1. First run the ‘AddPaths.m’ file.

Example experiment folder:

On a current path directory, the pipeline looks for the input of an experiment name which corresponds to a folder name. Within a experiment folder, there will be dataset folders. The dataset folders is where the data should be. The intuition behind this is that an experiment could have change in experimental conditions providing multiple datasets.

So, once the fNIRS files are preprocessed by Homer3, a ‘homerOutput’ folder should be created. Place the ‘homerOutput’ folder in a newly created experimental folder.

Than run the function where the current directory shows the experimental folder:

* Homer2AnalysisPipeline({‘Experiment Name’})

Note: Multiple experimental folders can be done in one go, just increase the cell array by 1 x n.

After this has run, entering the experimental folder will show multiple datasets depending on the number of experimental conditions.

From this, a ‘TEscript.m’ will need to be copied from pipeline/templates and then pasted in each dataset folder. The parameters for each script must be finetuned to each dataset.

After this has been done, all that is need to be executed is (with the experiment folder being in the current directory):

* TEGCAnalysisPipeline({‘ExperimentName’})

This process can be done individually if the results are not wanted by Granger Causality etc. Just view the ‘TEGCAnalysisPipeline.m’ file and call the commands one by one.