**Analysis scripts written by Jun Yin, Ningbo University, China**

Start by opening the script called ‘run\_temp\_pair’. This script will call ‘fNIRS\_Stat' which will show the statistics in figures.

Edit the input to fNIRS\_Stat to reflect the GroupResults file you want Matlab to use, as well as the time window length, and channels you want to use for the analyses.

Channels.txt file: this file tells the scripts the channel numbers of each source-detector pair. You need to edit this depending on your SD configuration.

Then edit ‘fNIRS\_Stat’ from lines 39-41 to reflect your study’s variables. The scripts can only compare two conditions, so if you have more than two conditions, you need to specify which one you want to compare. Note that the condition numbers are the same as in Homer.

Use fNIRS\_Stat if you use data processed using Homer2\_2\_1. If you end up using or these scripts for data pre-processed with newer versions of Homer you will need to use fNIRS\_Stat\_new.

Running run\_temp\_pair will give you three plots, one for oxyhemoglobin, one for deoxyhemoglobin, and one for the total hemoglobin. On the left y-axis you see the concentrations and on the right y-axis the p-values. The solid lines plot the chromophore concentrations and the dotted lines the p-values for these levels. So whenever the dotted line is lower than the *p* =.05 line the activation in that condition, or the difference in activation between the two conditions is significantly different from zero.

If you run the SaveScript after the fNIRS\_Stat script it will save the t- and p-values for the specified time bins.

If you run the SaveScriptAmp after the fNIRS\_Stat scripts it will save the amplitudes for all the time bins. This output would allow you to perform your own repeated measures analyses on the data instead of relying on the t-tests that are outputted by the script.

'export2Txt' exports the data into text files according to the channels and time range you selected. This output file is especially handy if you want to create your own plots of the data. You have to edit lines 4-8 in this script to reflect your study variables. You edit line 40 to specify whether you want to export HbO or Hbb values.

Further notes from Jun:   
(1) conditionROI = [1 2]; in line 40 of 'fNIRS\_Stat' are conditions which  
you are planning to analyze. They map to the indexes of conditions in Homer.  
  
(2) the first parameter of inputFileName in 'fNIRS\_Stat' is the output from  
Homer after computing the mean for all participants.  
  
(3) fileName = 'groupResultsAVG.mat'; in line 4 of 'export2Txt' is the file  
generated by calling ' fNIRS\_Stat '.