

## Homework 3: Group analysis

### Background:

Listen to the lecture on Data formats (Voxel and affine transformation matrices, nifti formats) and group analysis (Group Analysis, Anatomical Normalization, Multiple Testing problem, Randomization Tests).

Also, at least skim over the Eklund et al. (PNAS, 2016) paper to get a feel for the current debate in the field.

### Data homework:

Your task is to conduct a group analysis from a subset of the task-based Human connectome project (<https://www.humanconnectome.org/study/hcp-young-adult/project-protocol/task-fmri>). For this study you are given the contrast between reward vs. punishment from the gambling task for N=25 subjects (see Barch et al. for meaning of this contrast). The zip-files contains the data from all these 25 subjects in NIFTI format + the anatomical normalization template in MNI space.

GA\_RewardvsPunish\_xx.nii:

Contrast from the gambling task reward-punishment for s01-s25

MNI152\_T1\_2mm.nii:

Anatomical template image in MNI space

mask\_GA.nii:

Mask for the gambling task - marking all within-brain voxels

1. Load and plot horizontal slice  $z=0$ ,  $z=-20$ , and  $z=40$  of the MNI standard template. To translate the MNI coordinates to voxel coordinates in the image, you need to consider the affine transformation matrix in the header of the image (see lectures of data format).
2. Calculate a group t-test for the contrast Reward>Punishment and of Punishment>Reward. For each of the contrasts, what is the peak t-value and at what MNI coordinate can they be found? What is the uncorrected p-value? Plot the slice with the maximal t-value for each contrast. Only consider voxels where binary\_mask.nii is 1.
3. Is the peak t-value for each contrast significant when correcting for multiple tests using Bonferroni correction over the number of voxels considered (within the mask)? For each hypothesis use a one-sided test.
4. Obtain a Null-distribution of the peak t-value in an image through a randomization test. For each contrast, flip the sign of the contrast image for each subject separately. Try at least 1000 ways of flipping the data randomly.
  - a) What is your Null-hypothesis for each test and why is the way you conduct the randomization test justified under this null-hypothesis (i.e. what is exchangeable?).
  - b) Plot a histogram of the Null-distribution and mark the value of the real maximal t-values in the histogram with a vertical line.
  - c) Calculate and report the corrected p-value by determining from the randomized t-distribution how likely it is that the peak t-value (or a larger value) has occurred under the null-hypothesis?

Tips:

A. A free image viewer for NIFTI for Mac and PC is MRICroN (<http://www.mccauslandcenter.sc.edu/mricro/mricron/>)

B. Under the free SPM package (Matlab), you can load nift-files using the commands

```
V=spm_vol('filename');
```

```
X=spm_read_vols(V);
```

The affine transformation matrix will be in  
V.mat

Barch, D. M., Burgess, G. C., Harms, M. P., Petersen, S. E., Schlaggar, B. L., Corbetta, M., . . . Van Essen, D. C. (2013). Function in the human connectome: task-fMRI and individual differences in behavior. *Neuroimage*, *80*, 169-189. doi:10.1016/j.neuroimage.2013.05.033