Playing with data from lab

Getting data off the scanner

From the **Patient Browser**, select the folder for the study you want (or within that study, the set of images you want), and then from the **Transfer** menu, select **Send to *neudrei***. From *neudrei* (the PC in the console room, which controls the Matrix switcher, among other things), you can burn a CD/DVD, copy the data to a zip drive, or use WinSCP to transfer the data to /labs/olmanlab/PSY5065 on BLiSS (bliss.socsci.umn.edu).

Converting from DICOM to Nifti

The data come off the scanner in DICOM format, which can be read directly into many programs (e.g. Brain Voyager). For FSL and SPM, however, the data need to be converted to Nifti format.

MRIcro is an application for the Windows platform that can do this. On BLiSS, the program dinifti is installed – this is a simple commandline tool for doing the conversion. The syntax is `dinifti [-options] DICOMDIR outFile`

For example, here is a series of commands that convert the data from the first experiment on Dec. 7:

```
% dinifti –f ‘n2’ MR-SE002-t1_mpr_ns_sag_p2_iso_prescan/
t1anat
% dinifti –f ‘n2’ MR-SE003-ep2d_bold_moco/ testEPI
% dinifti –f ‘n2’ MR-SE005-ep2d_bold_moco/ run1
% dinifti –f ‘n2’ MR-SE006-gre_field_mapping/ mag
% dinifti –f ‘n2’ MR-SE007-gre_field_mapping/ ph
% dinifti –f ‘n2’ MR-SE008-ep2d-diff-mddw-12/ dwi
```

And a screenshot of the directory contents after conversion:

```
caolman@ignorance:/labs/olmanlab/PSY5065/20071207-ST001-Olman_Subject 50% ls
dwi.hdr                              MR-SE005-ep2d_bold_moco                    run1.img
dwi.img                              MR-SE006-gre_field_mapping                 SR-SE099-PhoenixZIPReport
mag.hdr                              MR-SE007-gre_field_mapping                 t1anat.hdr
mag.img                              MR-SE008-ep2d-diff-mddw-12                 t1anat.img
MR-SE001-localizer                   MR-SE101-_MPR_Range_Native_(MR)_Anatomy[1]_ testEPI.hdr
MR-SE002-t1_mpr_ns_sag_p2_iso_prescan ph.hdr                                    testEPI.img
MR-SE003-ep2d_bold_moco              ph.img
MR-SE004-ep2d_bold_moco              run1.hdr
caolman@ignorance:/labs/olmanlab/PSY5065/20071207-ST001-Olman_Subject 51%
```

It’s normal to get warnings about only one timepoint when doing anatomical data; I consider that a bug, but the authors probably set it up as a feature.

Looking at anatomical data

For many of our datasets, we just want to look at the high-resolution (1 mm isotropic) T_1-weighted anatomical scan (MP-RAGE). On a PC, you can load it

with MRIcro. On BLiSS, you can use fslview once the data are converted to Nifti format (as above).

Distortion compensation in functional data

We acquire a fieldmap with every experiment, usually with a slice prescription identical to the functional data. Using the same experiment (above) as an example, here's the commands necessary for removing distortion. (These commands are collected in a text file, FLS_unwarp.txt in the experiment directory.)

Use the Brain Extraction Tool to get rid of the skin signal and make a mask of brain tissue:

```
% bet mag mag_stripped -m
```

Use the commandline fslmaths utilities to convert the data from the 12-bit integer format (scaled from 0 to 4095) to radians (measure of phase evolution between 2 echo times in fieldmap acquisition). Input file is the phase part of the fieldmap, output is a file named ph_rad:

```
% fslmaths_32R ph –sub 2048 –div 2048 –mul 3.1415927
  ph_rad
```

Use PRELUDE to unwrap the phase map (spins that evolve more than pi during the delta echo time (2.46ms in our sequence) cause discontinuities in the fieldmap):

```
% prelude -i ph_rad -a mag -m mag_stripped_mask -o
  ph_unwrapped
```

Finally, convert the unwrapped phase map into a fieldmap, by dividing by the delta echo-time from the fieldmap sequence:

```
% fslmaths_32R ph_unwrapped -div 2.46 ph_rad_ms
```

At last, use FUGUE to undistort the EPI image, using your independent knowledge of the echo spacing (time to read out one line) and the phase encode direction:

```
% fugue -i run1 --loadfmap=ph_rad_ms --dwell=0.47 --
  unwarpdir=y -o run1u
```

To check the results of distortion compensation, open the original EPI data (run1) in FSLVIEW, then **Add** the corrected data (run1u).

NB: the FSL_unwarp.txt is actually written as a very simple shell script, so if you type `% sh FSL_unwarp.txt` at the command prompt in the directory with mag, ph and run1, it will execute all the specified commands and generate the unwarped EPI file.

Analyzing functional data

This is beyond the scope of the course, but for a simple demonstration we can set up the design matrix in FSL and look for functional activation.

If you type `fsl` at the command prompt, a small GUI will open up, and one button says FEAT FMRI analysis. Clicking that button will bring up a tabbed GUI that guides you through analysis. At the top, you can select first-level (single-scan) or higher-level (multi-scan or multi-subject) analysis, and whether you want to do a full analysis or only bits. The example here describes a full first-level analysis.

Data.

Setting the number of inputs to the number of scans (1 for first-level analysis), click the "Select 4D data" button to browse for the unwarped data. FEAT automatically sees how many volumes there are, but doesn't read the TR, so set this to 2s. The output directory will by default be in your current directory: run1u.feat. If this directory exists, it will append a + to the name.

Pre-stats.

The defaults are good as they are – this will do spatial smoothing and temporal filtering to remove drift, as well as motion correction (MCFLIRT). We've done the B0 warping (distortion correction) already, but we could have used the GUI. If you have time to spare, do the MELODIC ICA data exploration – it can take from 20 minutes to more than an hour, but helps build intuition for what's going on.

- To look at ICA before doing the rest of the analysis, pre-stats only were run with the output directory of run1u_prestats.feat.
- ICA can also be used for denoising. In this data set, the 1st 2 ICA components look like motion & respiration or cardiac noise. Descending into this directory, the command:
  ```
  % fsl_regfilt -i filtered_func_data -o denoised_data -d filtered_func_data.ica/melodic_mix -f="1,2"
  ```
  creates a new "denoised" file which was can be used as input for the rest of the analysis.
- The design.fsf file in run1u_prestats.feat should show only the prestats, and the design.fsf file in run1u.feat should show the rest of the analysis (including registration).

Stats.

The hardest part is setting up the design matrix. For all but the simplest designs, you want to create your own text file(s) with a different program, and use the Full model setup to input it here, using the 3-column format. This is the basis of the design matrix:

- first column is the onset time of an event
- second column is the duration
- third column is the value

One text file is created for each explanatory variable. Here, 2 explanatory variables were created: reading (blocks of time during which the subject was

reading text) and conflict (isolated events during which the subject might have detected a lack of global coherence in the text).

Post-stats
This is for display purposes only – the Thresholding setting most likely to yield instant gratification is Uncorrected, $p < 0.05$.

Registration
This accomplishes both the alignment of the EPI data to the anatomical data, and the resampling of the individual data into a standardized atlas space. Select Main structural image and browse for the Nifti file that corresponds to the anatomical reference image. Then set style of search to Full Search, 6 DOF.

Clicking GO launches a browser that keeps track of progress, and links to a html report when everything's done.

FSL has atlases built into it, and registration allows you to resample the functional data into standard anatomical space. Typing
`% Renderhires`
at the command prompt launches a GUI which lets you select a FEAT directory for which you want to re-sample all the functional data into standard space to pick out structures. The output files are found in a directory labeled hr in the selected FEAT directory. Opening these in **FSLVIEW**, and opening the Atlas Toolbar from the **Tools** menu lets you select the atlas you want for naming structures.

Analyzing DTI data

DTIFIT will take diffusion weighted data and calculate diffusion tensors for each voxel, as well as fractional anisotropy. A rough outline of the process from raw (DICOM) data to FA and eigenvector images is:

- use dinifti to convert data. The output is a 128 x 128 x 64 x 39 matrix – 2mm isotropic resolution of the brain.
    - The pulse sequence acquires 12 directions and 1 b=0 (not diffusion weighted) image, for a total of 13 volumes. This is repeated 3 times.
- use FUGUE to remove distortions, since DTI images are EPI-based
- use eddy_correct to correct for remaining distortions caused by eddy currents (and accomplish motion compensation)
- use Matlab (or some more appropriate tool) to average together the 3 volumes.
- use bet to extract a brain-only mask
- Generate text files listing b-values for each of the 13 images (0 for the first and 1000 for the rest) and (x,y,z) coordinates of directions for each image.
- Run dtifit with the following inputs:
    - Diffusion-weighted data (13 volumes)
    - Brain mask (1 volume)

  - Text-file listing b-values
  - Text-file listing diffusion directions

Details are collected in FSL_DTI_notes.txt; caoGetBvals.m will get the b-values and vectors from the dicom header information and write text files in the right format for DTIFIT.

For viewing, FSLVIEW has settings for DTI data:

- load dti_V1s.img (the primary eigenvector data – it's 128 x 128 x 64 x 3, w/ relative (x,y,z) indicating the orientation of the primary eigenvector in each voxel)
- Add dti_FAs.img (the fractional anisotropy map, which will be used to mask the eigenvector data; in this and the previous filenames, the s indicates that I swapped the data around so they look better in FSLVIEW)
- By clicking the "i" icon in the Overlay Settings toolbar, set the eigenvector data to be visualized as RGB and modulated by fractional anisotropy.