

Single Subject Demo Data Instructions

http://mindhive.mit.edu/filedrop/gablab/conn_demo/conn_demo.tar.gz

- 1) Click "New" and answer "No" to the "spatially preprocess" question.
- 2) In "Basic" enter "1" subject, "6" seconds TR, and "1" session
- 3) In "Functional" go to the functional folder and select all of the files in there (you should see two axial images, and read "62 files" in the left plots)
- 4) In "Structural" go to the structural folder and select the "ws*.img"
- 5) In "Rois" go to the structural folder, then first select the "Grey matter" ROI in the ROIs list (at the left) and select the "mwc1*.img" file in the files list (at the right), then select the "White matter" and the "mwc2*.img" file, and then select the "CSF" and the "mwc3*.img" file. The rest of the ROIs are already defined by default (to point to the conn/rois folder) so you can leave those unchanged.
- 6) In "Conditions", enter "rest" as condition name, then enter "0" as onset, and "inf" as duration
- 7) In "covariates->first-level" enter "motion" as covariate name, and then select the "rp_*.txt" file in the realign folder
- 8) Press "done" (and enter a new name for the project if you have not already done so), this will take a couple of minutes or so to complete...
- 9) In the "Preprocessing" tab, enter the "band-pass" filter "0.008 0.09", and change the "White matter" and "CSF" confounds to "3" dimensions (it still has the old default of "5"), then press "Done" (this should take only a few seconds to process).
- 10) In the "Analyses" tab, remove the entire BA* rois in the "sources" list (this is just to speed up the computations), to perform the analyses using our Fox sources as seeds. Then press "Done" (this should take again only a few seconds to process).
- 11) In the "results" tab, you can select the different fox "sources" to display the connectivity results for this subject (you can also use the "ROI view" button, but not the "Whole brain" button which is only in 2nd level stats).