Manual quality control procedure for structural T1-weighted scans processed in FreeSurfer

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Background information

Manual quality check (QC) procedures of T1 MRI scans are 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-weighted scans. Therefore, a step-by-step approach of out in house developed manual QC procedure is provided in this protocol. In addition, examples of MRI scans that we consider of sufficient and insufficient quality are included.

Tissue classification and anatomical labeling was performed on the basis of the T1-weighted MR image using the well-validated and well-documented FreeSurfer v6.0.0 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 the website https://surfer.nmr.mgh.harvard.edu/.

In this manual, we discuss our manual quality control procedure of FreeSurfer-processed T1-weighted anatomical scans. 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 manually controlled for 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 the present paper includes a longitudinal dataset, we used the longitudinal pipeline (http://freesurfer.net/fswiki/LongitudinalProcessing).

1.1 Start FreeSurfer and tkmedit (in Linux environment)
To start quality control procedure for a specific scan from a participant, open FreeSurfer:

module load freesurfer/6.0.0

Set up path for your subject directory:

export SUBJECTS_DIR=/[subjects folder]/

After this set-up, the following steps can be repeated for each individual scan. The code below opens the brainmask, the original T1-weighted scan as auxiliary image and overlays the reconstructed pial and gm/wm boarder surfaces of a processed T1 image:

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

Below an example of a script that automatizes this process, only the scan ID should be entered.

echo "Please enter scan ID"
read scanID
echo "Starting quality control for {scanID}"

for dir in /$SUBJECTS_DIR /*/;

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do
  if [[ $dir == *"{scanID}"* ]]
  then
    CorrectDir=${dir#/$SUBJECTS_DIR/}
fi
done
view="tkmedit $CorrectDir brainmask.mgz -surfs -aux wm.mgz
eval $view
```

This code opens an image of the parcellated brain in TkMedit (see Figure M1) (https://surfer.nmr.mgh.harvard.edu/fswiki/TkMeditGuide). Two surfaces are displayed: the pial surface is indicated in red and the division between grey/white matter (GM/WM) boarder is indicated in yellow. The original T1 scan (including skull) is opened as auxiliary file; you can easily switch to this scan using the TkMedit gui (button 4, see Figure M2).
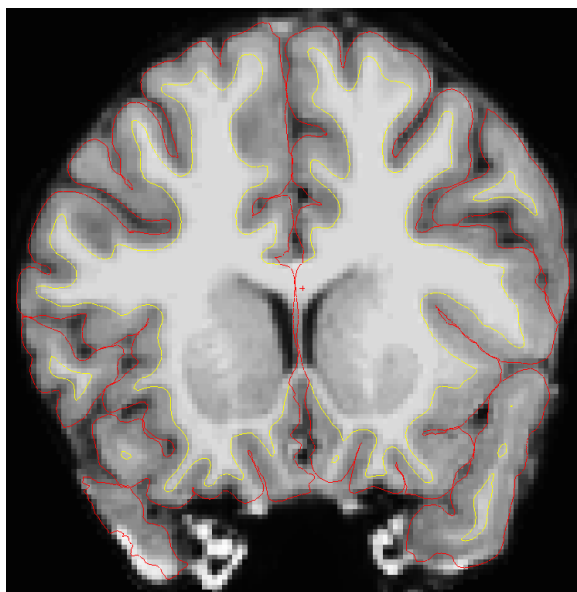

Figure M1. Example of parcellated scan opened in tkmedit, with pial surface (red) and WM/GM division (yellow).

1.2 Set-up TkMedit window

For quality control, we scroll through 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. Either type "215" in box 1 (see Figure M2), scroll to the anterior regions using the "+" button or type "Slice 215" in the command line. Next, use the "-" button to scroll towards the posterior part of the brain in a slow pace, or use the arrow keys. To ensure comparability between subjects, make sure that when you enlarge the TkMedit window it is always approximately the same size. You can also zoom in on the brain (if necessary) (see button in TkMedit interface shown in Figure M2.2). In addition, you can activate the cursor so you can move the image around to inspect relevant parts (button in TkMedit interface shown in Figure M2.3).
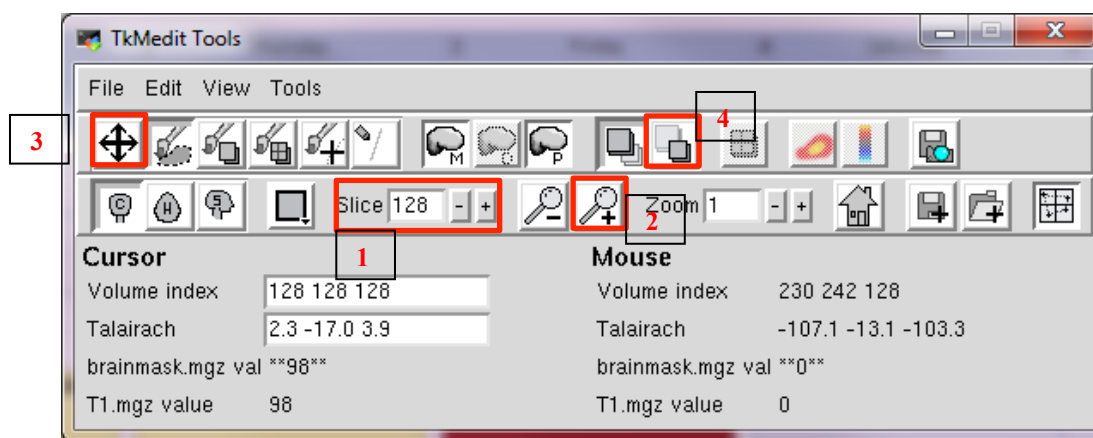
Figure M2. Example of TkMedit interface, with highlighted areas indicating slice selector (1), zoom in button (2), cursor activation button (3) and auxiliary file activation button (4).

2. 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. Four criteria are used to assess scan quality:

1) Is the reconstructed image affected by movement?
2) Is (part of) the temporal pole missing in the reconstruction?
3) Is non-brain tissue (e.g. dura/skull) included in the reconstruction of pial surface (red line)?
4) Are parts of the cortex missing in the reconstruction (other than temporal poles)?

For each criterion 0 is entered when the answer is No, no errors are visible, 1 is entered when the answer is Yes, errors are visible. We only score 1 if the criterion is met in at least 3 consecutive slices.

Each criterion has to be assessed for the left and right hemisphere separately. As such, we inspect each MRI scan twice (e.g. first scrolling back and forth through the left hemisphere, then repeating the procedure for the right hemisphere). Together, these criteria (more details are provided below) lead to a final evaluation of the scan, expressed in a numerical rating of overall quality (1-4: Excellent (1), Good (2), Poor (3), Failed (4)).

2.2 Keeping track of QC

To keep track of QC for each T1 scan, we used a datafile (see template on https://github.com/Qoala-T/QC). Each line contains information on a single T1 scan, where each quality criteria is represented in the columns (see Figure M3):

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

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

Columns C-M: 4 criteria for both left and right hemispheres (LH = left hemisphere, RH = right hemisphere)

Column N (*Notes)*: additional comments

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

Figure M3. Example of quality control file, with individual lines with information for each scan.

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

Below we provide step-by-step details of the four quality 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 is sometimes visible as rings (like growth rings on a tree; see Figure M4 for an example). Even though reconstruction has been completed, it is clearly not a good reconstruction. *Excessive movement* (column C) is therefore scored with "1".
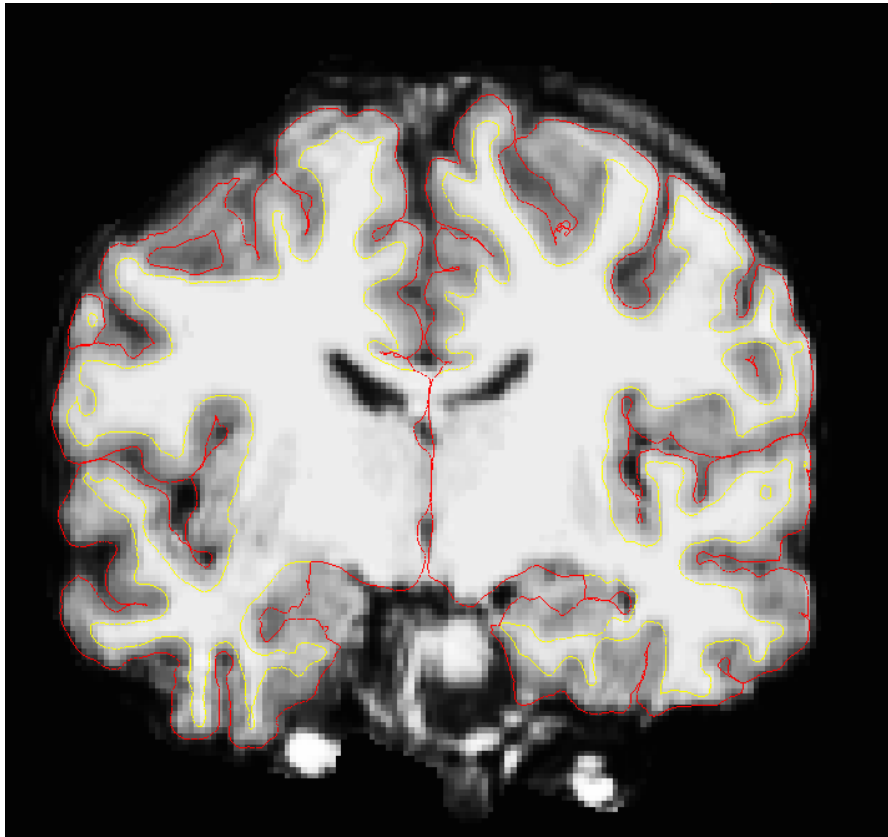

Figure M4. Example of a FreeSurfer processed image affected by movement.

Criterion 2: Is (part of) the temporal pole missing in the reconstruction?

(0=NO, 1=YES)

A particularly often-detected error is missing pial surface reconstruction at the temporal poles. An example can be seen in Figure M5. The pial surface of the temporal pole should be constructed from the first visible slice of the temporal pole. Although in Figure M5 the left temporal pole is clearly visible, the pial surface (red line) is reconstructed (highlighted by left square). If this is visible on three or more consecutive slices *Temp Pole Miss LH* (column D) is scored "1". The right temporal pole showed poor reconstructed (highlighted by right square), however this is not

observed on three consecutive slices, so *Temp Pole Miss RH* (column E) is scored as "0".
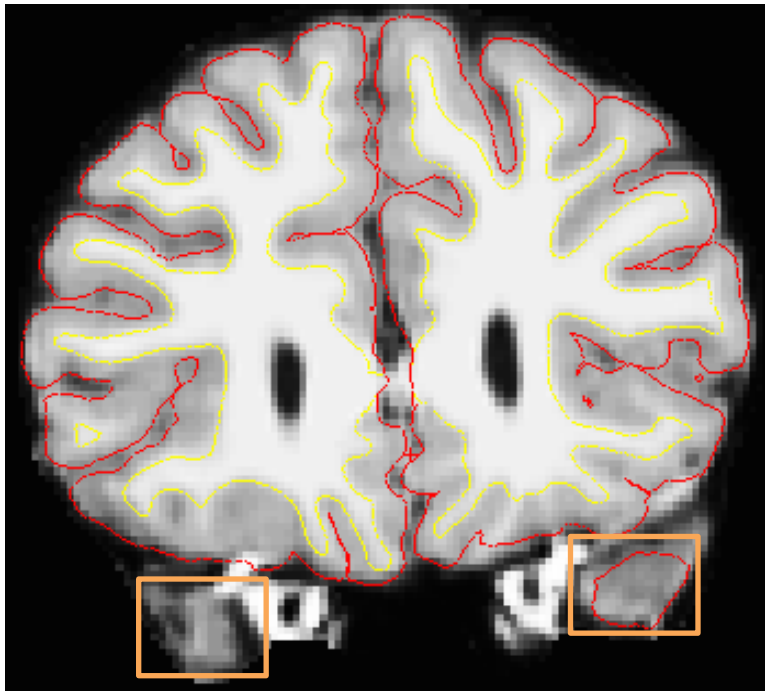
Figure M5. Example of temporal pole missing in reconstruction.

Criterion 3: Is non-brain tissue (e.g. dura/skull) included in the reconstruction of pial surface (red line)?

(0=NO, 1=YES)

Some brainmask.mgz files show skull or dura (see example in Figure M6). If dura is included in the reconstruction of the pial surface (see example on the right), *Dura LH* (column F) is scored "1". If no dura is included in the reconstruction of the pial surface (see example on the left), *Dura RH* (column G) is scored "0".
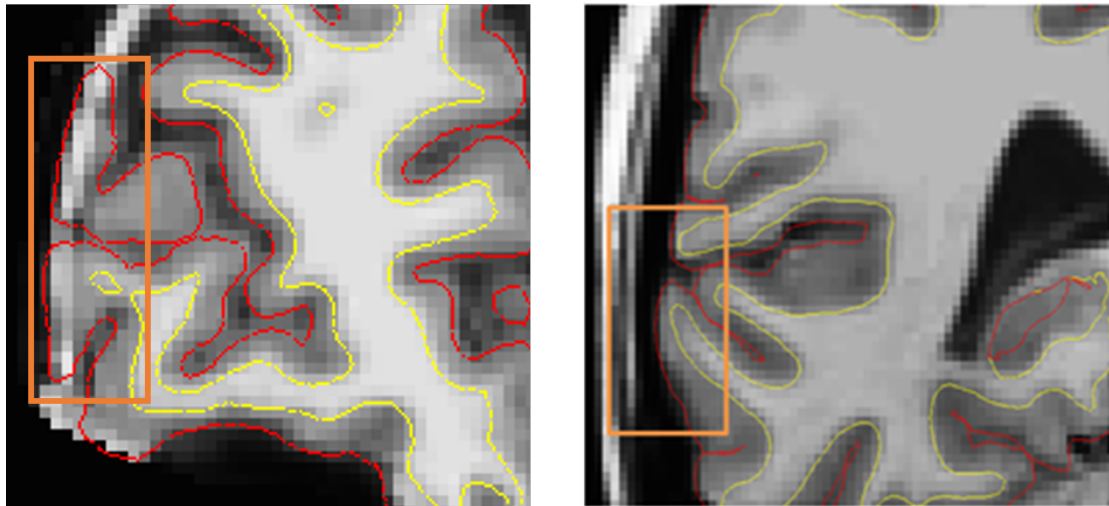
Figure M6. Example of dura included (left) and not included (right) in pial surface reconstruction.

Criterion 4: Are parts of the cortex missing in the reconstruction (other than temporal poles)?

(0=NO, 1=YES)

This criterion is aimed to evaluate whether parts of the cortex were not included in the reconstruction. We distinguished between anterior, superior/medial, and posterior areas of the brain. Again, this criterion is scored separately for the left and right hemispheres and is only indicated with a "1" if reconstruction errors are observed on 3 consecutive slices. An example of a slice with poor reconstruction is provided in Figure M7. 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 M7 did not follow the outer border of the cortex, leaving out some folds of the cortex. Therefore, *Missing Superior/Medial LH* (column J) has to be scored "1". In comparison, the right hemisphere is reconstructed well, and *Missing Superior/Medial RH* (column K) has to be scored "0".
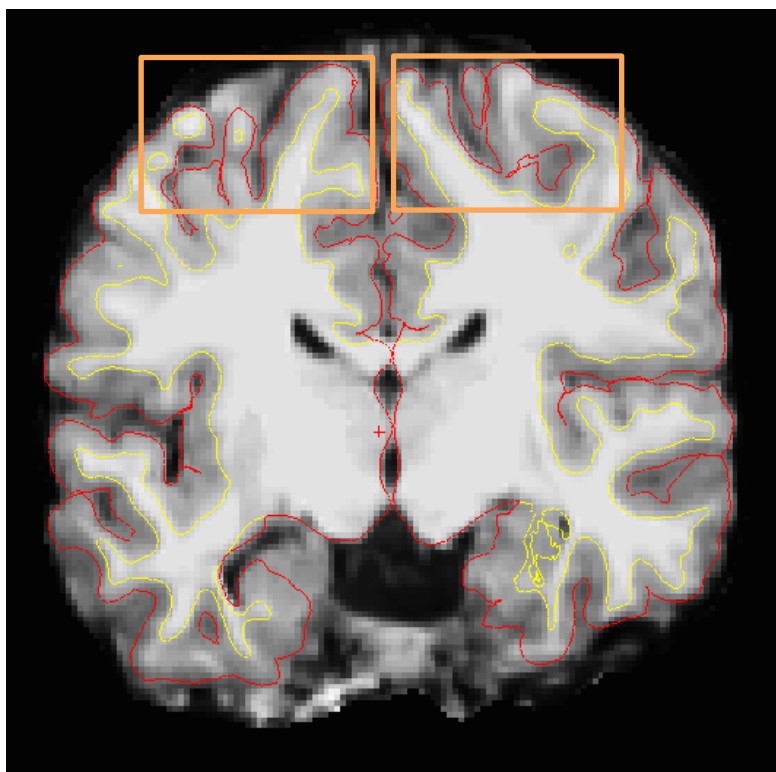
Figure M7. Example of cortical reconstruction error missing cortical brain tissue.

2.4 Final score

Each scan is rated with a final score, based on the assessment criteria described above. This score can range from 1-4 and gives information on the quality of the scan:

1 = Excellent

2 = Good

3 = Poor

4 = Failed

In general, if all criteria were rated with 0, the scan should get a final score of 1. For each "1" score in the criteria, an extra score is added to the final score. Thus, 2 (Good) if there were parts of the cortex not included in the in the reconstruction (e.g. Missing pial). If an additional criterion would also be violated (e.g. temporal pole missing), we recommend scoring the scan as a 3, etc.

There is one exception to this rule: If the criterion *Excessive movement* is scored with 1 (i.e. there is excessive movement), we would recommend that the scan is always scored as 4 (Failed).