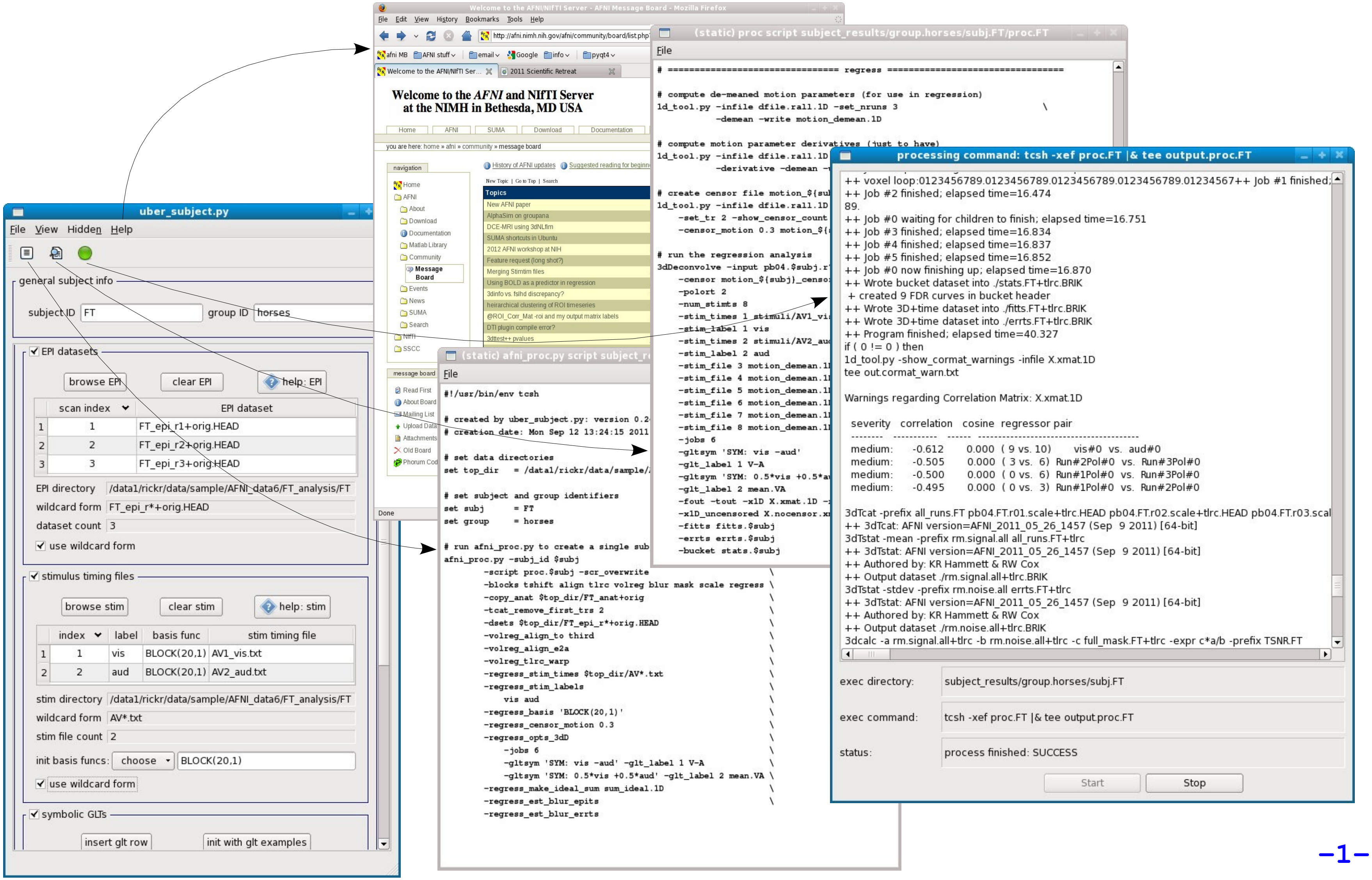
AFNI Start to Finish:
How to Analyze Data with AFNI



Welcome to the *AFNI* and NIfTI Server at the NIMH in Bethesda, MD USA

you are here: home » afni » community » message board

Topics
New AFNI paper
AlphaSim on groupana
DCE-MRI using 3dNLfim
SUMA shortcuts in Ubuntu
2012 AFNI workshop at NIH
Feature request (long shot?)
Merging Stimtim files
Using BOLD as a predictor in regression
3dinfo vs. fslhd discrepancy?
heirarchical clustering of ROI timeseries
@ROI_Corr_Mat -roi and my output matrix labels
DTI plugin compile error?
3dttest++ pvalues

uber_subject.py

subject ID: FT group ID: horses

☑ EPI datasets

	scan index	EPI dataset
1	1	FT_epi_r1+orig.HEAD
2	2	FT_epi_r2+orig.HEAD
3	3	FT_epi_r3+orig.HEAD

EPI directory: /data1/rickr/data/sample/AFNI_data6/FT_analysis/FT
wildcard form: FT_epi_r*+orig.HEAD
dataset count: 3
☑ use wildcard form

☑ stimulus timing files

	index	label	basis func	stim timing file
1	1	vis	BLOCK(20,1)	AV1_vis.txt
2	2	aud	BLOCK(20,1)	AV2_aud.txt

stim directory: /data1/rickr/data/sample/AFNI_data6/FT_analysis/FT
wildcard form: AV*.txt
stim file count: 2
init basis funcs: choose BLOCK(20,1)
☑ use wildcard form

☑ symbolic GLTs

(static) afni_proc.py script subject_r

```
#!/usr/bin/env tcsh

# created by uber_subject.py: version 0.2
# creation date: Mon Sep 12 13:24:15 2011

# set data directories
set top_dir   = /data1/rickr/data/sample/

# set subject and group identifiers
set subj      = FT
set group     = horses

# run afni_proc.py to create a single sub
afni_proc.py -subj_id $subj
        -script proc.$subj -scr_overwrite                          \
        -blocks tshift align tlrc volreg blur mask scale regress \
        -copy_anat $top_dir/FT_anat+orig                           \
        -tcat_remove_first_trs 2                                   \
        -dsets $top_dir/FT_epi_r*+orig.HEAD                        \
        -volreg_align_to third                                     \
        -volreg_align_e2a                                          \
        -volreg_tlrc_warp                                          \
        -regress_stim_times $top_dir/AV*.txt                       \
        -regress_stim_labels                                       \
            vis aud                                                \
        -regress_basis 'BLOCK(20,1)'                               \
        -regress_censor_motion 0.3                                 \
        -regress_opts_3dD                                          \
            -jobs 6                                                \
            -gltsym 'SYM: vis -aud' -glt_label 1 V-A               \
            -gltsym 'SYM: 0.5*vis +0.5*aud' -glt_label 2 mean.VA \
        -regress_make_ideal_sum sum_ideal.1D                       \
        -regress_est_blur_epits                                    \
        -regress_est_blur_errts
```

(static) proc script subject_results/group.horses/subj.FT/proc.FT

```
# ================================ regress =================================

# compute de-meaned motion parameters (for use in regression)
1d_tool.py -infile dfile.rall.1D -set_nruns 3                          \
           -demean -write motion_demean.1D

# compute motion parameter derivatives (just to have)
1d_tool.py -infile dfile.rall.1D
           -derivative -demean -

# create censor file motion_${su
1d_tool.py -infile dfile.rall.1D
    -set_tr 2 -show_censor_count
    -censor_motion 0.3 motion_${

# run the regression analysis
3dDeconvolve -input pb04.$subj.r
    -censor motion_${subj}_censo
    -polort 2
    -num_stimts 8
    -stim_times 1 stimuli/AV1_vi
    -stim_label 1 vis
    -stim_times 2 stimuli/AV2_au
    -stim_label 2 aud
    -stim_file 3 motion_demean.1
    -stim_file 4 motion_demean.1
    -stim_file 5 motion_demean.1
    -stim_file 6 motion_demean.1
    -stim_file 7 motion_demean.1
    -stim_file 8 motion_demean.1
    -jobs 6
    -gltsym 'SYM: vis -aud'
    -glt_label 1 V-A
    -gltsym 'SYM: 0.5*vis +0.5*a
    -glt_label 2 mean.VA
    -fout -tout -x1D X.xmat.1D -
    -x1D_uncensored X.nocensor.x
    -fitts fitts.$subj
    -errts errts.$subj
    -bucket stats.$subj
```

processing command: tcsh -xef proc.FT |& tee output.proc.FT

```
++ voxel loop:0123456789.0123456789.0123456789.0123456789.01234567++ Job #1 finished;
++ Job #2 finished; elapsed time=16.474
89.
++ Job #0 waiting for children to finish; elapsed time=16.751
++ Job #3 finished; elapsed time=16.834
++ Job #4 finished; elapsed time=16.837
++ Job #5 finished; elapsed time=16.852
++ Job #0 now finishing up; elapsed time=16.870
++ Wrote bucket dataset into ./stats.FT+tlrc.BRIK
 + created 9 FDR curves in bucket header
++ Wrote 3D+time dataset into ./fitts.FT+tlrc.BRIK
++ Wrote 3D+time dataset into ./errts.FT+tlrc.BRIK
++ Program finished; elapsed time=40.327
if ( 0 != 0 ) then
1d_tool.py -show_cormat_warnings -infile X.xmat.1D
tee out.cormat_warn.txt

Warnings regarding Correlation Matrix: X.xmat.1D

  severity   correlation   cosine  regressor pair
  --------   -----------   ------  ----------------------------------------
  medium:      -0.612      0.000  ( 9 vs. 10)      vis#0  vs.  aud#0
  medium:      -0.505      0.000  ( 3 vs.  6)  Run#2Pol#0  vs.  Run#3Pol#0
  medium:      -0.500      0.000  ( 0 vs.  6)  Run#1Pol#0  vs.  Run#3Pol#0
  medium:      -0.495      0.000  ( 0 vs.  3)  Run#1Pol#0  vs.  Run#2Pol#0

3dTcat -prefix all_runs.FT pb04.FT.r01.scale+tlrc.HEAD pb04.FT.r02.scale+tlrc.HEAD pb04.FT.r03.scal
++ 3dTcat: AFNI version=AFNI_2011_05_26_1457 (Sep  9 2011) [64-bit]
3dTstat -mean -prefix rm.signal.all all_runs.FT+tlrc
++ 3dTstat: AFNI version=AFNI_2011_05_26_1457 (Sep  9 2011) [64-bit]
++ Authored by: KR Hammett & RW Cox
++ Output dataset ./rm.signal.all+tlrc.BRIK
3dTstat -stdev -prefix rm.noise.all errts.FT+tlrc
++ 3dTstat: AFNI version=AFNI_2011_05_26_1457 (Sep  9 2011) [64-bit]
++ Authored by: KR Hammett & RW Cox
++ Output dataset ./rm.noise.all+tlrc.BRIK
3dcalc -a rm.signal.all+tlrc -b rm.noise.all+tlrc -c full_mask.FT+tlrc -expr c*a/b -prefix TSNR.FT
```

exec directory: subject_results/group.horses/subj.FT
exec command: tcsh -xef proc.FT |& tee output.proc.FT
status: process finished: SUCCESS

Goal: run group analysis on single subject response magnitudes

- how do we get there?
  - create beta (response magnitude) maps for each subject
    - should be aligned, probably to a well known template
  - run group analysis program (e.g. **`3dttest++`**, **`3dMEMA`**, **`3dANOVA`***)
    - can use **`uber_ttest.py`** to run single group tests

- how do we create aligned beta maps?
  - write single subject processing script: pre-processing through regression
    - inputs: anat, EPI, stimulus timing
    - controls: processing decisions like blur size and alignment template
    - outputs: beta weights (and t-stats, contrasts, blur estimates, etc.)

- how do we write single subject processing scripts?
  - **`afni_proc.py`** can be used to generate processing scripts
  - **`uber_subject.py`** can be used to generate **`afni_proc.py`** command
    - can also run the **`afni_proc.py`** command (generates proc script)
    - can also run the proc script (i.e. actually analyze the data)

General suggestions

- picture this experiment as your own
  - decisions on processing were made by you (and your colleagues)
    - hopefully before acquiring any data
  - there is no single "correct" way to analyze data, just reasonable ways

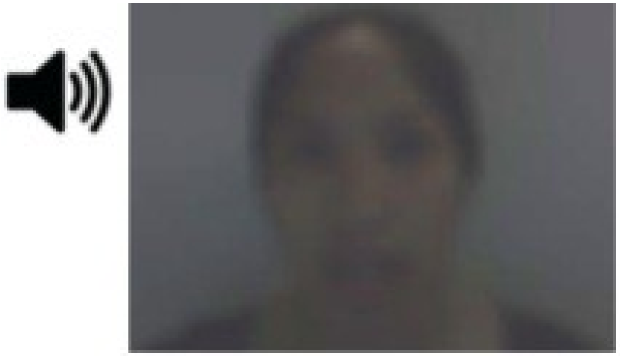
- focus on understanding the processing steps
  - in light of your having chosen which steps to perform

- practice the good habit of reviewing results
  - do the initial images look good?
  - review each processing step along with data
  - are the EPI and anat well aligned by the end?
  - do the statistical results look reasonable?

- create scripts for any processing step
  - they are a record of how data was processed
  - easy to apply to any new subjects
  - easy to repeat
    - expect to re-analyze everything (mistake, new decision, etc.)
    - keep original data and all processing scripts

Review of stimulus conditions

- Speech Perception Task: Subjects were presented with audiovisual speech that was presented in a predominantly auditory or predominantly visual modality.
- A digital video system was used to capture auditory and visual speech from a female speaker.
- There were 2 types of stimulus conditions:



(1) **Auditory-Reliable**

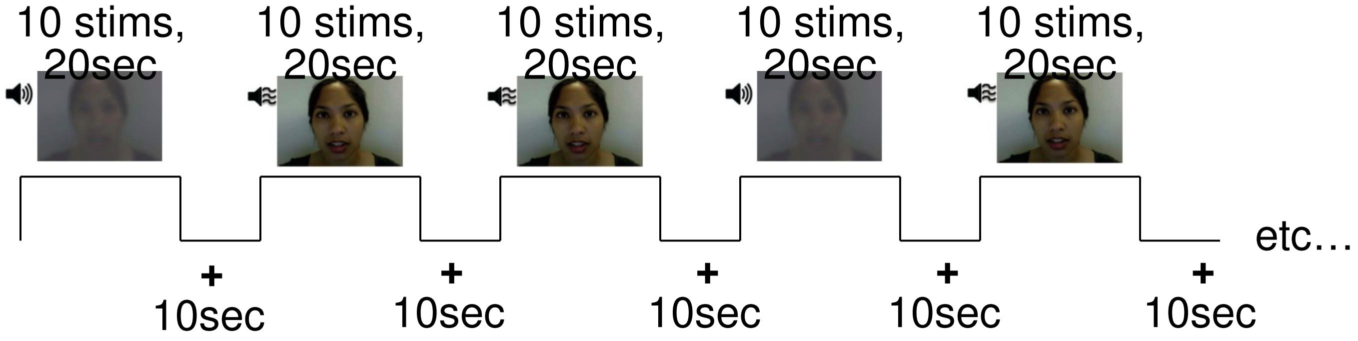
Example: Subjects can clearly *hear* the word "cat," but the video of a woman mouthing the word is degraded.

(2) **Visual-Reliable**

Example: Subjects can clearly *see* the video of a woman mouthing the word "cat," but the audio of the word is degraded.

Experiment Design:

- There were 3 runs in a scanning session.
- Each run consisted of 10 blocked trials:
  - 5 blocks contained Auditory-Reliable (*Arel*) stimuli, and
  - 5 blocks contained Visual-Reliable (*Vrel*) stimuli.
- Each block contained 10 trials of *Arel* stimuli OR 10 trials of *Vrel* stimuli.
  - Each block lasted for 20 seconds (1 second for stimulus presentation, followed by a 1-second inter-stimulus interval).
- Each baseline block consisted of a 10-second fixation point.



10 stims, 20sec

10 stims, 20sec

10 stims, 20sec

10 stims, 20sec

10 stims, 20sec

+ 10sec

+ 10sec

+ 10sec

+ 10sec

+ 10sec

etc…

Data Collected:

- 2 Anatomical datasets for each subject, collected at 3 tesla.
  - 175 sagittal slices
  - voxel dimensions = 0.938 x 0.938 x 1.0 mm

- 3 Time Series (EPI) datasets for each subject.
  - 33 axial slices x 152 volumes = 5016 slices per run
  - TR = 2 sec; voxel dimensions = 2.75 x 2.75 x 3.0 mm

- Sample size, n = 10 (all right-handed subjects)

afni_proc.py
uber_subject.py

- What is **`afni_proc.py`**?
  - a program used to generate processing scripts for single subject analysis
    - command-line program
  - generated scripts are in **`tcsh`** syntax
  - scripts are written to be easily read and modified

- What is **`uber_subject.py`**?
  - for running single subject analysis
  - a graphical user interface to **`afni_proc.py`**
  - quickly create processing scripts
  - can analyze all subjects from GUI
  - good for learning
    - FMRI processing, shell scripting, AFNI commands
    - can compare against manually generated scripts
      - for sanity, bug detection, quick evaluation

Overview of remaining steps

- **`cd AFNI_data6/FT_analysis`**
  - review directory contents and note subject data under directory **`FT`**
- from home directory, run **`uber_subject.py`** and analyze subject **`FT`**
  - set subject ID, group ID
  - specify inputs: anat, EPI, stimulus timing files (all under **`FT_analysis/FT`**)
  - controls: BLOCK(20,1), init GLTs, remove first 2 TRs
  - peruse other options, e.g. multiple CPUs for 3dDeconvolve?
  - create afni_proc.py command
  - execute afni_proc.py command (to create proc script)
  - execute proc script (analyze subject data)
- briefly review processing script
- review proc script in modest detail, while viewing processed data
  - run **`afni`** from **`FT.results`** directory and follow script
  - run resulting **`@ss_review_driver`** script
- run group analysis (**`3dttest++, 3dMEMA or 3dANOVA2`**)
  - run **`uber_ttest.py`** on data under **`AFNI_data6/group_results`**
  - or run existing **`s1.3dANOVA2`** script

Additional comments

- inputs for subject **`FT`** are under **`AFNI_data6/FT_analysis/FT`**

- results from **`uber_*.py`** go where the program was run
  - **`uber_subject.py`**: **`subject_results/group.GROUP/subj.SUBJECT`**
  - **`uber_ttest.py`**: **`group_results/test.INDEX.PROGRAM`**
  - so in class, these directory trees should end up under the home directory

- it is not necessary to master all shell script details
  - but want to understand processing steps

- when analyzing data, run **`@ss_review_driver`** for every subject
  - script represents the **minimum** of what to look at for each subject
  - for the first few subjects analyzed, look at all results in detail
    - in more detail than the level of this class
    - before acquiring many subjects

Note what is under **AFNI_data6/FT_analysis**

FT - subject data directory
s01.ap.simple - basic **afni_proc.py** script
s02.ap.align - more advanced script
s09.cleanup - remove analysis results
s11.proc.FT - result of **s01.ap.simple**
s12.proc.FT.align - result of **s01.ap.align**

under **FT**

AV1_vis.txt - visual reliable timing
AV2_aud.txt - auditory reliable timing
FT_anat+orig.BRIK/HEAD - anatomical dataset
FT_epi_r1+orig.BRIK/HEAD - EPI run 1
FT_epi_r2+orig.BRIK/HEAD - EPI run 2
FT_epi_r3+orig.BRIK/HEAD - EPI run 3

`AV1_vis.txt`:

```
60 90 120 180 240
120 150 180 210 270
0 60 120 150 240
```

AFNI Start to Finish

(the horror continues...)

- To continue reviewing the data on your own, please see the corresponding tutorial that continues under the data directory:

    - **`AFNI_data6/FT_analysis/tutorial`**

- Alternatively, this can be viewed from the AFNI web site:

  http://afni.nimh.nih.gov/pub/dist/edu/data/CD.expanded/AFNI_data6/FT_analysis/tutorial

- or from the Help menu of **`uber_subject.py`**
    - ❖ Help --> Browse --> web: tutorial-single subject analysis