**CSN T1 and fMRI Connectivity processing QC sheet**

Subject ID:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_ Processed by:\_\_\_\_\_\_\_\_\_ Pipeline Version Number:\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

*NOTE: Working your way down the QC sheet, place check marks and fill in parameters next to completed steps.*

Create a symbolic links to the dicom series on global\_data within the subject T1 and REST directories. For unwarping of fMRI data create link to field map dicom directories, within unwarp directory.

Example: ln –s /path/to/global\_data/data/mprage DICOMS #

Dicom directory link path: /portal01/global\_data/clinical/YODER\_KARMEN/­­­­: \_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

**T1\_prepare\_A Date ran:**

T1 link path: portal01/kkyoder/CONN\_MR/­­­­­­­­­­­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_­­­­­­­­­­­­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

Check the following for quality overlaid on *T1\_fov\_denoised.nii*

\_\_\_\_\_\_ *T1\_brain\_mask\_filled.nii.gz*

If the mask is bad (e.g. does not cover the whole brain) change the bet parameters and run the bet flag again. Alternatively, the mask can be manually edited in MRIcron.

Final BET parameters used: Bet –f \_\_\_\_\_\_\_\_\_ Bet –g \_\_\_\_\_\_\_\_\_

Was the mask manually edited? YES NO

\_\_\_\_\_\_If YES, re-run the T1.brain flag only of T1\_prepare\_A to re-extract brain with the new mask before proceeding to T1\_prepare\_B.

**T1\_prepare\_B Date ran:**

From batch script global flags: flags.shen\_org = \_\_\_\_\_\_ ( 1 or 0; Indicated the parcellation used)

Open the following image: [connectivity pipeline path]/templates/MNIparcs/*MNI152T1\_1mm.nii.gz*

Overlay the following image on top to ensure proper transformation into MNI space.

\_\_\_\_\_\_\_ [subject T1 directory]/registration/*T1\_warped.nii.gz*

Check the following for quality overlaid on *T1\_fov\_denoised.nii*

\_\_\_\_ *T1\_GM\_parc\_shen.nii.gz*

\_\_\_\_ *T1\_GM\_parc\_yeo7.nii.gz*

\_\_\_\_ *T1\_GM\_parc\_yeo17.nii.gz*

**fMRI\_A Date ran: BASELINE SALINE ETHANOL**

fMRI link path: portal01/kkyoder/CONN\_MR/­­­­­­­­­­­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_­­­­­­­­­­­­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

In the fMRI directory for the subject, open the following: *2\_epi\_meanvol.nii.gz*

Overlay the following images on top to check for quality.

\_\_\_\_\_ *rT1\_brain\_dof6.nii.gz \_\_\_\_\_ rT1\_GM\_parc\_shen\_clean.nii.gz*

\_\_\_\_\_ *rT1\_brain\_mask\_FC.nii.gz \_\_\_\_\_ rT1\_GM\_parc\_yeo7\_clean.nii.gz*

*\_\_\_\_\_ rT1\_GM\_parc\_yeo17\_clean.nii.gz*

In the GS\_reg\_(select one: YES NO) open the *motion\_parameters\_all.png*

*NOTE: This figure should provide motion estimates for the subject and give a sense in the subject will be dropped due to excessive scrubbing.*

Fill in the motion parameter cut-offs used from the batch file.

FD:\_\_\_\_\_ DVARS:\_\_\_\_\_ SD:\_\_\_\_\_

**fMRI\_B Date ran: BASELINE SALINE ETHANOL**

In the subject fMRI directory within the global signal (GS) directrory:

YES NO Was the figures directory created and did it contain fig1 – fig8.

If no, check the motion plots in the GS directory to see if subject was dropped due to excessive motion scrubbing.

\_\_\_\_\_ Check over the figures to ensure the network matrices look reasonable.

**fMRI\_A Date ran: BASELINE SALINE ETHANOL**

fMRI link path: portal01/kkyoder/CONN\_MR/­­­­­­­­­­­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_­­­­­­­­­­­­­­\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_\_

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\_\_\_\_\_ *rT1\_brain\_mask\_FC.nii.gz \_\_\_\_\_ rT1\_GM\_parc\_yeo7\_clean.nii.gz*

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