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HST.583 Functional Magnetic Resonance Imaging: Data Acquisition and Analysis
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Laboratory 2: Introduction to fMRI Data and Analysis

SOLUTIONS

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Exercises and Questions

1. After overlaying the activation map on the anatomical/structural volume in exercise 4 (page 25), adjust the threshold and opacity parameters such that only activated regions of the overlay can be seen. What parameter values did you use?

This of course will vary based on your criteria; a threshold value of between 20 and 25 does a reasonable job of showing true regions of activation, and masking false activations (e.g. from motion or noise). The opacity value was more subjective; a high enough value should have been used such that the spectral activation regions could be easily seen.

2. Do the activations appear to be in the right places (roughly) based on how the visual fields map to the visual cortex? Why or why not?

Yes. Based on what we know about the mapping of visual fields to contralateral visual (occipital) cortex, the activations do appear in the right place (given the contrast of $[1 \ -1]$). The positive values on the $-\log(p)$ map correspond to positive values of the effect $\beta_1 - \beta_2 > 0$, indicating that the right visual cortex is significantly more activated by the left hemifield stimulus than the right hemifield stimulus. The negative $-\log(p)$ values, corresponding to effect $\beta_1 - \beta_2 < 0$, are found in the left visual cortex, indicating that the right hemifield stimulus produces more of an effect than the left hemifield stimulus, in the left visual cortex. .

3. Instead of using $[1 \ -1]$ to set the Left - Right contrast, use $[1 \ 0]$ and then $[0 \ 1]$ when applying the linear model. What do these activation maps tell you? How is this information different from the map produced with $[1 \ -1]$? What if $[-1 \ 1]$ is used? How is the $-\log(p)$ map different in this case? Does this contrast setting provide any additional useful information?

The $[1 \ 0]$ contrast simply shows you the regions that are activated ONLY during the left hemifield stimulus. In other words, the $-\log(p)$ maps depend on the left hemifield stimulus (β_1) exclusively. Therefore, most of the activation we see is in the right visual cortex. We do, however, see some ipsilateral activation in the right visual cortex, likely due to the fact that the left hemifield stimulus does not exclusively isolate the right visual field. To a small extent, the left hemifield stimulus is seen by the left visual field, and there is some activation in the right visual cortex. The same logic holds true for the $[0 \ 1]$ activation, except now we are examining the effects of only a right hemifield stimulus.

The $[1 \ 0]$ and $[0 \ 1]$ contrasts are indeed different from $[1 \ -1]$, which looks at the difference in effect size for the left versus right stimulus ($\beta_1 - \beta_2$), as opposed to effects individually. All three contrasts provide distinct and useful information. On the other

hand, $[-1\ 1]$ provides the same information as $[1\ -1]$, save for the fact the activation maps will be inverted (since we are now looking at $(\beta_2 - \beta_1)$).

4. Would it be correct to just use one of the two design blocks to try to fit the data? What would such a map tell you? In other words, if just the left hemifield design block was used for linear modeling, what would be the significance of the resulting $-\log(p)$ map?

Using just one of the design blocks is wrong, wrong, wrong! If we have a stimulus we MUST model its effect!! Even if the effect is small it must be modeled (this is the whole point of using a stimulus). Now, there is a distinction between modeling the effect, and using the effect size to compute the statistical map (be it $-\log(p)$ or T) - these are separate steps. In this experiment, we must model both hemifield stimuli. Our contrasts, however, allow us to ignore the effect size of one of the stimuli, as we have done with the $[1\ 0]$ and $[0\ 1]$ contrasts. Another way of thinking about it is like this: if we model just one of the hemifields, but the effect of the other one is still present, the model fit to the first hemifield would not be accurate (since the GLM would be trying to fit both effects with a single model. If there is any confusion on this, please see me, it is an important concept and can be understood easily with a visual example.

5. Give two reasons why it is beneficial to spatially smooth before performing a general linear model analysis? Would it still be useful if fMRI activations were not spatially correlated? Why or why not?

1. *Since all fMRI activations are spatially correlated, due to functional similarity of adjacent brain regions and blurring introduced by blood flow. Thus, spatial smoothing will increase functional SNR and increase significance of activations (both in terms of detection and extent of activation).*
2. *Spatial smoothing can reduce false positive rates by reducing the number of activations caused by chance alone (which are often single, spatially isolated voxels).*

If fMRI activations were NOT spatially correlated, smoothing would actually decrease SNR, and decrease the analysis power. See your textbook (pg 277) for more information.

6. What is the major drawback of spatially smoothing?

Spatially smoothing decreases spatial resolution (try this yourself; it is immediately noticeable).

7. Perform GLM analysis without spatially smoothing. Are the results consistent with what you would expect?

Without spatial smoothing, the activations have less significance and there are more activations due to chance scattered throughout the brain.

8. Perform GLM analysis without performing any motion correction. What are the major differences in the activation maps?

Although this subject did not move much, the un-motion corrected maps do show weaker activation in the visual cortices, and more activation near the edges of the brain (which are not true activations).

9. On the "Model" page of the Linear Modeling action, it is possible to remove polynomial drift, up to the third order. What is the benefit of having a non-zero drift order? Extra credit: Give an example when using a non-zero drift order may not benefit the analysis.

Often in an fMRI scan, the signal is not completely stable over the time course (even in a phantom). This can be the result of many factors, such as drift due to thermal heating of the gradient coils over the course of the scan or other system noise inherent to the scanner's electronics. Including drift terms into the linear model allows for these terms to be accounted, such that they have less impact on the fit of our stimulus-based design matrices.

If the drift term(s) is NOT orthogonal to the stimulus-based model functions, inclusion could actually worsen the fit estimate (see Buxton, pg 479).

10. Change the original EPI time series (i.e. `ge_functionals8_64`) to a spectral colormap. Then, overlay this series (*not* the $-\log(p)$ map) onto the structural. Make the opacity of the overlay about 0.35 and take a look at a mid-cortical axial slice. Do you notice any spatial differences between the EPI image and the anatomical image? Extra credit: Why is this occurring and how could it be minimized? (hint: check the types of scans acquired in lab 1; review the purpose of each one).

The most obvious problem is the distortion in the EPI images, near the frontal lobes of the brain, and in general, near regions of air-tissue interface. This occurs because there are large magnetic field inhomogeneities in these regions (i.e. regions of high susceptibility), which lead to spin dephasing and signal loss. Distortions can be improved in several ways:

- 1. Acquisition of a field map, which can be subsequently used to correct the EPI images (since a field map allows estimation of the regional magnetic fields).*
- 2. Shorten the echo-spacing (i.e. increase the bandwidth) of the EPI scan, which results in less time for spins to dephase.*
- 3. Use higher-order shims before scanning to improve the magnetic field homogeneity, even in regions of high susceptibility.*