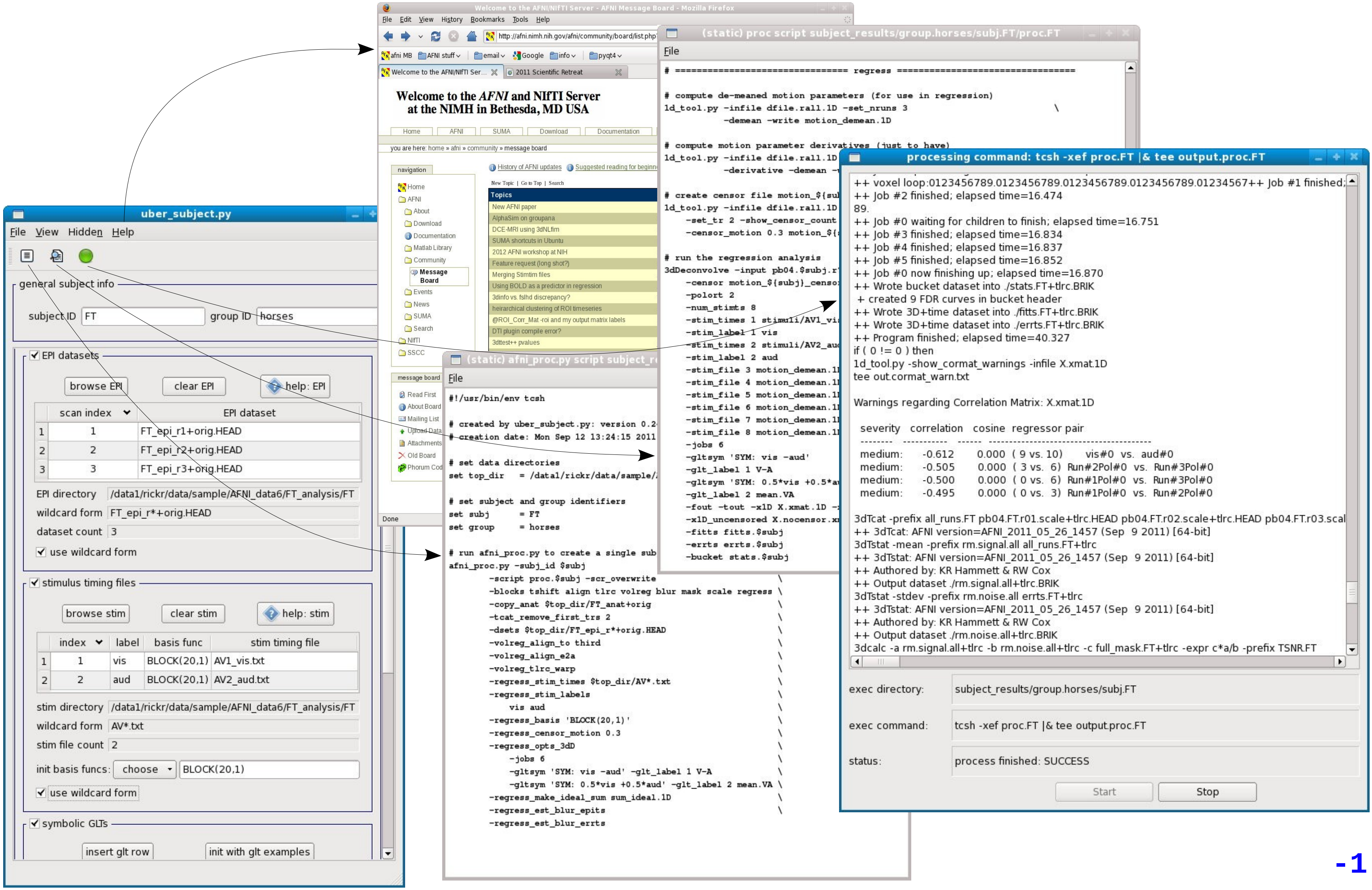
# AFNI Start to Finish:
# How to Analyze Data with AFNI



subject ID: FT
group ID: horses

| | 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

| | 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

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http://afni.nimh.nih.gov/afni/community/board/list.php
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2011 Scientific Retreat

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

```
#!/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
File

```
# ================================ 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`**, **`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 contrasts, t-stats, 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

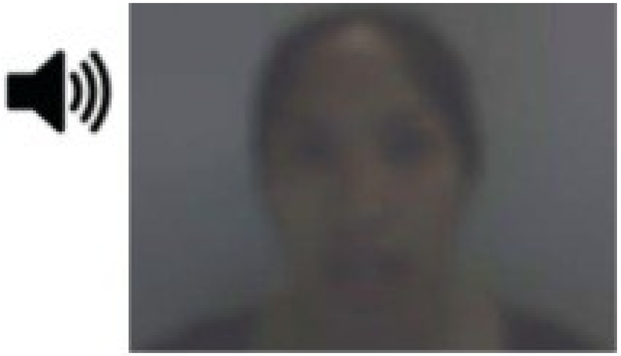
- focus on understanding the processing steps
    - in light of your having chosen which steps to perform

- 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 data (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>**

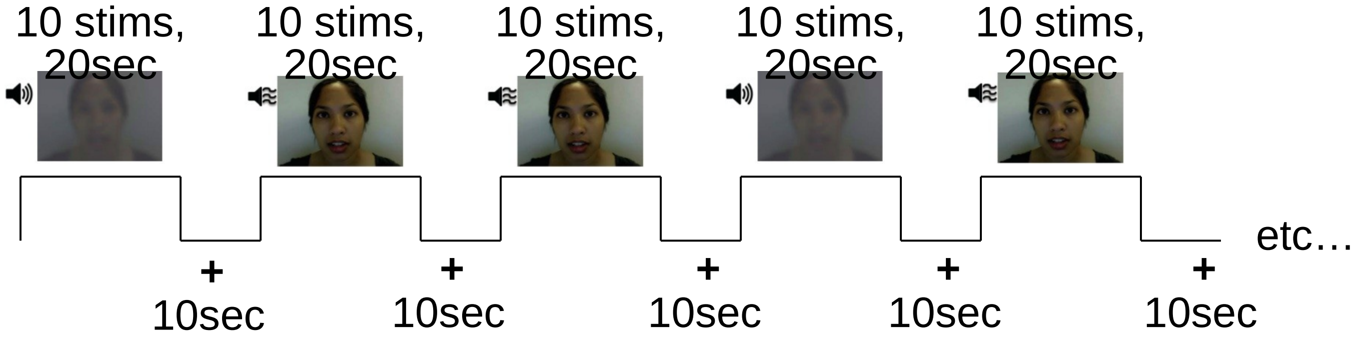
Example: Subjects can clearly *hear* the word “cat,” but the video of a woman mouthing the word is degraded.

(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**
# **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`**
- run **`uber_subject.py`** and analyze this subject
  - set subject ID, group ID
  - specify inputs: anat, EPI, stimulus timing files
  - controls: BLOCK(20,1), init GLTs, remove first 2 TRs
  - peruse other options, e.g. use 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
  - perhaps 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 script **`s1.3dANOVA2`**

1. Note what is under **AFNI_data6/FT_analysis**.

| | | |
|---|---|---|
| **FT** | - | subject data directory |
| **s01.ap.simple** | - | class 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** | - | autidory 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