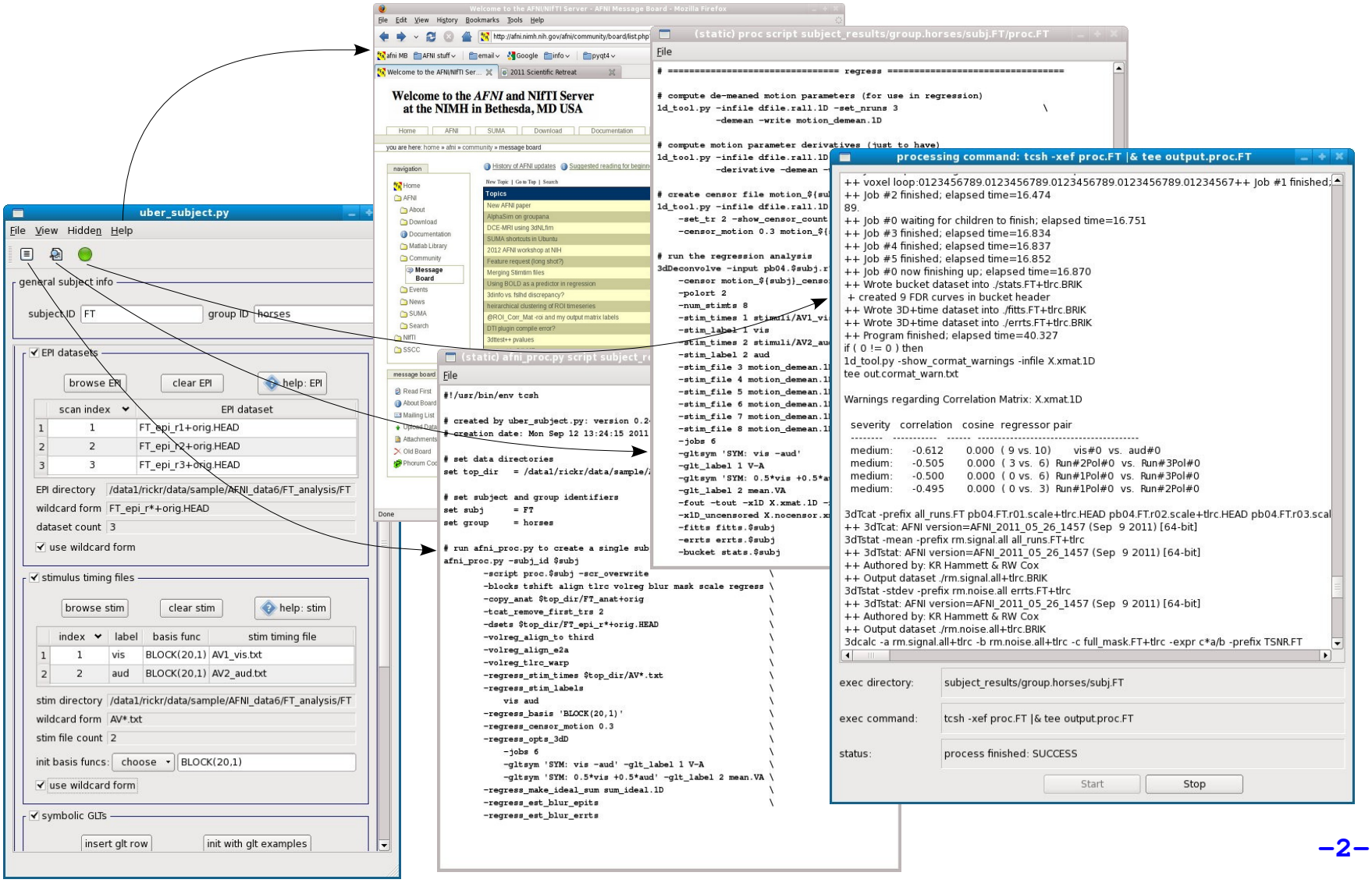
AFNI

Didactics and Demonstrations

AFNI Start to Finish:
FMRI Analysis with AFNI

Turning the pain level up to 11...

AFNI Start to Finish:
FMRI Analysis with AFNI



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.)

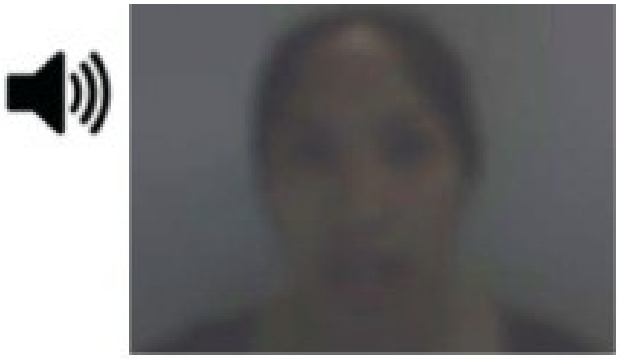
- how do we write single subject processing scripts?
  - **afni_proc.py** can be used to generate processing scripts
    - an **afni_proc.py** command can be included in publication
      - ✓along with the **AFNI** version (e.g. **AFNI_17.2.09**)
    - proc scripts are meant to be clear records of the 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?
  - do the resulting statistical maps look reasonable?
- 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

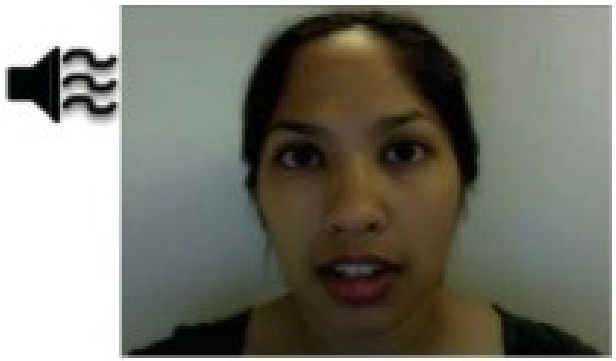
Review of stimulus conditions

- 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) **Auditory-Reliable**

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

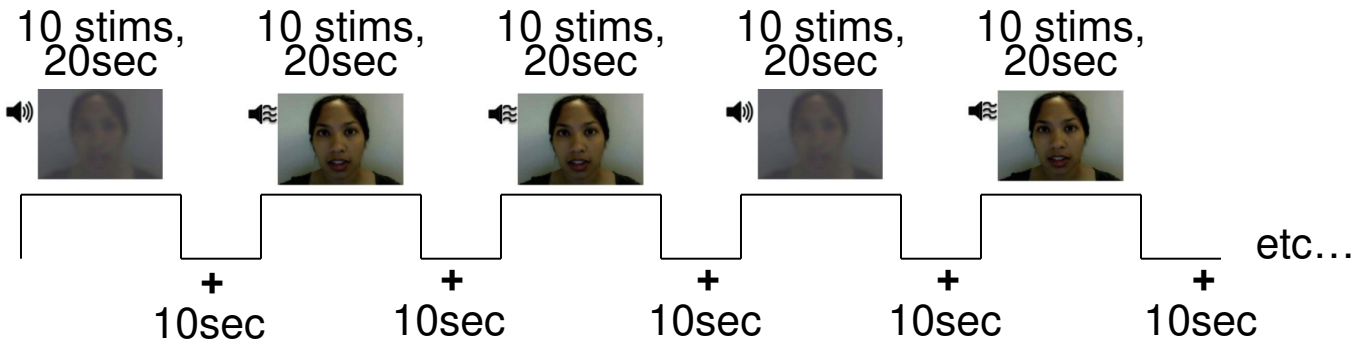


(2) **Visual-Reliable**

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.



❖ 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 **@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

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`**
- run quality control review script, **`@ss_review_driver`**
  - **`tcsh @ss_review_driver`**
- 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

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