

Resting State Html Data Checking

Subject ID _____

@SS_Warper Data Checking

Navigate to SS_Warper folder

Open QC_anatSS.\$subj.jpg to check skull strip

Open QC_anatQQ.\$subj.jpg to check spatial normalization

If you have any questions ask the study data manager

Who checked this data?

- ☐ RA_1
☐ RA_2
☐ Postdoc/PI
☐ Other

Is the skull strip ok?

- ☐ Good
☐ Missing brain
☐ Extra skull/dura
☐ Unsure

Is the alignment of the anatomical dataset and template ok?

- ☐ Good
☐ Unsure
☐ Bad

Do skull strip issues interfere with alignment of the anatomical data to the template?

- ☐ Yes
☐ No
☐ Unsure
☐ N/A

Troubleshooting:

1) If skull strip issues interfere with alignment, check 3dSkullStrip help file and options and rerun.

2) If skull strip issues do NOT interfere with alignment, proceed with caution paying close attention to alignment in the following QC steps.

3) If alignment is bad, check @SS_Warper help file and options and rerun. Consider adding -giant_move or other options

Notes about @SS_Warper:

(Include notes regarding whether the script needed to be rerun and what changes were made to the analysis script)

RS Data Checking

Navigate to \$subject_rs.results folder (ex. 101_rs.results)

Open QC_\$subj folder

Open (double click) index.html file.

Scroll through html file step by step!

If you have any questions ask data manager
email:

Who checked this data?

- ☐ RA_1
☐ RA_2
☐ Postdoc/PI
☐ Other

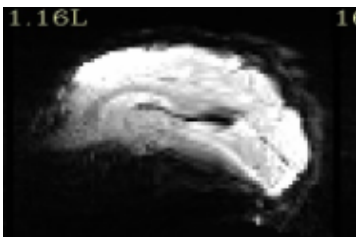
Step 1: Check original data

1) Check vols in original space

2) Check Anatomical in original space

3) Check initial overlap with and without obliquity

Example of warped image



How do the EPI images look?

- ☐ Ok, clear
☐ Images appear to have rows of darker/lighter voxels
☐ Images appear blurry
☐ Images appear stretched or warped
☐ Unsure

Notes about vols in original space:

How do the anat images look?

- ☐ Ok, clear
☐ Images appear to have rows of darker/lighter voxels
☐ Images appear blurry
☐ Images appear stretched or warped
☐ Unsure

Notes about anat in original space:

How do the underlay/overlay images look?

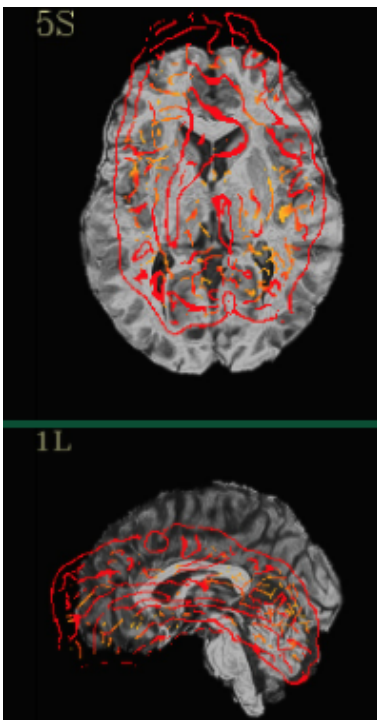
- ☐ Both with and without obliquity are aligned - Good
- ☐ Without obliquity are not aligned, with obliquity are - Okay (applied 40 degree angle)
- ☐ With obliquity are not aligned, without obliquity are - Not okay, this should not happen, something is wrong, check preprocessing script and output.
- ☐ Both with and without obliquity are not aligned - Bad, something failed in preprocessing, rerun.
- ☐ Unsure

Notes about underlay/overlay images:

Step 2: Check alignment EPI to anatomy

Check vol alignment (EPI to anat)

Example of bad alignment



How do the epi to anat images look?

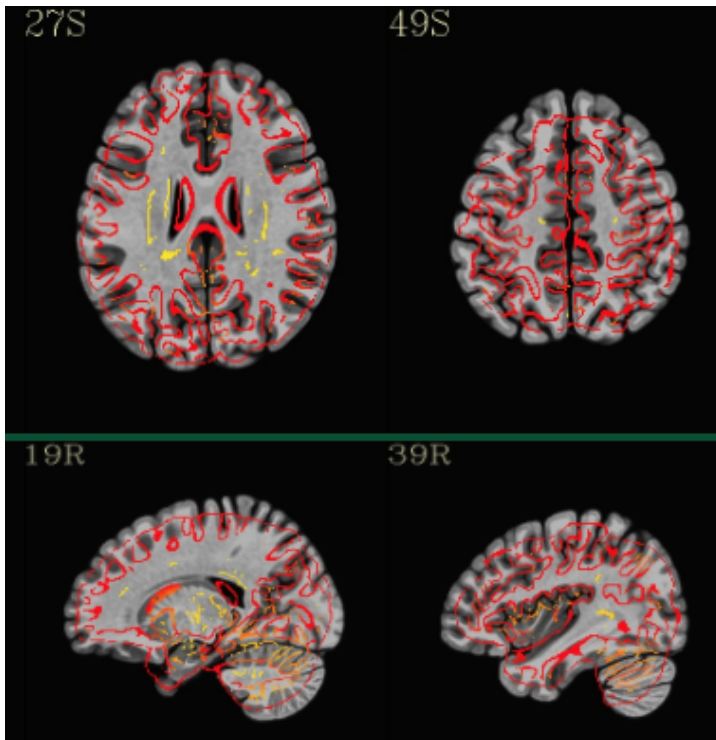
- ☐ Good (red line matches brain outline)
- ☐ Ok (red line somewhat matches brain outline)
- ☐ Bad (red line does not match brain outline)
- ☐ Unsure

Notes about alignment of EPI to anat

Step 3: Check alignment anatomy to mni template

Check vol alignment (anat to template)

Example of mismatched template = poor alignment



How do the anat to template images look?

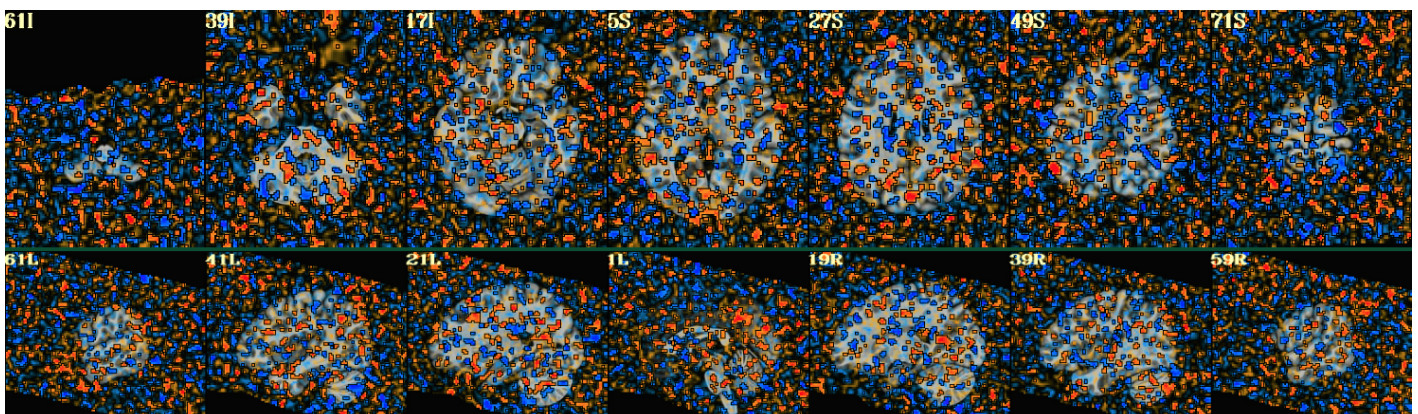
- ☐ Good (red line matches brain outline)
 - ☐ Ok (red line somewhat matches brain outline)
 - ☐ Bad (red line does not match brain outline)
 - ☐ Unsure
- (*Note these images should match exactly 98% of the time)

Notes about alignment of anat to template

Step 4:

Check statistics vols (and effect estimates)

Example of noise (activation) outside of brain



How do the images look? (lh-PCC)

- ☐ Good (activation only in the brain)
☐ Ok (activation mainly in the brain)
☐ Bad (lots of activation outside of the brain)
☐ Unsure

Notes about lh-PCC statistics

How do the images look? (rh-cort-vis)

- ☐ Good (activation only in the brain)
☐ Ok (activation mainly in the brain)
☐ Bad (lots of activation outside of the brain)
☐ Unsure

Notes about rh-cort-vis statistics

How do the images look? (rh-cort-aud)

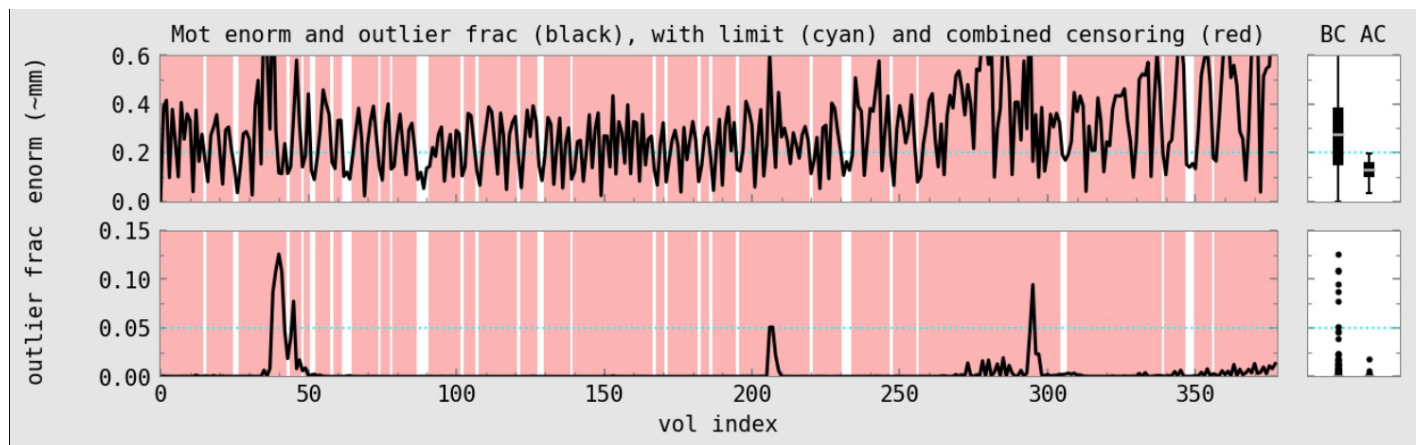
- ☐ Good (activation only in the brain)
☐ Ok (activation mainly in the brain)
☐ Bad (lots of activation outside of the brain)
☐ Unsure

Notes about rh-cort-aud statistics

Step 5:

Check motion and outliers

Example of highly censored data (motion and outliers)

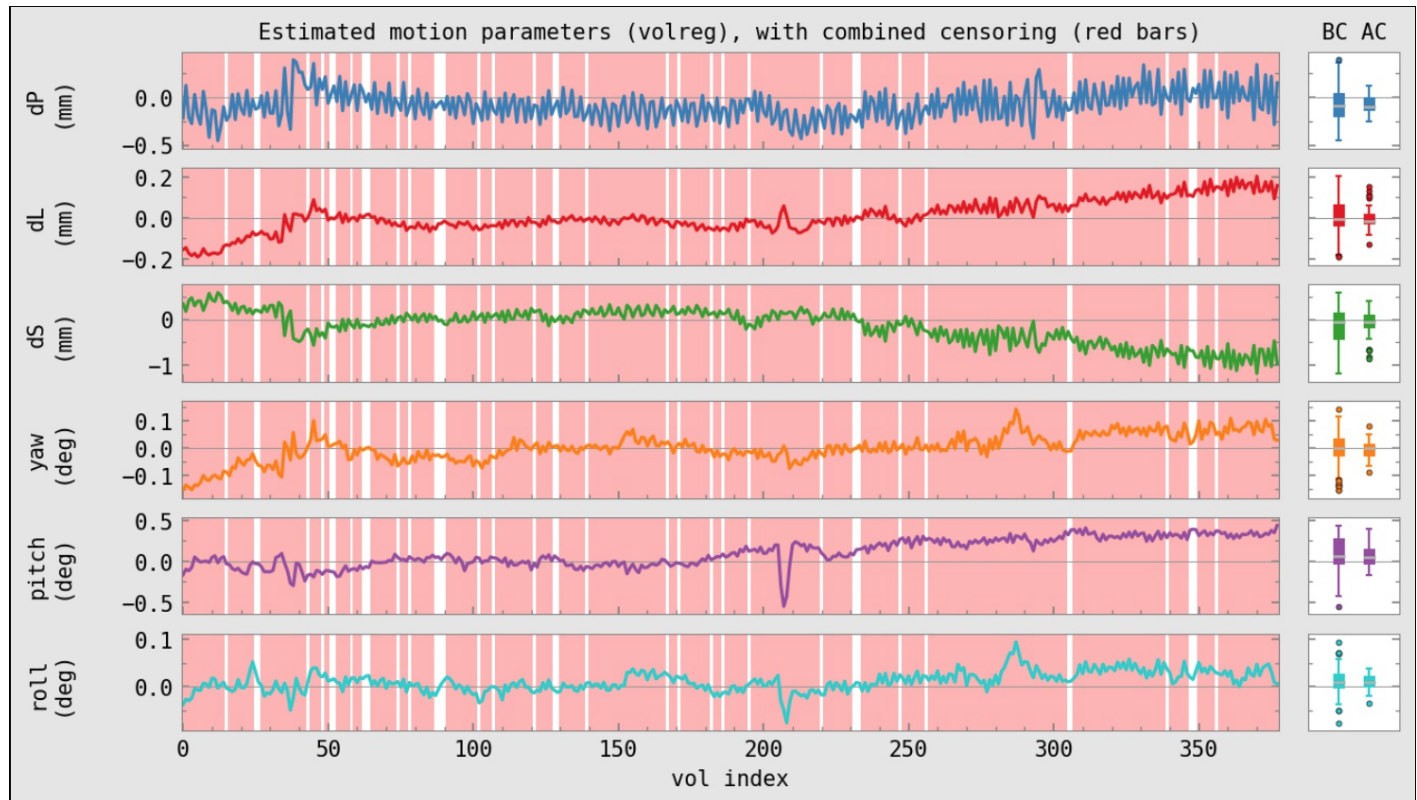


How does the motion enorm and outlier plot look?

- ☐ OK
☐ Some censoring but not too bad (e.g. a few red lines throughout)
☐ lots of time points censored for motion (e.g. lots of red lines top plot)
☐ lots of time points censored as outliers (e.g. lots of red lines bottom plot)
☐ overall plot shows lots of censoring (e.g. lots of red indicating censored data)
☐ Unsure

Notes about motion/outlier censoring

Example of highly censored data (estimated motion parameters)

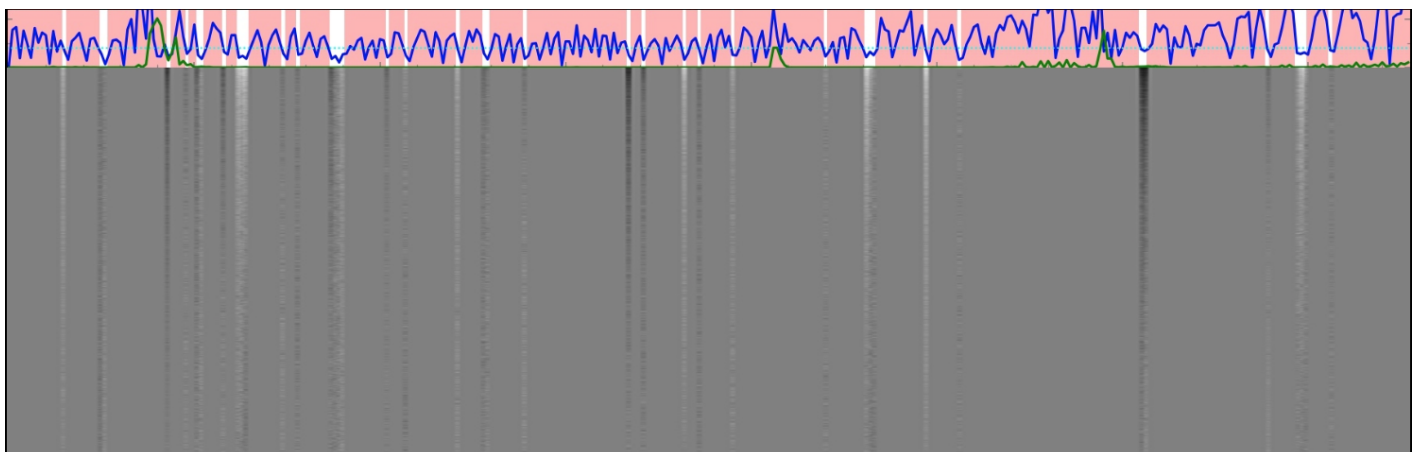


How does the 6 volume registration motion parameters plot look?

- ☐ OK
- ☐ Some censoring but not too bad (e.g. a few red lines throughout)
- ☐ more time points censored for motion than not (e.g. lots of red lines)
- ☐ overall plot is mostly censored (e.g. entire plot is red)
- ☐ Unsure

Notes about estimated motion parameters censoring

Example of highly censored data (Grayplot)



How does the Grayplot look?

- ☐ OK
☐ Some censoring but not too bad (e.g. a few red lines throughout top, very little missing data)
☐ more time points censored for motion than not (e.g. lots of red lines, lots of missing data)
☐ overall plot is mostly censored (e.g. entire plot is red, very little data left)
☐ Unsure

Notes about Grayplot

Step 6:

Check regressors, DFs and residuals

What is the final degrees of freedom (DF) percent?

Degrees of freedom notes

*If low percentage, copy and paste .html output

Do you see activation (large orange or blue blobs) in the brain?

- ☐ Yes - the whole brain is orange or blue!
☐ Yes - several activations throughout the brain
☐ Yes - a few activations throughout the brain
☐ No - no activation present
☐ Unsure
 (Check the corr of WB-average)

Whole brain activation notes

Step 7:

Check all warnings from processing

Check the severity of the regression matrix correlation warnings:

- ☐ None
☐ Mild
☐ Medium
☐ Severe

Matrix warning notes

(*copy and paste any warnings in the .html file)

Check the severity of the general censor fraction warnings:

- ☐ None
☐ Mild
☐ Medium
☐ Severe

General censor fraction warning notes

(*copy and paste any warnings in the .html file)

Check the severity of the pre-steady state warnings:

- ☐ None
☐ Mild
☐ Medium
☐ Severe

Pre-steady state warnings notes

(*copy and paste any warnings in the .html file)

Check the severity of the left-right flip check warnings:

- ☐ None
☐ Mild
☐ Medium
☐ Severe

Left-right flip check warning notes

(*copy and paste any warnings in the .html file)

Are the left and right hemispheres flipped?

- ☐ Yes
☐ No
 (Check the flip guess NO_FLIP = No or DO_FLIP = Yes)

Check flip Notes

Step 8:**Check summary quantities from @ss_review_basic**

Final Voxel Resolution = 2.5 x 2.5 x 2.5

- ☐ Yes
☐ No

Average Motion per TR

- ☐ < 0.3 mm
☐ 0.3 - 1 mm
☐ 1 - 3 mm
☐ > 3 mm

Max Motion Displacement

- ☐ < 3 mm
☐ 3-6 mm
☐ > 6 mm

Max Motion Value

Max Censored Displacement = Max Motion Displacement

- ☐ Yes
☐ No

Max Censor Displacement Value

(What is the max censor displacement?)

Num of Runs = 1

- ☐ Yes
☐ No

Censor Fraction

- ☐ < 5%
☐ 5-10%
☐ 10-15%
☐ 15-20%
☐ > 20%

Censor Fraction Value

Notes for @ss_review_basic

(List and describe any notes from the SS Review Basic)

Step 9:

HTML Review Summary

Overall, how do the data look?

Check all that apply

- ☐ Everything looks good
☐ Alignment is off between anat and epi
☐ Alignment is off between anat and template
☐ Little activation present
☐ Low degrees of freedom
☐ Medium or Severe warnings
☐ Left and right hemispheres are flipped
☐ Very high correlations in brain
☐ High max displacement
☐ High censor fraction
☐ Unsure

If there is a lot of motion, high censor percentage, or high max displacement, check the epi by doing the following:

1) Open Terminal

2) navigate to participant's data folder (e.g., \$subj.results)

3) tcsh @epi_review return

EPI Review Run 1

- ☐ Ok
☐ Image jumps between timepoints
☐ Image appears to have rows of darker/lighter voxels at some timepoints
☐ Unsure

EPI Review Notes:

If you see any major alignment issues, missing data, or any warping in the brain, check the brain data by reviewing the various outputs from the @ss_review_driver command

1) Open Terminal

2) navigate to participant's data folder (e.g., \$subj.results)

3) tcsh @ss_review_driver

You have already checked the basic review, so you can skip to the next step.

Follow the instructions within the review driver.

Do the motion plots look bad?

- ☐ OK
☐ a lot of drift throughout the scan
☐ large spikes throughout the scan
☐ Unsure

Do the plots look bad?

- ☐ OK
☐ lots of time points censored as outliers (e.g. lots of green lines in red plot)?
☐ lots of time points censored for motion (e.g. lots of green lines in black plot)?
☐ overall plot shows lots of censoring (e.g. lots of green lines on plot in second window)?
☐ Some censoring but not too bad?
☐ Unsure

Notes on censor plots

Alignment of anatomy to functional scans

- ☐ good
☐ ok
☐ bad
☐ unsure

Notes on Alignment

Regression warnings

- ☐ Smallest FDR warning
☐ Tent_warn.txt warning
☐ Correlation Matrix warning
☐ Other
☐ No warning

Notes on Regression Warnings: Cut and paste warnings from Terminal

Matrix plots look ok?

This will look weird. You are looking at the physiological data.

- ☐ Yes
☐ No
☐ Unsure

Notes on Matrix Plots

Review Normalized Brain

- ☐ Ok
☐ Lots of non-brain left after skull strip?
☐ Lots of cortex cut off with skull strip?
☐ Brain appears warped or stretched?
☐ Unsure

Notes on Normalized Brain

Recommendation

Include in group analysis?

- ☐ Yes
☐ No
☐ Unsure

Notes on decision to include/exclude in group analysis

Final Review

Final Reviewer

- ☐ RA_1
☐ RA_2
☐ PostDoc/PI
☐ Other

Other Reviewer

(Name)

Final Decision: Include in group analysis?

- ☐ Yes
☐ No

Final Review Notes

(Include reason for excluding or including participant)