Bramen-NITP-Lab

Background: You piloted an experiment using a flashing checkerboard As an ancillary aim, you wanted to take a look at the estimated hrf in different patient populations, but you aren't sure if it is worth the power you lose running an ER designed experiment. Another big worry you have is how reliable the data are. Your last data set was an ER designed experiment, and when you changed small preprocessing parameters, you noticed huge changes in your results. Therefore, you also collected data using a block design to determine whether the ability to inspect the shape of the HRF is worth the tradeoff.

This lab will show you how 1) preprocessing choices such as smoothing kernel, modeling of motion parameters, and hrf selection change your results. Also, 2) how design choices like using an event-related or block design impact results. Lastly, you will also learn how to 3) model the average hrf in an event-related design using finite impulse response (FIR) modeling, and 4) see how parameters such as start, length of estimated hrf, and number of impulses impact your modeled hrf.

Your data is in a folder called:
BramenLab_NITP2013

Subfolders are:
behavior – contains your events in 3 column text format (start time, duration, height)

canned_outputs – I ran feat using a lot of different parameters we will want to inspect. Sparse feat directories are located in here. You will use fslview to inspect results.

nifti – your functional and structural data

student_outputs – this is where I suggest you save your feat outputs

/Users/jbramen/Documents/Courses-Lectures/NITP-block-v-er-lab/data-7-2013/

RUNNING FEAT

1) Brain Extract MPRAGE (coMPRAGE.nii.gz), Bandwidth Matched T2 (T2MBW4.nii.gz) , and BOLD (VISBLOCK.nii.gz; VISEVENT.nii.gz) data using BET.

a) Open MPRAGE in fslview and find the center of the volume. Use the top of the brain, not the skull, as your upper border. Log the x, y, z coordinates.

- Open the BET GUI
  - fsl &
    -Select BET
    - Select the MPRAGE in the "Input Image" field
    -Click Advanced Options
    -Deselect "Output brain-extracted image. We will only save a mask. When we get the mask right, we will apply it to the data.
    -Select "output binary brain mask image"
    -Enter your x, y and z coordinate on the bottom line
    -Click GO

    Note – in your terminal, it will output the full command. You can simply alter parameters in the terminal until you get them right. This will also make it a lot easier to script your brain extractions when you have multiple subjects.

    -Return to fslview
    -select file->add-><your brain mask>
    -The top of he brain is cut off, but it is only a couple of slices. I think this brain extraction is ok. If you get a brain extraction that leaves too much skull or cuts off too much brain:
    -type bet in the terminal to get the usage
    -To make the outline larger, use the –f flag
    -To change how large the brain is on top relative to the bottom of the image use the –g flag
    -Apply the mask to the image using fslmaths
    -type fslmaths to find usage.
    NAME OUTPUT "coMPRAGE_brain"

b) The T2 images are usually straightforward. In a new BET window, load T2MBW4.nii.gz. Use the default settings and click Go. Inspect the result in fslview.

c) For both 4D BOLD images, use BET and in the dropdown menu, select "Apply to 4D data" and inspect results with fslview.

2) Use FEAT to run the GLM on ER data using these smoothing kernels:

Start with the default (5mm) smoothing kernel and a double gamma hrf. Do not model the motion parameters.

Turn OFF brain extraction (you already ran it on the BOLD data)

Leave the defaults on
Stats Tab ->Full Model Setup -> Basic Shape=Custom (3Col format)
Select Double-Gamma HRF
Select <evs_visevent.txt>
Select your skull stripped data in Registration tab.
Make sure the initial hires is set at 6DOF
Change BBF to 7DOF under Main structural image line
Select Nonlinear under standard space
For the utput, select the directory your data is in
Name the output – "5mm-dg-nomps"
In the post Stats tab, change z to 2 and p to 1. This will give you a threshold of about $p < 0.05$, uncorrected.

Click "Go"

You will use these same exact parameters, only

1) Turn OFF registration by deselecting all the lines in the registration tab (click the yellow boxes)
2) Run the following 3 smoothing kernels for the next analyses: 6mm, 8mm, 12mm
3) When your analyses have run, copy the reg folder from your 5mm analysis to the other directories. Make sure you are in the directory with your outputs
   - for I in 6mm*feat 8mm*feat 12mm*feat; do cp -R 5mm-dg-nomps.feat/reg $i;done

5) Apply registration so that you can view results on the T1-weighted high resolution MPRAGE

   - cd student_outputs
   - for i in *feat; do fsl_sub flirt -in $i/thresh_zstat1.nii.gz -ref $i/reg/highres.nii.gz -applyxfm -init $i/reg/example_func2highres.mat -out $i/thresh_zstat1_2_T1;donels

INSPECT RESULTS USING DIFFERENT PREPROCESSING PARAMETERS AND DESIGN CHOICES:

Using FSLVIEW: JEN WILL DEMO THIS

To inspect how the smoothing kernals impact results, we will start in native space. Registering the data adds additional smoothing. We can also inspect how this effects results.

Open fslview:

- fslview &

-File – > Open -> 5mm-dg-nopm.feat/example_func
-File – > Add -> thresh_zstat1

-rename the overlay: click the little "I", delete the text "zstat1" and type 5mm-dg-nomp

Open another fslview:

- fslview &

-File – Open -> coMPRAGE
-File – Add -> thresh_zstat1_2_T1
-repeat using the registered data

Questions:

1) What happenes to results in regions such as the thalamus, frontal lobe, and visual cortex as you smooth the data more?
2) What happens to the data when you display it on the high resolution T1?
3) Would these change you interpretations of the findings?

NEXT:

Using fslview (and either the example_func or the T1, depending on how you feel about inspecting results on a low resolution brain), inspect how the following parameters change results:

1) gamma vs double gamma hrf
2) modeling motion parameters versus not.
3) Modeling motion parameters and the temperal derivatives, and squares of both original and TD (extended motion parameters)
4) Block design – temporal filtering (100 versus 75)
5) Block versus ER
    a. Repeat inspecting these parameters, only using the block designed data
    b. Do results from the block designed study change as much as the ER analysis when you make slightly different preprocessing decisions?

FIR: Stats this at 4:30pm

We will set up the FIR modeling in 3 different ways. I ran these already, but I still want to go over the decisions I made

I used a 6mm smoothing kernel, standard motion parameters and the event-related data. I ran FIR modeling using 3 sets of modeling parameters:
Phase= 0
Number=8

Duration = 16

Phase=2
Number=4
Duration = 12

Phase=2
Number=8
Duration =16

Lets set up on of these together. Do not click Go. It will slow your computer down.

After you run FIR modeling, you need to create a time series

eg –
> cd 6mm-FIR-mps-P0-N8_W16.feat/stats
> fslmerge -t FIR-timeseries pe1 pe2 pe3 pe4 pe5 pe6 pe7 pe8 pe9 pe10 pe11 pe12 pe13 pe14

Now you can open FIR-timeseries in fslview. If you want structural information, either open example_func, or register the FIR time course to the T1, and open the T1 with registered data. You can then surf around the brain.