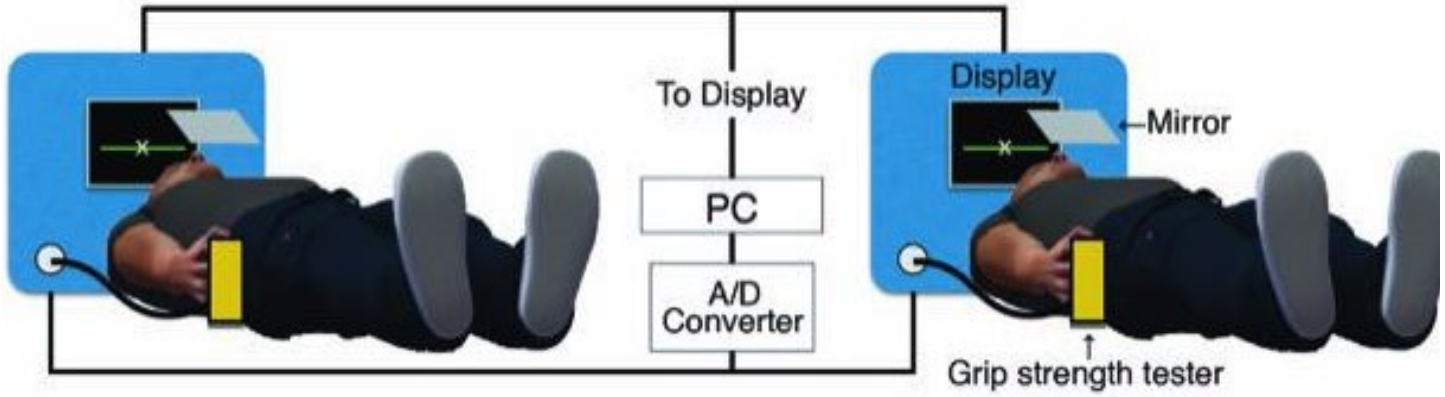
How is task fMRI different from resting state?

1. There's no free lunch
2. Often requires participants to get hooked up to more stuff
    a) Eyetracker, gsr, other physiological measures
    b) Stimulus recorders like grip tester, button, joystick
3. Getting hooked up to more stuff means more can go wrong

Basically during resting state you rest and during task MRI you do a task

DURING BOTH YOU MUST KEEP AS STILL AS POSSIBLE!



Let’s walk through an fMRI task

fMRI Task Step-by-Step

1. P. shows up, does paperwork, removes all metal, goes through safety procedures & instructions

2. P. gets into MRI bed, gets comfy & safe, gets relevant machines & stimulus recorders attached

3. If not already done, an anatomical scan is run on P.

4. P. is read task instructions over intercom. Performs task while moving as little as possible
   - May require restarts if moving is bad

5. If necessary other scans are collected before P. is removed from scanner, unhooked, & debriefed

Image: MIT mcgovern institute

fMRI Task Designs

BLOCK DESIGN VS EVENT-RELATED DESIGN

Questions to ask yourself if you want to do a task MRI (other than 'why am I masochistic?')

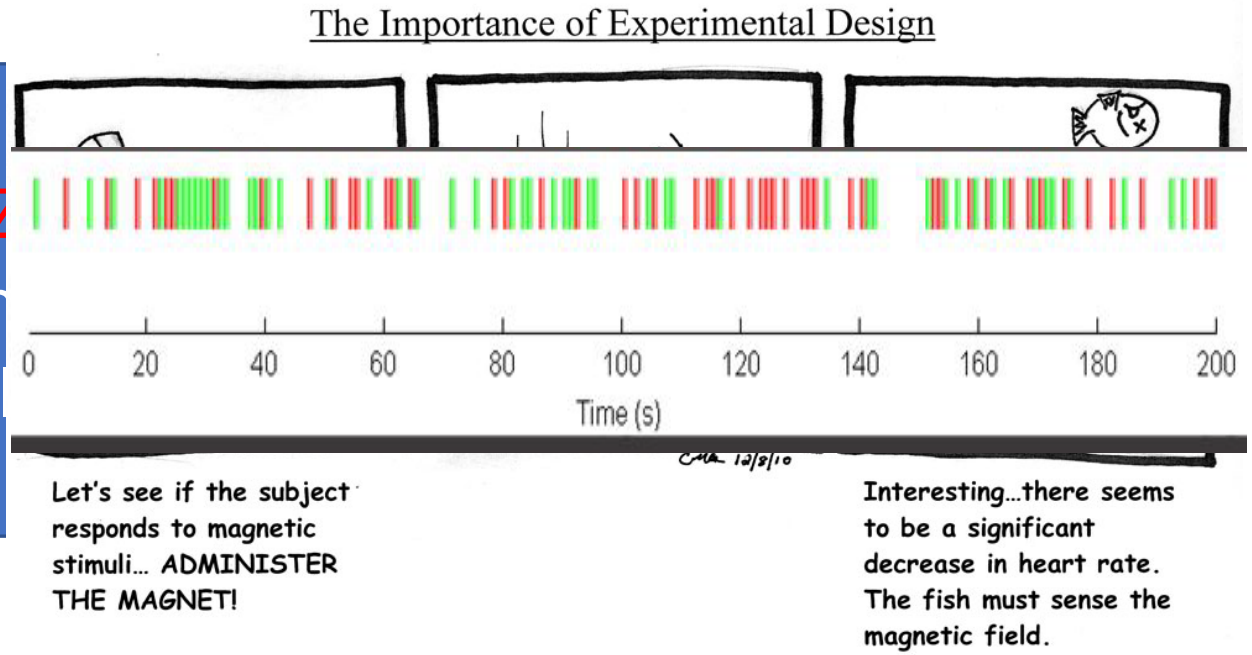
1. Imaging Parameters and Experimental Design are

THERE IS NO OPTIMIZ

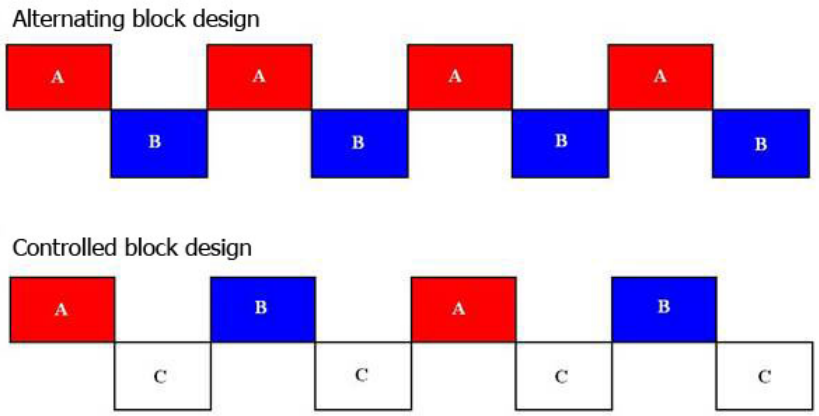
Just THINK, ASK your tech question

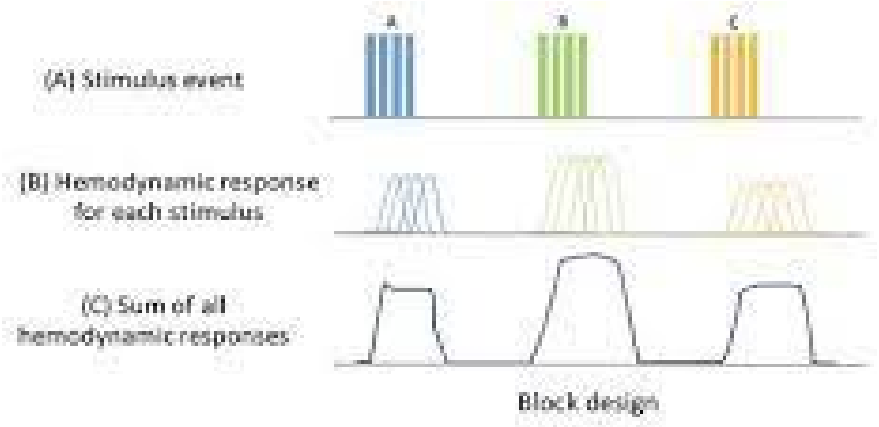
SPECIF

3. How long are the runs?
   a. Longer = more problems (after 6-9m or so?)
4. How long will each trial be?
   a. Within a trial how long will different stimulus presentations be?



10. AND MUCH MUCH MORE



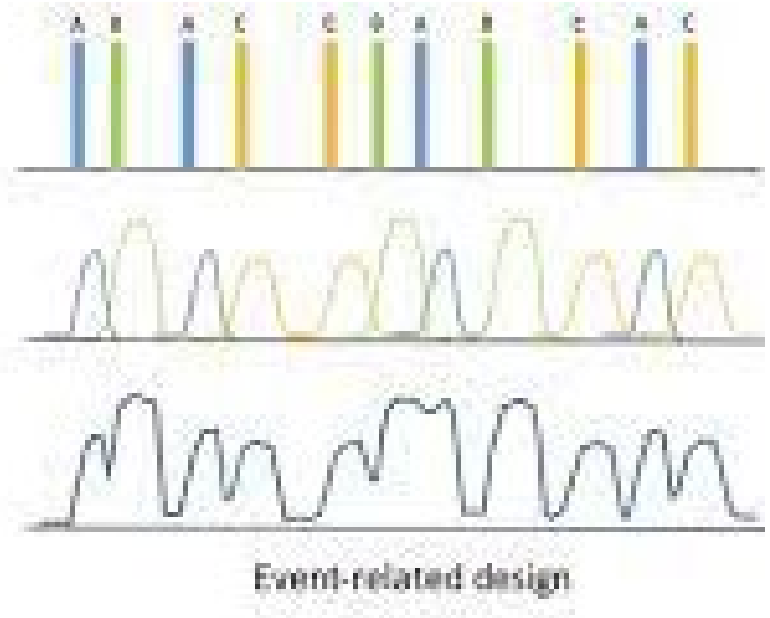


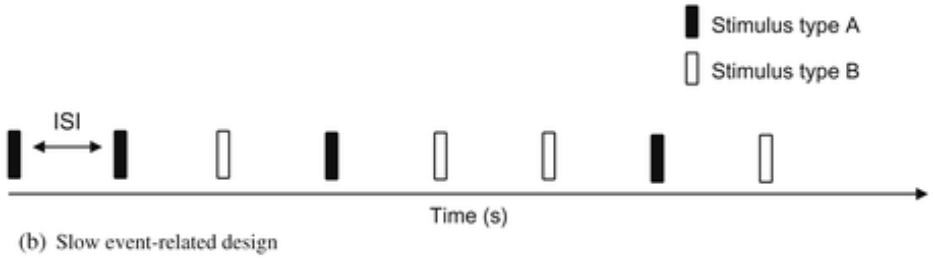
Block Design

- Stimuli of the same kind are presented together **IN A BLOCK**
  - This means stimuli are NOT interspersed
- It's good because…
  - Big brain responses
  - Easier to make/interpret
- It's bad because…
  - Boring for participants
  - Really limits what you can do

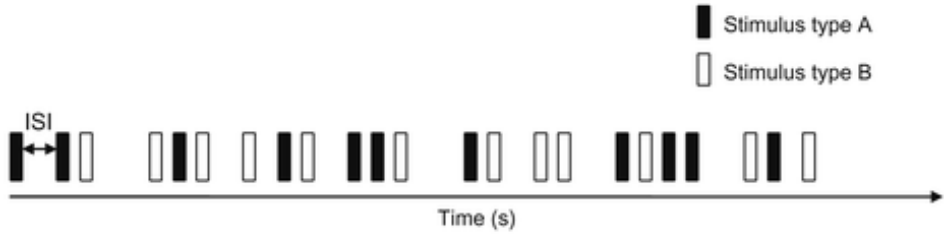
Event-Related Design

- Stimulus presentations are intermixed into single **EVENTS**
  - Time between stimulus presentations is fixed or jittered
- It's good because…
  - Design can be way more complex
  - If done right, estimates HRF well and can look at single events
- It's bad because…
  - Not great signal-to-noise ratio
  - Requires more thought on the front end



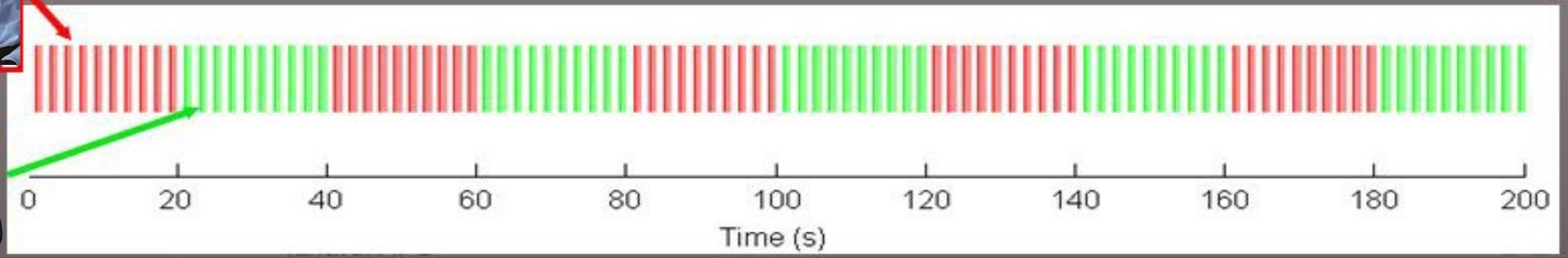


(b) Slow event-related design

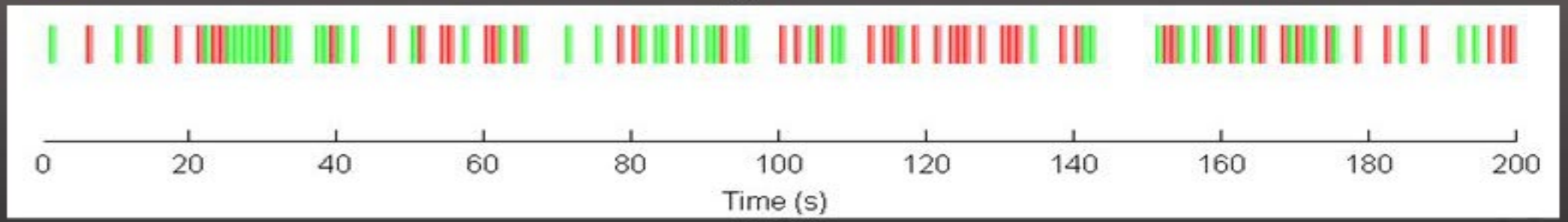


(c) Rapid event-related design

- Block design: Similar events are grouped



- Event-related design: Events are mixed



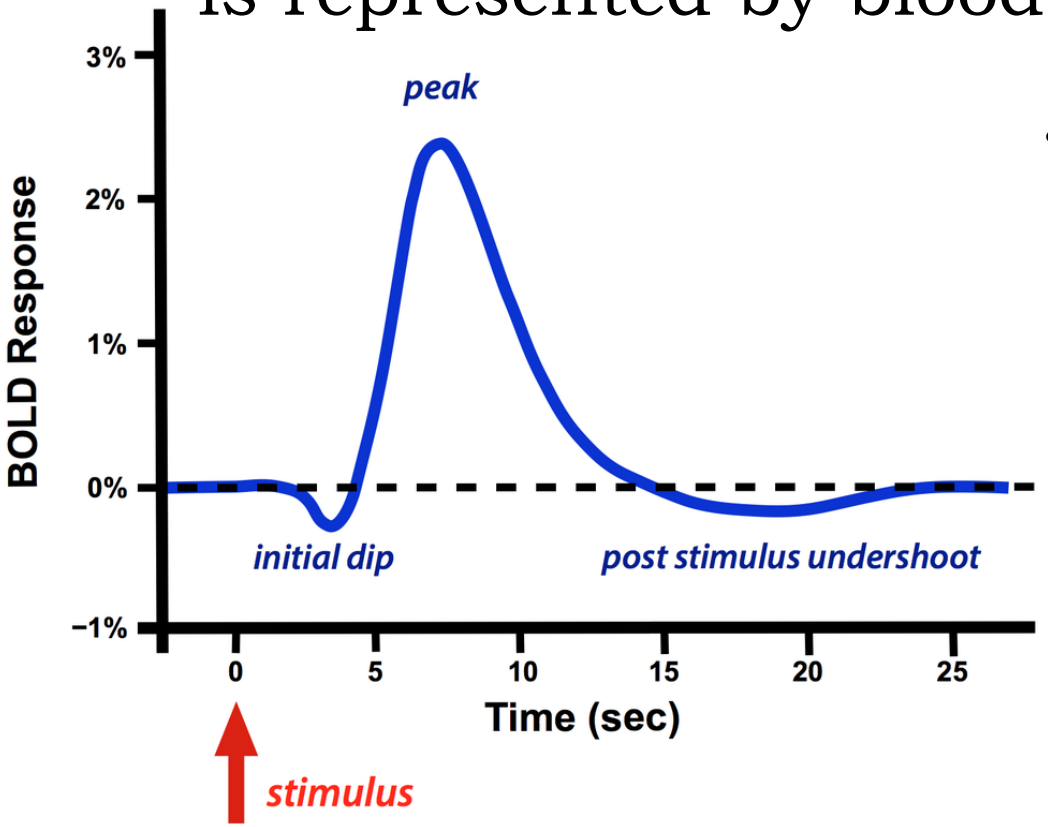
Which is best for you depends on your experimental question!

So no I can't tell you what your design should be, sorry.

What Are We Measuring During Task MRI

INTRODUCTION TO THE HEMODYNAMIC RESPONSE FUNCTION (HRF)

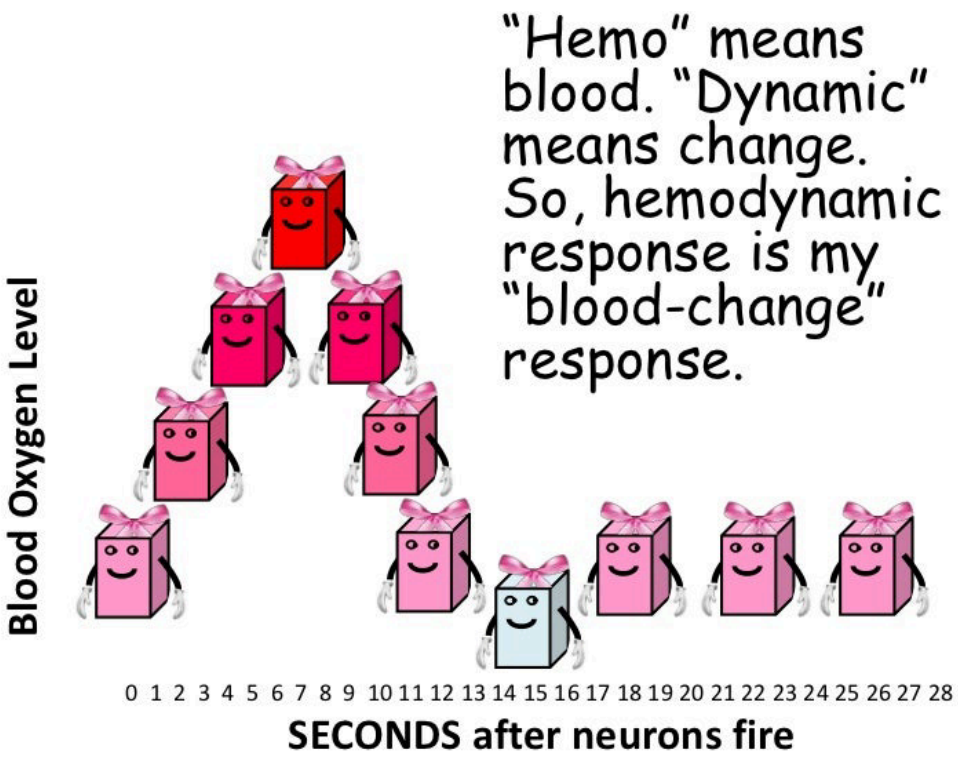
The HRF is our model of how neural activity is represented by blood flow changes in the brain

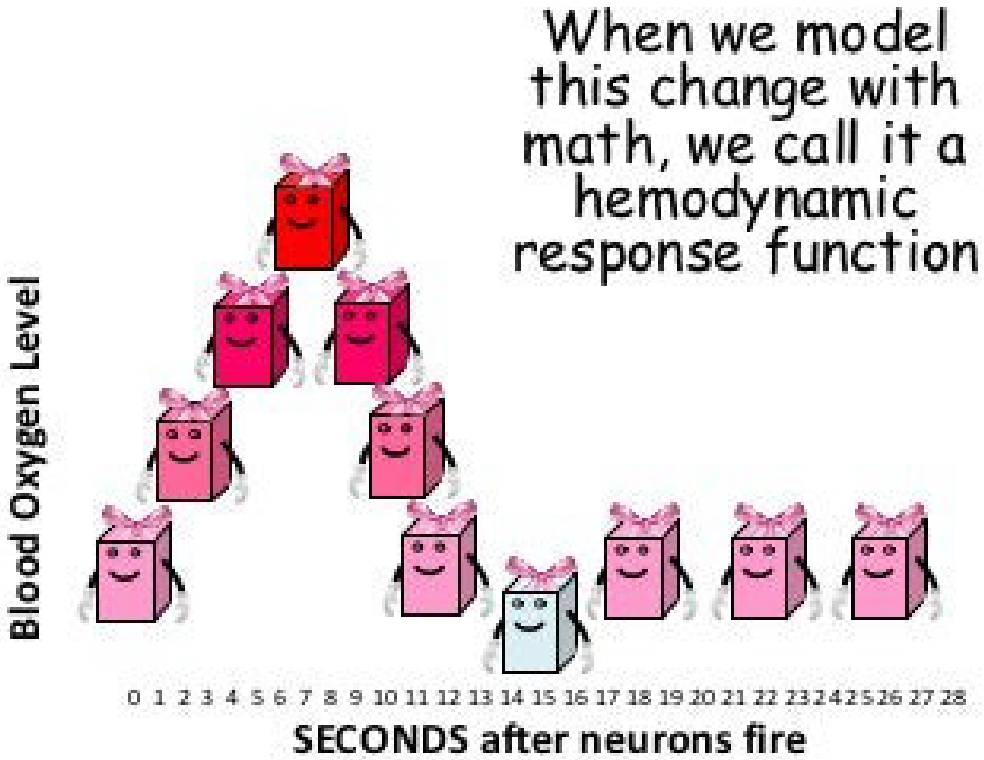


- The Hemodynamic Response Function has certain properties:
  1. Initial dip
  2. Peak at ~ 6s post stimuli
  3. Often an undershoot before return to baseline

The HRF

THE REAL MVP OF FMRI



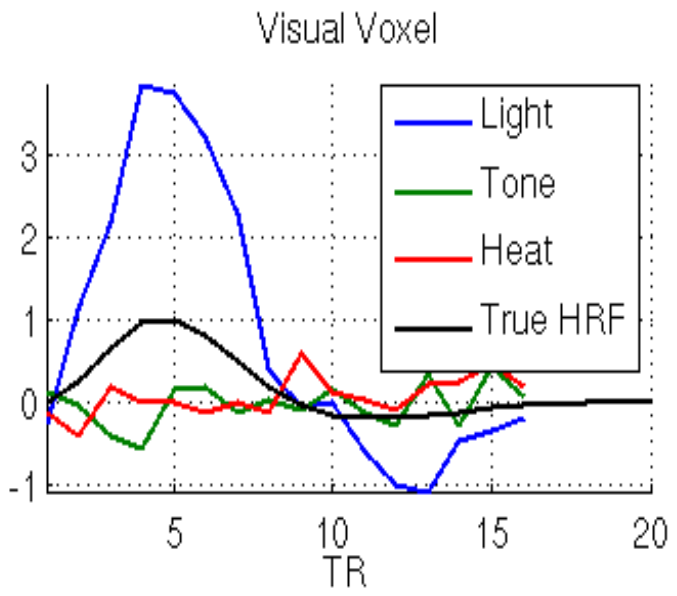


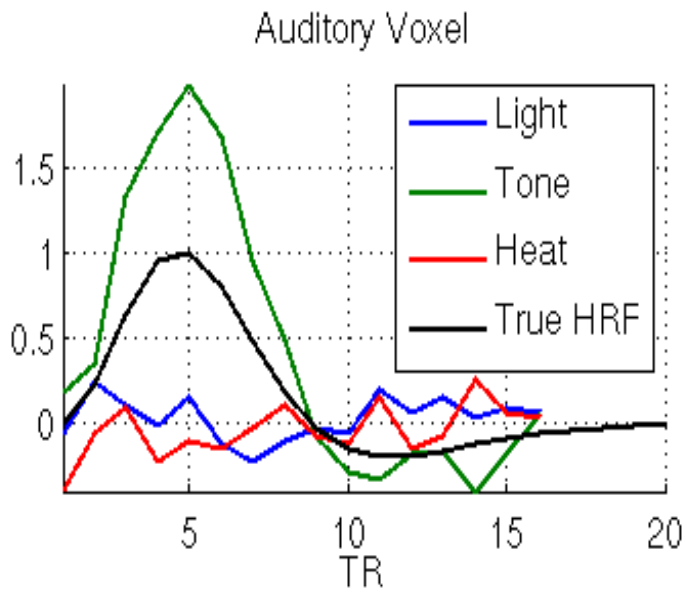
Breaking Down the HRF with Vicki

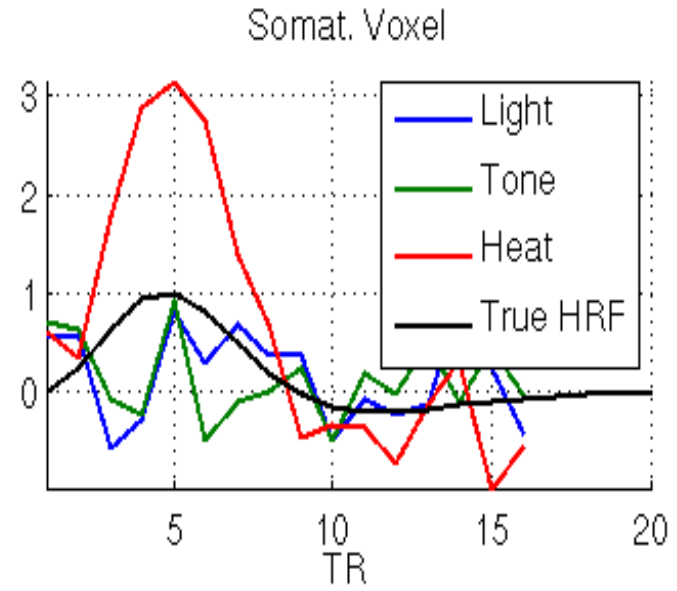
IMAGES VIA RUSSELL JAMES

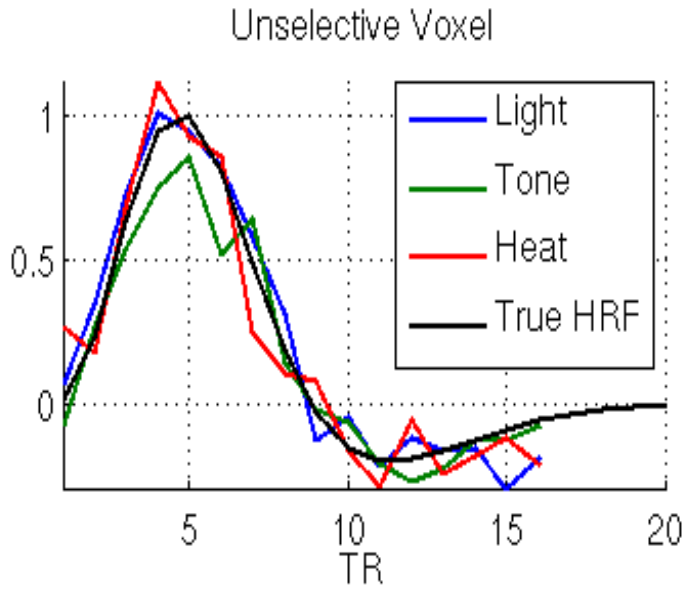
Each voxel will produce unique HRFs for different stimuli

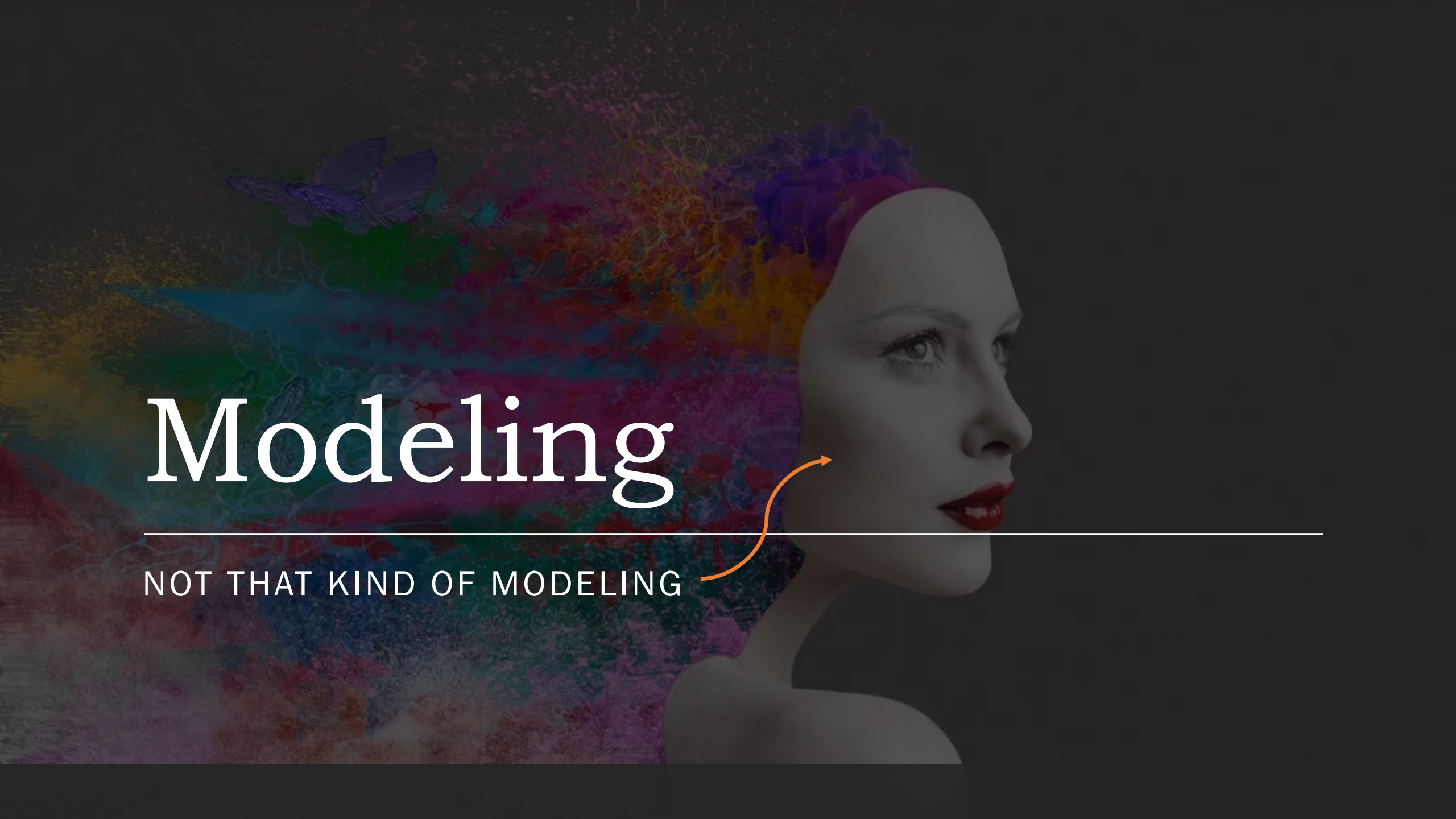
This fact is important for modeling later.







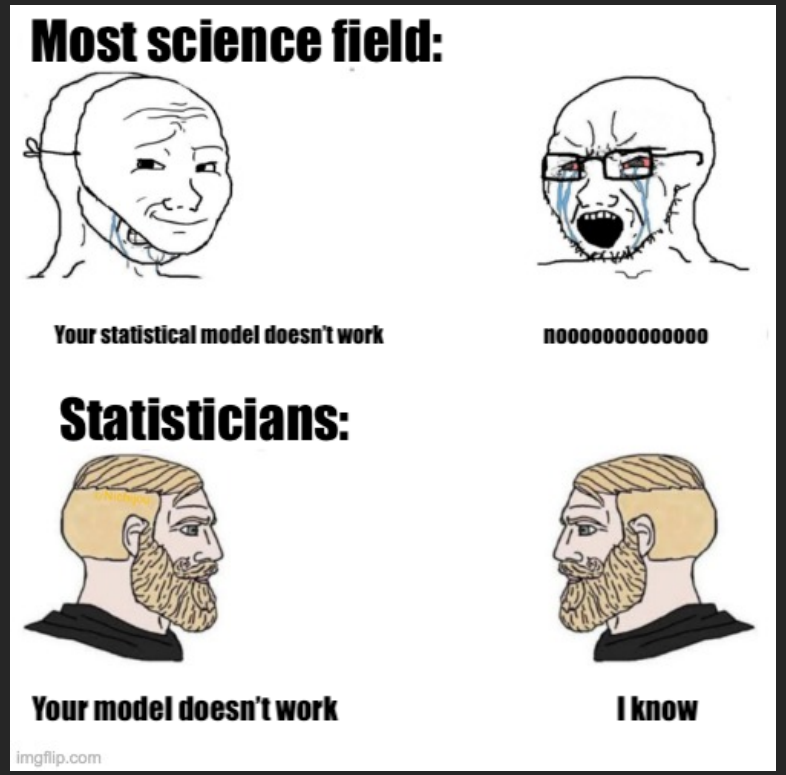




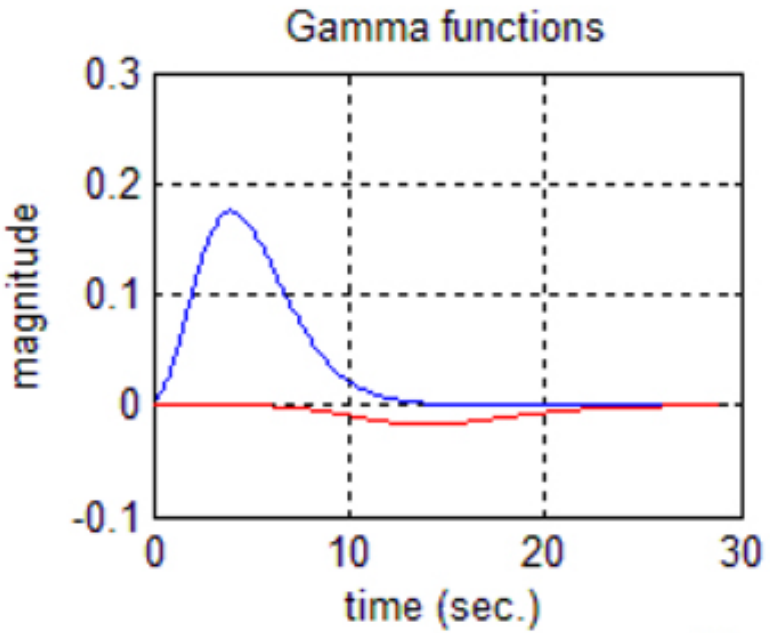
Modeling

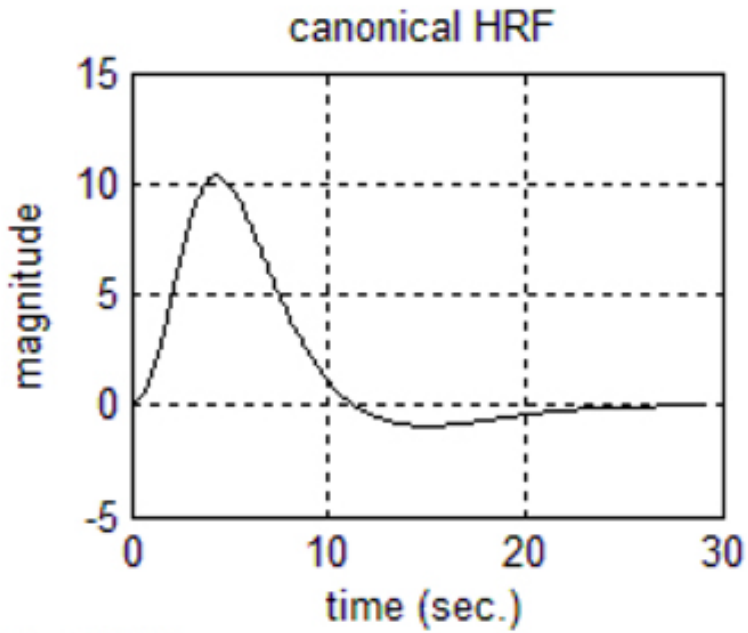
NOT THAT KIND OF MODELING

What does the HRF have to do with Modeling



- The HRF doesn't necessarily look like I said but we ASSUME it does
- The HRF is modeled with the (double) Gamma Distribution
  - Gamma well models decay of signal over time

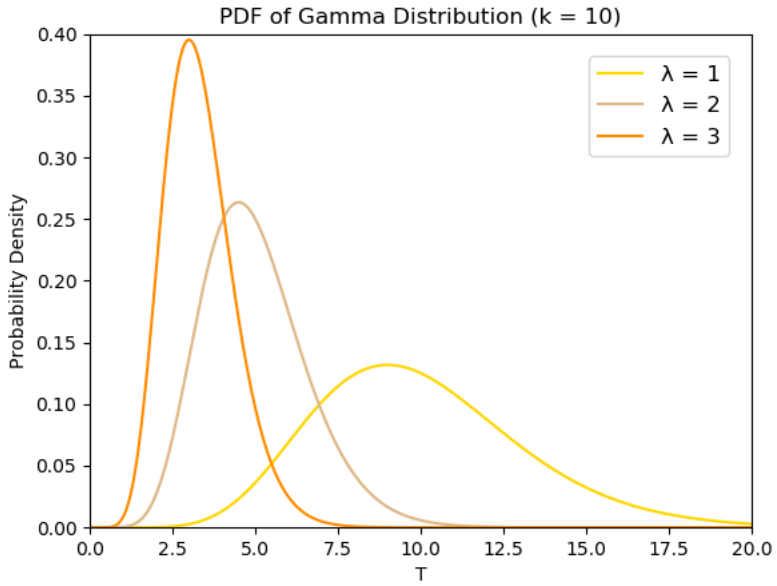




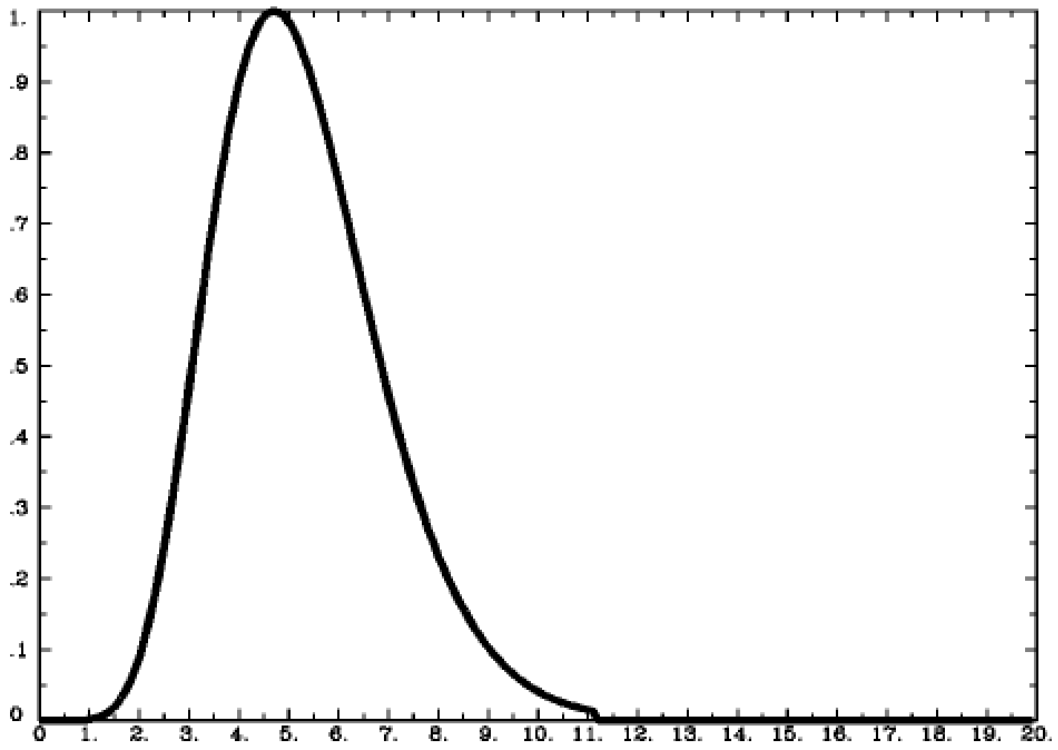
What does the HRF have to do with Modeling

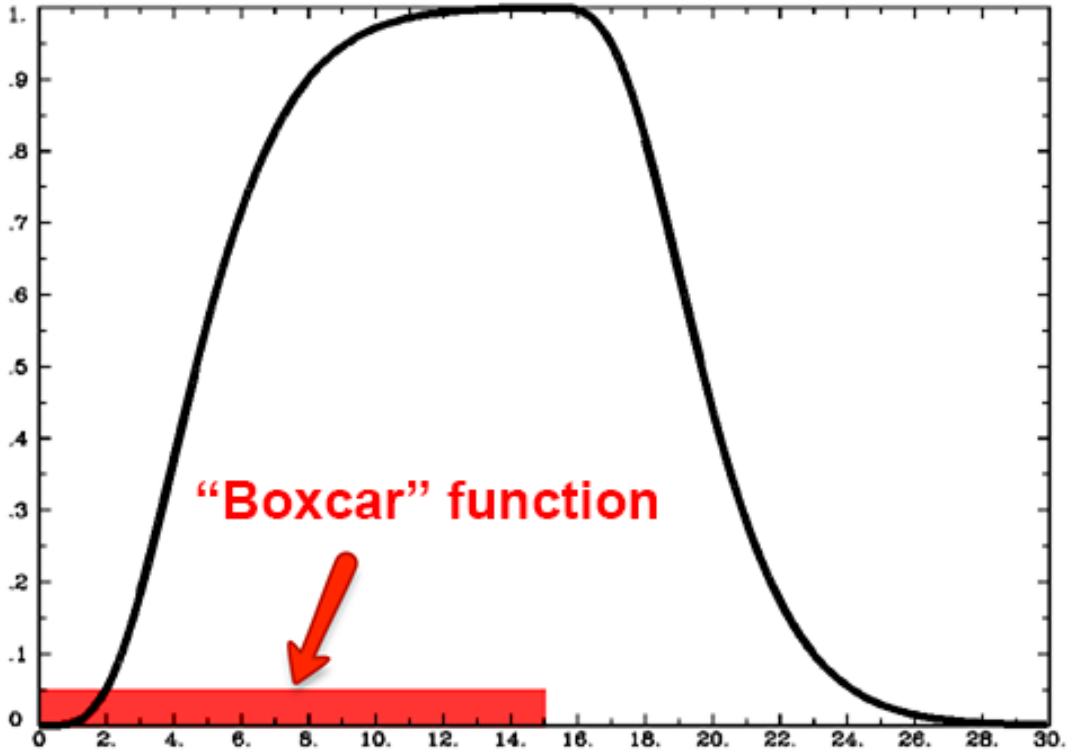
HELPFUL NOTE: If you're confused by what the **basis function is,** it's just the math function we use to make the same shape as the HRF

- The HRF doesn't necessarily look like I said but we ASSUME it does
- The HRF is modeled with the Gamma Distribution
  - Gamma well models decay of signal over time

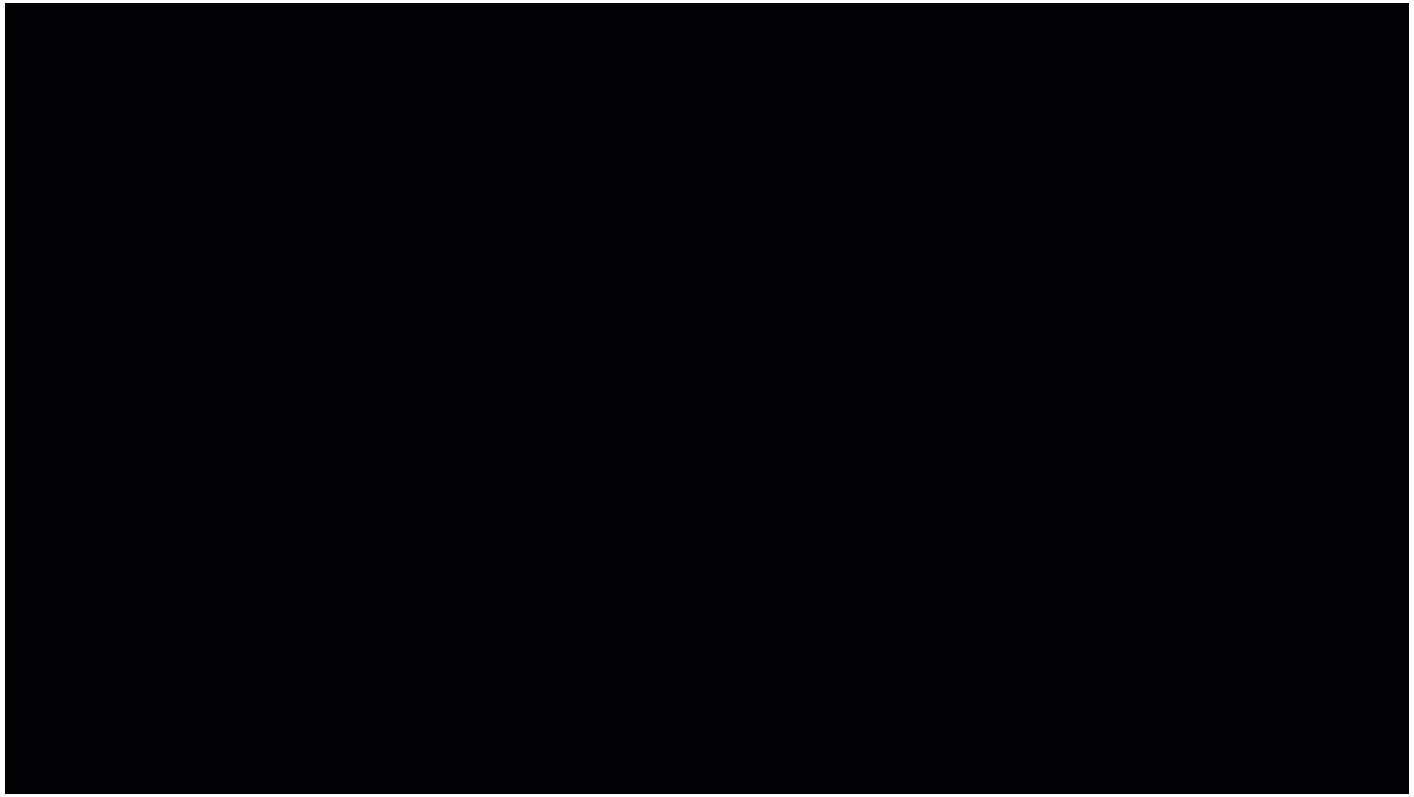


  - When applied to fMRI the Gamma Distribution is called a **BASIS FUNCTION** & we will use it for modeling

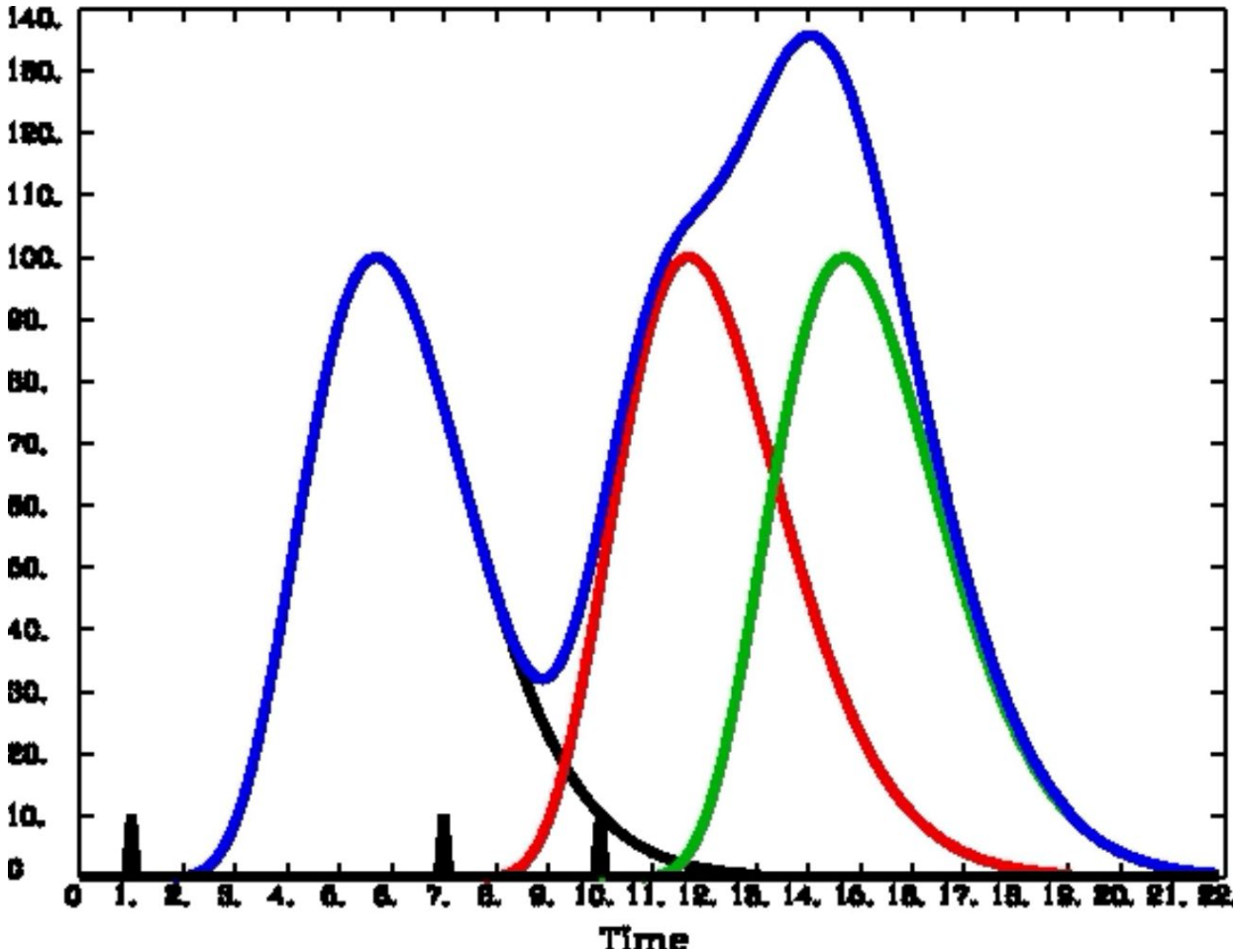


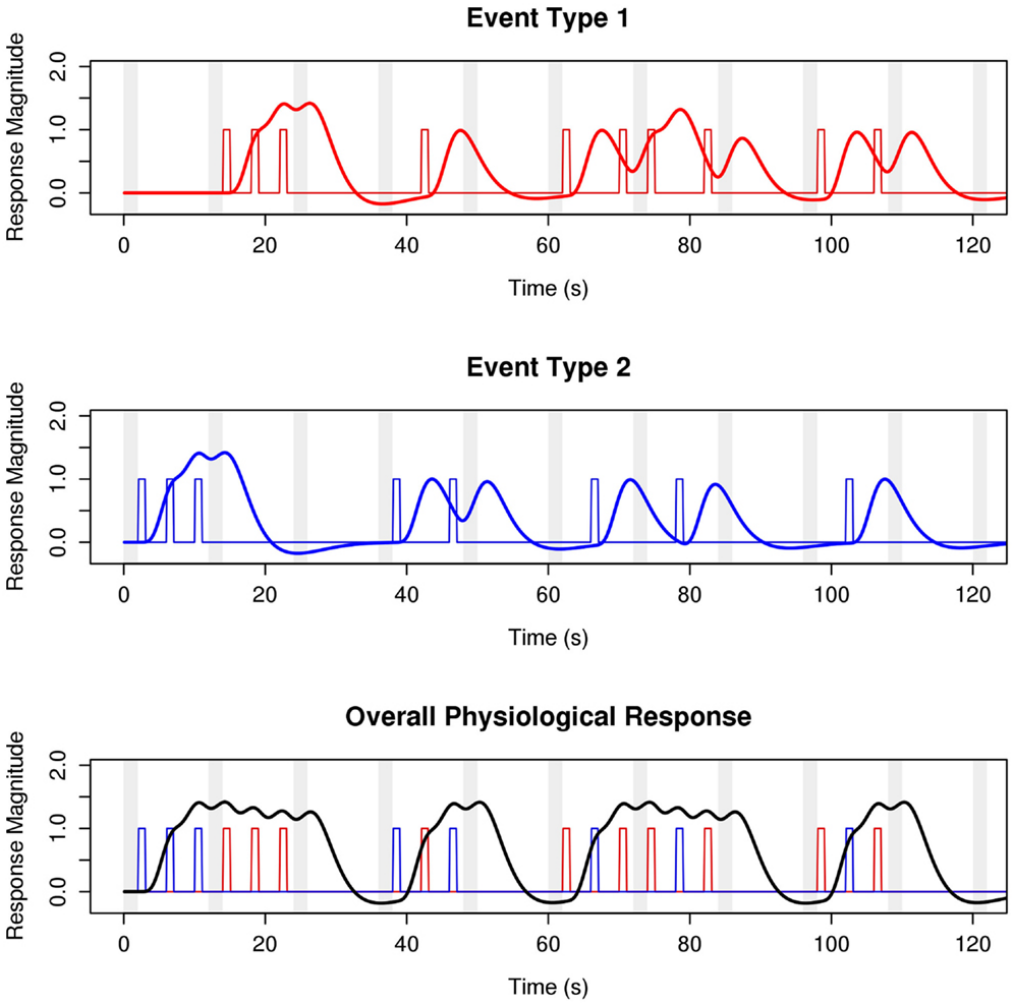


How do we use this "basis function" to model brain responses?



How do we use this “basis function” to model brain responses?





What if stimuli overlap?

YOU AVERAGE ‘EM UP

What does this matter for modeling?

WE USE THE PRINCIPLES HERE TO MODEL WHAT WE THINK “IDEAL” BRAIN RESPONSES TO DIFFERENT STIMULUS PRESENTATIONS WILL BE

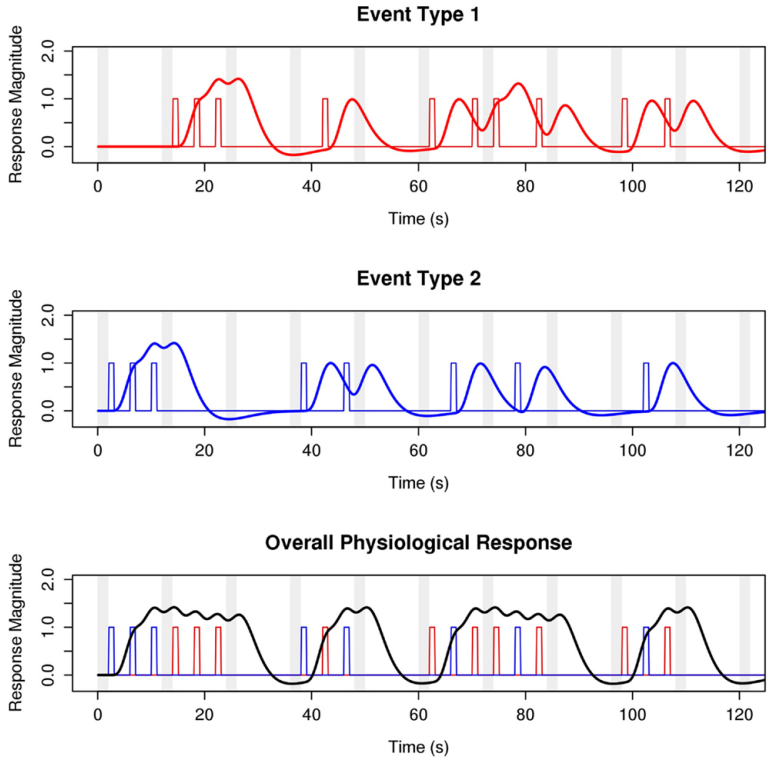
Wait, Ideal What?

So we've got:

1. Information about our experiment including a) number of trials, b) trial duration, c) trial onsets, etc.
2. A math way to model what the fMRI brain response to stimuli is

So what do we do?

- We take the fMRI response model and basically 'overlay' it on top of our stimuli



THIS IS OUR 'IDEAL TIMESERIES.'

THIS IS BASICALLY OUR BEST GUESS TO WHAT THE BRAIN RESPONSE TO OUR EXPERIMENT WILL BE GIVEN THOSE PARAMETERS WE HAVE.

How to create models of responses to a stimulus

1. Create text (or csv) file with 3 column
   1. Onset time, in seconds, relative to the start of the scan;
   2. Duration of the trial, in seconds;
   3. Parametric modulation OR Trial Type
2. Use scripting tools to make timing files for each subject, run, and stimulus

Timing Files

A

SUB-01_TASK-FLANKER_RUN-1_EVENTS.TSV DOWNLOAD

onset	duration	tri…	res…	co…
0.0	2.0	incongrue…	1.095	correct
10.0	2.0	incongrue…	0.988	correct
20.0	2.0	congruent…	0.591	correct
30.0	2.0	congruent…	0.499	correct
40.0	2.0	incongrue…	0.719	correct
52.0	2.0	congruent…	0.544	correct
64.0	2.0	congruent…	0.436	correct
76.0	2.0	incongrue…	0.47	correct
88.0	2.0	congruent…	0.409	correct

B

onset	duration	trial_type
0.0	2.0	incongruent_correct
10.0	2.0	incongruent_correct
20.0	2.0	congruent_correct
30.0	2.0	congruent_correct
40.0	2.0	incongruent_correct
52.0	2.0	congruent_correct
64.0	2.0	congruent_correct
76.0	2.0	incongruent_correct
88.0	2.0	congruent_correct
102.0	2.0	incongruent_correct
116.0	2.0	congruent_correct

C

```
0.0 2.0 1
10.0 2.0 1
40.0 2.0 1
76.0 2.0 1
102.0 2.0 1
150.0 2.0 1
164.0 2.0 1
174.0 2.0 1
208.0 2.0 1
220.0 2.0 1
232.0 2.0 1
260.0 2.0 1
```

incongruent_run1.txt

What do the numbers mean?

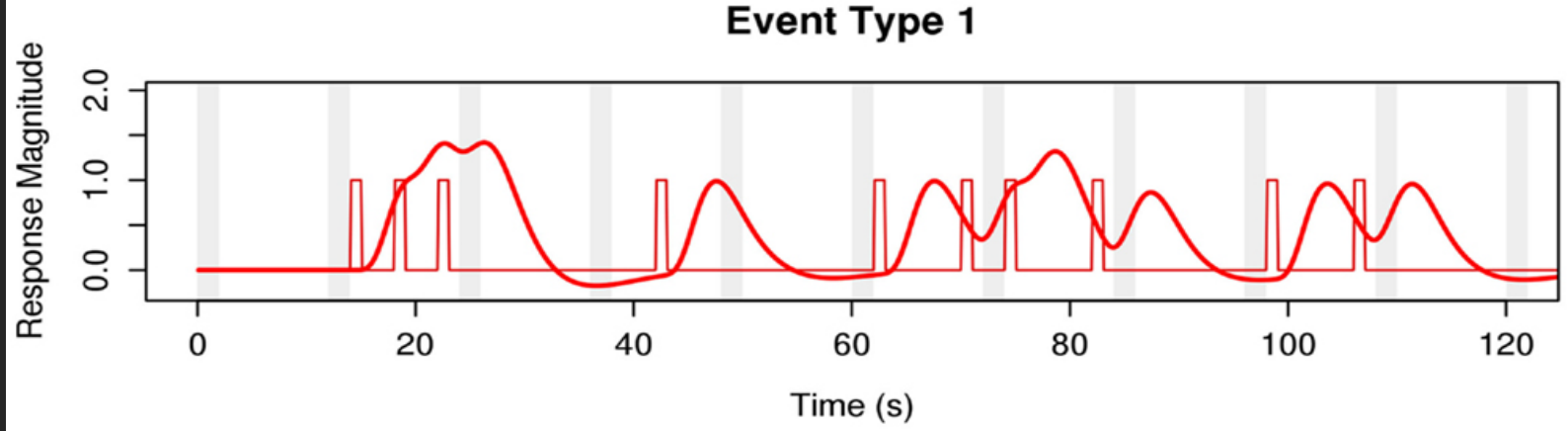
B

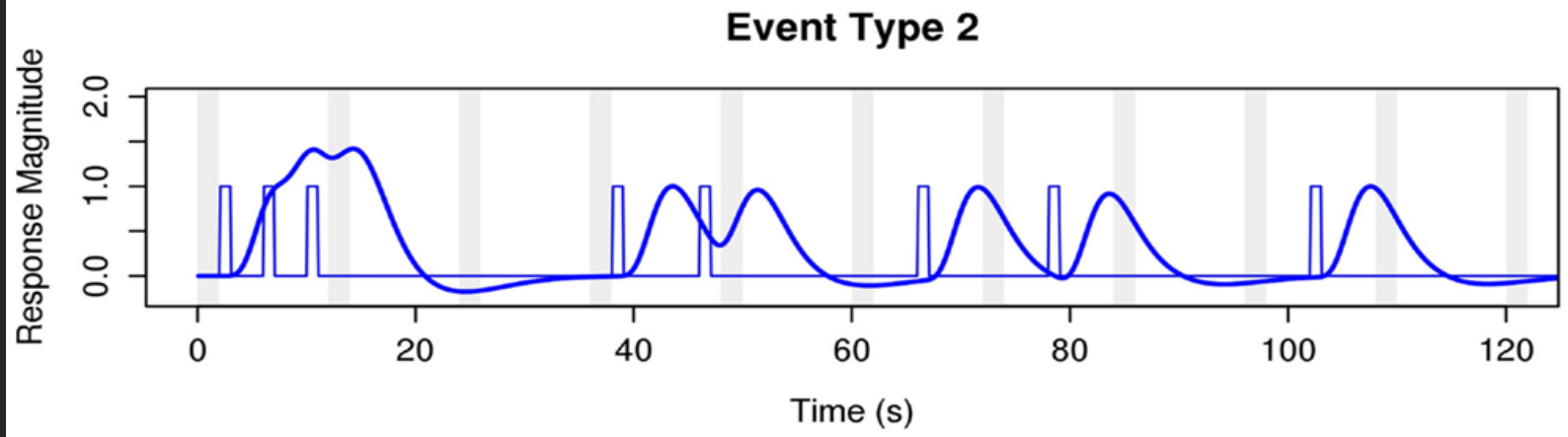
onset	duration	trial_type
0.0	2.0	incongruent_correct
10.0	2.0	incongruent_correct
20.0	2.0	congruent_correct
30.0	2.0	congruent_correct
40.0	2.0	incongruent_correct
52.0	2.0	congruent_correct
64.0	2.0	congruent_correct
76.0	2.0	incongruent_correct
88.0	2.0	congruent_correct
102.0	2.0	incongruent_correct
116.0	2.0	congruent_correct

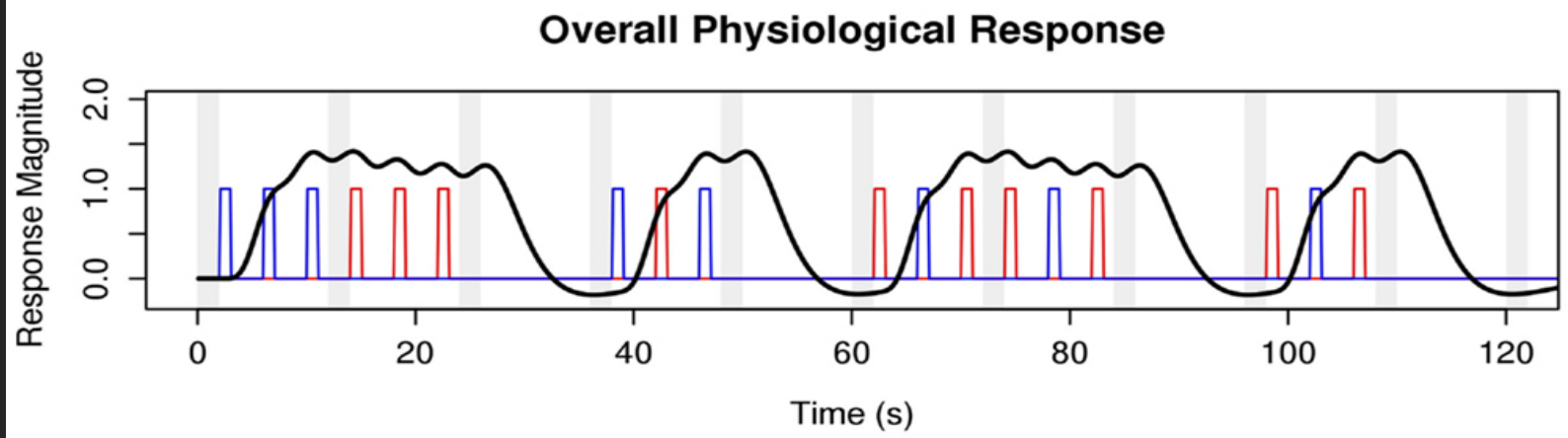
C

incongruent_run1.txt

```
0.0 2.0 1
10.0 2.0 1
40.0 2.0 1
76.0 2.0 1
102.0 2.0 1
150.0 2.0 1
164.0 2.0 1
174.0 2.0 1
208.0 2.0 1
220.0 2.0 1
232.0 2.0 1
260.0 2.0 1
```







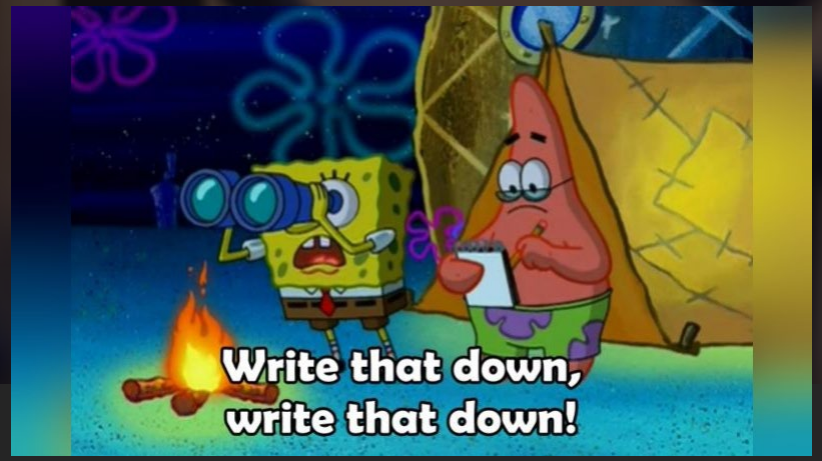
Deconvolution

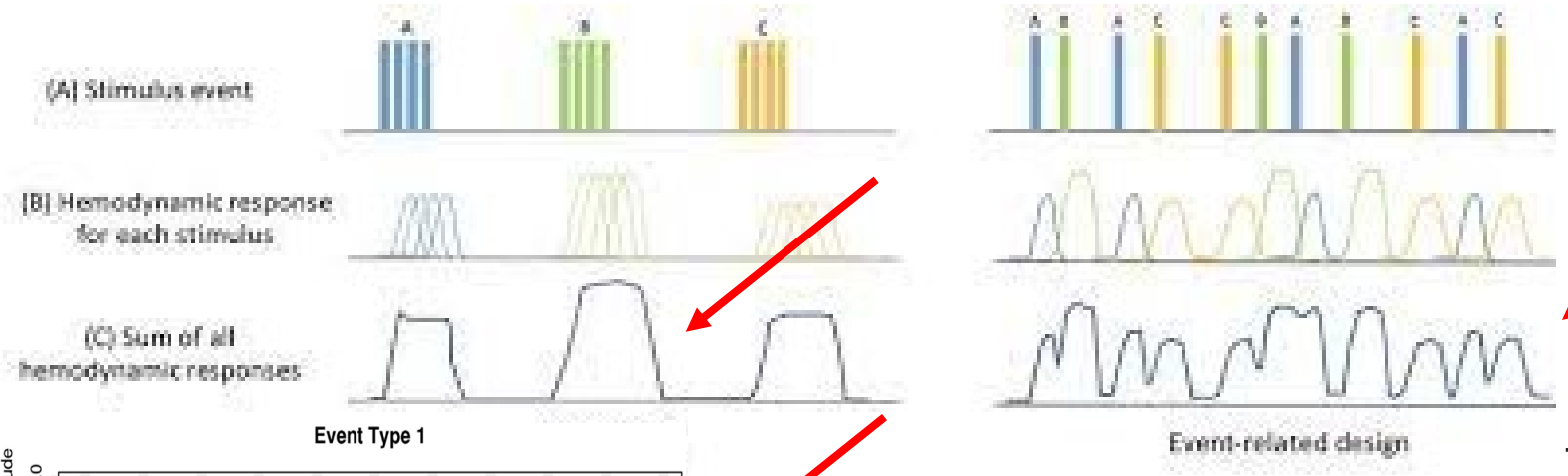
OH BOY HERE WE GO

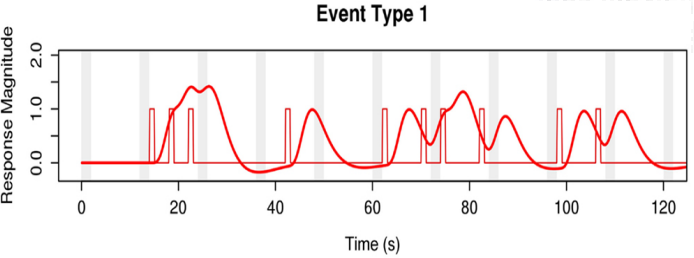
I am going to be murdered for this slide but…

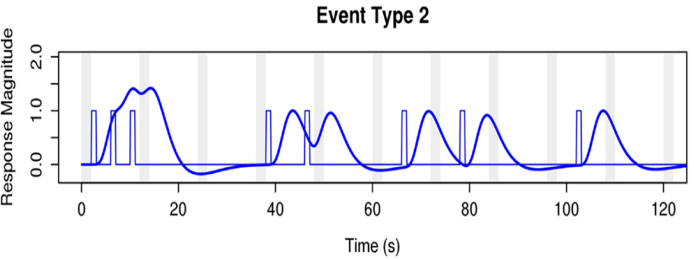
CONVOLUTION = MIXING STUFF UP

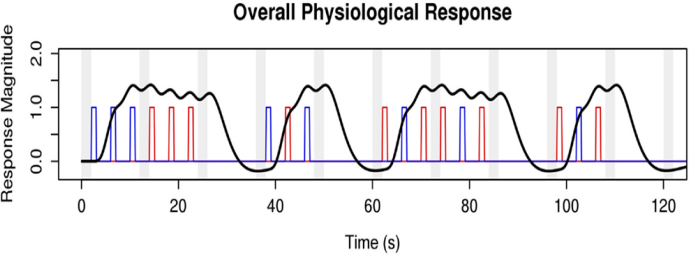
DECONVOLUTION = SEPARATING THE MIXED UP STUFF INTO ITS PARTS

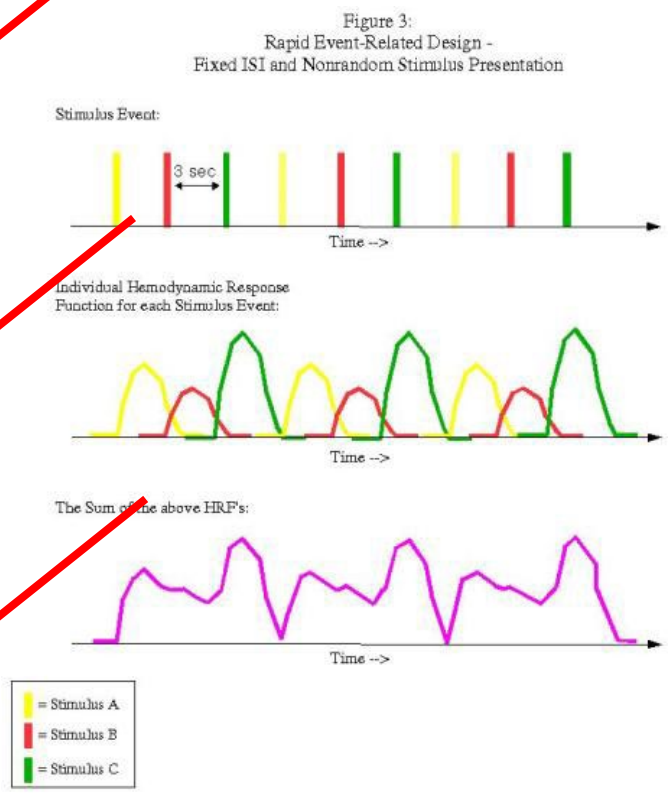








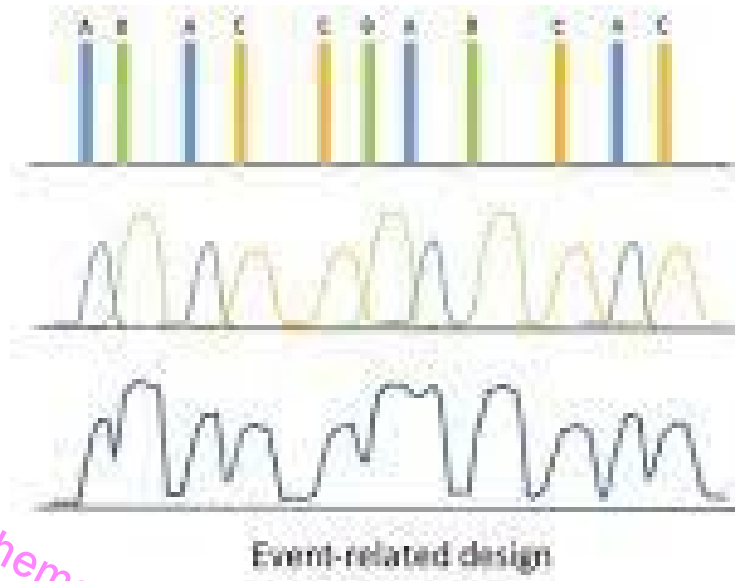




Every time I showed you a figure with squiggly lines over bars, that was a **CONVOLVED** stimulus time series!

But the problem is:

THE ACTUAL SIGNAL MEASURED FROM IN BRAIN NEVER LOOKS LIKES THIS

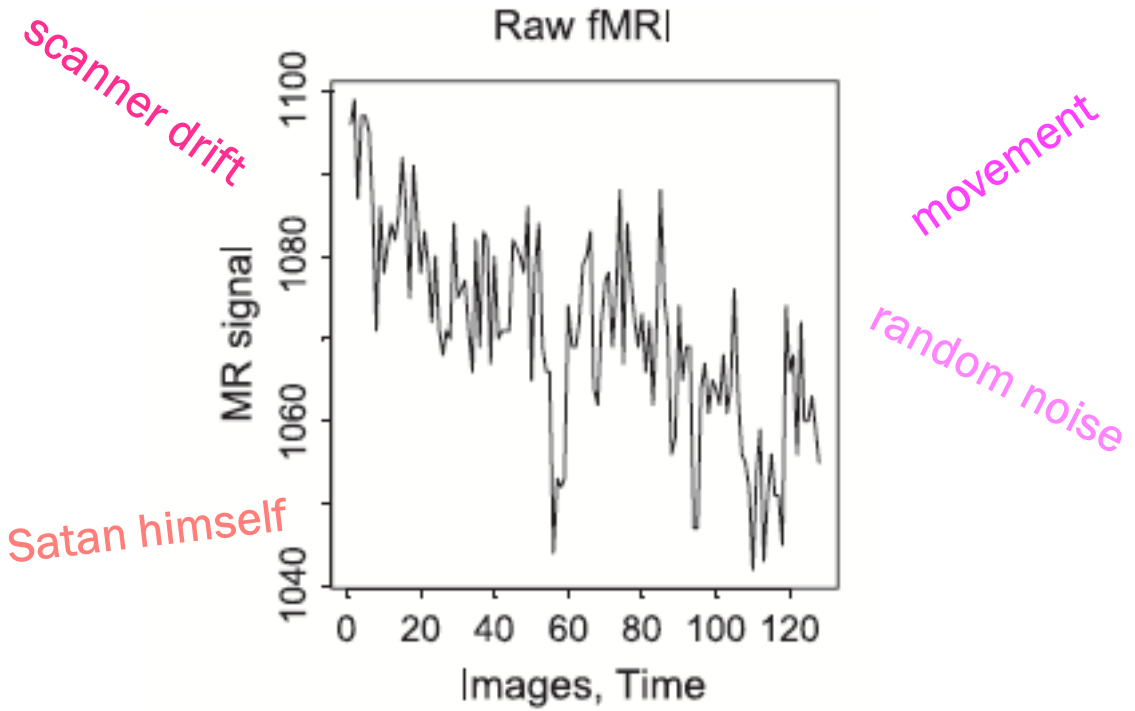


smooth

nice

mathematically optimal

IT ACTUALLY LOOKS LIKE THIS BECAUSE THE SIGNAL IS FILLED WITH VARIOUS SOURCES OF NOISE



scanner drift

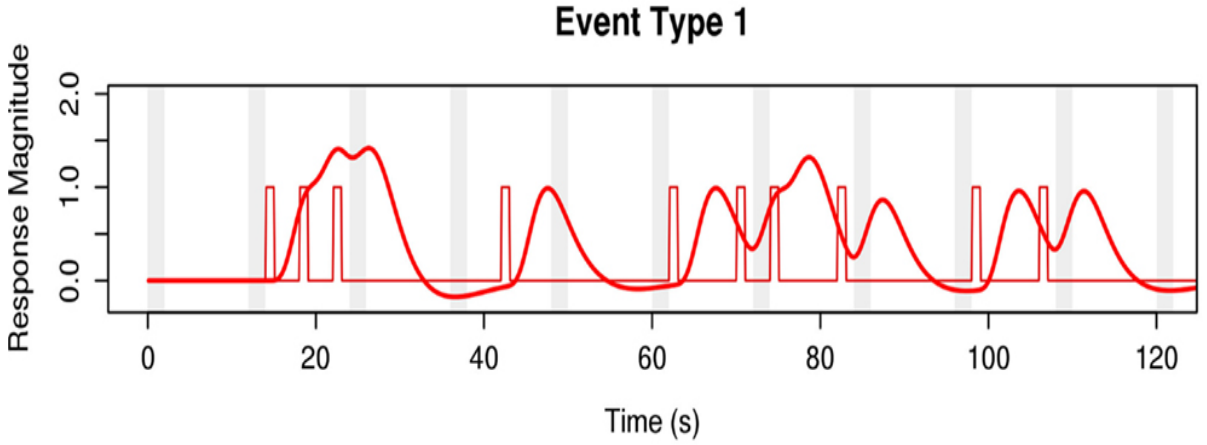
movement

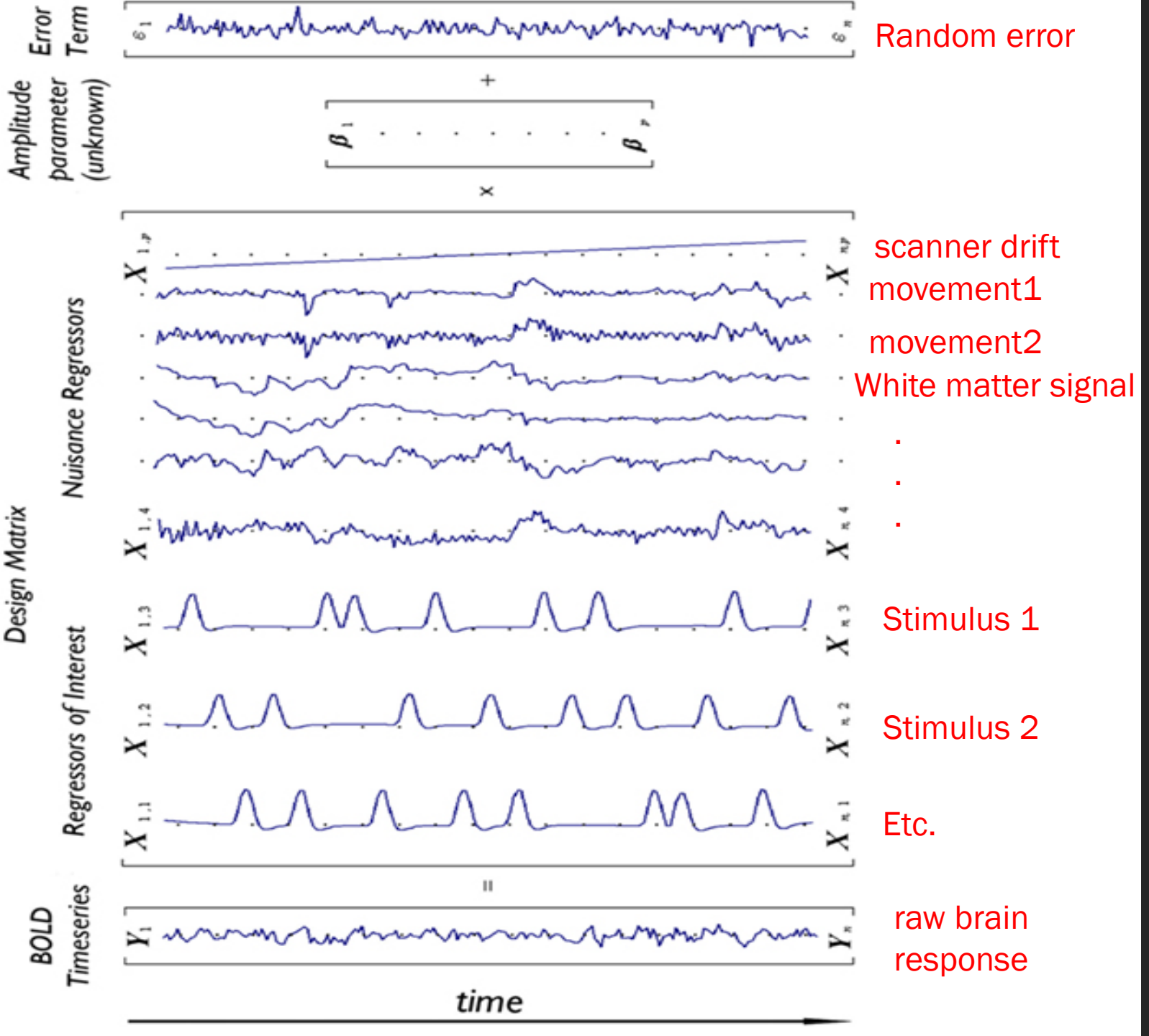
random noise

Satan himself

So what does the MEASURED signal of an active voxel look like?

- The brain signal from a voxel we assume is responsive to a specific event (e.g. event type 1) is the modeled response to that stimulus…





…convolved with all the noise we can account for

So it ends up looking like the jagged, messy, raw timeseries you usually see that comes out of the MRI

So what is deconvolution

Deconvolution is us using regression (GLM) to un-mix the fMRI signal, removing the noise to find each voxel's "response" to each different stimulus we presented

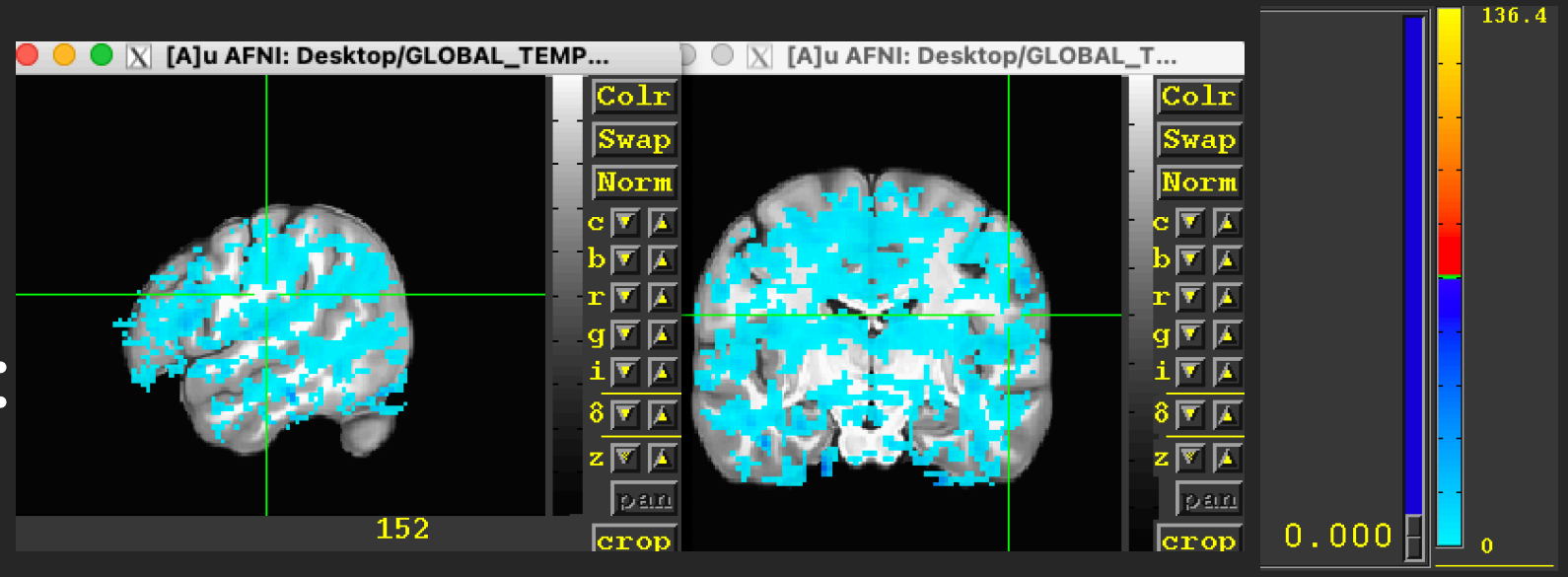
In deconvolution we:

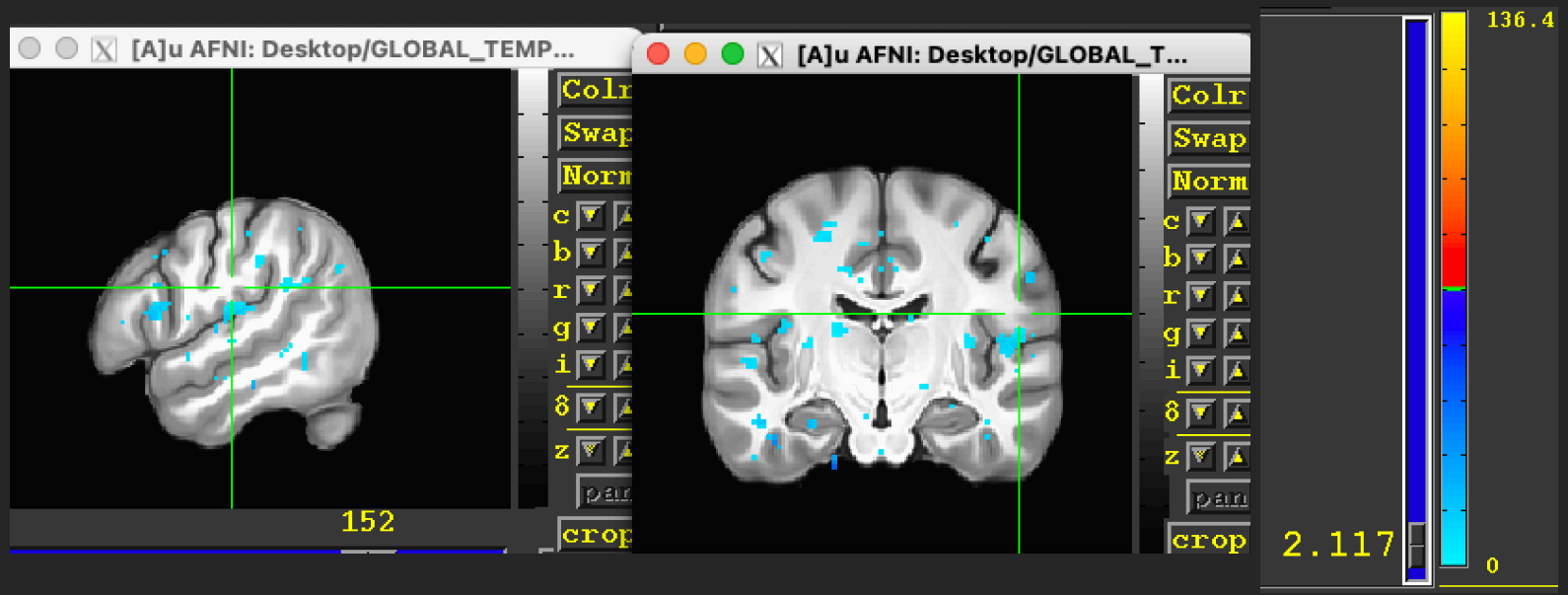
1. Create a model with all stimuli and noise
    1. We already have our “ideal timeseries”
    2. We know certain sources of noise that will be present and can calculate them
2. Fit the model to all voxels
    a. Noise regressors are “removed”

```
#!/bin/csh
#
set ptid = $1
set run = $2
set tdir = $3
cd ${tdir}/${ptid}.results/
sed '1,2d' ${ptid}MSwav > ${ptid}MSCwav
PkCensorSD outcount.r01.1D 2 ${ptid}${run}Censor.1D
3dDeconvolve \
-input pb05.${ptid}.r01.scale+tlrc \
-censor ${ptid}${run}Censor.1D \
-polort A \
-num_stimts 12 \
-stim_file 1 ${ptid}'MSCwav[0]' -stim_label 1 EasyC \
-stim_file 2 ${ptid}'MSCwav[1]' -stim_label 2 MedC \
-stim_file 3 ${ptid}'MSCwav[2]' -stim_label 3 HardC \
-stim_file 4 ${ptid}'MSCwav[3]' -stim_label 4 EasyE \
-stim_file 5 ${ptid}'MSCwav[4]' -stim_label 5 MedE \
-stim_file 6 ${ptid}'MSCwav[5]' -stim_label 6 HardE \
-stim_file 7 dfile.r01.1D'[0]' -stim_label 7 Roll \
-stim_file 8 dfile.r01.1D'[1]' -stim_label 8 Pitch \
-stim_file 9 dfile.r01.1D'[2]' -stim_label 9 Yaw \
-stim_file 10 dfile.r01.1D'[3]' -stim_label 10 dX \
-stim_file 11 dfile.r01.1D'[4]' -stim_label 11 dY \
-stim_file 12 dfile.r01.1D'[5]' -stim_label 12 dZ \
-num_glt 10 \
-gltsym 'SYM: +.33*EasyC +.33*MedC +.33*HardC -.33*EasyE +.33*MedE -.33*HardE ' -glt_label 1
-gltsym 'SYM: +.5*EasyE +.5*EasyC ' -glt_label 2 "Easy" \
-gltsym 'SYM: +.5*MedE +.5*MedC ' -glt_label 3 "Med" \
-gltsym 'SYM: +.5*HardE +.5*HardC ' -glt_label 4 "Hard" \
-gltsym 'SYM: -EasyC +HardC ' -glt_label 5 "Hard-Easy_C" \
-gltsym 'SYM: -MedC +HardC  ' -glt_label 6 "Hard-Med_C" \
-gltsym 'SYM: +MedC -EasyC  ' -glt_label 7 "Med-Easy_C" \
-gltsym 'SYM: -EasyE +HardE ' -glt_label 8 "Hard-Easy_E" \
-gltsym 'SYM: -MedE +HardE  ' -glt_label 9 "Hard-Med_E" \
-gltsym 'SYM: +MedE -EasyE ' -glt_label 10 "Med-Easy_E" \
-errts ${ptid}${run}_error_ts \
-GOFORIT 4 -tout -bout -nofull_first \
-bucket ${ptid}${run}.buc
```

In deconvolution we:

1. Create a model with all stimuli and noise
2. Fit the model to all voxels
   a. Noise regressors are “removed”
3. Look at whole brain maps to see how all voxels responded to any given stim. of interest
   1. The voxel colors represent their numbers
   2. The numbers are beta weights
   3. Beta weights represent how much a stimulus affects the voxel’s BOLD – effect amplitude
   4. Higher number = more voxel ”responds” to stimulus
4. Look for voxels that have larger betas to find areas of interest





Note: Each different stimulus can have its own map (e.g. the Bulbasaur map) – the brain map outputs will be whatever you asked for in the code

In the end…

- We do this same thing to all participants to get the same maps
- To look at different brain responses to 2 different stimuli, we'd take all the maps of stimulus 1 and compare them to all the maps of stimulus 2

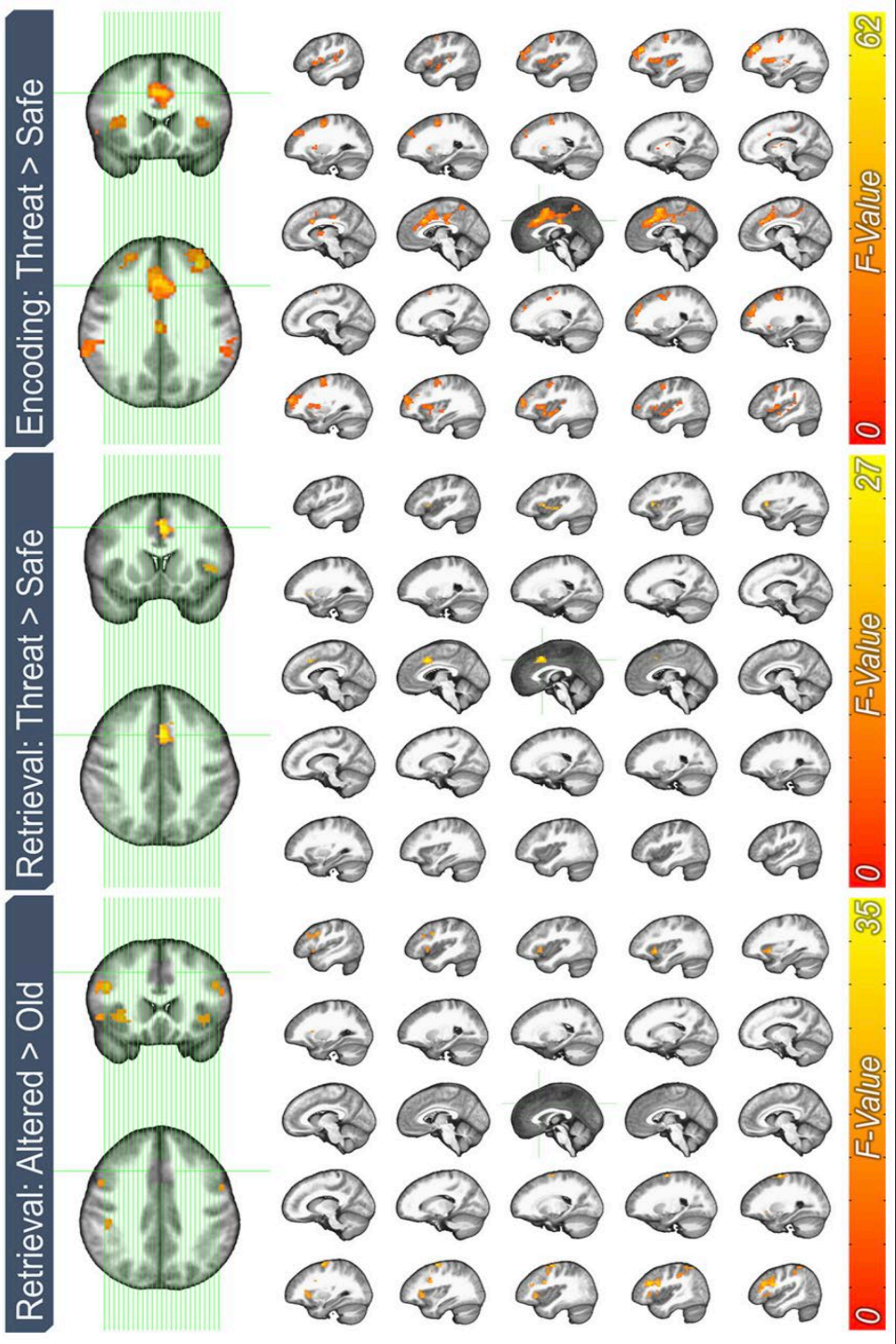
OR

- To look at differences in a task between a control and patient group, we'd take all the control brain maps and compare them to all of the patient maps.

- These comparisons are simply another level of stats. (e.g. t-test, mixed-effects ANOVA) between the stimuli or groups buT THAT'S FOR MY MODELING TALK, I HAVE BECOME AN OMEN OF BAD TALKS

In the end…

- And that is where you get maps like this in a journal near you…



Any questions?

(IM SORRY)