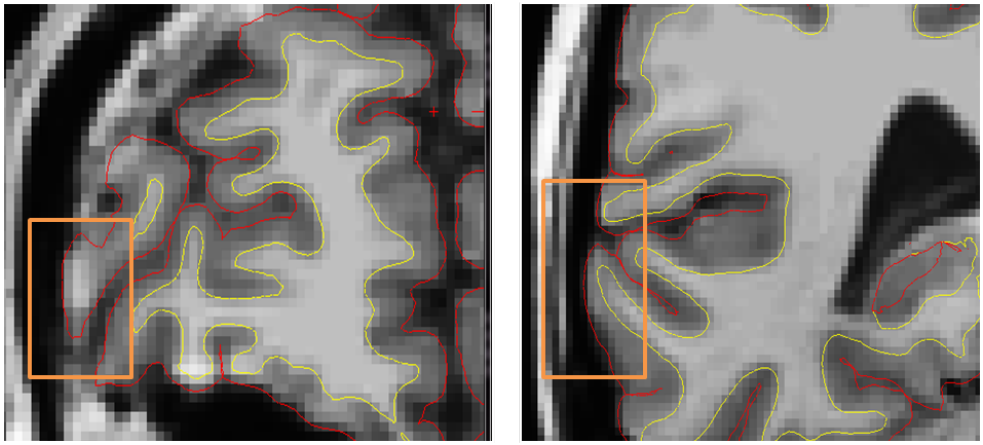


Criterion 3: Is dura/skull included in the reconstruction of pial surface (red line)?

(0=NO, 1=YES)

When the T1 scan is processed in FreeSurfer, one of the steps is the stripping of skull and dura from the image, so that only the actual brain remains. When this skull strip has gone wrong, the pial surface might include the leftover skull/dura (for an example see Figure 6). If dura was included in the reconstruction of the pial surface (see example on the right), *Dura LH* (column F) was scored as 1. If no dura was included in the reconstruction of the pial surface (see example on the left), *Dura RH* (column G) was scored as 0.

Figure 6. Example of dura included (left) and not included (right) in pial surface reconstruction.



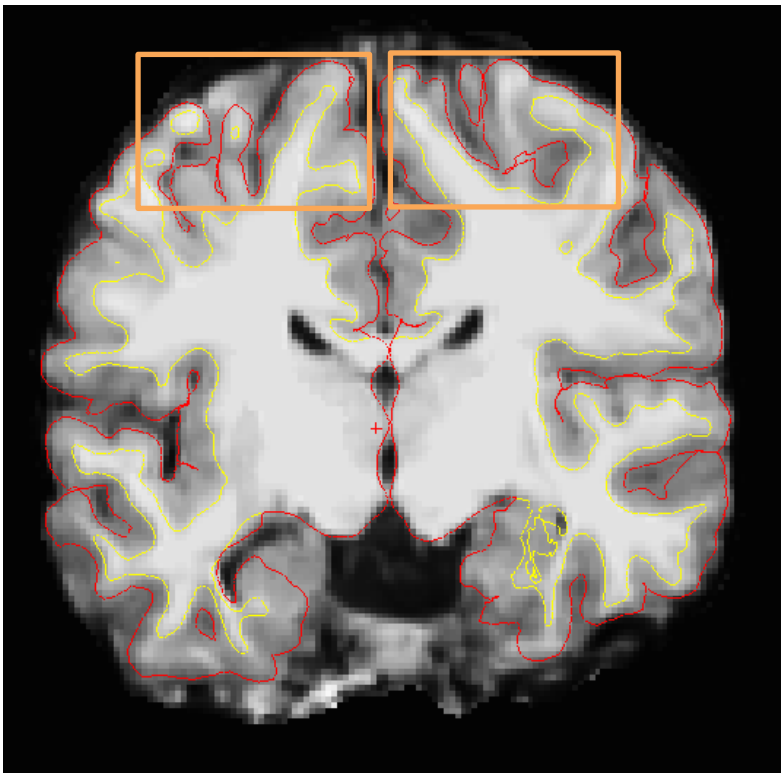
Criterion 4: Are other parts of the brain missing in the reconstruction of pial surface (red line) and gray matter/white matter division (yellow line)?

(0=NO, 1=YES)

With this criterion we aimed to check whether the entire brain was included in the reconstruction, or whether some parts were missing. To be more regionally specific, for this criterion we distinguished between missing areas in distinct parts of the brain: anterior, superior/medial, and posterior. Again, the criterion should be scored for the left and right hemisphere separately and only if the criterion was violated for three consecutive slices. An example of a slice with missing brain regions in the medial part of the brain is provided in Figure 7. The pial surface (indicated by the red line) should follow the outer border of the cortex as

close as possible. The pial surface (red line) in the left hemisphere in Figure 7 did not follow the outer border of the cortex, leaving out some folds of the cortex. Therefore, *Missing Superior/Medial LH* (column J) was scored as 1. In comparison, the right hemisphere is reconstructed well, and *Missing Superior/Medial RH* (column K) was scored as 0.

Figure 7. Example of brain part missing in reconstruction pial surface.



2.4 Determining final score

Based on the assessment criteria described above one final score should be given to each participant. This score can range from 1 – 4 and gives information on the quality of the scan:

1 = Excellent

2 = Good

3 = Poor

4 = Bad

To determine the final score, the earlier scored criteria should be taken into account. If the criterion *Excessive movement* was scored with 1 (i.e. there is excessive movement), we recommend that the scan is scored as 4 (exclusion).
In comparison, we recommend that a score of 1 for the temporal poles criteria (i.e. temporal poles are not included in the reconstruction) will not always lead to exclusion, but to a final score of 1 or 2 (depending on the severity of the misreconstruction). If an additional criterion would also be violated (e.g. other parts of the brain missing in reconstruction), we recommend scoring the scan as a 3, to indicate a poor quality.