

Deconvolution Approach to Modeling

- Deconvolution + regression

- ★ What is deconvolution in the context of fMRI regression?
- ★ How different from shape-prefixed approach?
- ★ Pros and cons
- ★ Implementation via TENT basis function in 3dDeconvolve
- ★ Collinearity issue
- ★ Complications for group analysis

- Example of HRF modeling with TENT basis function

- ★ Preprocessing steps
- ★ Regression model with 3dDeconvolve
- ★ Stimulus timing setup
- ★ Specifications for general linear testing: t and F

Deconvolution vs. Convolution

- Convolution + regression

- ★ Impulse response © stimulus = BOLD response (speed X time = dist.)
- ★ Known: impulse response, stimulus, and BOLD response to a stimulus
- ★ Use convolution to create regressors (waver or 3dDeconvolve)
- ★ Then response strength (β) estimated via regression
- ★ Regression with each condition modeled with one basis function

- Deconvolution + regression

- ★ Deconvolution: derive impulse response or stimulus when the other 2 known in impulse response © stimulus = BOLD response
- ★ Known: stimulus and BOLD response; unknown: impulse response
- ★ Have to estimate average BOLD response to stimuli
- ★ Set a yardstick at each sliding window
- ★ Stimulus response as a linear combination of multiple yardsticks
- ★ Combination of multiple yardsticks © stimulus = regressors
- ★ Deconvolution: combination weights (β) estimated via regression

Fixed vs. flexible shape modeling

- Basic or Fixed-shape regression (previous talks):
 - ★ Conservative: fix the shape of the HRF — amplitude varies
 - ★ Generally used in block or some event-related experiments
 - ★ Use `-stim_times` to generate regressors from stimulus timing
 - ★ Find “average” response amplitude in each voxel — solution to the set of linear equations = β weights
- Deconvolution or Variable-shape regression (now):
 - ★ Liberal: Allow HRF shape to vary in each voxel, for each stimulus class
 - ★ Generally used in event-related or occasionally some block designs
 - ★ Appropriate when you don’t want to over-constrain the solution by assuming an HRF shape
 - ★ **Caveat** : need to have enough time points during the HRF in order to resolve its shape (e.g., $TR \leq 3$ s)
- There’s always a middle ground
 - ★ Moderate: some wiggle room in shape modeling

Deconvolution: Pros & Cons (+ & -)

- + Likely to have more accurate response estimate: allowing for subject and regional variability in hemodynamics
- + Can test subtle shape difference (e.g., later time points more “active” than earlier? Undershoot?)
- Need to estimate more parameters for each stimulus class (e.g., 4-15 vs. 1)
- Need more data to get same statistical power (assuming fixed-shape model used was in fact “correct”)
- May lead to weird HRF shapes that are difficult to interpret
- Overfitting: noise, head motion, or other regressors may leak into shape estimate
- Challenging for group analysis with multiple β s per regressor: [3dLME](#)

Expressing HRF via Regression Unknowns

- The tool for expressing an unknown function as a finite set of numbers that can be fit via linear regression is an **expansion in basis functions**

$$h(t) = \beta_0\psi_0(t) + \beta_1\psi_1(t) + \beta_2\psi_2(t) + \dots = \sum_{q=0}^{q=p} \beta_q\psi_q(t)$$

- ★ Basis functions $\psi_q(t)$ & expansion order p are known
 - Larger $p \Rightarrow$ more complex shapes & more parameters
- ★ Unknowns: weight β_q for each $\psi_q(t)$
- Regressors created through convolution of stimulus timing with $h(t)$
- β s solved with the regressors in **3dDeconvolve**

3dDeconvolve with “Tent Functions”

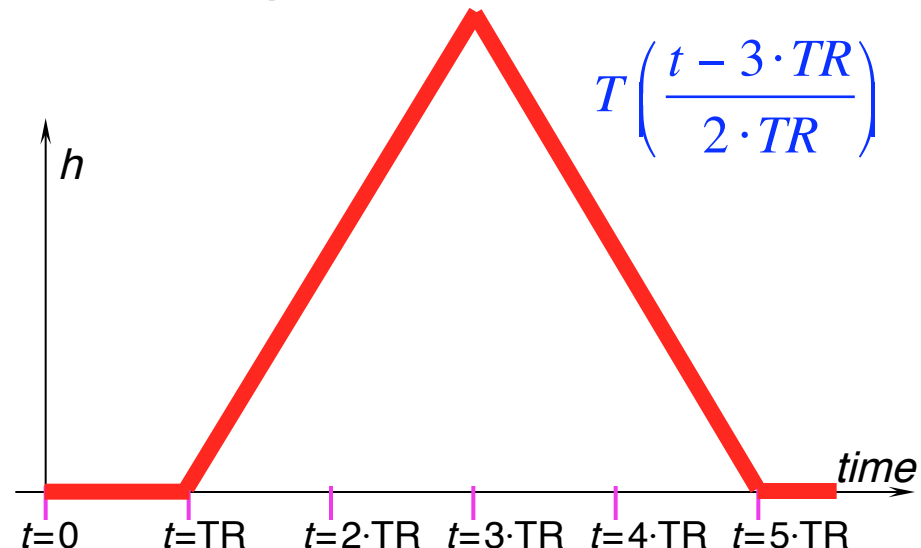
- Need to describe HRF shape and magnitude with a finite number of parameters
 - ★ **Convolution**: allows for calculation of $h(t)$ at any arbitrary point in time after the stimulus times:

$$r_n = \sum_{k=1}^K h(t_n - \tau_k) = \text{sum of HRF copies}$$

- Simplest set of such functions are tent functions
 - ★ Also known as “piecewise linear splines”

$$T(x) = \begin{cases} 1 - |x| & \text{for } -1 < x < 1 \\ 0 & \text{for } |x| > 1 \end{cases}$$

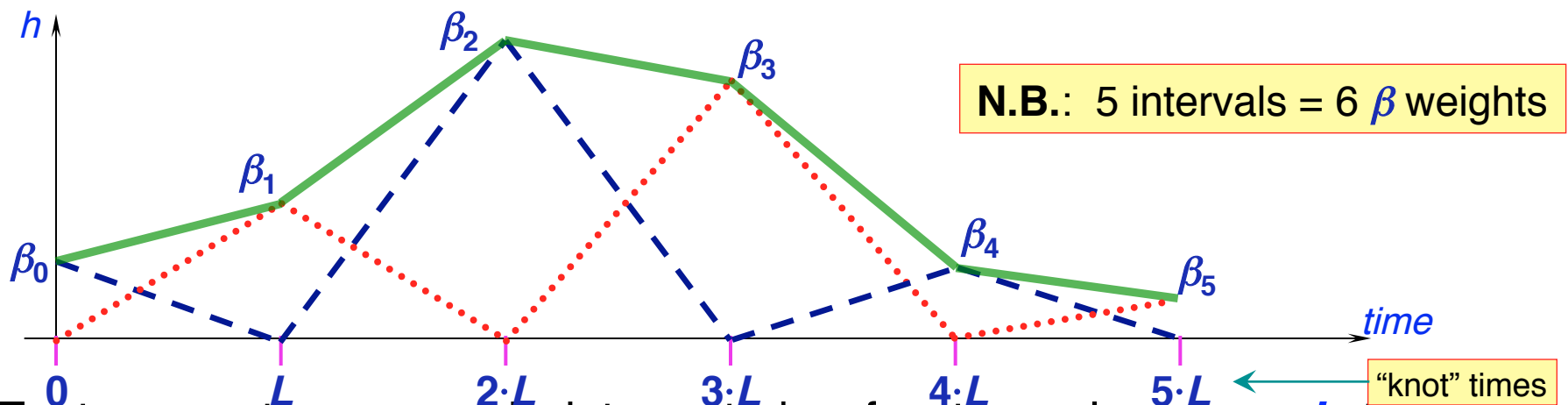
N.B.: cubic splines are also available



Tent Functions = Linear Interpolation

- Expansion of HRF in a set of spaced-apart tent functions is the same as linear interpolation between “knots”

$$h(t) = \beta_0 \cdot T\left(\frac{t}{L}\right) + \beta_1 \cdot T\left(\frac{t-L}{L}\right) + \beta_2 \cdot T\left(\frac{t-2 \cdot L}{L}\right) + \beta_3 \cdot T\left(\frac{t-3 \cdot L}{L}\right) + \dots$$



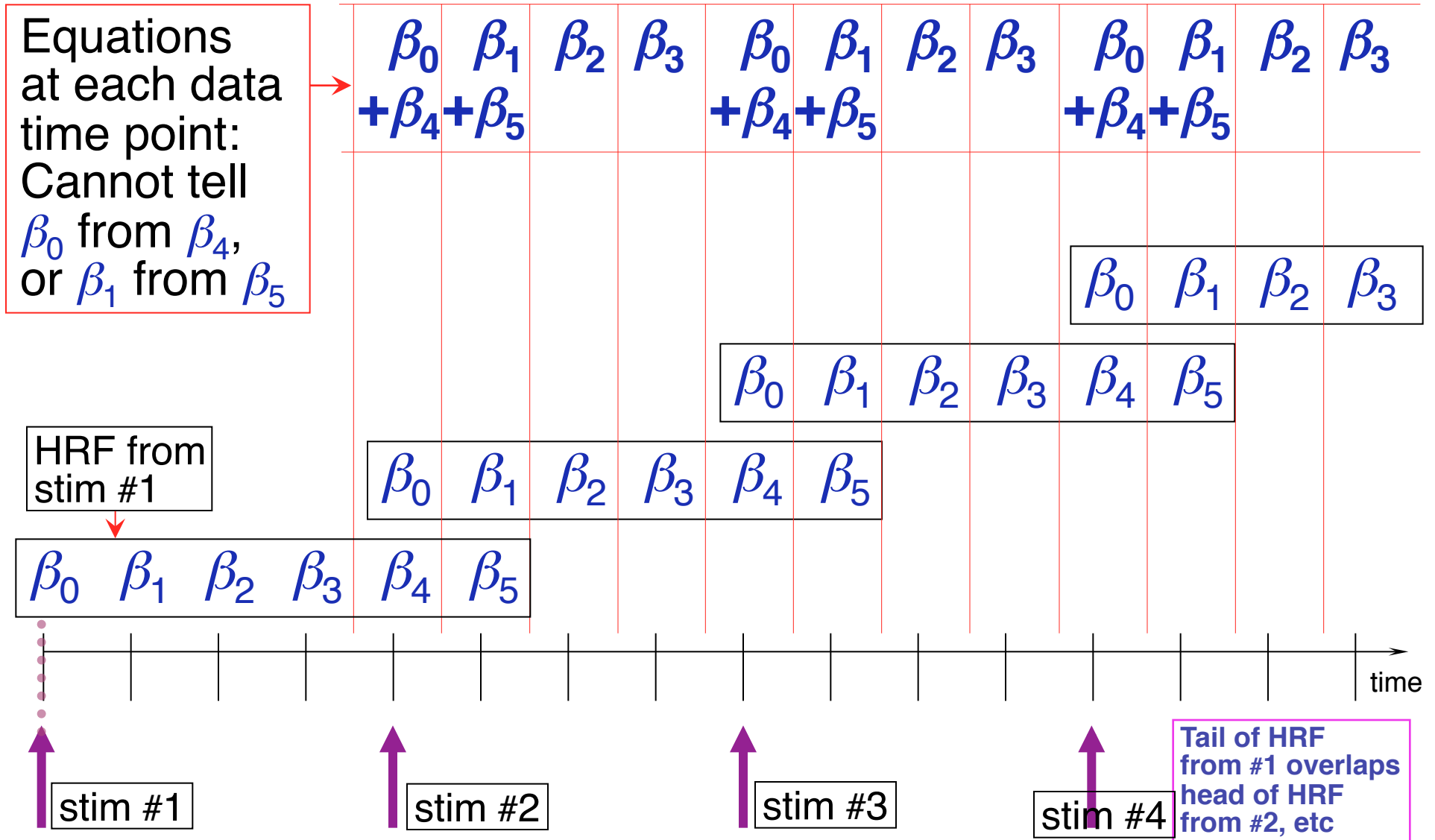
- Tent parameters are easily interpreted as function values (e.g., L : tent radius; β_2 = response (tent height) at time $t = 2 \cdot L$ after stim = tent width)
- User must decide on relationship of tent function grid spacing L and time grid spacing TR (usually would choose $L \geq TR$)
- In **3dDeconvolve**: specify duration (D) of HRF and number (n) of β parameters (details shown a few slides ahead): radius $L = D/(n-1)$ in $(n-2)$ full tents + 2 half tents, each tent overlaps half with two neighboring ones

Tent Functions: Average Signal Change

- For group analysis, may compute average signal change
 - ★ Over entire duration of HRF (usual): in previous slide, with 6 β weights, average signal change is $\frac{1}{2}\beta_0 + \beta_1 + \beta_2 + \beta_3 + \beta_4 + \frac{1}{2}\beta_5$
 - ★ Over a sub-interval of the HRF duration (sometimes)
- Or feed all β s into group analysis using **3dLME** so that serial correlation is accounted for
 - ★ More cumbersome than fixed-shape modeling
- First and last β weights are scaled by half since they only affect half as much of the duration of the response
 - ★ To assume a HRF of D seconds duration with 0 value at beginning & end, use **TENT($L, D-L, n-2$)**, not **TENT(0, D, n)**
- All β weights (for each stimulus class) are output into the “bucket” dataset produced by **3dDeconvolve**

Deconvolution and Collinearity

- Regular stimulus timing can lead to collinearity!



Deconvolution Example - The Data

- **cd AFNI_data2**
 - ★ data is in **ED/** subdirectory (10 runs of 136 images each; TR=2 s)
 - ★ script = **s1.afni_proc_command** (in **AFNI_data2/** directory)
 - stimuli timing and GLT contrast files in **misc_files/**
 - ★ this script runs program **afni_proc.py** to generate a shell script with all AFNI commands for single-subject analysis
 - Run by typing **tcsh s1.afni_proc_command** ; then copy/paste **tcsh -x proc.ED.8.glt |& tee output.proc.ED.8.glt**
- Event-related study from Mike Beauchamp
 - ★ 10 runs, four classes (2x2 design) of stimuli (short videos)
 - Tools moving (e.g., a hammer pounding) - **ToolMovie**
 - People moving (e.g., jumping jacks) - **HumanMovie**
 - Points outlining tools moving (no objects, just points) - **ToolPoint**
 - Points outlining people moving - **HumanPoint**
 - ★ Goal: find brain area that distinguishes natural motions (**HumanMovie** and **HumanPoint**) from simpler rigid motions (**ToolMovie** and **ToolPoint**)

Text output from programs goes to screen *and* file

Master Script for Data Analysis

afni_proc.py

```
-dsets ED/ED_r??+orig.HEAD
-subj_id ED.8.glt
-copy_anat ED/EDspgr
-tcat_remove_first_trs 2
-volreg_align_to first
-regress_stim_times misc_files/stim_times.*.1D
-regress_stim_labels ToolMovie HumanMovie
                    ToolPoint HumanPoint
-regress_basis 'TENT(0,14,8)' or 'TENT(2,14,6)'
-regress_opts_3dD
-gltsym ../misc_files/glt1.txt -glt_label 1 FullF
-gltsym ../misc_files/glt2.txt -glt_label 2 HvsT
-gltsym ../misc_files/glt3.txt -glt_label 3 MvsP
-gltsym ../misc_files/glt4.txt -glt_label 4 HMvsHP
-gltsym ../misc_files/glt5.txt -glt_label 5 TMvsTP
-gltsym ../misc_files/glt6.txt -glt_label 6 HPvsTP
-gltsym ../misc_files/glt7.txt -glt_label 7 HMvsTM
```

- \ ← Master script program
- \ ← 10 input datasets
- \ ← Set output filenames
- \ ← Copy anat to output dir
- \ ← Discard first 2 TRs
- \ ← Where to align all EPs
- \ ← Stimulus timing files (4)
- \ ← Stimulus labels
- \
- \ ← HRF model
- \ ← Specifies that next lines are options to be passed to **3dDeconvolve** directly (in this case, the GLTs we want computed)

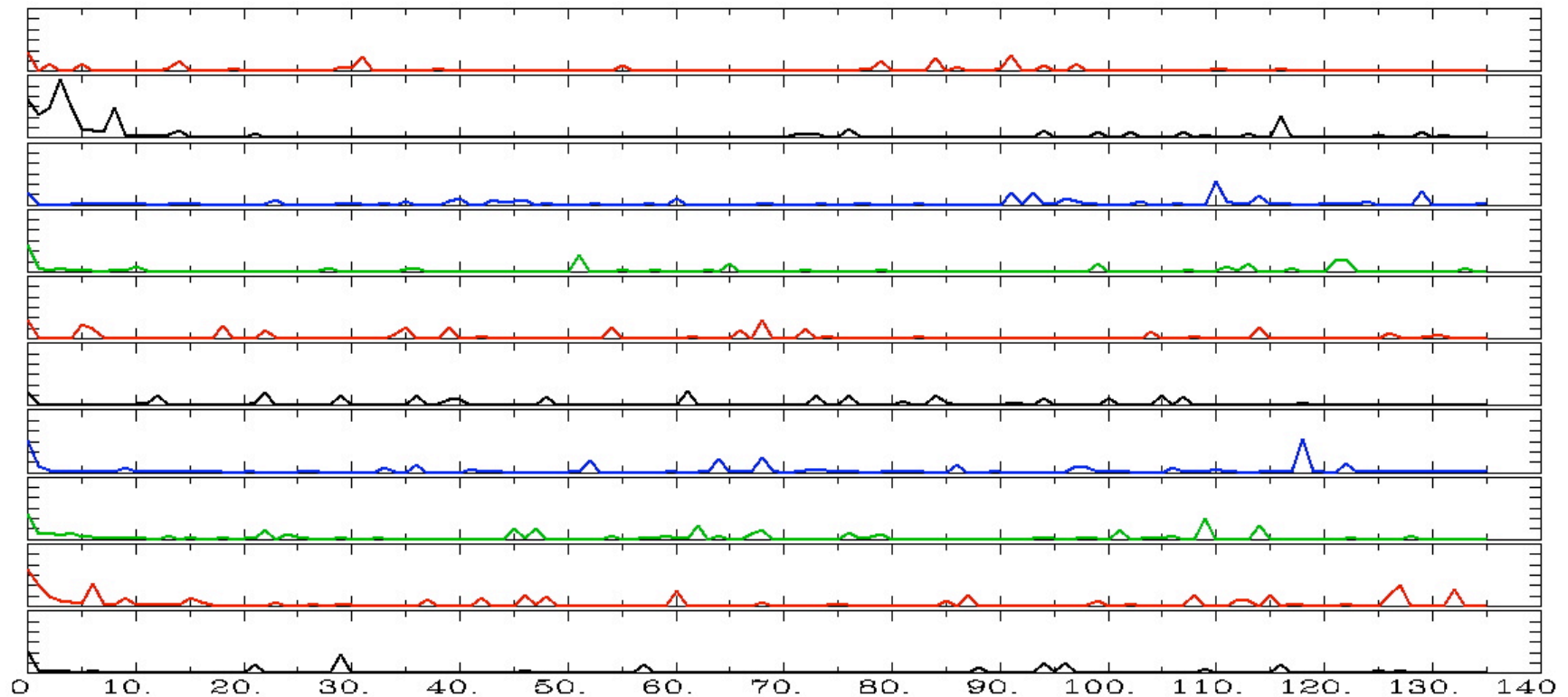
This script generates file `proc.ED.8.glt` (180 lines), which contains all the AFNI commands to produce analysis results into directory `ED.8.glt.results/` (148 files)

Shell Script for Deconvolution - Outline

- Copy datasets into output directory for processing
- Examine each imaging run for outliers: **3dToutcount**
- Time shift each run's slices to a common origin: **3dTshift**
- Registration of each imaging run: **3dvolreg**
- Blurring: **3dmerge**, **3dBlurToFWHM**, **3dBlurInMask**
- Create a brain mask: **3dAutomask** and **3dcalc**
- Rescale each voxel time series in each imaging run so that its average through time is 100: **3dTstat** and **3dcalc**
 - ★ β_q of 1.6 indicates 1.6% change at tent function knot # q after stimulus
 - ★ Biophysics: believe % signal change is relevant physiological parameter
- Catenate all runs into 1 dataset (1360 time points): **3dTcat**
 - ★ This dataset is useful for plotting **-fitts** output from **3dDeconvolve** and visually examining time series fitting
- Compute HRFs and statistics: **3dDeconvolve**

Script - 3dToutcount

```
# set list of runs
set runs = (`count -digits 2 1 10`)
# run 3dToutcount for each run
foreach run ( $runs )
  3dToutcount -automask pb00.$subj.r$run.tcat+orig > outcount_r$run.1D
end
```



Via `1dplot outcount_r??.`1D
3dToutcount searches for “outliers” in data time series;
You should examine noticeable runs & time points

Script - 3dTshift

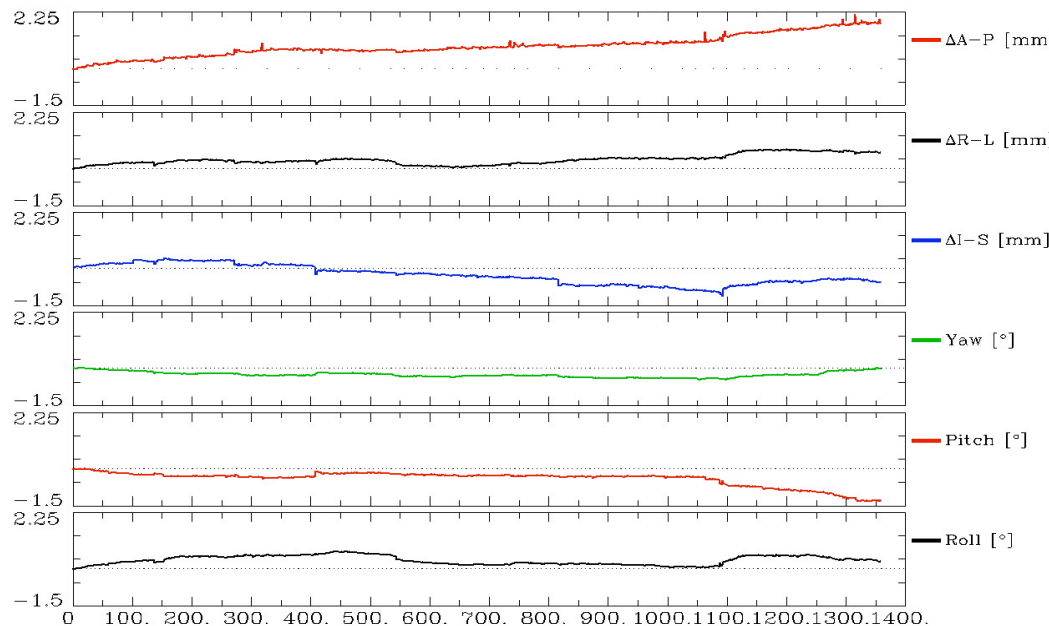
```
# run 3dTshift for each run
foreach run ( $runs )
    3dTshift -tzero 0 -quintic -prefix pb01.$subj.r$run.tshift \
            pb00.$subj.r$run.tcat+orig
end
```

- Produces new datasets where each time series has been shifted to have the same time origin
- **-tzero 0** means that all data time series are interpolated to match the time offset of the first slice
 - Which is what the slice timing files usually refer to
 - Quintic (5th order) polynomial interpolation is used
- **3dDeconvolve** will be run on these time-shifted datasets
 - This is mostly important for Event-Related fMRI studies, where the response to the stimulus is briefer than for Block designs
 - (Because the stimulus is briefer)
 - Being a little off in the stimulus timing in a Block design is not likely to matter much

Script - 3dvolreg

```
# align each dset to the base volume
foreach run ( $runs )
  3dvolreg -verbose -zpad 1 -base pb01.$subj.r01.tshift+orig'[0]' \
    -1Dfile dfile.r$run.1D -prefix pb02.$subj.r$run.volreg \
    pb01.$subj.r$run.tshift+orig
end
```

- Produces new datasets where each volume (one time point) has been aligned (registered) to the #0 time point in the #1 dataset
- Movement parameters are saved into files `dfile.r$run.1D`
 - Will be used as extra regressors in `3dDeconvolve` to reduce motion artifacts



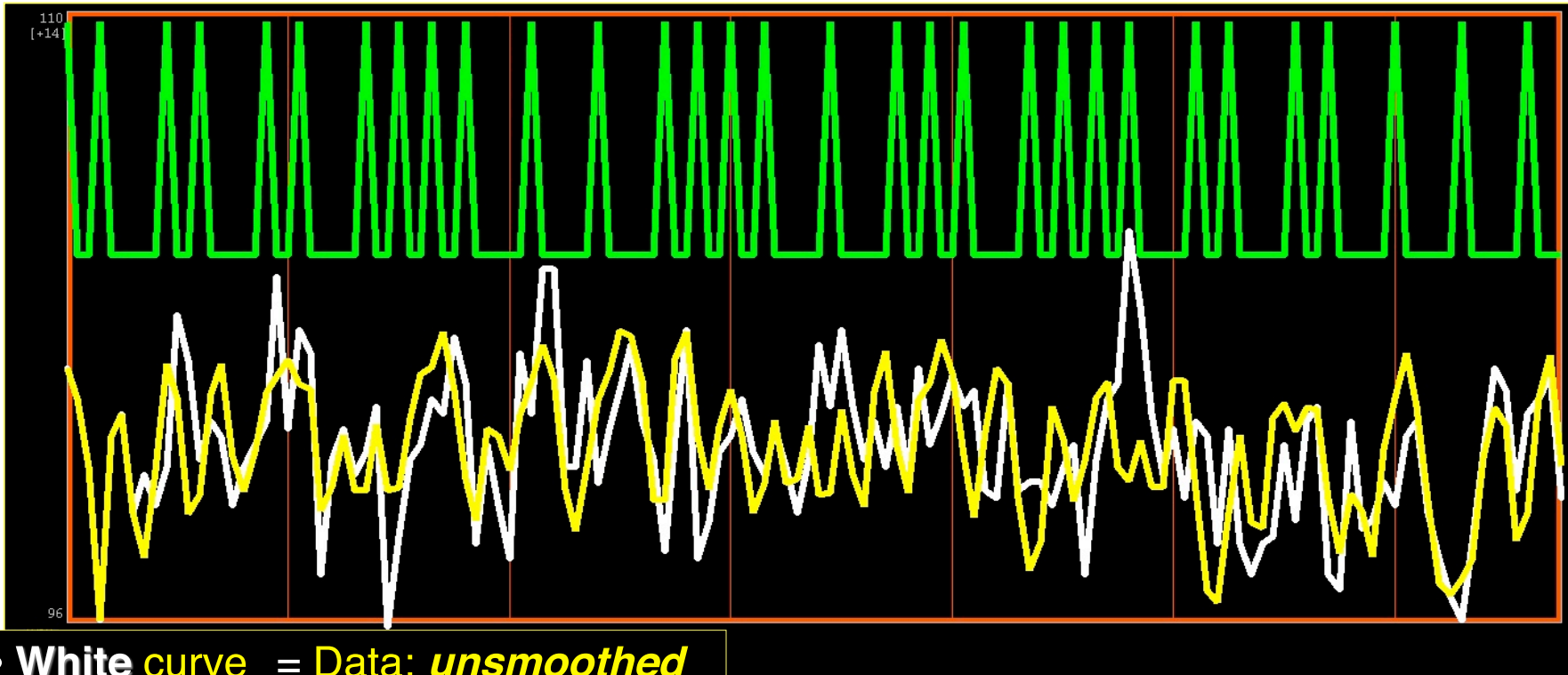
`1dplot -volreg dfile.rall.1D`

- Shows movement parameters for all runs (1360 time points) in degrees and millimeters
- **Very** important to look at this graph!
- Excessive movement can make an imaging run useless — `3dvolreg` won't be able to compensate
 - Pay attention to scale of movements: more than about 2 voxel sizes in a short time interval is usually bad

Script - 3dmerge

```
# blur each volume
foreach run ( $runs )
    3dmerge -1blur_fwhm 4 -doall -prefix pb03.$subj.r$run.blur \
    pb02.$subj.r$run.volreg+orig
end
```

- **Why Blur?** Reduce noise by averaging neighboring voxels time series

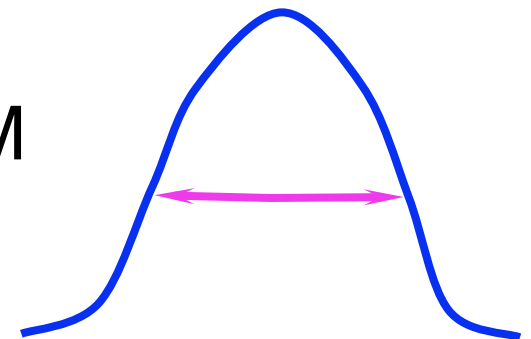
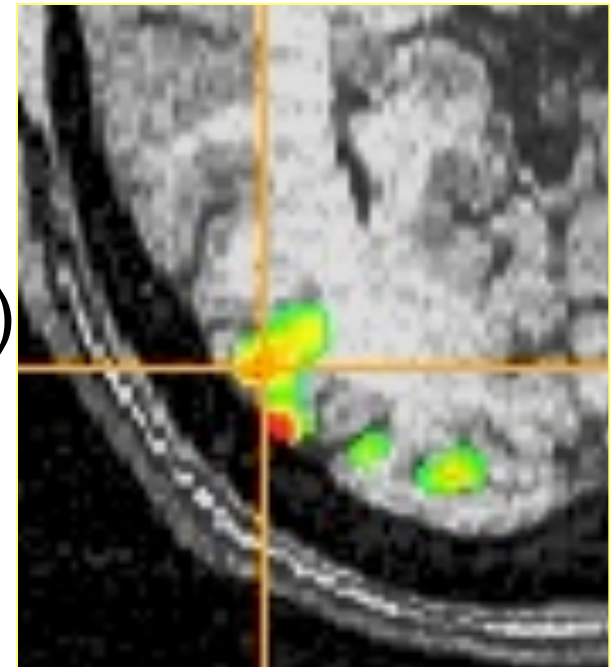


- **White** curve = Data: *unsmoothed*
- **Yellow** curve = Model fit ($R^2 = 0.50$)
- **Green** curve = Stimulus timing

This is an extremely good fit for ER FMRI data!

Why Blur? - 2

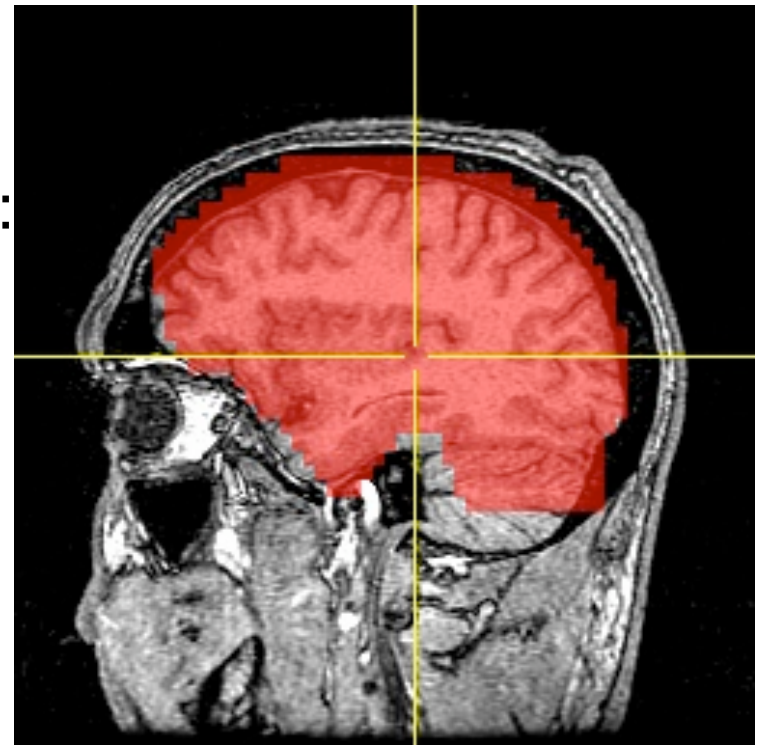
- fMRI activations are (usually) blob-ish (several voxels across)
- Averaging neighbors will also reduce the fiendish multiple comparisons problem
 - ★ Number of independent “resels” will be smaller than number of voxels (*e.g.*, 2000 vs. 20000)
- Why not just acquire at lower resolution?
 - ★ To avoid averaging across brain/non-brain interfaces
 - ★ To project onto surface models
- Amount to blur is specified as FWHM (Full Width at Half Maximum) of spatial averaging filter (4 mm in script)



Script - 3dAutomask

```
# create 'full_mask' dataset (union mask)
foreach run ( $runs )
  3dAutomask -dilate 1 -prefix rm.mask_r$run pb03.$subj.r$run.blur+orig
end
# get mean and compare it to 0 for taking 'union'
3dMean -datum short -prefix rm.mean rm.mask*.HEAD
3dcalc -a rm.mean+orig -expr 'ispositive(a-0)' -prefix full_mask.$subj
```

- **3dAutomask** creates a mask of contiguous high-intensity voxels (with some hole-filling) for each run separately: common mask for all runs/subjects
- **3dMean** and **3dcalc** are used to create a mask that is the union of all the individual run masks
- **3dDeconvolve** analysis will be limited to voxels in this mask
 - Will run faster, since less data to process

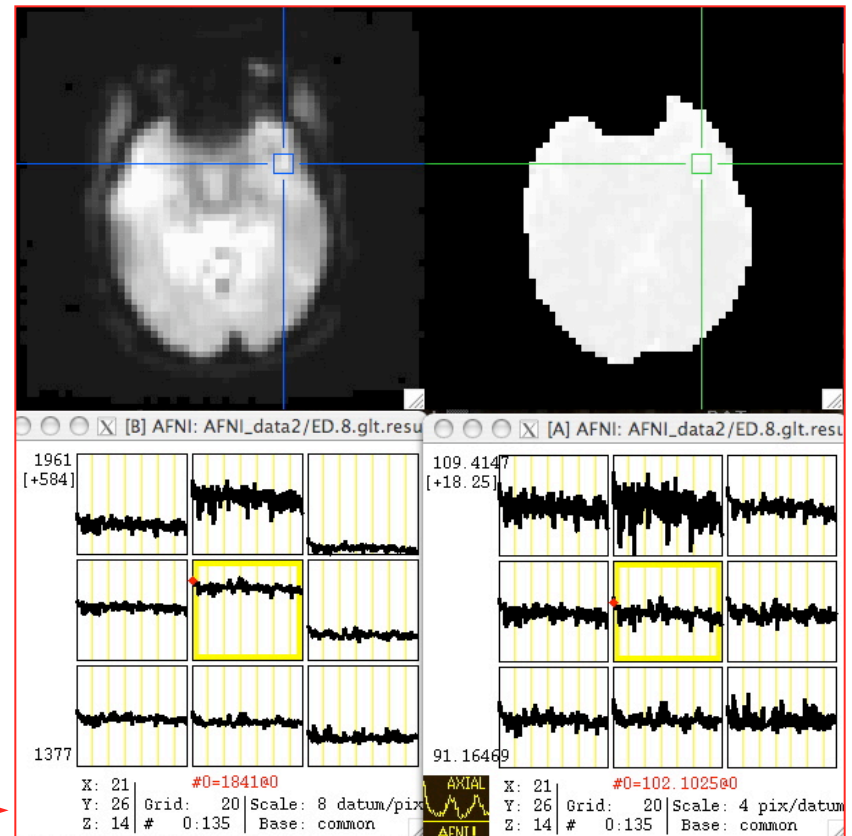


Automask from EPI shown in red

Script - Scaling

```
# scale each voxel time series to have a mean of 100
# (subject to maximum value of 200)
foreach run ( $runs )
    3dTstat -prefix rm.mean_r$run pb03.$subj.r$run.blur+orig
    3dcalc -a pb03.$subj.r$run.blur+orig -b rm.mean_r$run+orig \
        -c full_mask.$subj+orig \
        -expr 'c * min(200, a/b*100)' -prefix pb04.$subj.r$run.scale
end
```

- **3dTstat** calculates the mean (through time) of each voxel's time series data
- For voxels in the mask, each data point is scaled (multiplied) using **3dcalc** so that it's time series will have mean=100
- If an HRF regressor has max amplitude = 1, then its β coefficient will represent the % signal change (from the mean) due to that part of the signal model
- Scaled images are very boring to view
 - No spatial contrast by design!
 - Graphs have common baseline now →



Script - 3dDeconvolve

```
3dDeconvolve -input pb04.$subj.r??.scale+orig.HEAD -polort 2 \
  -mask full_mask.$subj+orig -basis_normall 1 -num_stimts 10 \
  -stim_times 1 stimuli/stim_times.01.1D 'TENT(0,14,8)' \
  -stim_label 1 ToolMovie \
  -stim_times 2 stimuli/stim_times.02.1D 'TENT(0,14,8)' \
  -stim_label 2 HumanMovie \
  -stim_times 3 stimuli/stim_times.03.1D 'TENT(0,14,8)' \
  -stim_label 3 ToolPoint \
  -stim_times 4 stimuli/stim_times.04.1D 'TENT(0,14,8)' \
  -stim_label 4 HumanPoint \
  -stim_file 5 dfile.rall.1D'[0]' -stim_base 5 -stim_label 5 roll \
  -stim_file 6 dfile.rall.1D'[1]' -stim_base 6 -stim_label 6 pitch \
  -stim_file 7 dfile.rall.1D'[2]' -stim_base 7 -stim_label 7 yaw \
  -stim_file 8 dfile.rall.1D'[3]' -stim_base 8 -stim_label 8 dS \
  -stim_file 9 dfile.rall.1D'[4]' -stim_base 9 -stim_label 9 dL \
  -stim_file 10 dfile.rall.1D'[5]' -stim_base 10 -stim_label 10 dP \
  -iresp 1 iresp_ToolMovie.$subj -iresp 2 iresp_HumanMovie.$subj \
  -iresp 3 iresp_ToolPoint.$subj -iresp 4 iresp_HumanPoint.$subj \
  -gltsym ../misc_files/glt1.txt -glt_label 1 FullF \
  -gltsym ../misc_files/glt2.txt -glt_label 2 HvsT \
  -gltsym ../misc_files/glt3.txt -glt_label 3 MvsP \
  -gltsym ../misc_files/glt4.txt -glt_label 4 HMvsHP \
  -gltsym ../misc_files/glt5.txt -glt_label 5 TMvsTP \
  -gltsym ../misc_files/glt6.txt -glt_label 6 HPvsTP \
  -gltsym ../misc_files/glt7.txt -glt_label 7 HMvsTM \
  -fout -tout -full_first -x1D Xmat.x1D -fitts fitts.$subj -bucket stats.$subj
```

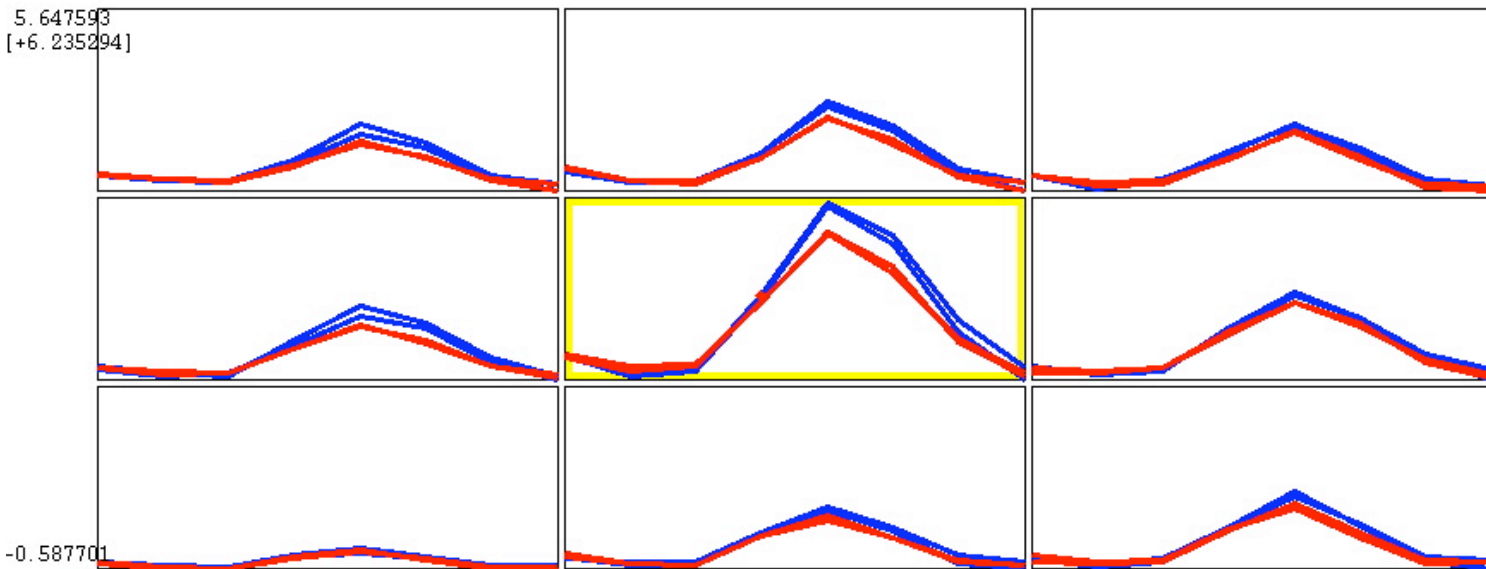
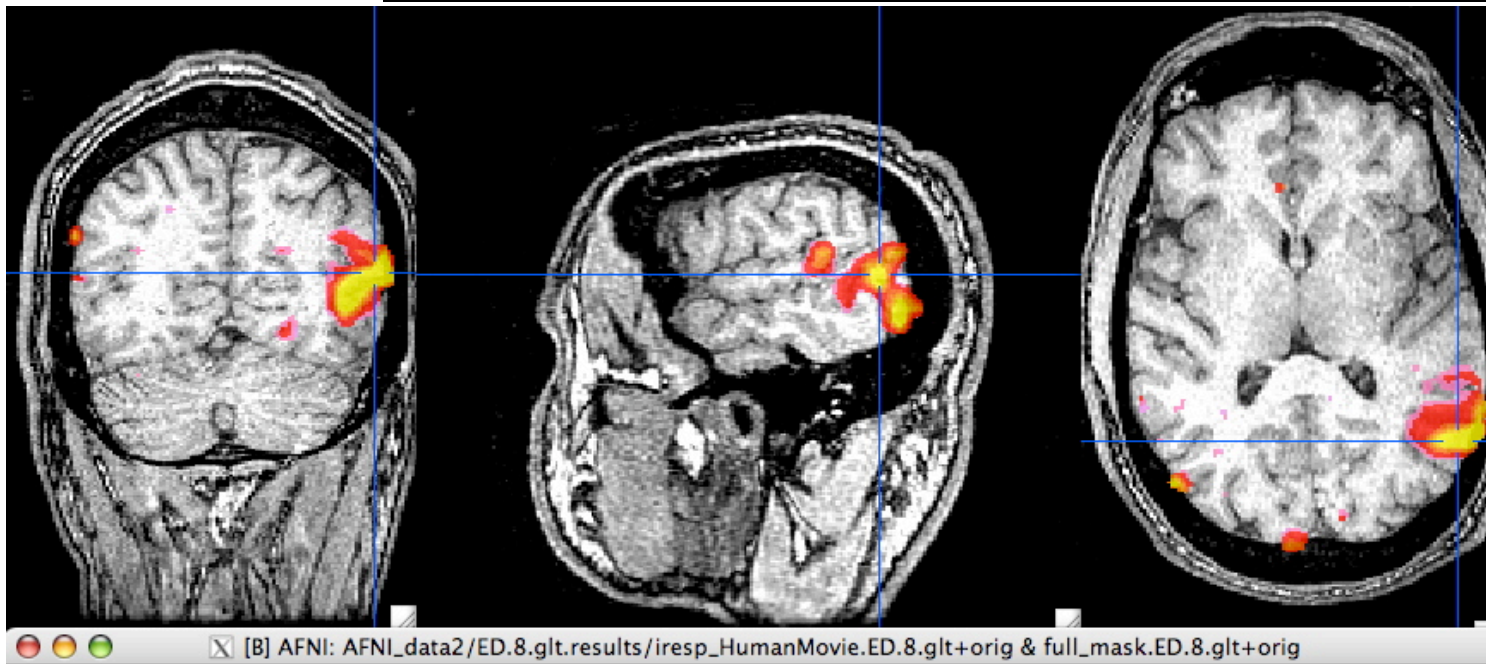
4 stim types

motion params

HRF outputs

GLTs

Results: Humans vs. Tools



- Color overlay:
HvsT
GLT
contrast

- **Blue**
(upper)
graphs:
Human
HRFs

- **Red**
(lower)
graphs:
Tool
HRFs

Script - X Matrix



Via `lgrayplot -sep Xmat.x1D`

Script - Random Comments

- `-polort 2`
 - ★ Sets baseline (detrending) to use quadratic polynomials—in each run
- `-mask full_mask.$subj+orig`
 - ★ Process only the voxels that are nonzero in this mask dataset
- `-basis_normall 1`
 - ★ Make sure that the basis functions used in the HRF expansion all have maximum magnitude=1
- `-stim_times 1 stimuli/stim_times.01.1D`
`'TENT(0,14,8)'`
 - `-stim_label 1 ToolMovie`
 - ★ The HRF model for the **ToolMovie** stimuli starts at 0 s after each stimulus, lasts for 14 s, and has 8 (6 full + 2 half) basis tents
 - Which have knots (breakpoints) spaced $14/(8-1)=2$ s apart
- `-iresp 1 iresp_ToolMovie.$subj`
 - ★ The HRF model for the **ToolMovie** stimuli is output into dataset `iresp_ToolMovie.ED.8.glt+orig`

Script - GLTs

- `-gltsym ../misc_files/glt2.txt -glt_label 2 HvsT`
 - File `../misc_files/glt2.txt` contains 1 line of text:
 - `-ToolMovie +HumanMovie -ToolPoint +HumanPoint`
 - This is the “Humans vs. Tools” **HvsT** contrast shown on Results slide
- This GLT means to take all 8 β coefficients for each stimulus class and combine them with additions and subtractions as ordered:

$$LC = -\beta_0^{TM} - \dots - \beta_7^{TM} + \beta_0^{HM} + \dots + \beta_7^{HM} - \beta_0^{TP} - \dots - \beta_7^{TP} + \beta_0^{HP} + \dots + \beta_7^{HP}$$

- This test is looking at integrated (summed) response to “Human” stimuli and subtracting it from integrated response to “Tool” stimuli
- Combining subsets of the β weights is also possible with `-gltsym`:
 - `+HumanMovie[2..6] -HumanPoint[2..6]`
 - This GLT would add up #2,3,4,5, & 6 β s for one type of stimulus and subtract sum of #2,3,4,5, & 6 β s for another type of stimulus
 - And also produce F - and t -statistics for this linear combination
 - Alternatively F-test for composite hypothesis: `-gltsym '+HumanMovie [[2..6]] -HumanPoint[[2..6]]' -glt_label 2 HvsT`
 - $H_0: \beta_2^{TM} = \beta_2^{TP}, \beta_3^{TM} = \beta_3^{TP}, \dots, \beta_6^{TM} = \beta_6^{TP}$

Script - Multi-Row GLTs

- GLTs presented up to now have had one row
 - ★ Testing if some linear combination of β weights is nonzero; test statistic is t or F ($F=t^2$ when testing a single number)
 - ★ Testing if the X matrix columns, when added together to form one column as specified by the GLT (+ and -), explain a significant fraction of the data time series (equivalent to above)

- Can also do a single test to see if several different combinations of β weights are *all* zero

```
-gltsym ../misc_files/glt1.txt  
-glt_label 1 FullF
```

4 rows

```
+ToolMovie  
+HumanMovie  
+ToolPoint  
+HumanPoint
```

- ★ Tests if *any* of the stimulus classes have nonzero integrated HRF (each name means “add up those β weights”) : $DOF = (4, 1292)$
- ★ Different than the default “Full F-stat” produced by **3dDeconvolve**, which tests if any of the *individual* β weights are nonzero: $DOF = (32, 1292)$

Two Possible Formats for `-stim_times`

- If you don't use `-local_times` or `-global_times`, `3dDeconvolve` will *guess* which way to interpret numbers:

4.7
9.6
11.8
19.4

- A single column of numbers (**GLOBAL** times)
 - ★ One stimulus time per row
 - ★ Times are relative to first image in dataset being at **$t=0$**
 - ★ May not be simplest to use if multiple runs are catenated

- One row for each run within a catenated dataset (**LOCAL** times)
 - ★ Each time in j^{th} row is relative to start of run $\#j$ being **$t=0$**
 - ★ If some run has NO stimuli in the given class, just put a single “*” in that row as a filler
 - Different numbers of stimuli per run are OK
 - At least one row must have more than 1 time

(so that the **LOCAL** type of timing file can be told from the **GLOBAL**)

4.7	9.6	11.8	19.4
*			
8.3	10.6		

- Two methods are available because of users' diverse needs
 - ★ **N.B.:** if you chop first few images off the start of each run, the inputs to `-stim_times` must be adjusted accordingly!
 - Better to use `-CENSORTR` to tell `3dDeconvolve` just to ignore those points

**More information
about -stim_times
and its variants
is in the
afni07_advanced talk**

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