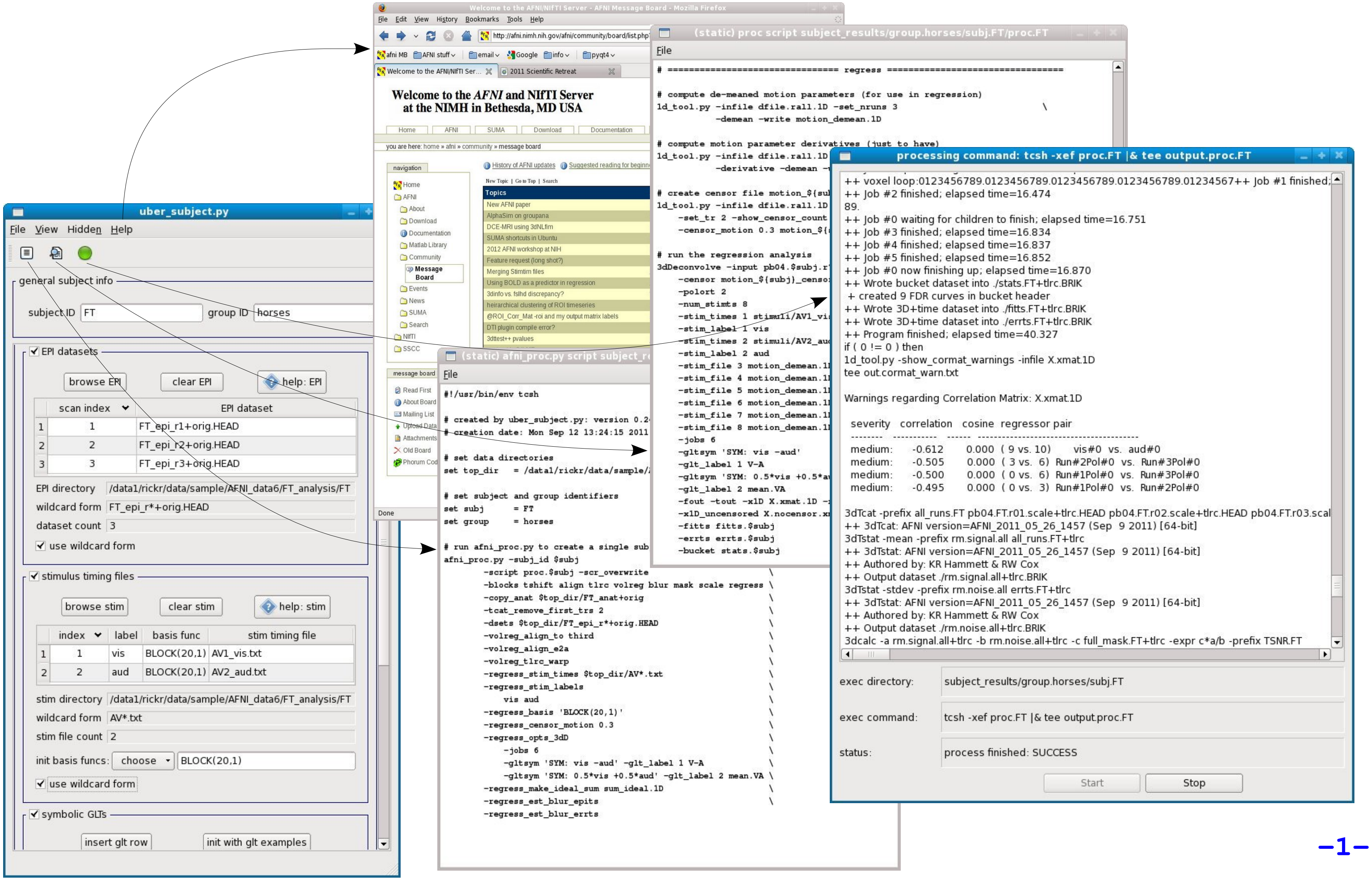
AFNI Start to Finish:
FMRI Analysis with AFNI



uber_subject.py
File View Hidden Help
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http://afni.nimh.nih.gov/afni/community/board/list.php
afni MB
AFNI stuff
email
Google
info
pyqt4
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2011 Scientific Retreat
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Done
(static) afni_proc.py script subject_r
(static) proc script subject_results/group.horses/subj.FT/proc.FT
processing command: tcsh -xef proc.FT |& tee output.proc.FT
File
browse EPI
clear EPI
help: EPI
browse stim
clear stim
help: stim
insert glt row
init with glt examples
Start
Stop

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History of AFNI updates   Suggested reading for beginn

New Topic | Go to Top | Search

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

general subject info

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

```
#!/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
```

```
# ================================ 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
```

```
++ 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`**, **`3dMVM`**)
    - can use **`gen_group_command.py`** to run simple 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
    - an **`afni_proc.py`** command can be included in publication
      - ✓along with the **`AFNI`** version (e.g. **`AFNI_21.2.09`**)
    - proc scripts are meant to be clear records of the processing

General suggestions

- picture this experiment as your own (i.e. feel responsibility)
  - 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

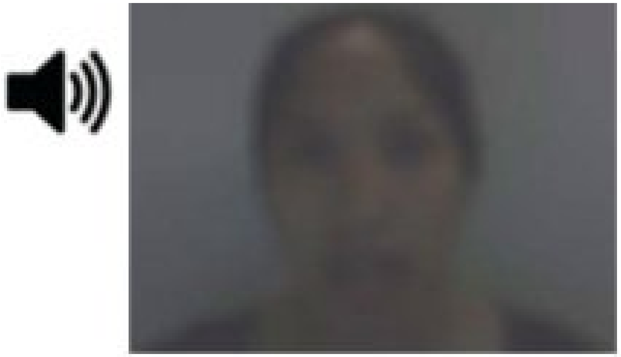
- focus on understanding the processing steps
  - in light of your having chosen which steps to perform

- 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?
  - review (at least) the afni_proc.py HTML QC for every subject

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

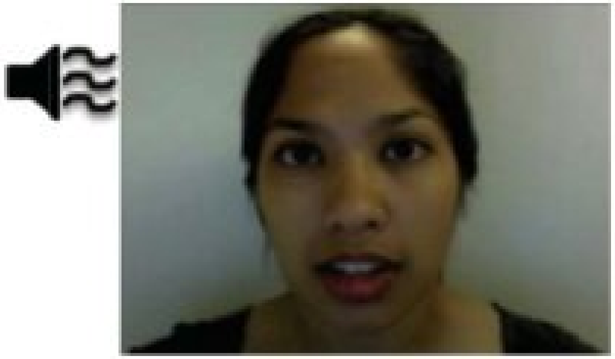
Review of stimulus conditions

- 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) **<u>Auditory-Reliable</u>**

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

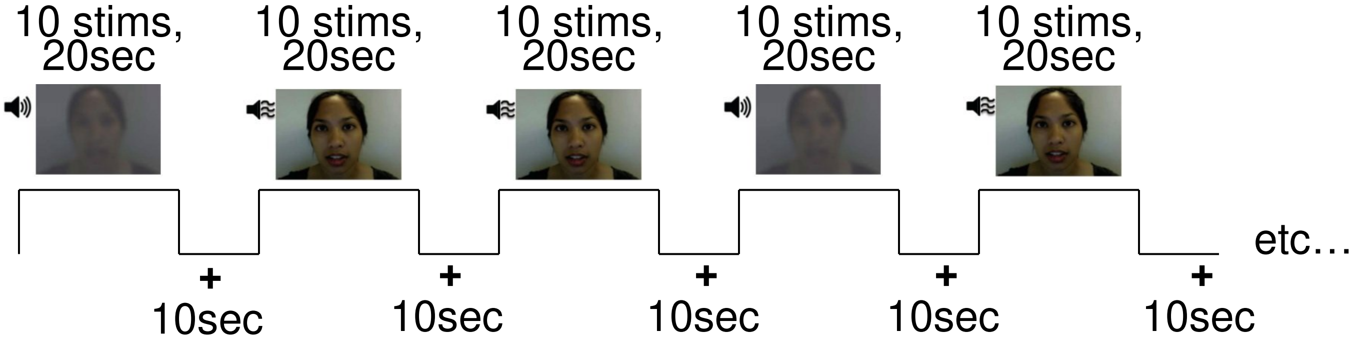


(2) **<u>Visual-Reliable</u>**

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.



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

- What is **afni_proc.py**?
  - a program used to generate processing scripts for single subject analysis
    - a short command can generate a long processing script to:
      - copy inputs into new ‘results’ directory
      - process data (e.g. tshift/align/tlrc/volreg/blur/scale/regress)
      - leave results in place to allow review of processing
      - create HTML report and **@ss_review_*** scripts, for quality control
    - many options for control over processing steps
    - many examples (in -help output) for getting started
  - generated scripts are in **tcsh** syntax
  - scripts are written to be easily read (good idea) and modified (bad idea)
  - preferable to run **afni_proc.py** (generating proc script) per subject
    - rather than running one (modified?) proc script across all subjects
    - graphical user interfaces exist (e.g. **uber_subject.py**), for those who prefer such things, but they are not recommended

Overview of remaining steps

- `cd AFNI_data6/FT_analysis`
  - review directory contents and note subject data under directory **`FT`**
  - review the **`afni_proc.py`** command in **`s05.ap.uber`**
- `tcsh s05.ap.uber`
  - runs **`afni_proc.py`** to generate proc script **`proc.FT`**
  - executes **`proc.FT`**, saving text output to **`output.proc.FT`**
  - processed results are under **`results.FT`** directory
- review proc script **`proc.FT`** while viewing processed data
  - `cd FT.results  ;  afni`
- review quality control HTML report
  - `afni_open -b FT.results/QC_FT/index.html`
- run group analysis (**`3dttest++, 3dMEMA or 3dANOVA2`**)
  - from the **`AFNI_data6/group_results`** directory:
  - `tcsh s6.ttest.covary`

Note what is under **AFNI_data6/FT_analysis**

FT	-	subject data directory
s01.ap.simple	-	basic **afni_proc.py** script
s05.ap.uber	-	more advanced script
s09.cleanup	-	remove analysis results
s11.proc.FT	-	result of **s01.ap.simple**
s15.proc.FT.uber	-	result of **s05.ap.uber**

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
SUMA	-	FreeSurer output for suma

AV1_vis.txt:

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

Single Subject Analysis: FT

- change to analysis directory and review **`afni_proc.py`** command
  - **`cd AFNI_data6/FT_analysis`**
  - **`cat s05.ap.uber`**
- execute that command, which also processes the data
  - **`tcsh s05.ap.uber`**
- review processing script and results
  - review the **`proc.FT`** script while looking at the results under **`FT.results`**
    - **`afni_open -e proc.FT`**
    - **`cd FT.results`**
    - **`ls`**
    - **`afni`**
- run automatically generated quality control review script
  - **`tcsh @ss_review_driver`**
    - considered a **minimal** data review (run for every subject)
    - for each step in the review:
      - ✓read prompt text in each black window and follow instructions
      - ✓close any windows newly opened by the script
      - ✓click “OK” to move on to the next step

Group Analysis: paired t-test (Vrel-Arel)

- `cd AFNI_data6/group_results`

- review the **`3dttest++`** script and possibly the covariates file
  - `cat s6.ttest.covary`
  - `cat covary.toe.gap.txt`

- execute the **`3dttest++`** command script
  - `tcsh s6.ttest.covary`

- view the results, in all their glory
  - `afni`
    - set OverLay to **`stat.6.covary`**
    - set OLay/Thr volumes to #0/#1, for Vrel-Arel and Tstat
    - threshold at p<0.005 (right-click on T-t above threshold slider)
    - set color range scale to 1.0
    - Clusterize (with defaults) and open Rpt (cluster report) window
    - jump to CMass (center of mass) locations

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