**Instructions for going from group analysis to extraction of data from individual image files**

After group analysis, it can be useful to extract individual time series from the significant clusters to show a block average time series that NIRS folks are used to. Here’s how to do this.

1. Start with the clust\_order\*.nii file for the effect you want to examine

* e.g., clust\_order\_6Hb\_l1\_01.nii
* copy these ‘clust’ files to a new folder that will store the output of the current analysis

1. Create a new .prn file, adding a new column to the original .prn file that specifies the full path of the output folder (the new folder you created in step 1)
2. Run registerCommonDriver\_Invert.sh (or registerCommonDriver\_Invert\_wFixOrientation.sh if you are working with a data set that has issues with the orientation…Sara’s data has this; I think Courtney’s data as well).

* This resamples the headvol for each subject to 2mm resolution
* Then it creates a subject-specific clust file by inverting the original affine transformation applied to the data to get to group space. So the end result is a mask with the clusters in each ‘clust’ file moved to subject-specific space.
* If you are using the ‘fixOrientation’ version, a second set of ‘prefix’ files will be generated. These are temp files (that can ultimately be deleted).
* Example:

bash registerCommonDriver\_Invert.sh Y1\_finalComboSubjListGroup.prn

1. run ExtractHbFromMask.m

* To be used for extracting a weighted average time series for each subject for each effect from each cluster for each regressor for each chromophore
* Input example in matlab

ExtractHbFromMask('Combo\_finalSubjListGroup.prn',[1,2,3],'Test',10,10,3,0,0)

* Input file name (.prn file)
* Regressor List – the conditions from the original GLM that you want to extract block averages for
* A name for the analysis (for the output file). The name is also a column in the .csv file which can be useful for tagging ‘Y1’ vs. ‘Y2’ (e.g., if you ultimately want to combine across years)
* newSamplingFreq: the sampling frequency of the image recon files
* HRFDuration: the duration of the HRF window (in seconds)
* MaxMaskValue = the max mask cluster value across all clust\_order files to analyse
* checkAlignment – flag to display the headvol, the cluster mask, and the ‘GoodVox’ as overlays. Useful for checking a handful of subjects initially, but set to 0 for full runs
* showHRF – flag to plot the resultant time series data for each subject. Again, most useful for initial explorations, but set to 0 for full runs.