

# HW2 Report — Daehyun Cho

## [1] Preprocessing and GLM

### **(a) Preprocess and GLM**

(b) Review overall results with afni\_proc.py QC with a html format.

## [2] Statistical Analysis

(a) One-sample t-test

(b) Paired t-test for all pairs of tasks

(c) One-way repeated ANOVA

## [3] Discuss Overall results obtained from [1] and [2]

## [1] Preprocessing and GLM

### (a) Preprocess and GLM

Here is my `afni_proc.py` command and I've automated them into one tcsh file since it's very exhausting to type the command every time(12 subjects \* 4 tasks).

```
#!/bin/tcsh

foreach subj (s*)
    foreach task (ad_evt lh_evt rh_evt vs_evt)

        set prefix = $subj$task
        afni_proc.py \
            -subj_id $prefix \
            -dsets ./$subj/$task+orig.HEAD \
            -copy_anat ./$subj/anat/anat_orig/anat_$subj.nii.gz \
            -blocks despoke tshift align tlrc volreg blur mask scale

        regress \

            -tlrc_base /home/jj/abin/MNI152_T1_2009c+tlrc.BRIK.gz \
            -volreg_align_to MIN_OUTLIER \
            -volreg_align_e2a \
            -volreg_warp_dxyz 3 \
            -mask_epi_anat yes \
            -blur_size 8 \
            -regress_reml_exec \
            -regress_apply_mask \
            -html_review_style pythonic \
            -execute

    end
end
```

Required preprocessing steps and their corresponding commands are below

—

1. **despiking** `-blocks despike`
2. **slice timing correction** `-blocks tshift`
3. **motion correction** `-blocks align`
4. **spatial normalization to the MNI space** `-blocks tlrc volreg`  
 with **3mm isotropic voxel size** `-volreg_warp_dxyz 3`
  - so this needed an extra option `-tlrc_base`  
`/home/jj/abin/MNI152_T1_2009c+tlrc.BRIK.gz` because I thought the default was Talairach space. But later found out that the default space was MNI. What a waste of time...
  - `-volreg_align_to MIN_OUTLIER` It's to specify the base position for volume reg but normally we use third. Since I didn't know when MP data was taken, I chose `MIN_OUTLIER`
  - `-volreg_align_e2a` Aligned EPI to anatomy at volreg step.
5. **Spatial smoothing** `-blocks -blur`  
 using **8mm isotropic FWHM Gaussian kernel** `-blur_size 8`
6. **Scaling** of the voxel intensity to an average of 100 `-blocks scale`
  - default average was 100, no extra options needed.
  - `-blocks mask` and `-mask_epi_anat` options were added since default scaling processes were set to extended mask, which is not our desirable results.
7. **temporal detrending**
  - I understood the documentation of `afni_proc.py` to have
8. **General Linear Model** `-blocks regress`
  - `-regress_reml_exec` Option that runs GLM code during tcsh run.
  - `-regress_apply_mask` Since default setting wasn't using the mask but the extent one, this option was added.

## (b) Review overall results with afni\_proc.py QC with a html format.

This was done with `-html_review_style pythonic`

I am keep trying to find out how to save that self-quality check results, but that save button doesn't work. Since it's relatively new function to show up, it

looks like a bug...

## [2] Statistical Analysis

The first thing to do was to resample all the `stats.` files after GLM since they had number of voxels and stuffs. I referenced the link below. Beforehand, I've put all the `stats.` from the same task into same folder(i.e. to have auditory tasks GLM results were all in the `ad` folder)

```
----- hw2
|      -- mask_anat.s02ad_evt+orig.BRIK.gz
|-- ad
|   |-- res.
|   |   -- stats.s02ad_evt # resampled ones
|   |-- stats.s02ad_evt ...
|   -- stats.s03ad_Evt ...
|-- lh
|-- rh
--- vs
```

Re: T-Test Error: "Does match first one in size"

I'm currently in the process of adding more data to my current sample. The new data was collected during a different session. I am having issues with the t-test (one and two sample) and keep getting this error (see below, "does match first one in size") for ONLY the newly added data.

<https://afni.nimh.nih.gov/afni/community/board/read.php?1,107517,148717#msg-148717>

With `tcsh` script below, I've gone through all the resampling process. I've resampled with master dataset of the first subjects auditory tasks' masked data which is the result from `afni_proc.py`.

Reason I chose the masked data as master is it took too much memory while doing the t-test due to the voxels outside the brain region.

```
#!/bin/tcsh

foreach file (*.gz)

    echo $file
    3dresample -master ../mask_anat.s02ad_evt+orig.BRIK.gz \
              -prefix res$file \
              -input $file

end
```

## (a) One-sample t-test

Command — `3dttest++ -setA STATS*` ← file that starts with stats, results from GLM

```
3dttest++ -setA ad/res./stats* -prefix ad_onesample
3dttest++ -setA lh/res./stats* -prefix lh_onesample
3dttest++ -setA rh/res./stats* -prefix rh_onesample
3dttest++ -setA vs/res./stats* -prefix vs_onesample
```

## (b) Paired t-test for all pairs of tasks

Command — `3dttest++ -setA STATSforTask1 -setB STATSforTask2 -paired` ← two file

```
3dttest++ -setA ad/res./stats* -setB lh/res./stats* -paired -prefix ad_lh_paired
3dttest++ -setA ad/res./stats* -setB rh/res./stats* -paired -prefix ad_rh_paired
3dttest++ -setA ad/res./stats* -setB vs/res./stats* -paired -prefix ad_vs_paired

3dttest++ -setA lh/res./stats* -setB rh/res./stats* -paired -prefix lh_rh_paired
3dttest++ -setA lh/res./stats* -setB vs/res./stats* -paired -prefix lh_vs_paired

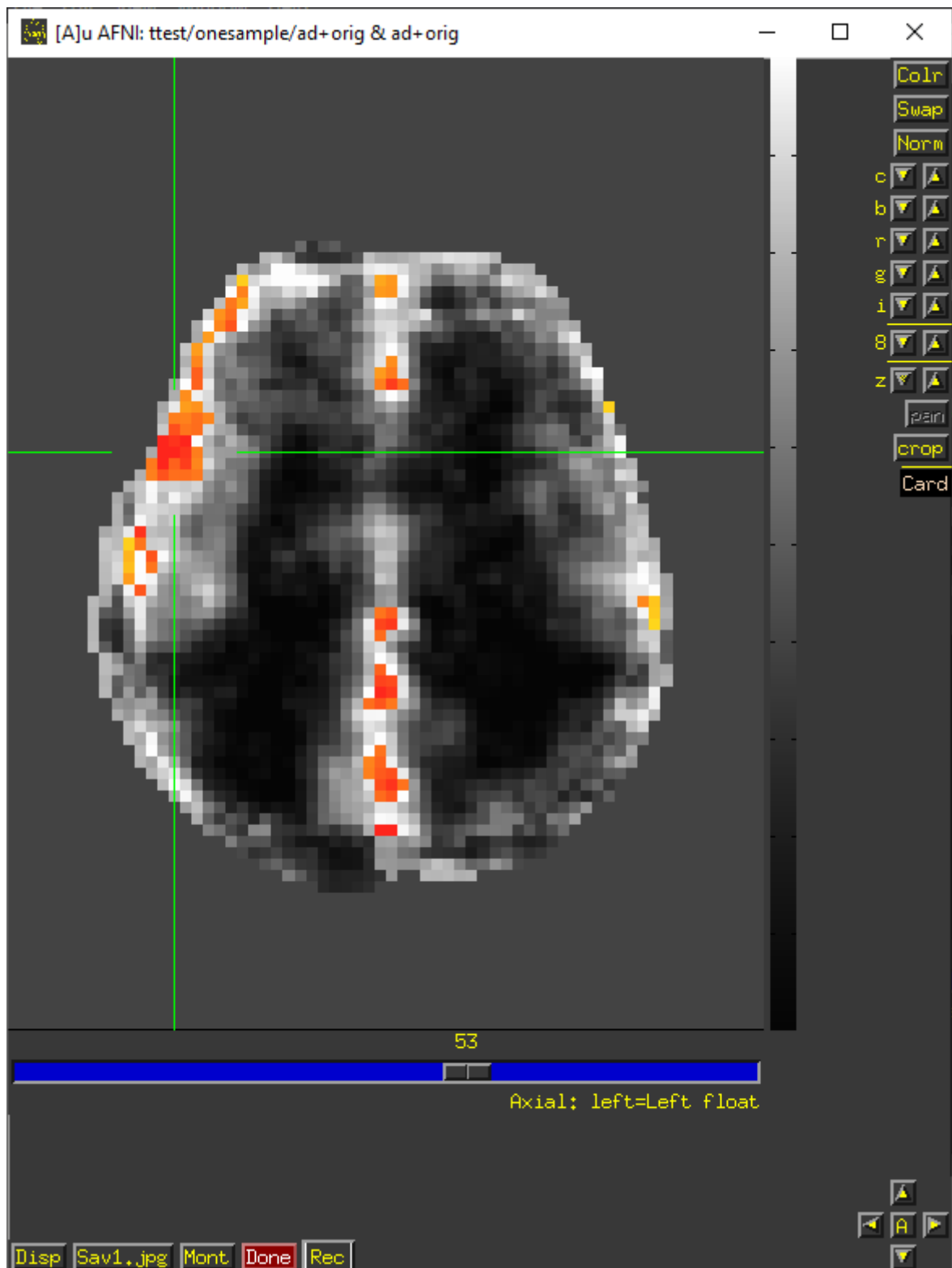
3dttest++ -setA rh/res./stats* -setB vs/res./stats* -paired -prefix rh_vs_paired
```

## (c) One-way repeated ANOVA

```
3dANOVA -levels 4 -dset 1 ad/res./stats* -dset 2 lh/res./stats* -dset 3 rh/res./stats* -dset 4 vs/res./stats* -contr 1 1 1 -1 ALRVV -contr 1 1 -1 1 ALVVR -contr 1 -1 1 1 ARVVL -contr -1 1 1 1 LRVVA
```

## [3] Discuss Overall results obtained from [1] and [2]

***Better than Expectation***



This is the results of one-sampled t-test from auditory task and it looks pretty okay with the real auditory activation field.

### ***Gap between theory and practice***

Even though I get to know what's going on in theory, I can't directly match

them to practice right away. There are too many exceptions, extra options for minor edge cases which is good, but documentations are not intuitive to newly-users, which is sad...

### ***tcsh***

I used bash more than 5 years ago and it was good to automate some works with tcsh script file.