

1. CES CONN Instructions
 - a. Running CONN script
 - i. Log into lens workstation using a unique NIC ID and password.
 - ii. Navigate to the study specific code directory using the “cd” command.
 - iii. Run CONN script: “./run_CONN21a.sh” enter
 - iv. The CONN Toolbox graphical user interface (GUI) will open
 - b. Importing Project: *This section will be a one-time process*
 - i. Click “New(import)” > fMRIPrep dataset
 - ii. Navigate to fMRIPrep directory in right-hand window > click Import
 1. Note: Bottom of the screen: change “copy to DERIVATIVES folder and import” to “import selected files”
 - iii. Click Import
 - c. Opening Project:
 - i. Project Tab in top left > Open/Open Recent > Click the path to project <nameofproject>.mat
 - d. SETUP Page:
 - i. Check to make sure the correct number of subjects listed in the “Basic” tab
 - ii. Under “Number of sessions or runs”: verify number of sessions is correct.
 1. Note: I recommend saving frequently.
 - e. Structural Scans:
 - i. Quality Check (QC) to ensure structural images look normal (i.e., brain is not cut off or any unusual artifacts are on the brain)
 - ii. QC each session
 - f. Functional Scans:
 - i. QC functional images as you did above
 1. Note with this dataset, some subjects do not have mid or post scans. Recommend keeping a subject list regarding which CES subject corresponds to CONN subject nomenclature and number of sessions per subject.
 - g. ROI:
 - i. Segmented GM, WM and CSF have already been generated from fMRIPrep
 - h. Conditions
 - i. Conditions may have already been generated, need to verify
 - ii. Click on the conditions tab
 - iii. In the blue Conditions window ensure that bl, mid and post conditions are present
 - iv. If not, at the bottom of the blue “Conditions” bar click “new” and name these Conditions “mid” and “post”
 - v. With Conditions bl and Session 1 highlighted use the “Condition definition” menu to specify that the “condition spans entire session”

- vi. With Conditions bl and Session 2 highlighted use the “Condition definition” menu to specify that the “condition is not present in selected session(s)”
 - vii. With Conditions bl and Session 3 highlighted use the “Condition definition” menu to specify that the “condition is not present in selected session(s)”
 - viii. With Conditions mid and Session 1 highlighted use the “Condition definition” menu to specify that the “condition is not present in selected session(s)”
 - ix. With Conditions mid and Session 2 highlighted use the “Condition definition” menu to specify that the “condition spans entire session”
 - x. With Conditions mid and Session 3 highlighted use the “Condition definition” menu to specify that the “condition is not present in selected session(s)”
 - xi. With Conditions mid and Session 1 highlighted use the “Condition definition” menu to specify that the “condition is not present in selected session(s)”
 - xii. With Conditions mid and Session 2 highlighted use the “Condition definition” menu to specify that the “condition is not present in selected session(s)”
 - xiii. With Conditions post and Session 3 highlighted use the “Condition definition” menu to specify that the “condition spans entire session”
 - xiv. Once complete, look at the rectangular graph under “Study design: with bl and Session 1 highlighted the upper left bar should be red. With mid and Session 2 highlighted the second middle bar should be red. With post and Session 3 highlighted the bottom right bar should be red.
- i. First-level Covariates
 - i. 1st-level covariates have been generated
 - j. Second-level Covariates
 - i. Bottom of the blue panel > click new
 - ii. Create 2 new covariates: True and Sham
 - iii. For the True covariate, change the values to a 1 if the subject is in that condition and a 0 if they are not (ex. [1 1 0 1 0 0 0...])
 - iv. Do the opposite for the Sham covariate (ex. [0 0 1 0 1 1 1...])
 - k. Options
 - i. Unclick Voxel-to-Voxel and Dynamic Circuits for enabled analyses
 - ii. Under Optional output files > click Create confound-corrected time-series, first level seed-to-voxel r-maps and first-level seed-to-voxel p-maps
 - iii. Then at the bottom left of the screen click “Preprocessing”. Find the “functional smoothing (spatial convolution with Gaussian kernel). Then click Start. A pop-up will ask for kernel size, just click ok.

- iv. The preprocessing step should begin. And this will take a while (hours). After that has been completed, check the functional images, they should look smoothed (i.e. blurred).
 - v. Next click “Done” at the bottom of the screen. This will also take some time.
- l. Denoising
 - i. After preprocessing has been completed, you will be taken to the Denoising tab
 - ii. On the left you should see covariates CONN wants to include in the denoising phase.
 - iii. If the “effect of pre”, “effect of mid” and “effect of post” are under the Confounds list, highlight them then click the right arrow button in the middle to remove them from the confounds list
 - iv. Right hand side, go through each subject and ensure that the brain heat map completely covers the brain underlay
 - v. Click “DONE” at the bottom left of the screen. This will take a while
- m. Analysis (1st-Level)
 - i. After Denoising, you will be taken to the Analysis page. This is for individual subject results. Click Done to proceed to the group-level analysis results
- n. Results (2nd-level)
 - i. The Results page displays Seed-to-Voxel (SBC) between-subjects functional connectivity analysis for every subject effect
 - ii. To run SBC analysis: Cntrl+click True and Sham under Subject effects
 - iii. To setup contrasts: under “Between-subjects contrast” set True to 1 and Sham to -1, alternatively click the “Effect of” drop-down menu and click “Difference True > Sham”
 - iv. To ensure that the contrasts are correct, the between-subjects model specifications should be: $y \sim True + Sham (1 -1)$
 - v. Under Conditions: Cntrl+click post and bl
 - vi. Conditions contrasts: 1 for post, -1 for bl
 - vii. Once you have selected the subject-effects/conditions you want to analyze, click which seeds/sources you want to analyze (these will be based on research aims)
 - viii. Once Subjects effects, Conditions, and Seeds/Sources have been selected click “compute results”
 - ix. This will begin the analysis and pull up a results GUI
- o. In results explorer GUI:
 - i. Click the top drop-down menu and click “customize advanced family-wise error control settings”. You will then be able to set statistical measures: voxel threshold and cluster threshold.
 - ii. For voxel-threshold: $p < .005$ p-uncorrected
 - iii. Cluster threshold: change .05 to 100 and the drop-down change to cluster size

- iv. On the righthand side of the GUI are multiple image viewers for the connectivity results that can be exported as images