**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 something like a block average time series that NIRS folks are used to. Here’s an emerging pipeline to do this.

1. Start with the .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 explorations

1. Create a new .prn file, adding a new column to the original .prn file that specifies the output folder (the new folder you created in step 1)
2. Run registerCommonDriver\_Invert.sh (or registerCommonDriver\_Invert\_wUnfix.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 ‘unfix’ version, a second set of ‘unfix’ files will be generated. These should be used for subsequent steps.

1. [in development] run ExtractHbFromMask.m

* To be used for extracting the time series data from each cluster
* At present, run line-by-line
* MaxMaskValue = the max mask value in the original clust file
* Line 74 will read in the image recon file for the specified run
* Lines 77 and 82 need to be updated to match your clust file and headvol file
* Commented code in 86-89 can be used to check alignment of data
* Lines 104-115 show an example of plotting the time series data for the mean over the cluster, adding in particular stim marks from the design matrix
* Lines 143-157 show an example of calculating the block average for particular stims