

Hands-On Session: Regression Analysis

- What we have learned so far

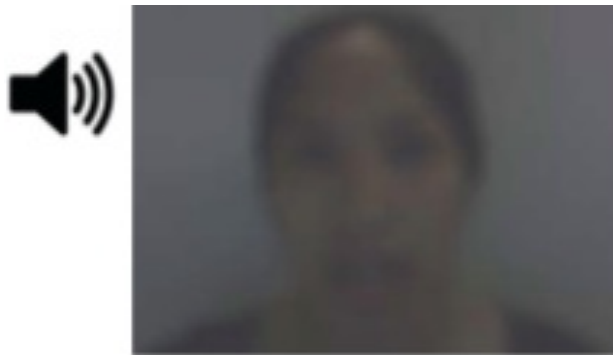
- Use data viewer 'afni' interactively
- Model HRF with a **shape-prefixed** basis function
 - ❑ Assume the brain responds with the **same shape**
 - in any active regions
 - regardless stimulus types
 - ❑ Differ in **magnitude**: β (and its significance) is what we focus on

- What we will do in this session

- Data pre-processing overview for time series regression analysis
- Basic concepts of regressors, design matrix, and confounding effects
- Statistical significance testing in regression analysis
- Navigation with GUI '**afni**'
 - ❑ Spot check for the original data
 - ❑ Statistics 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)

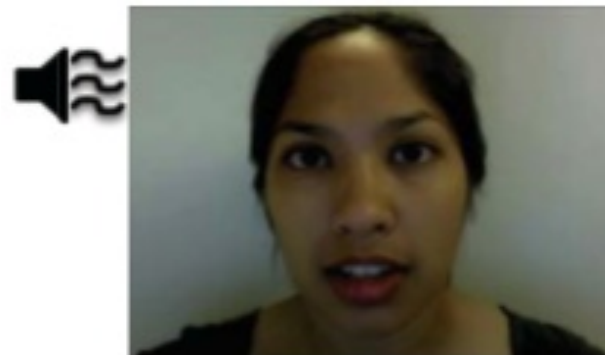
A Case Study

- ◆ **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

- ◆ 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* 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

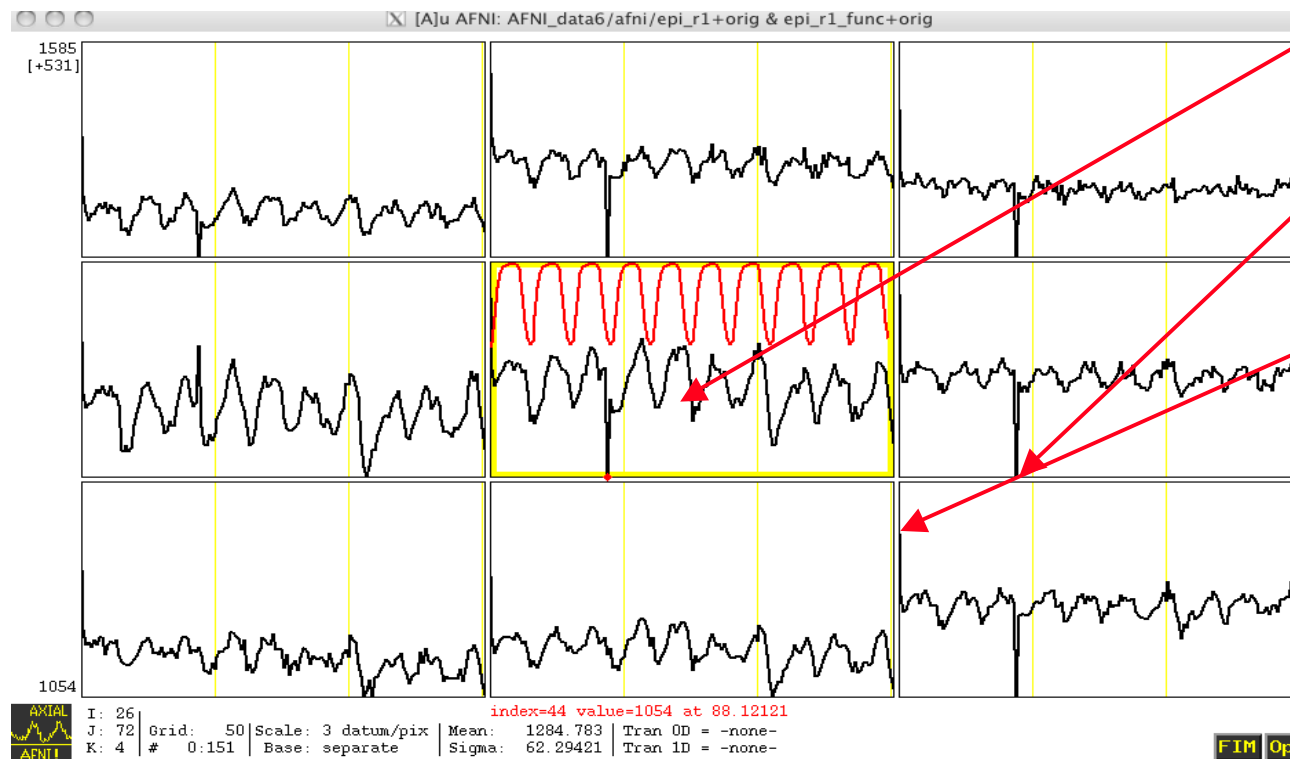
- ◆ 2 anatomical datasets for each subject from a 3T
 - 175 sagittal slices
 - voxel dimensions = $1.0 \times 0.938 \times 0.938$ mm

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

- ◆ Sample size, $n = 10$ (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
 - `a`: automatic scaling
 - `v`: video mode
 - `m/M`: voxel matrix sizing on Graph window

Preparing Data for Analysis

- Eight preparatory steps are common:
 - 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

- Run script by typing **tcsh rall_regress** (takes a few minutes)

```
3dDeconvolve -input rall_vr+orig \
  -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?**

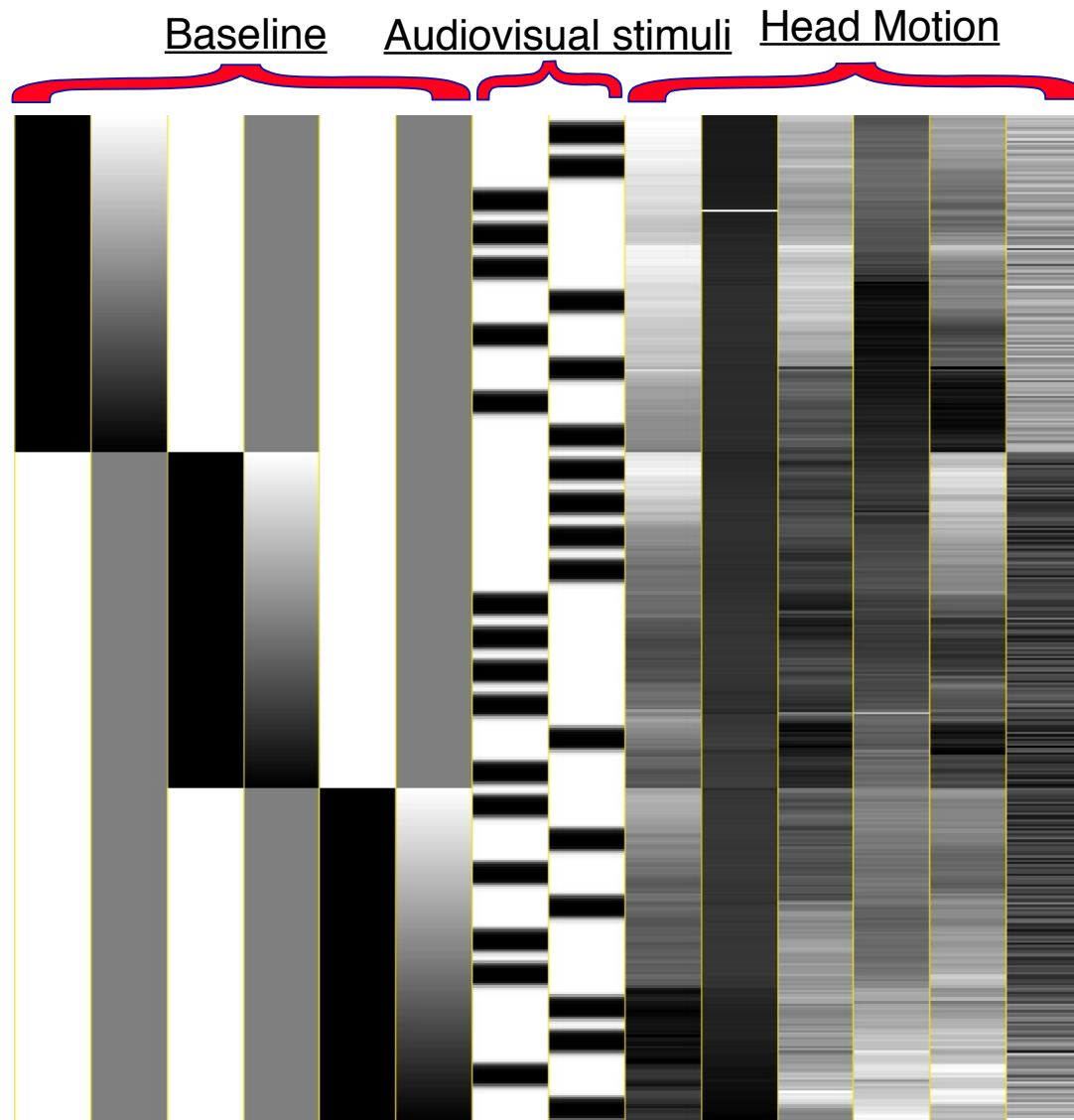
- › May remove the confounding effects due to motion artifacts
- › 6 motion parameters as covariates via **-stim_file + -stim_base**
- › **motion.1D** generated from **3dvolreg** with the **-1Dfile** option
- › Test the significance of head motion parameters
 - › Switch from **-stim_base** to **-stim_label roll ...**
 - › 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 `tcsch -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 for This Script (via -xjpeg)

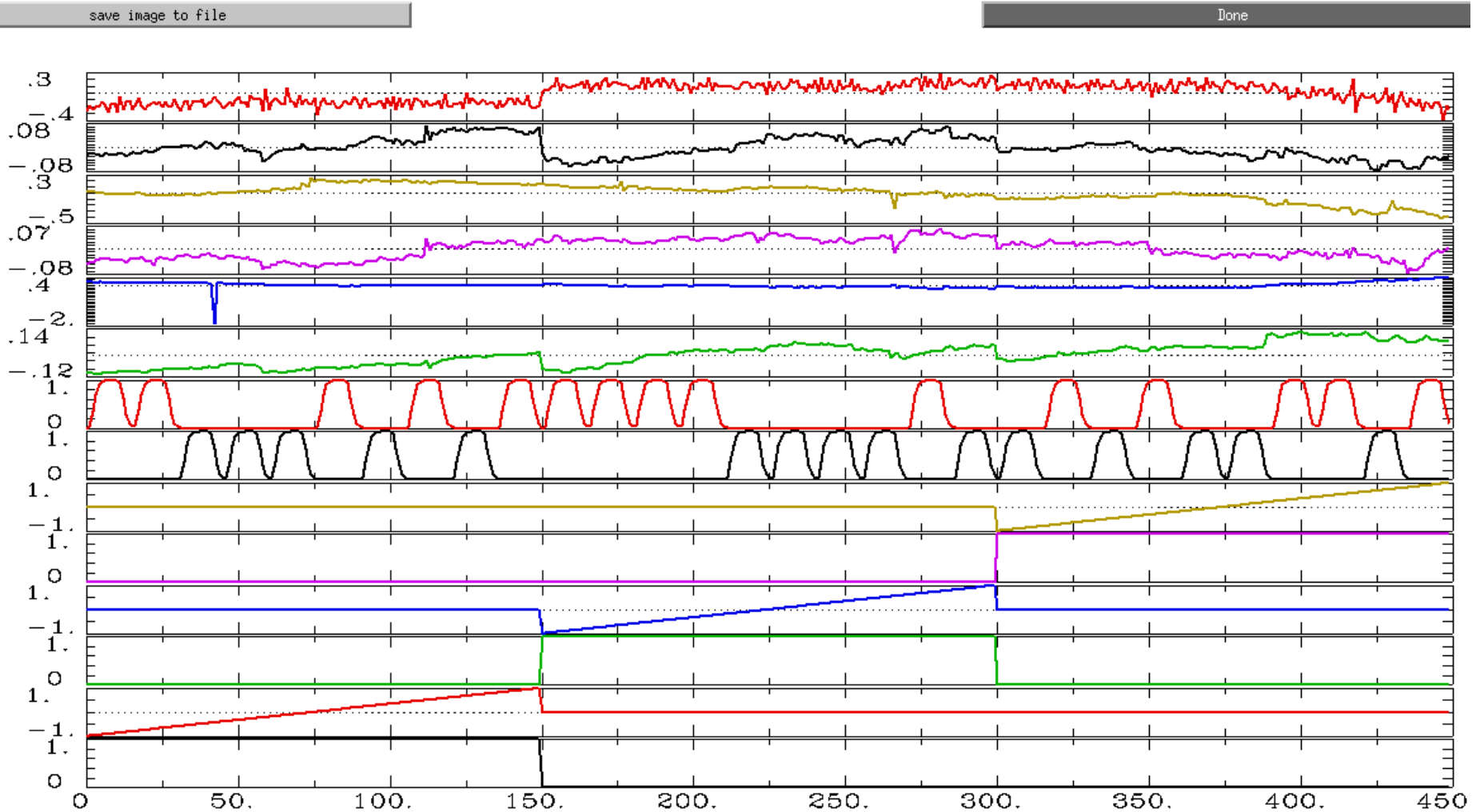


- 6 drift effect regressors
 - linear baseline
 - 3 runs times 2 params/run
- 2 regressors of interest

- 6 head motion regressors
 - 3 rotations and 3 shifts

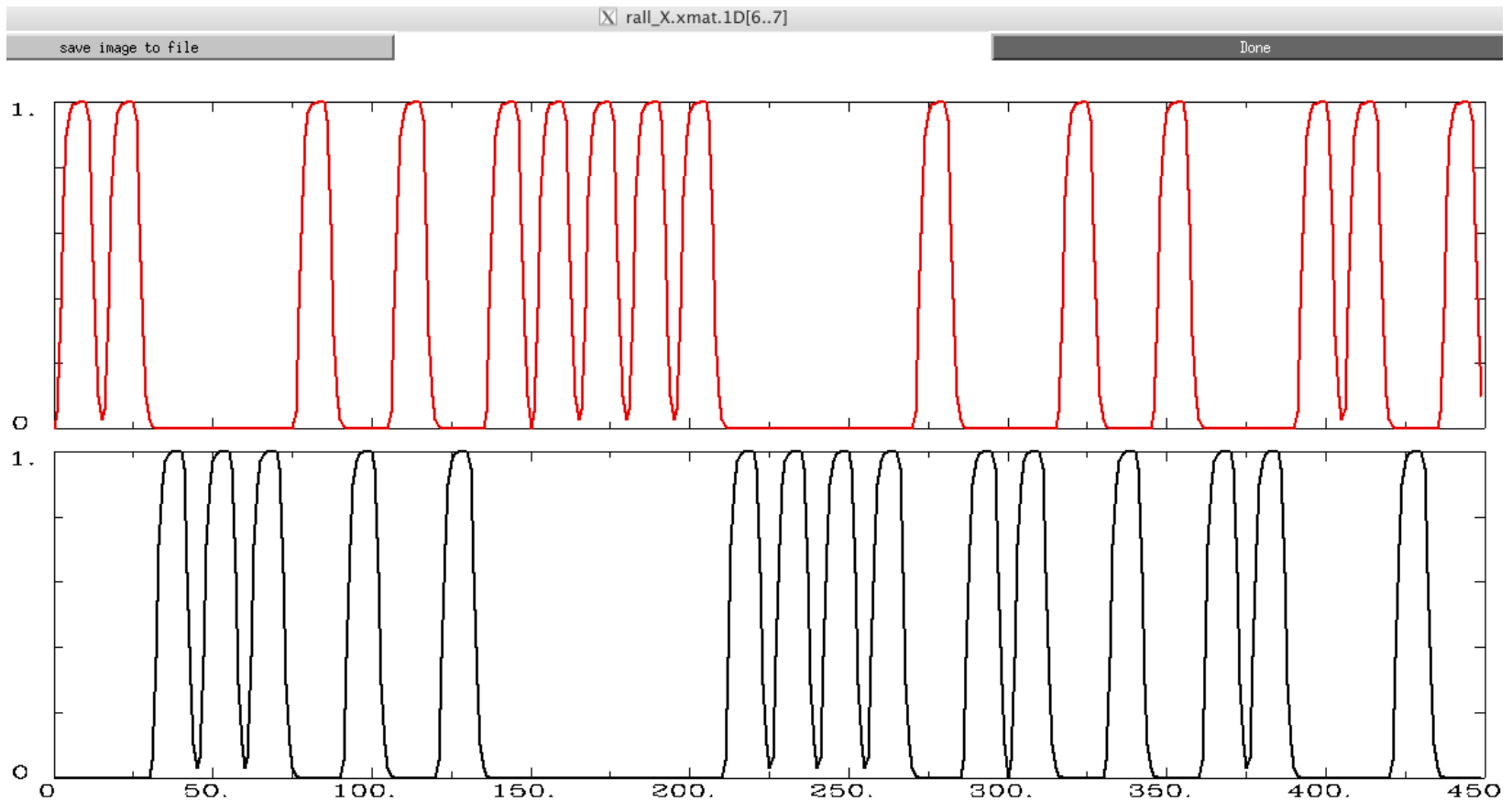
`aiv_rall_xmat.jpg`

Showing All Regressors (via -x1D)



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

Showing 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
```

- **GLTs**: 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. On the left, three brain scan windows show results in different views: Sagittal (top), Axial (middle), and Coronal (bottom). Each window shows a brain slice with colored regions (yellow, orange, red, blue) indicating statistical significance. The top window is labeled 'Sagittal: left=Anterior short [2%-98%]' and the middle 'Axial: left=Right short [2%-98%]'. The bottom window is labeled 'Coronal: left=Right short [2%-98%]'. To the right of the top window is a control panel with various settings: 'Original View' (AC-PC Aligned, Talairach View), 'Define Markers', 'Define Overlay', 'Define Datamode', 'DataDir', 'UnderLay', 'OverLay', 'Control Surface', 'New Views', 'BHHelp', 'done'. Below this is a menu window titled 'menu' with the following text: '----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'. To the right of the menu window is a list of bullet points: '• Images showing results from third GLT contrast: **VrelvsArel**', '• Menu showing labels from **3dDeconvolve**', '• Play with these results yourself!'. The top right window shows a 'T-t' plot with a color scale from -1.00 to 1.00, and a 'Background' section with 'Clusters' and 'Clusterize' buttons. The 'Clusters' section shows 'Ulay #0 #0', '0Lay #6 V-A_GLT#0_Tstat', and 'Thr #6 V-A_GLT#0_Tstat'. The 'Background' section shows 'Ulay 0: 4111', '0Lay -10.16891: 15.29865', and 'Thr -10.16891: 15.29865'. The 'T-t' plot shows a value of 2.757. The 'Background' section also shows 'p=.0061*', 'q=.0343', '# 10', 'Ulay = 423', '0Lay = 11.22595', and 'Thr = 11.22595'.

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

• Menu showing labels from **3dDeconvolve**

• Play with these results yourself!

Compare 3dDeconvolve and 3dREMLfit

The screenshot displays the AFNI software interface. The top row shows two windows side-by-side, labeled [A] and [B]. Both windows have a similar layout with control panels on the left and right, and a central display area. The left panel contains options for 'Original View' (AC-PC Aligned, Talairach View), 'Define Markers', 'Define Overlay', 'Define Datamode', 'DataDir', 'Switch', 'Read', 'UnderLay', 'EditEnv', 'OverLay', 'NIML+PO', and 'Control Surface'. The right panel contains 'T-t Inten' (with a color scale from -1.00 to 1.00), 'Background', 'Clusters', 'bkgd:ULay', 'Clusterize', 'Clear', 'Rpt', 'ULay #0 #0', 'OLay #6 V-A_GLT#0_Tstat', 'Thr #6 V-A_GLT#0_Tstat', 'ULay 0: 4111', 'OLay -10.16891: 15.29865', 'Thr -10.16891: 15.29865', 'autoRange: 15.29865', 'ULay = 732', 'OLay = 12.3577', 'Thr = 12.3577', 'p=.0088*', 'q=.0437', '#**', 'ULay = 732', 'OLay = 12.3577', 'Thr = 12.3577', 'ULay = 732', 'OLay = 6.437695', 'Thr = 6.437695', 'p=.0088*', 'q=.2002', '#**', 'ULay = 732', 'OLay = 6.437695', 'Thr = 6.437695'. The central display area shows three brain slices (axial, sagittal, coronal) with colored overlays. The bottom right window is a terminal window with the following text:

```

Terminal - afni - 74x30
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