

Hands-On Session: Regression Analysis

File: [afni05_regression.pdf](#)

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Overview

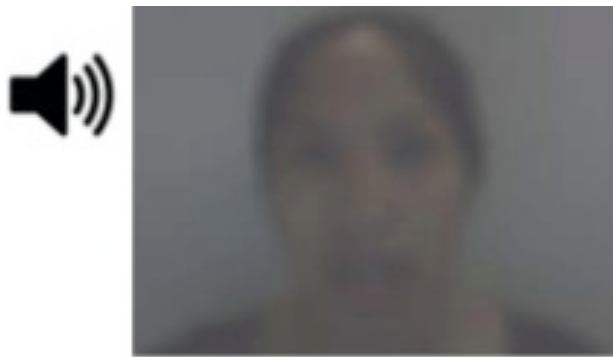
- What we have learned so far
 - Use data viewer ‘afni’ interactively
 - Model HRF with a **shape-prefixed** basis function (*e.g.*, Gamma variate)
 - Assume the brain responds with the **same shape**
 - Across **subjects**, any activated **regions**, stimulus **conditions/tasks**, **trials**
 - Differ in **magnitude**: β (and its significance) is what we focus on
- What we will do in this hands-on session
 - Data pre-processing overview for time series regression analysis
 - Basic concepts
 - Regressors, design matrix, and confounding effects
 - Statistical significance testing in regression analysis
 - Navigation with GUI ‘**afni**’
 - Spot check for the original data
 - Statistic thresholding with data viewer ‘**afni**’ (**two-sided** vs. **one-tailed** with t)
 - Model performance (visual check of curve fitting and test via full F or R^2)

FMRI Regression Analysis

- Voxel-wise regression model: $y = X\beta + \varepsilon$
 - y : signal (time series) at a voxel – **different** across voxels
 - X : explanatory (independent) variables (regressors) – **same** across voxels
 - β : regression coefficients (response strength) – **different** across voxels
 - ε : residuals (anything we can't account for) – **different** across voxels
- Regressors in design matrix $X = [x_1, x_2, \dots, x_k]$
 - Regressors of interest: hemodynamic responses (HDR)
 - Regressors of no interest: drift effect (polynomials), head motion, *etc.*
- Association between stimulus and BOLD signal: HDR/HRF
 - Pre-fixed shape regardless of subjects, brain regions, stimuli: regression
 - No assumption about the HDR shape: deconvolution + regression
 - Middle ground: regression
- Residuals
 - White noise: OLS – 3dDeconvolve
 - Serially correlated: ARMA(1,1)+REML – 3dREMLfit

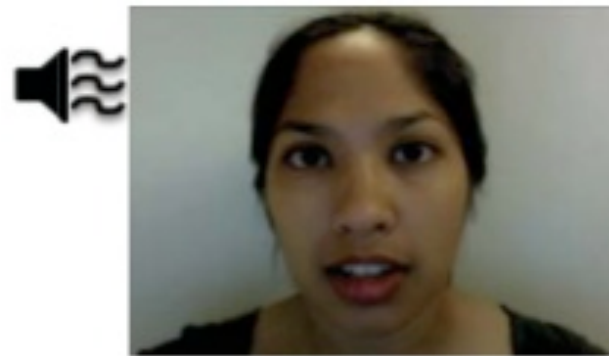
A Case Study

- ◆ **Speech Perception Task:** Subjects were presented with audiovisual speech 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.
- ◆ 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.

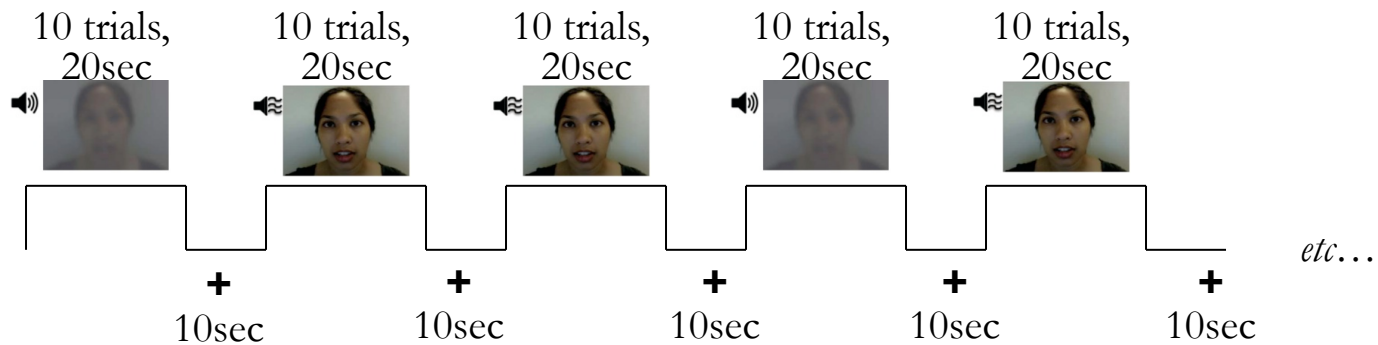


(2) **Visual-Reliable**

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

Experiment Design

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



Data Collected

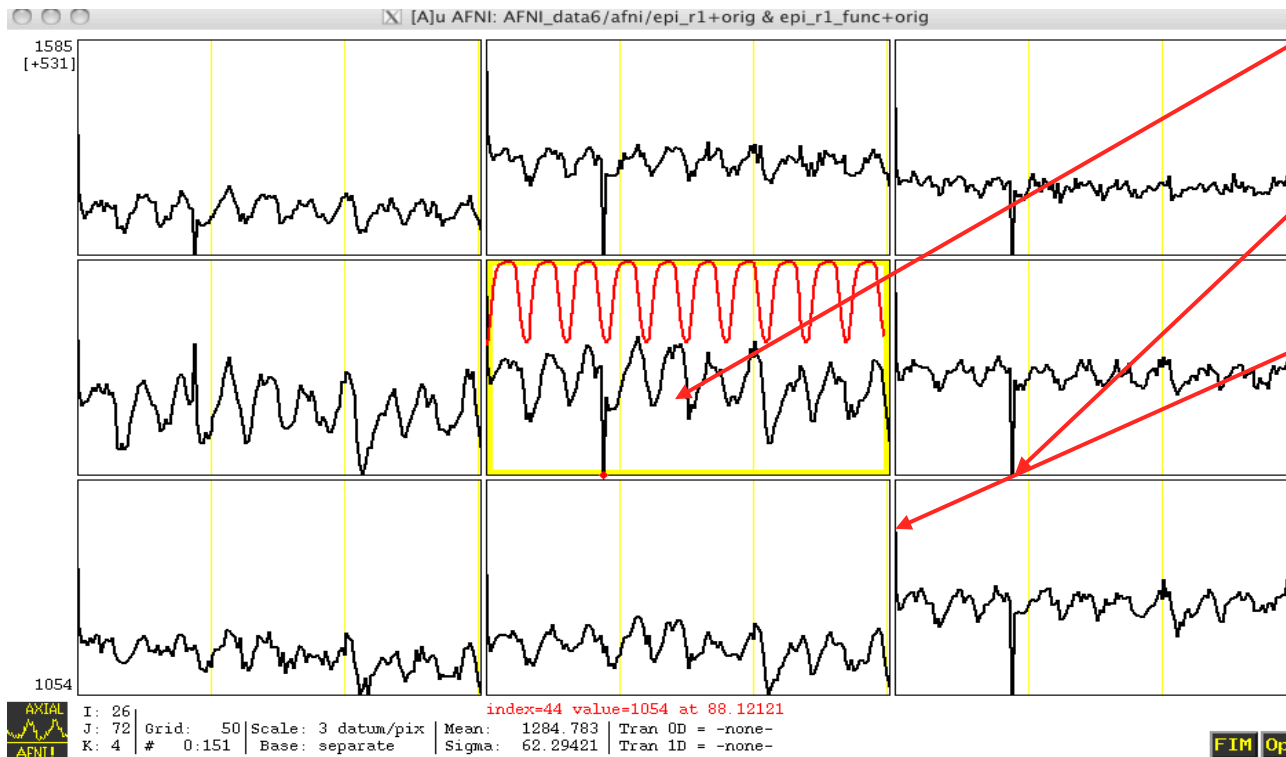
- ◆ 2 anatomical datasets for each subject from a 3T
 - 175 sagittal slices
 - voxel dimensions = $1.0 \times 0.938 \times 0.938 \text{ mm}^3$

- ◆ 3 time series (EPI) datasets for each subject
 - 33 axial slices \times 152 volumes (TRs) per run
 - TR = 2s; voxel dimensions = $2.75 \times 2.75 \times 3.0 \text{ mm}^3$

- ◆ Sample size, $\underline{n} = 10$ (all right-handed subjects)

Data Quality Check

- To look at the data: type `cd AFNI_data6/afni`, then `afni &`
- **Switch Underlay** to dataset `epi_r1`
 - Then **Axial Image** and **Graph**
 - **FIM**→**Pick Ideal** ; then click `afni/epi_r1_ideal.1D` ; then **Set**
 - Right-click in image, **Jump to (ijk)**, then `26 72 4`, then **Set**



- Data clearly has activity in sync with reference
 - 20s blocks
- Data also has a big spike at 89s
 - Head motion
- Spike at $t=0$
- Some tricks with keyboard
 - `oa`: automatic scaling
 - `ov`: video mode
 - `om/M`: voxel matrix sizing on Graph window

Preparing Data for Analysis

- Following preparatory steps are common (e.g., `afni_proc.py`):
 - Outliers: `3dToutcount` (or `3dTqual`), `3dDespike`
 - Temporal alignment or slice timing correction (sequential/interleaved): `3dTshift`
 - Image/volume registration (aka realignment, head motion correction): `3dvolreg`
 - Spatial normalization (standard space conversion): `adwarp`, `@auto_tlrc`, `align_epi_anat.py`
 - Blurring/smoothing: `3dmerge`, `3dBlurToFWHM`, `3dBlurInMask`
 - Masking: `3dAutomask`
 - Global mean scaling*: `3dROIstats` (or `3dmaskave`) and `3dcalc`
 - Temporal mean scaling: `3dTstat` and `3dcalc`
- Not all steps are necessary or desirable in any given case

Regression Analysis

- Regression model: $y = X\beta + \varepsilon$
- Run script by typing **tcs** **rall_regress** (takes a few minutes)

```
3dDeconvolve -input rall_vr+orig -polort 1 \
  -concat '1D: 0 150 300' \
  -num_stimts 8 \
  -stim_times 1 stim_AV1_vis.txt 'BLOCK(20,1)' -stim_label 1 Vrel \
  -stim_times 2 stim_AV2_aud.txt 'BLOCK(20,1)' -stim_label 2 Arel \
  -stim_file 3 motion.1D'[0]' -stim_base 3 -stim_label 3 roll \
  -stim_file 4 motion.1D'[1]' -stim_base 4 -stim_label 4 pitch \
  -stim_file 5 motion.1D'[2]' -stim_base 5 -stim_label 5 yaw \
  -stim_file 6 motion.1D'[3]' -stim_base 6 -stim_label 6 dS \
  -stim_file 7 motion.1D'[4]' -stim_base 7 -stim_label 7 dL \
  -stim_file 8 motion.1D'[5]' -stim_base 8 -stim_label 8 dP \
  -gltsym 'SYM: Vrel -Arel' -glt_label 1 V-A \
  -tout -x1D rall_X.xmat.1D -xjpeg rall_X.jpg \
  -fitts rall_fitts -bucket rall_func \
  -jobs 2
```

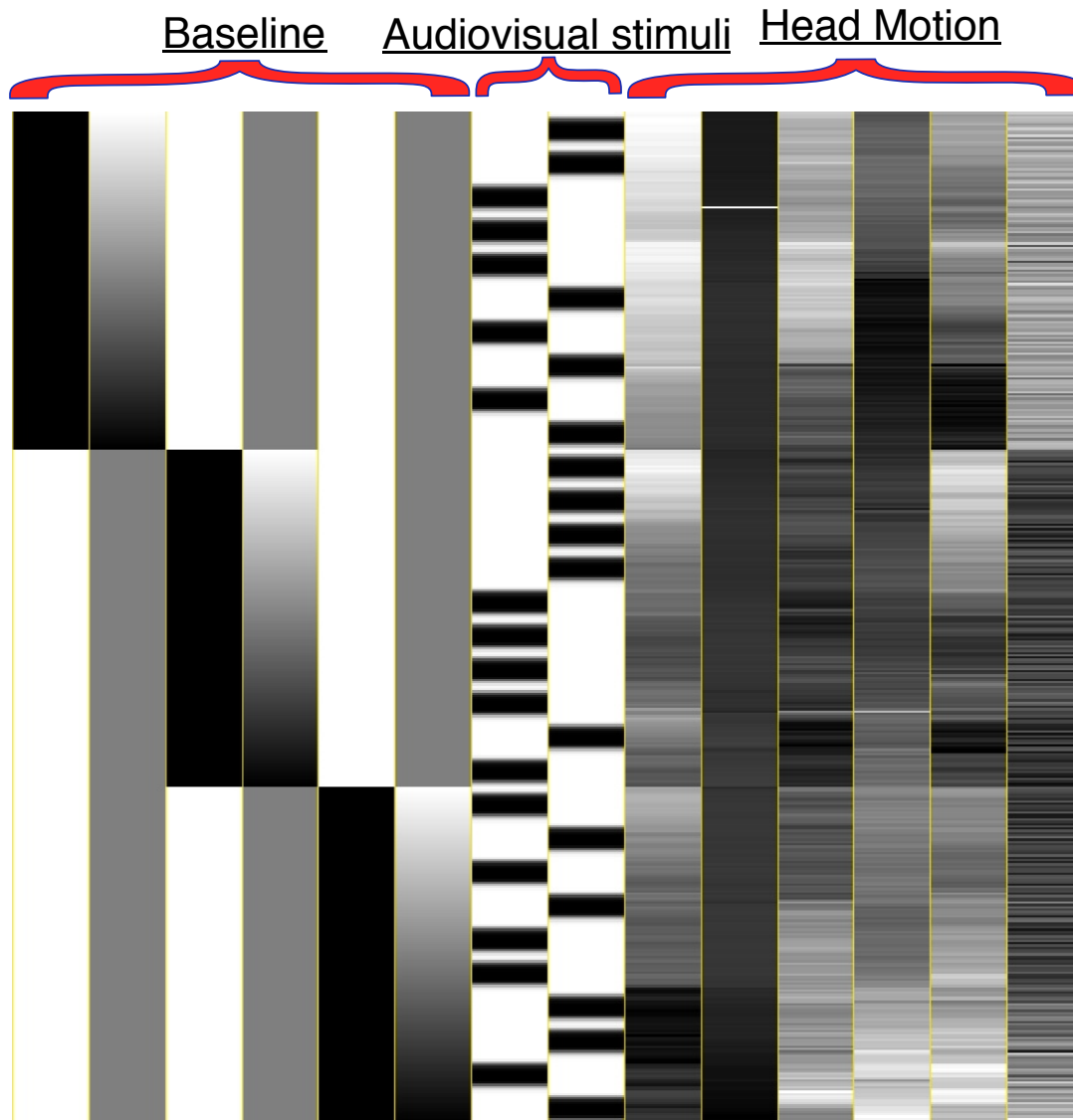
- 2 audiovisual stimulus classes were given using **-stim_times**
- **Important to include motion parameters as regressors?**
 - › May remove the confounding effects due to motion artifacts
 - › 6 motion parameters as covariates via **-stim_file + -stim_base**
 - › **motion.1D** generated from **3dvolreg** with the **-1Dfile** option
 - › Test the significance of head motion parameters
 - › Add **-bout** or remove **-stim_base**
 - › Use **-gltsym 'SYM: roll \ pitch \yaw \dS \dL \dP'**

Modeling Serial Correlation in the Residuals

- Temporal correlation exists in the residuals of the time series regression model
- Within-subject variability (or statistical value) would get deflated (or inflated) if temporal correlation is not accounted for in the model
- Better correct for the temporal correlation if bringing both effect size and within-subject variability to group analysis
- ARMA(1, 1) assumed in `3dREMLfit`
- Script automatically generated by 3dDeconvolve (may use `-x1D_stop`)
 - ★ File `rall_func.REML_cmd` under `AFNI_data6/afni`
 - ★ Run it by typing `tcsh -x rall_func.REML_cmd`

```
3dREMLfit -matrix rall_X.xmat.1D -input rall_vr+orig \  
-tout -Rbuck rall_func_REML -Rvar rall_func_REMLvar \  
-Rfitts rall_fitts_REML -verb
```

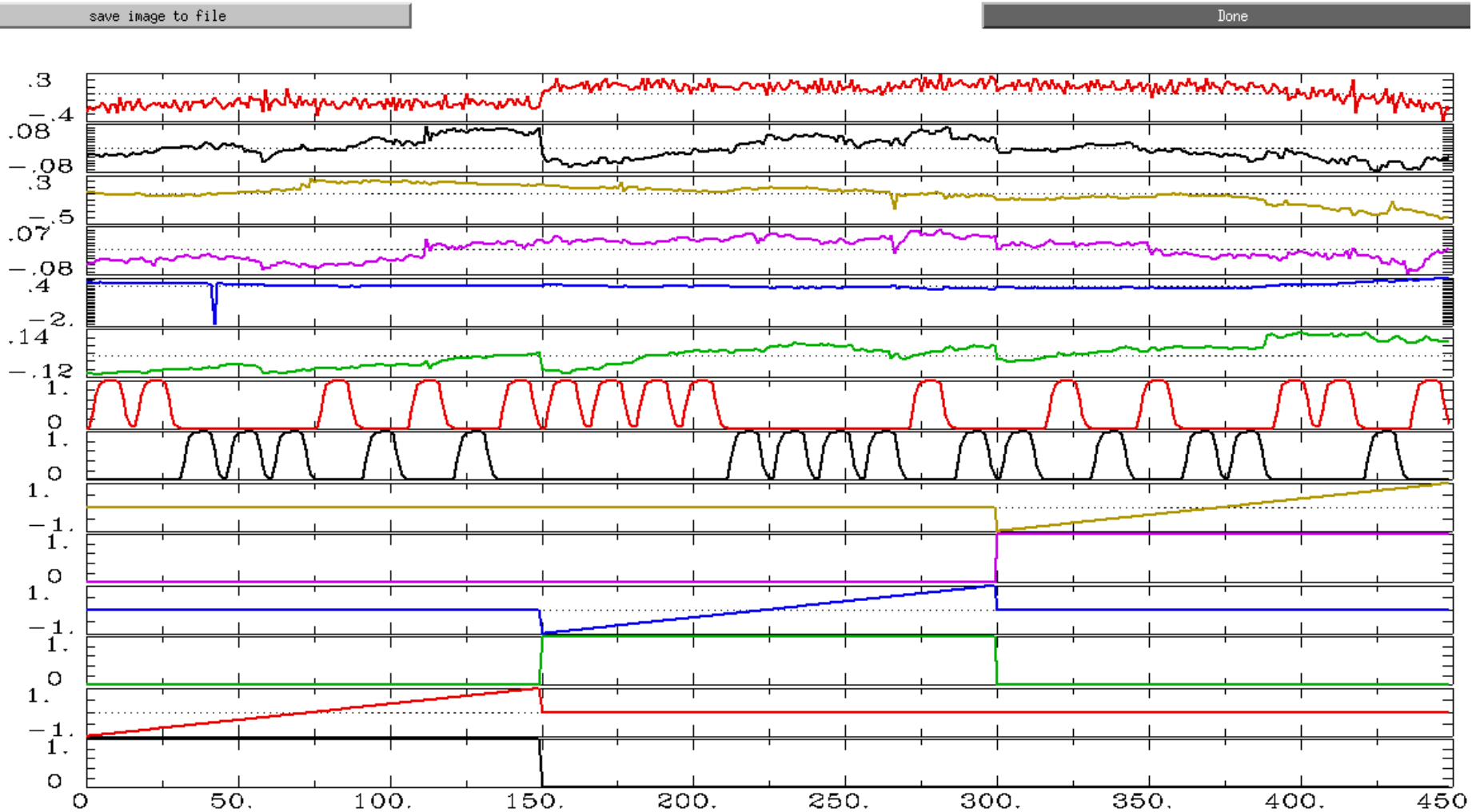
Regressor Matrix X for This Script (via -xjpeg)



- 6 drift effect regressors
 - linear baseline
 - 3 runs times 2 params/run
- 2 regressors of interest
- 6 head motion regressors
 - 3 rotations and 3 shifts

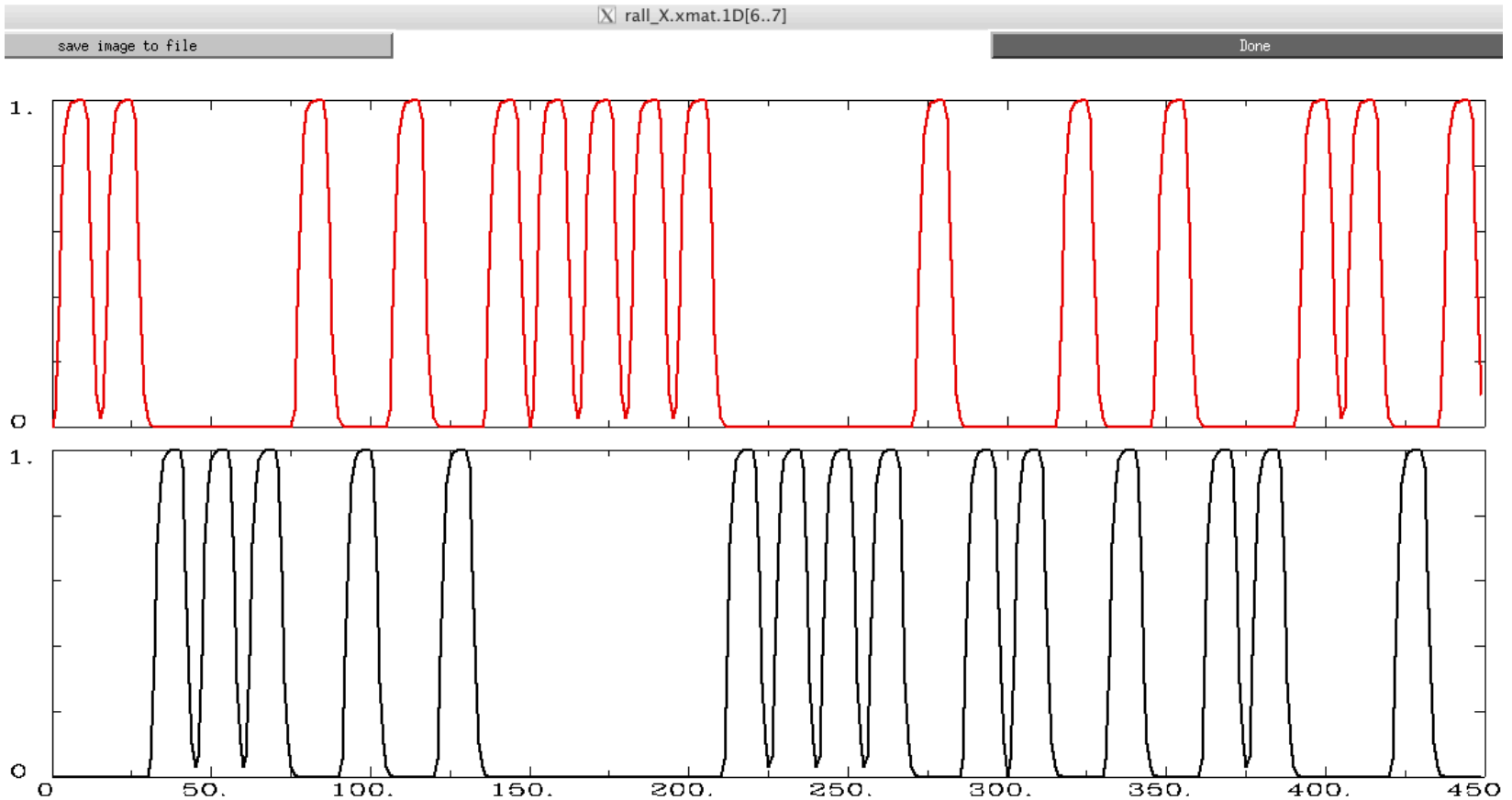
`aiv_rall_xmat.jpg`

Showing All Regressors (via -x1D)



All regressors: **1dplot -sepscl rall_X.mat.1D**

Plotting Regressors of Interest



Regressors of Interest: `1dplot rall_X.mat.1D'[6..7]'`

Options in 3dDeconvolve - 1

```
-concat '1D: 0 150 300'
```

- “File” that indicates where distinct imaging runs start inside the input file
 - Numbers are the time (TR) **indexes** inside the dataset file for start of runs
 - These time points are considered as **discontinuities** in the model
 - In this case, a text format .1D file put directly on the command line
 - Could also be a filename, if you want to store that data externally

```
-num_stimts 8
```

- 2 audiovisual stimuli (+6 motion), thus 2 `-stim_times` below
- Times given in the `-stim_times` files are *local* to the start of each run

```
-stim_times 1 stim_AV1_vis.txt 'BLOCK(20,1)' -stim_label 1 Vrel
```

- Content of `stim_AV1_vis.txt`

```
60 90 120 180 240
```

```
120 150 180 210 270
```

```
0 60 120 150 240
```

- ★ Each of 3 lines specifies start time in **seconds** for stimuli within the run

Options in 3dDeconvolve - 2

```
-gltsym 'SYM: Vrel -Arel' -glt_label 1 V-A
```

- **GLT**s: **General Linear Tests**
- **3dDeconvolve** provides test statistics for each regressor separately, but to test combinations of the β weights in each voxel, we need **-gltsym** option
- Example above tests the difference between the β weights for the **Virtual-reliable** and the **Audio-reliable** responses
 - **SYM:** means symbolic input is on command line
 - Otherwise inputs will be read from a file
 - Symbolic names for each regressor taken from **-stim_label** options
 - Stimulus label can be preceded by **+** or **-** to indicate sign to use in combination of β weights
 - **Leave space after each label!**
- Goal is to test a linear combination of the β weights
 - Null hypothesis $\beta_{Vrel} = \beta_{Arel}$
 - e.g., does **Vrel** get different response from **Arel**?
- What do **'SYM: 0.5*Vrel +0.5*Arel'** and **'SYM: Vrel \ Arel'** test?

Options in 3dDeconvolve - 4

-fout -tout = output both F - and t -statistics for each stimulus class (**-fout**) and stimulus coefficient (**-tout**) — but not for the baseline coefficients (use **-bout** for baseline)

- The full model statistic is an F -statistic that shows how well all the regressors of interest explain the variability in the voxel time series data
 - Compared to how well *just* the baseline model time series fit the data times (in this example, we have 12 baseline regressor columns in the matrix — 6 for the linear drift, plus 6 for motion regressors)
 - $F = [SSE(r) - SSE(f)] / df(n) \div [SSE(f) / df(d)]$
- The individual stimulus classes also will get individual F - (if **-fout** added) and/or t -statistics indicating the significance of their individual *incremental* contributions to the data time series fit
 - If $DF=1$ (e.g., F for a single regressor), t is equivalent to F : $t(n) = F^2(1, n)$

Results of **rall_regress** Script

The image displays the AFNI software interface. At the top, three windows show brain slices in sagittal, axial, and coronal views, each with colored overlays representing statistical results. The sagittal view is labeled 'Sagittal: left=Anterior short [2%-98%]' with slice 55. The axial view is labeled 'Axial: left=Right short [2%-98%]' with slice 144. The coronal view is labeled 'Coronal: left=Right short [2%-98%]' with slice 233. To the right is a control panel with various settings. At the bottom center is a menu window titled 'menu' with the following content:

```
-----Choose One-----
0Lay
#0 Full_Fstat
#1 Vrel#0_Coef
#2 Vrel#0_Tstat
#3 Arel#0_Coef
#4 Arel#0_Tstat
#5 V-A_GLT#0_Coef
#6 V-A_GLT#0_Tstat
Quit Apply Set
Index 6
```

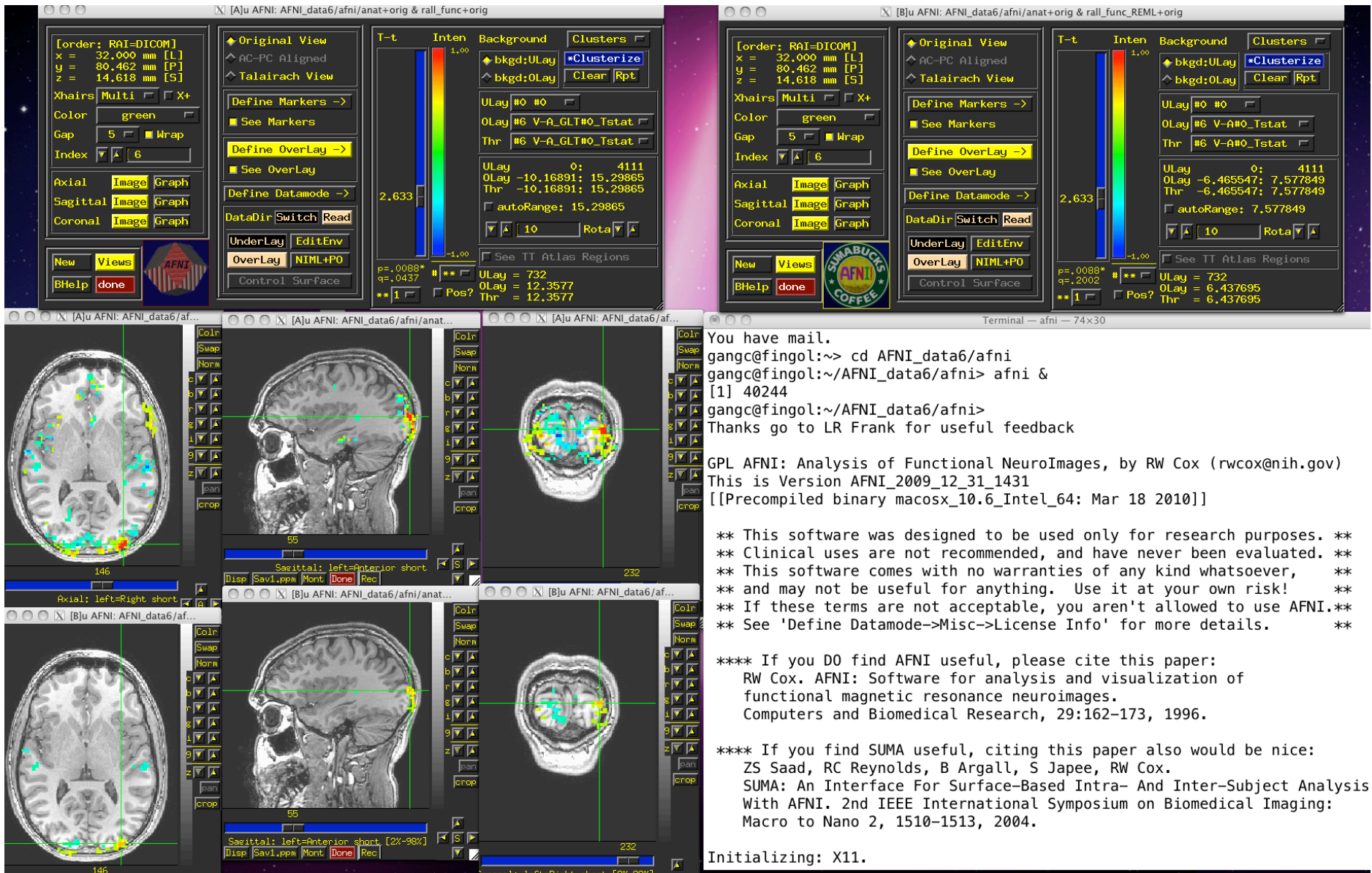
Blue arrows point from the menu window to the three brain scan windows, indicating that the menu options correspond to the data shown in the slices.

• Images showing results from third GLT contrast: **VrelvsArel**

• Menu showing labels from **3dDeconvolve**

• Play with these results yourself!

Compare 3dDeconvolve and 3dREMLfit



The image displays a comparison of AFNI software results for two different analysis methods: 3dDeconvolve (left) and 3dREMLfit (right). Both windows show a 3D brain slice with a color scale from -1.00 to 1.00. The left window shows a cluster of significant voxels in red and yellow, while the right window shows a similar cluster but with a different threshold. Below the windows is a terminal window with the following text:

```
You have mail.
gangc@fingol:~> cd AFNI_data6/afni
gangc@fingol:~/AFNI_data6/afni> afni &
[1] 40244
gangc@fingol:~/AFNI_data6/afni>
Thanks go to LR Frank for useful feedback

GPL AFNI: Analysis of Functional NeuroImages, by RW Cox (rwcox@nih.gov)
This is Version AFNI_2009_12_31_1431
[[Precompiled binary macosx_10.6_Intel_64: Mar 18 2010]]

** This software was designed to be used only for research purposes. **
** Clinical uses are not recommended, and have never been evaluated. **
** This software comes with no warranties of any kind whatsoever, **
** and may not be useful for anything. Use it at your own risk! **
** If these terms are not acceptable, you aren't allowed to use AFNI.**
** See 'Define Datamode->Misc->License Info' for more details. **

**** If you DO find AFNI useful, please cite this paper:
RW Cox. AFNI: Software for analysis and visualization of
functional magnetic resonance neuroimages.
Computers and Biomedical Research, 29:162-173, 1996.

**** If you find SUMA useful, citing this paper also would be nice:
ZS Saad, RC Reynolds, B Argall, S Japee, RW Cox.
SUMA: An Interface For Surface-Based Intra- And Inter-Subject Analysis
With AFNI. 2nd IEEE International Symposium on Biomedical Imaging:
Macro to Nano 2, 1510-1513, 2004.

Initializing: X11.
```

Group Analysis: will be carried out on β or GLT coef (+t-value) from single-subject analysis