FEAT pre-processing exercise

1. cd to fsl_course_data/fmri/ptt
   a. This directory contains sub folders for a number of participants who have performed a finger tapping experiment, with both left and right hand. With each hand, they performed
      i. index finger tapping
      ii. sequential tapping of multiple digits
      iii. random tapping
   b. The first level analysis has already been run for each of these participants, but you are going to repeat it in order to see the effects of manipulating the different pre-processing steps. You can see the .feat directories for the existing analyses in the file browser or using the terminal.
2. cd into one of the participant subfolders and then launch FEAT
3. In FEAT, load the unprocessed functional data for either the left or right hand version of the experiment. (No need to re-process both)
4. To set up a minimal analysis of the data, with no pre-processing and a very simple design matrix:
   a. Stats tab: full model set up, then create 3 original EV's.
      i. The first EV is set to Custom (3 column format). You need to choose a text file with the onset times and durations for this EV in it. To locate this file you can open the pre-existing feat directory for that participant, with the hand you have chosen. Then open the sub-directory called custom_timing_files. Choose ev1.txt
      ii. Repeat the above for the second and 3rd EV's, selecting the files ev1 and ev2.txt respectively.
   b. Name the three EV's index finger, sequential, and random
   c. For each EV de-select the temporal derivative option, set convolution to Gamma, and deselect apply temporal filtering
5. On the Contrasts & F tests tab specify 5 t contrasts
   a. index (just on its own versus the baseline)
   b. sequential (just on its own versus the baseline)
   c. random (just on its own versus the baseline)
   d. sequential - index
   e. random - sequential
6. On the registration tab, select the main structural image, which is in the same directory as the functional time series, and change the registration method from BBR to 12DOF (we don't have field maps and other info needed for BBR).
7. Now you are going to turn off all the features that are designed to improve your chances of finding activation, and then run the analysis to see if you can still find any activation. Once you have done this you can try again, and again, adding more pre-processing options.
   a. Preprossing tab make sure the following are "off":
      i. motion correction

    ii.   BO unwarping (always leave this off today)

    iii.   Slice timing correction (always off today)

    iv.   BET

    v.   Set smoothing to 0

    vi.   Intensity normalization (best to leave this off today)

    vii.   Highpass

    viii.   Perfusion subtraction (leave this one off all day)

    ix.   MELODIC (always off today, unless you are very adventurous)

  b. Stats tab, turn off:

    i.   FILM

    ii.   Full model setup (you should already have set this up, but here is a list of the minimalist settings)

        1. convolution is gamma

        2. no temporal derivatives

        3. apply temporal filtering (to model) is off

8. Run the analysis. Did any of the 5 contrasts locate activation? Compare with your neighbour who may have selected a different participant. You can also compare your results with the ones in the .feat directory that was "done earlier" and had standard preprocessing by opening the report.html file for that analysis using the web browser. Note: if you are using your computer as a terminal to run FSL on MET cluster – with a program like MOBAXTERM – then to launch a web browser that will be able to access the .feat directories on MET cluster you can type `firefox &` at the command prompt.

  a. (Another good method of comparison is to load the filtered_func.nii.gz file from the original analysis in fslview, then overlay the filtered func from the new analysis that has reduced preprocessing. You can now use the timecourse view in fslview to look at voxel time series in the two 4D files that are at the same X,Y,Z coordinates. How different are they?)

9. Go back to FEAT and turn on one of the options that was turned off. Run the analysis again. Did it make a difference? (Each time you run the analysis again it will create a new folder with the same name as the last one but with + appended)

10. If you have time, then you could try another analysis where you turn off all of the preprocessing except MELODIC. This will perform an independent component analysis (ICA) on the data, and many of the resulting components will correspond to artefacts in the data, while some might correspond to activation. This is a good way to familiarise yourself with what motion artefacts look like in fMRI data.