

HowTo 03: stimulus timing design (hands-on)

- Goal: to design an effective random stimulus presentation
 - end result will be stimulus timing files
 - example: using an event related design, with simple regression to analyze
- Steps:
 0. given: experimental parameters (stimuli, # presentations, # TRs, etc.)
 1. create random stimulus functions (one for each stimulus type)
 2. create ideal reference functions (for each stimulus type)
 3. evaluate the stimulus timing design
- Step 0: the (made-up) parameters from HowTo 03 are:
 - 3 stimulus types (the classic experiment: "houses, faces and donuts")
 - presentation order is randomized
 - TR = 1 sec, total number of TRs = 300
 - number of presentations for each stimulus type = 50 (leaving 150 for fixation)
 - fixation time should be 30% ~ 50% total scanning time
 - 3 contrasts of interest: each pair-wise comparison
 - refer to directory: `AFNI_data1/ht03`

- Step 1: creation of random stimulus functions

→ RSFgen : Random Stimulus Function generator

→ command file: `c01.RSFgen`

```
RSFgen -nt 300 -num_stimts 3 \
      -nreps 1 50 -nreps 2 50 -nreps 3 50 \
      -seed 1234568 -prefix RSF.stim.001.
```

→ This creates 3 stimulus timing files:

```
RSF.stim.001.1.1D  RSF.stim.001.2.1D  RSF.stim.001.3.1D
```

- Step 2: create ideal response functions (linear regression case)

→ waver: creates waveforms from stimulus timing files

- effectively doing convolution

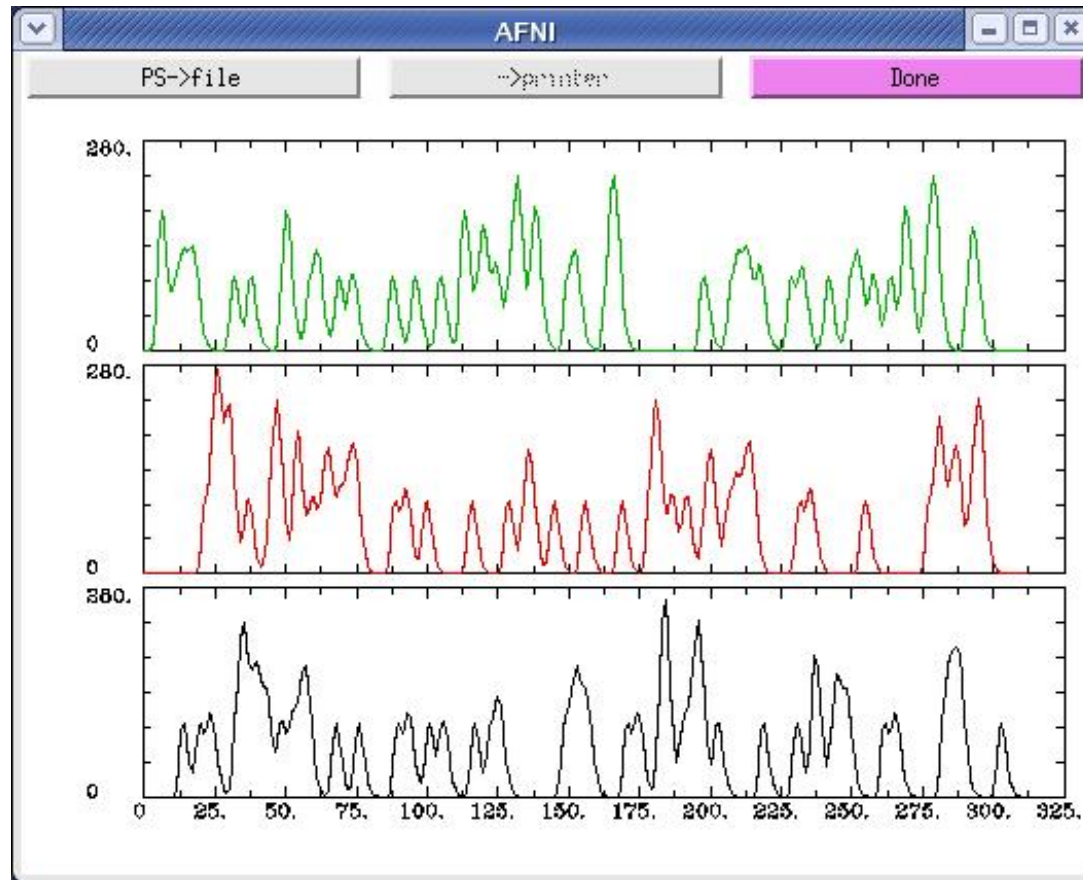
→ command file: `c02.waver`

```
waver -GAM -dt 1.0 -input RSF.stim.001.1.1D
```

→ this will output (to the terminal window) the ideal response function, by convolving the Gamma variate function with the stimulus timing function

→ output length allows for stimulus at last TR (= 300 + 13, in this example)

→ use '1dplot' to view these results, command: `1dplot wav.*.1D`



- the first curve (for `wav.hrf.001.1.1D`) is displayed on the bottom
- x-axis covers 313 seconds, but the graph is extended to a more "round" 325
- y-axis happens to reach 274.5, shortly after 3 consecutive type-2 stimuli
- the peak value for a single curve can be set using the `-peak` option in `waver`
 → default peak is 100
- it is worth noting that there are no duplicate curves
- can also use `'waver -one'` to put the curves on top of each other

- Step 3: evaluate the stimulus timing design
 - use '3dDeconvolve -nodata': experimental design evaluation
 - command file: `c03.3dDeconvolve`
 - command: `3dDeconvolve -nodata`

```
-nfirst 4 -nlast 299 -polort 1 \
-num_stimts 3 \
-stim_file 1 "wav.hrf.001.1.1D" \
-stim_label 1 "stim_A" \
-stim_file 2 "wav.hrf.001.2.1D" \
-stim_label 2 "stim_B" \
-stim_file 3 "wav.hrf.001.3.1D" \
-stim_label 3 "stim_C" \
-glt 1 contrasts/contrast_AB \
-glt 1 contrasts/contrast_AC \
-glt 1 contrasts/contrast_BC
```

- Use the 3dDeconvolve output to evaluate the normalized standard deviations of the contrasts.
- For this HowTo script, the deviations of the GLT's are summed. Other options are valid, such as summing all values, or just those for the stimuli, or summing squares.
- Output (partial):

```

Stimulus: stim_A
  h[ 0] norm. std. dev. = 0.0010
Stimulus: stim_B
  h[ 0] norm. std. dev. = 0.0009
Stimulus: stim_C
  h[ 0] norm. std. dev. = 0.0011
General Linear Test: GLT #1
  LC[0] norm. std. dev. = 0.0013
General Linear Test: GLT #2
  LC[0] norm. std. dev. = 0.0012
General Linear Test: GLT #3
  LC[0] norm. std. dev. = 0.0013

```

- What does this output mean?
 - What is `norm. std. dev.?`
 - How does this compare to results using different stimulus timing patterns?

Basics about Regression

- Regression Model (General Linear System)

→ Simple Regression Model (one regressor): $Y(t) = \alpha_0 + \alpha_1 t + \beta r(t) + \varepsilon(t)$

- Run `3dDeconvolve` with regressor $r(t)$, a time series IRF

→ Deconvolution and Regression Model (one stimulus with a lag of p TR's):

$$Y(t) = \alpha_0 + \alpha_1 t + \beta_0 f(t) + \beta_1 f(t-TR) + \dots + \beta_p f(t-p*TR) + \varepsilon(t)$$

- Run `3dDeconvolve` with stimulus files (containing 0's and 1's)

- Model in Matrix Format: $Y = X\beta + \varepsilon$

→ X : design matrix - more rows (TR's) than columns (baseline parameters + beta weights).

α_0	α_1	β		α_0	α_1	β_0	\dots	β_p

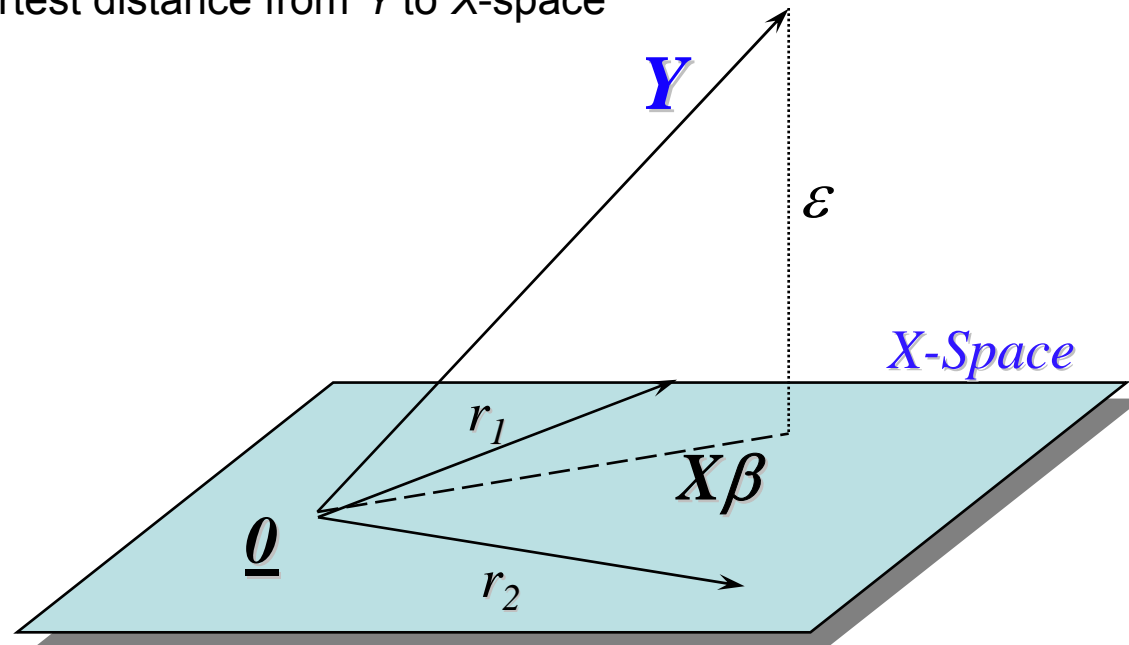
1	1	$r(0)$		1	p	f_p	\dots	f_0
1	2	$r(1)$		1	$p+1$	f_{p+1}	\dots	f_1
	\dots				\dots			
1	$N-1$	$r(N-1)$		1	$N-1$	f_{N-1}	\dots	f_{N-p-1}

→ ε : random (system) error $N(0, \sigma^2)$

- X matrix examples (based on modified HowTo 03 script, stimulus #3):
 - regression: baseline, linear drift, 1 regressor (ideal response function)
 - deconvolution: baseline, linear drift, 5 regressors (lags)

<u>regression</u>			<u>deconvolution - with lags (3-7)</u>						
1	0	0	1	0	0	0	0	0	0
1	1	0	1	1	0	0	0	0	0
1	2	0.14	1	2	0	0	0	0	0
1	3	9.11	1	3	0	0	0	0	0
1	4	56.05	1	4	1	0	0	0	0
1	5	136.9	1	5	1	1	0	0	0
1	6	188.2	1	6	0	1	1	0	0
1	7	174.2	1	7	0	0	1	1	0
1	8	121.9	1	8	0	0	0	1	1
1	9	78.1	1	9	0	0	0	0	1
1	10	80.63	1	10	1	0	0	0	0
1	11	104.4	1	11	0	1	0	0	0
1	12	112.9	1	12	0	0	1	0	0
1	13	124.9	1	13	1	0	0	1	0
1	14	136.4	1	14	0	1	0	0	1
1	15	130.6	1	15	0	0	1	0	0
1	16	133.2	1	16	1	0	0	1	0
1	17	139.8	1	17	0	1	0	0	1

- Solving the Linear System : $Y = X\beta + \varepsilon$
 - the basic goal of `3dDeconvolve`
 - Least Square Estimate (LSE): making sum of squares of residual (unknown/unexplained) error ε' minimal \rightarrow Normal equation: $(X'X)\beta = X'Y$
 - When X is of full rank (all columns are independent), $\hat{\beta} = (X'X)^{-1}X'Y$
- Geometric Interpretation:
 - project vector Y onto a space spanned by the regressors (the column vectors of design matrix X)
 - find shortest distance from Y to X -space



- Multicollinearity Problem

- `3dDeconvolve` Error: Improper X matrix (cannot invert $X'X$)

- $X'X$ is singular (not invertible) \leftrightarrow at least one column of X is linearly dependent on the other columns

- normal equation has no unique solution

- Simple regression case:

- mistakenly provided at least two identical regressor files, or some inclusive regressors, in `3dDeconvolve`
 - all regressors have to be orthogonal (exclusive) with each other
 - easy to fix: use `1dplot` to diagnose

- Deconvolution case:

- mistakenly provided at least two identical stimulus files, or some inclusive stimuli, in `3dDeconvolve`
 - easy to fix: use `1dplot` to diagnose
 - intrinsic problem of experiment design: lack of randomness in the stimuli
 - varying number of lags may or may not help.
 - running RSFgen can help to avoid this

- see `AFNI_data1/ht03/bad_stim/c20.bad_stim`

- Design analysis

- $X'X$ invertible but $cond(X'X)$ is huge → linear system is sensitive → difficult to obtain accurate estimates of regressor weights

- Condition number: a measure of system's sensitivity to numerical computation

- $cond(M)$ = ratio of maximum to minimum eigenvalues of matrix M

- note, `3dDeconvolve` can generate both X and $(X'X)^{-1}$, but not $cond()$

- Covariance matrix estimate of regressor coefficients vector β :

- $s^2(\beta) = (X'X)^{-1}MSE$

- t test for a contrast $c'\beta$ (including regressor coefficient):

- $t = c'\beta / \sqrt{c'(X'X)^{-1}c MSE}$

- contrast for condition A only: $c = [0 \ 0 \ 1 \ 0 \ 0]$

- contrast between conditions A and B: $c = [0 \ 0 \ 1 \ -1 \ 0]$

- $\sqrt{c'(X'X)^{-1}c}$ in the denominator of the t test indicates the relative stability and statistical power of the experiment design

- $\sqrt{c'(X'X)^{-1}c}$ = normalized standard deviation of a contrast $c'\beta$ (including regressor weight) → *these values are output by 3dDeconvolve*

- smaller $\sqrt{c'(X'X)^{-1}c}$ → stronger statistical power in t test, and less sensitivity in solving the normal equation of the general linear system

- RSFgen helps find out a good design with relative small $\sqrt{c'(X'X)^{-1}c}$

- A bad example: see directory `AFNI_data1/ht03/bad_stim/c20.bad_stim`
 - 2 stimuli, 2 lags each
 - stimulus 2 happens to follow stimulus 1

baseline	linear drift	S1 L1	S1 L2	S2 L1	S2 L2
1	0	0	0	0	0
1	1	0	0	0	0
1	2	0	0	0	0
1	3	1	0	0	0
1	4	0	1	1	0
1	5	0	0	0	1
1	6	1	0	0	0
1	7	0	1	1	0
1	8	0	0	0	1
1	9	0	0	0	0
1	10	1	0	0	0
1	11	0	1	1	0
1	12	1	0	0	1
1	13	1	1	1	0
1	14	0	1	1	1
1	15	1	0	0	1
1	16	0	1	1	0
1	17	1	0	0	1
1	18	0	1	1	0
1	19	0	0	0	1

- So are these results good?

```
stim A:  h[ 0] norm. std. dev. =  0.0010
stim B:  h[ 0] norm. std. dev. =  0.0009
stim C:  h[ 0] norm. std. dev. =  0.0011
GLT #1:  LC[0] norm. std. dev. =  0.0013
GLT #2:  LC[0] norm. std. dev. =  0.0012
GLT #3:  LC[0] norm. std. dev. =  0.0013
```

- And repeat... see the script: `AFNI_data1/ht03/@stim_analyze`
 - review the script details:
 - 100 iterations, incrementing random seed, storing results in separate files
 - only the random number seed changes over the iterations
 - execute the script via command: `./@stim_analyze`
 - "best" result: iteration 039 gives the minimum sum of the 3 GLTs, among all 100 random designs (see file `stim_results/LC_sums`)
 - the `3dDeconvolve` output is in `stim_results/3dD.nodata.039`
- Recall the Goal: to design an effective random stimulus presentation (while preserving statistical power)

→ Solution: the files `stim_results/RSF.stim.039.*.1D`

```
RSF.stim.039.1.1D  RSF.stim.039.2.1D  RSF.stim.039.3.1D12
```