1 Processing data with an isometric voxel size other than 1x1x1 mm^3 using FreeSurfer

- recon-all -autorecon1 -cm -noskullstrip -s <subject>
- change dir to subject/mri
- mri_convert -cs 1 nu.mgz nu.conformed.mgz
- mri_em_register -skull nu.conformed.mgz $FREESURFER_HOME/average/RB_all_withskull_2008-03-26.gca transform/talairach_with_skull.lta
- recon-all -skullstrip -s <subject>
  - Skull stripping looks okay? If not...
  - recon-all -skullstrip -clean-bm -wsatlas -wsthresh <threshold> -s <subject>
  - wsatlas should be used in most cases if the skull stripping is not great; sometimes produces further errors
  - wsthresh default is 10; lower values remove more skull, higher values leave more tissue
- recon-all -autorecon2 -s <subject>
  - if recon-all breaks on canorm stage
    - change dir to subject/mri
    - cp brainmask.mgz norm.mgz (brainmask.mgz is sufficient to replace norm.mgz)
    - recon-all -autorecon2-volonly -nocareg -nocanorm -s <subject>
  - if nu_noneck.mgz looks odd, which is needed for a correct aseg.mgz
    - change dir to subject/mri
    - mri_remove_neck -radius <radius> nu.mgz transforms/talairach.m3z $FREESURFER_HOME/average/RB_all_2008-03-26.gca nu_noneck.mgz
    - radius is a value in mm which refers to tissue that is being erased outside the "possible brain"; default 25
    - recon-all -skull-lta -calabel -s <subject>

- recon-all breaks on normalization2 stage, as aseg.mgz needs to be conformed
  - change dir to subject/mri
  - mri_normalize -noconform -mask brainmask.mgz norm.mgz brain.mgz
- one can run two instances of recon-all simustaneously to shorten processing time a lot
  - without two instances of recon-all
    - recon-all -autorecon2-cp -nonormalization2 -autorecon3 -s <subject>
  - with two instances of recon-all
    - recon-all -maskbfs -segmentation -fill -s <subject>
    - after this finishes run these two commands in different terminals
      - recon-all -autorecon2-perhemi -hemi lh -log <full path to subject dir>/scripts/lh.recon-all.log -s <subject>
      - recon-all -autorecon2-perhemi -hemi rh -log <full path to subject dir>/scripts/rh.recon-all.log -s <subject>
    - could break on cortribbon stage, as the left hemisphere needs to be finished before the right to run properly
      - if it breaks wait for left hemisphere to be finished
      - change dir to subject/mri
      - mri_volmask -label_left_white 2 -label_left_ribbon 3 -label_right_white 41 -label_right_ribbon 42 -save_ribbon -save_distance <subject>
    - recon-all -autorecon3 -s <subject>

2 Processing data with an isometric voxel size other than 1x1x1 mm^3 using FreeSurfer with modified mri_watershed by Krish S.

- recon-all -autorecon1 -cm -s <subject>
  - Skull stripping looks okay? If not...
  - recon-all -skullstrip -clean-bm -wsatlas -wsthresh <threshold> -s <subject>
  - wsatlas should be used in most cases if the skull stripping is not great; sometimes produces further errors
  - wsthresh default is 10; lower values remove more skull, higher values leave more tissue
- recon-all -autorecon2 -s <subject>
  - if recon-all breaks on canorm stage
    - change dir to subject/mri
    - cp brainmask.mgz norm.mgz (brainmask.mgz is sufficient to replace norm.mgz)
    - recon-all -autorecon2-volonly -nocareg -nocanorm -s <subject>
  - if nu_noneck.mgz looks odd, which is needed for a correct aseg.mgz
    - change dir to subject/mri
    - mri_remove_neck -radius <radius> nu.mgz transforms/talairach.m3z $FREESURFER_HOME/average/RB_all_2008-03-26.gca nu_noneck.mgz
    - radius is a value in mm which refers to tissue that is being erased outside the "possible brain"; default 25
    - recon-all -skull-lta -calabel -s <subject>
- recon-all breaks on normalization2 stage, as aseg.mgz needs to be conformed
  - change dir to subject/mri
  - mri_normalize -noconform -mask brainmask.mgz norm.mgz brain.mgz

- one can run two instances of recon-all simustaneously to shorten processing time a lot
  - without two instances of recon-all
    - recon-all -autorecon2-cp -nonormalization2 -autorecon3 -s <subject>
  - with two instances of recon-all
    - recon-all -maskbfs -segmentation -fill -s <subject>
    - after this finishes run these two commands in different terminals
      - recon-all -autorecon2-perhemi -hemi lh -log <full path to subject dir>/scripts/lh.recon-all.log -s <subject>
      - recon-all -autorecon2-perhemi -hemi rh -log <full path to subject dir>/scripts/rh.recon-all.log -s <subject>
    - could break on cortribbon stage, as the left hemisphere needs to be finished before the right to run properly
      - if it breaks wait for left hemisphere to be finished
      - change dir to subject/mri
      - mri_volmask -label_left_white 2 -label_left_ribbon 3 -label_right_white 41 -label_right_ribbon 42 -save_ribbon -save_distance <subject>
    - recon-all -autorecon3 -s <subject>

3 Improving inhomogeneity correction (and talairach registration) using FreeSurfer

- improves talairach registration significantly; should be used if tal-check fails or quality check is really low
- after normalization has finished (recon-all -motioncor -nuintensitycor -normalization -s <subject>)
- change dir to subject/mri
- mri_nu_correct.mni −−stop 0.0001 −−distance 25 −−i T1.mgz −−o nu.mgz
- delete all files in mri/transforms
- recon-all -talairach -tal-check -s <subject>
- mri_normalize -noconform -g 1 nu.mgz T1.mgz
- doing this once should be sufficient; if further improvements need to be done, one should do this after the skull stripping (see section 4)
- repeat if necessary
  - if used too often; might end up with bad skull stripping as skull might get the same intensity as white/gray matter

4 Further improvement of inhomogeneity correction using FreeSurfer

- once skull stripping has been made and especially temporal lobes and cerebellum are too bright compared to the other tissues
- change dir to subject/mri
- mri_nu_correct.mni −−stop 0.0001 −−distance 25 −−i brainmask.mgz −−o brainmask.new.mgz
- mri_normalize -noconform -g 1 brainmask.new.mgz brainmask.mgz
- repeat if necessary