Extracting data from your group analyses:

The purpose of this lab is to help you visualize your data for both your own sanity check (i.e. are there any problems with your data?) and for publication purposes. Unlike the last lab, you are not planning to run stats on these results, but rather display the data that has already been analyzed. Based on the last lab, you should know a lot of what you will need.

We will continue with the motor task from the fsl tutorial.
http://www.fmrib.ox.ac.uk/fslcourse/lectures/practicals/feat2/index.htm

We have completed the first-level and group analysis for you. It will be up to you to:

> **open up results of single subject analyses and scroll through your data to be sure there is nothing amiss.*
>
> *${DATA_DIR}/*`fmri/ptt/<SID>/<SID>_left.feat`
> *${DATA_DIR}/*`fmri/ptt/<SID>/<SID>_right.feat`
>
> ** open up results of group analysis (6 subjects, 2 conditions)*
> *${DATA_DIR}/*`fmri/ptt/ptt_ols.gfeat`
> **Create a small ROI of most active voxels within interesting regions (anything*
you would want to discuss)
> **Convert results to % signal change*
> **Extract data*
> **Plot data*

Before You Begin

Set Paths: Use yesterday's lab handout to set the paths for
DATA_DIR (path to fsl_course_data)
OUT_DIR (path to your outputs folder)
LAB_DIR (path to this lab's files, like ROI and pdfs. Probably outputs is inside here)

Move The Following Folder:
mv /Users/Shared/ptt_ols.gfeat $DATA_DIR/fmri/ptt/ptt_ols.gfeat

Data Quality

*It is critical that you **LOOK AT YOUR DATA.** Most of the plots you will need for publication are there to help others look at your major findings, since otherwise pretty statistical maps are difficult to believe (for example, results could be driven by an outlier or artifact). In addition to showing convincing plots, it is good practice to look at your data. It seems obvious, but many people don't really know where to begin.*

How do you look at your data? There are a lot of different tools for finding artifacts out there, and these will be covered too. BUT there is no substitute for simply opening files, scrolling through them, and making sure nothing looks fishy.

Things I have found using nothing fancier than visual inspection include:

1) Missing data: If you are missing data from any subject, that part of the brain will not be included in your group analysis, as it requires data from all subjects
   examples:
   a) Large of the occipital lobe is out of the field of view (cut off)
   b) Severe susceptibility artifact in the orbito-frontal cortex, a critical region in the study I was working on.
2) Extremely noisy data (the head coil was not totally closed while data was collected, so the images had black and white snow throughout
3) RF leak from devices like goggles and headphones.
4) Wrap-around artifact

Inspect results of first level analyses (6 subjects, 2 conditions)

1) Divide the inspection amongst the members of your group. Consult each other if you spot anything wrong with the data to determine whether the data are still useable
2) Create a list of scans (<SID>_<direction>) and take notes on below. Also make sure you have a column to simply track whether data will be dropped from the analysis.
3) Open feat reports (you can access both the group and single subject analysis reports from: $DATA_DIR/fmri/ptt/ptt_ols.gfeat/report.html

*Check registrations. If any look bad, double check the structural used. If there are a lot of distortions in the fmri data, do they seem to cause errors in regions we care about like motor cortex?
*Check input masks/ missing mask voxels
*Go to Inputs -> check each single-subject scan
   *motion more than ½ a voxel (1.5 mm)?
   *look at results of single-subject analyses. Do the results look reasonable? Or are they all localized in the edges of brain/ventricles (sign of excessive motion artifact)? Or do they look too non-specific (whole brain is red?)

4) Open all single-session filtered_func_data input files in fslview

*scroll through first time point in x y, z.
* Find a good point and scroll through in time. Does anything look really suspicious? EG – missing data/volumes/motion errors still visible after registration?

Once you are confident that all of the data included in the analysis has been looked at, and is ok to use…

Plot results
There are 5 contrasts in this analysis (C1: index, C2: sequential, C3: random, C4:random-sequential, C5: Sequential-Index).
For the purpose of this exercise, we will plot C2 (sequential)

$DATA_DIR/fmri/ptt/ptt_ols.gfeat/cope2.feat

Inside you will find
Thresh_zstat1 (left – right)
Thresh_zstat2 (right – left)

1) Create a 3x3x3 box in the center of any major clusters (anything you would discuss in a manuscript).
   Here, you will want one region for the left M1 and one for the right M1 if there are significant voxels in both regions for both contrasts. You are welcome to add any regions (SMA?) to the analysis
   > Open results in fslview:
   ➢ Open standard
   ➢ Add thresh_zstat1 (left > right)
   ➢ Find peak voxel
   ➢ File > Create mask
   ➢ Click Pencil
   ➢ Change pencil size to 3 (far right box)
   ➢ Click on the peak voxel
   ➢ Move one slice and click peak in slice
   ➢ Move one back (from peak) and click peak in slice
   ➢ File > Save As > $OUT_DIR/<region>_<contrast>

2) Run featquery to calculate %signal change inside this ROI in each subject
   a. Change Number of feat directories to …
   b. Load all 12 feat directories
   c. Change "Stats images of interest" to only the contrast(s) of interest
   d. Load on of your masks (3x3x3 boxes)
   e. Click convert PE/COPE value to %
   f. Unclick everything else
   g. Change the output directory name to your mask name
   h. Go
   i. Repeat for the rest of your masks
      i. NOTE if you look at the terminal when you run this, you will see the entire featquery command. You can run this as a for loop for subsequent masks. This is totally elective.
   j. Create a workbook or data file in matlab and plot your results.

NOTE – Featquery works well for a boxcar design like this. IF you have an event-related design, please refer to the following to extract data

http://mumford.fmripower.org/
Guide for Calculating Percent Change with Featquery: This guide describes how featquery calculates percent change and how for certain types of studies a different procedure is necessary to calculate interpretable percent changes.

How To Calculate % Signal Change Manually Using Jeanette Mumford's guide

Featquery uses the min/max value of the EVs in your design to scale results. Unfortunately, in most rapid event-related designs, the min/max range is often different from scan to scan, making the values you get for each subject difficult to combine into any analysis, or compare with other studies.

Please download and read Jeanette's description of this (above) as it is terrific, and she is a much better statistician than I am (because she is an actual biostatistician)

We are going to walk through this How To (pg 4-5) and convert the data we worked with yesterday to % signal change manually so that you know how to do it for future studies.

As A Class:
-I will walk through the steps you would need to take to calculate % signal change in her example (1 second stimulus, double-gamma HRF, and a contrast of [1 1 -1 -1]

Directions:
-Follow Jeanette's guide to calculate % signal change for cope1, cope2, and cope3 in the left and right M1 using yesterday's ROI
DATA:
$DATA_DIR/fmri/ptt/ac/ac_left.feat

-You should load the design.fsf file into feat
-The EVs used for this analysis are located in
$DATA_DIR/fmri/ptt/ac/ac_left.feat/custom_timing_files
and tell you start time, duration, and height (0 means it is off)

Likely the results will be similar to those you got with featquery today, but if you have anything besides a long block design, you should probably avoid featquery.

Calculating the HRF using FIR modeling

A few of you asked that we do this assignment today as a class. Unfortunealty, I do not currently have any data online that is appropriate for this type of analysis. It is also fairly time-consuming and not realistic in a 2-hour session with the rest of the assignments I had planned.

HOWEVER, if you are doing a project that would benefit from this, we can sit down and I can walk you through how to do it on your data. Please email/see me if you would like to schedule time (jbramen@gmail.com)