

fMRI Course, Day 5

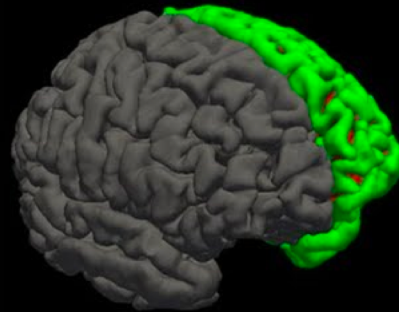
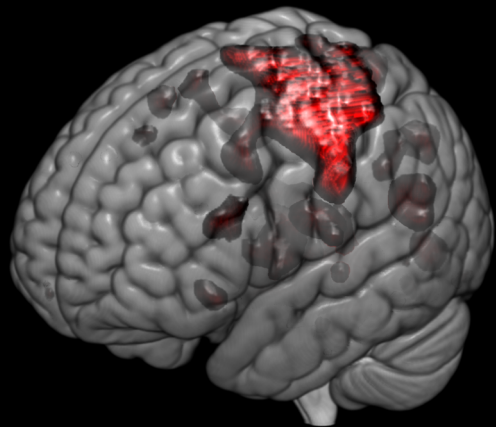
1st-Level Analysis

August 5th, 2022

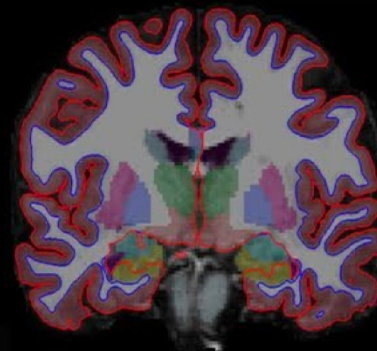
About Me

Neuroimaging Initiative (NII)

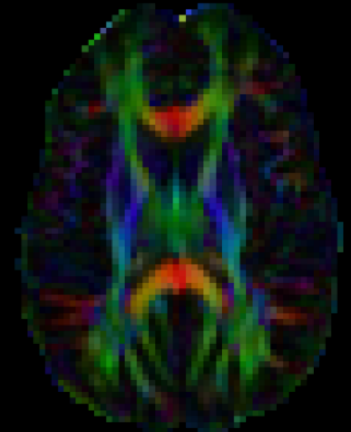
Consulting for anyone who does neuroimaging



Surface



Volume



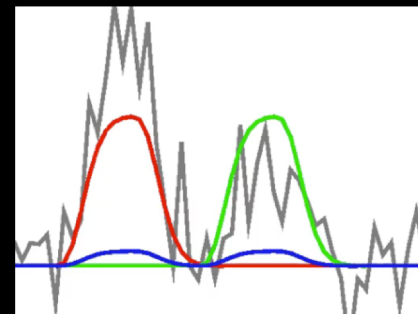
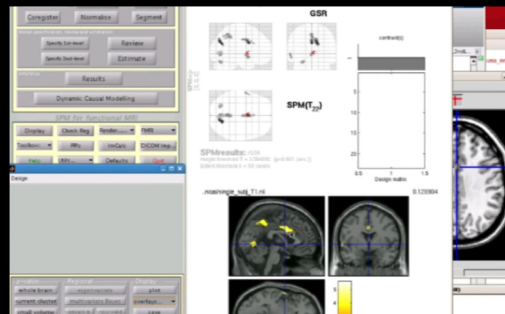
Goals

1. Understand how to do the steps

2. Understand why we did the steps



Both Remember Steps and Apply Concepts



Problem

**How to accommodate dozens of labs
spread across three campuses?**

**How to stay current with the
latest methods and tools?**

How to make sure the ideas “stick”?

Solutions

Illustrations and demonstrations using data

Goal is for you to analyze your own data

Feedback is highly appreciated!

About Me

🏠 Andy's Brain Book
latest

Search docs

INSTALL

Overview

UNIX FOR NEUROIMAGERS

What is Unix?

Unix Tutorial #1: Navigating the directory tree

Unix Tutorial #2: Copying and Removing Files

Unix Tutorial #3: Reading Text Files

Unix Tutorial #4: Shells and Path Variables

Unix Tutorial #5: For-Loops

Unix Tutorial #6: Conditional Statements

Unix Tutorial #7: Scripting

Unix Tutorial #8: The Sed Command

Unix Tutorial #9: Automating The Analysis


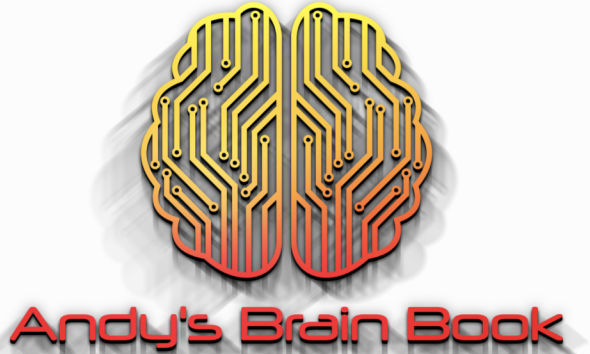
FMRI SHORT COURSE WITH FSL

Introduction

fMRI Tutorial #1: Downloading the Data

[Docs](#) » Welcome to Andy's Brain Book! [Edit on GitHub](#)

Welcome to Andy's Brain Book!



This resource is sponsored by the [University of Michigan](#).

This book, *Andy's Brain Book*, is the ReadTheDocs companion to [Andy's Brain Blog](#). It is intended for fMRI beginners, with more advanced imaging techniques being added later on. If this is your first

Overview of The Schedule

Friday 8/5/2022	8:30 AM – 12:30 PM	Level Analysis & Experimental Design	Andy Jahn University of Michigan
Monday 8/8/2022	8:30 AM – 12:30 PM	Contrasts, Group Analysis & Double Dissociations	Andy Jahn University of Michigan
	4:00 PM	Pattern Analysis & Classification via MVPA-virtual but live	Stephen LaConte Virginia Tech
Tuesday 8/9/2022	8:30 AM - 12:30 PM	Pitfalls in fMRI Research	Andy Jahn University of Michigan
Wednesday 8/10/2022	8:30 AM – 12:30 PM	Network Analysis & Tools	Scott Peltier University of Michigan Alex Jordan University of Michigan
Thursday 8/11/2022	8:30 AM – 12:30 PM	Part 1- Introduction to Open Science Part 2- BIDS, MRIQC & fMRI Prep	Andy Jahn University of Michigan Scott Peltier University of Michigan
Friday 8/12/2022	8:30 AM – 12:30 PM	Reproducibility	Andy Jahn University of Michigan

Overview of The Schedule

At regular intervals, I will be asking you to download software and data

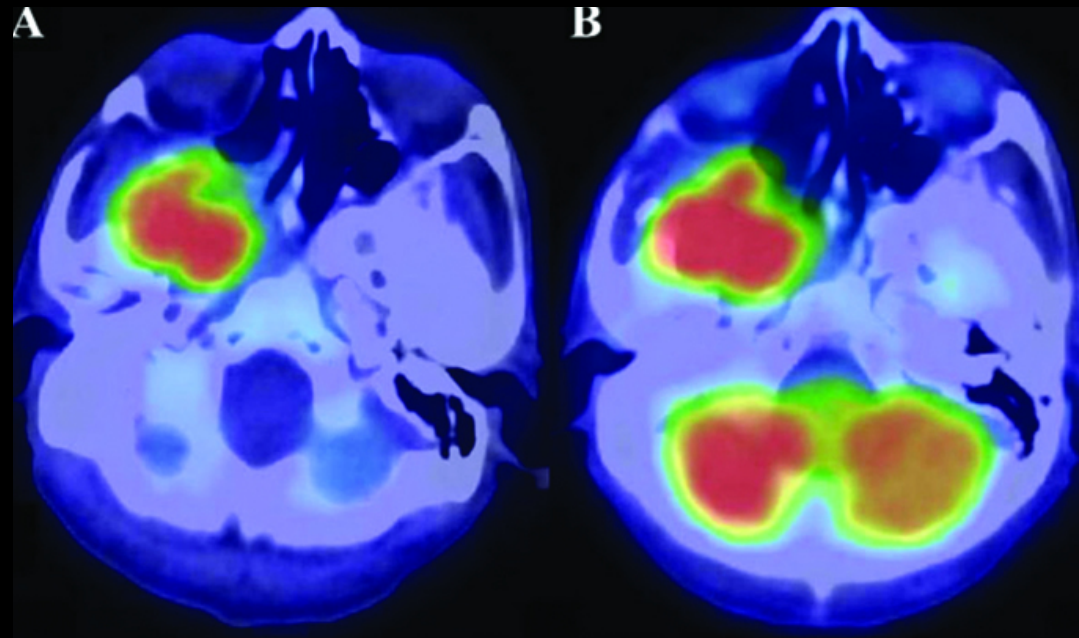
This is just to help with the demonstrations; don't worry if you are unable to download or install these!

Today's Agenda

- 1. Brief review of fMRI**
- 2. The BOLD Response**
- 3. Model Fitting and 1st-Level Analysis**
- 4. Other Modeling Options: Parametric Modulation and Finite Impulse Response**

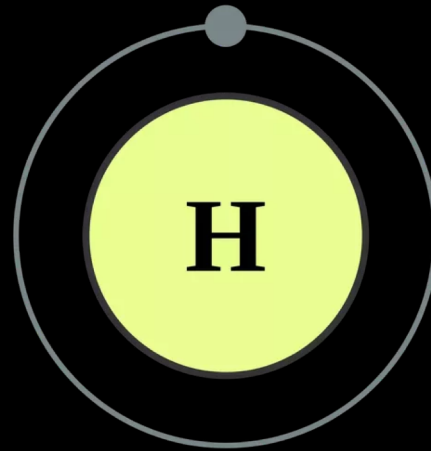
Review of fMRI

Neuroimaging Scene: The Early 1990's



Review of fMRI

MRIs: More powerful & More widespread

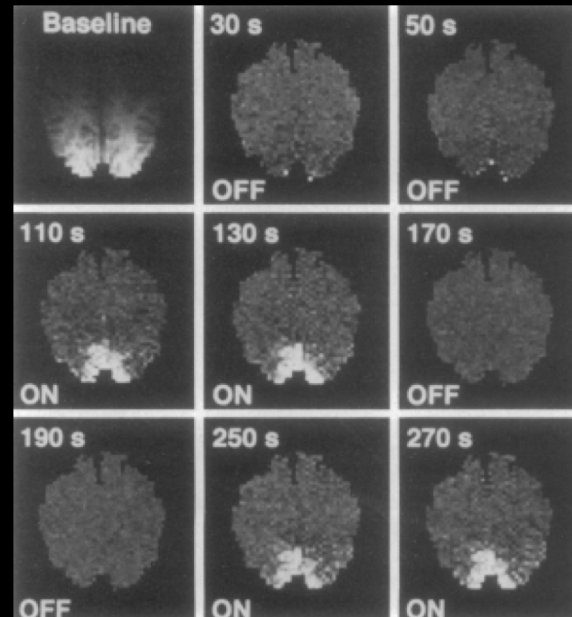
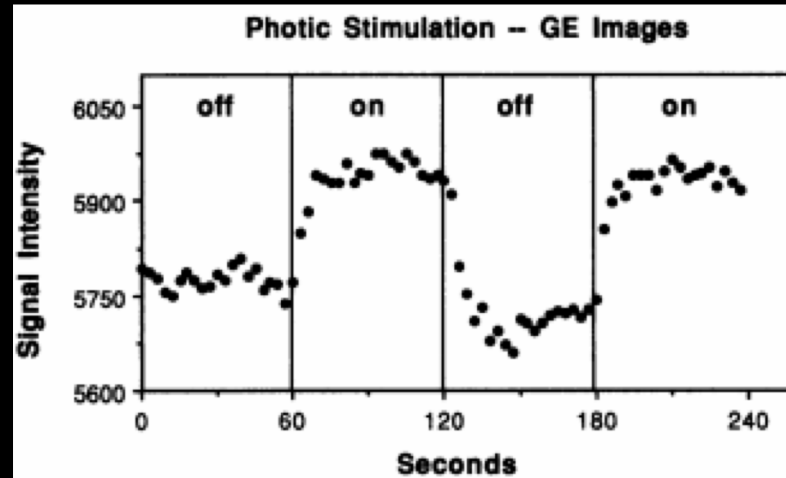


Deoxygenated blood = Lower signal

Oxygenated blood = Higher signal

Blood Oxygenation Level Dependent Signal (BOLD Signal)

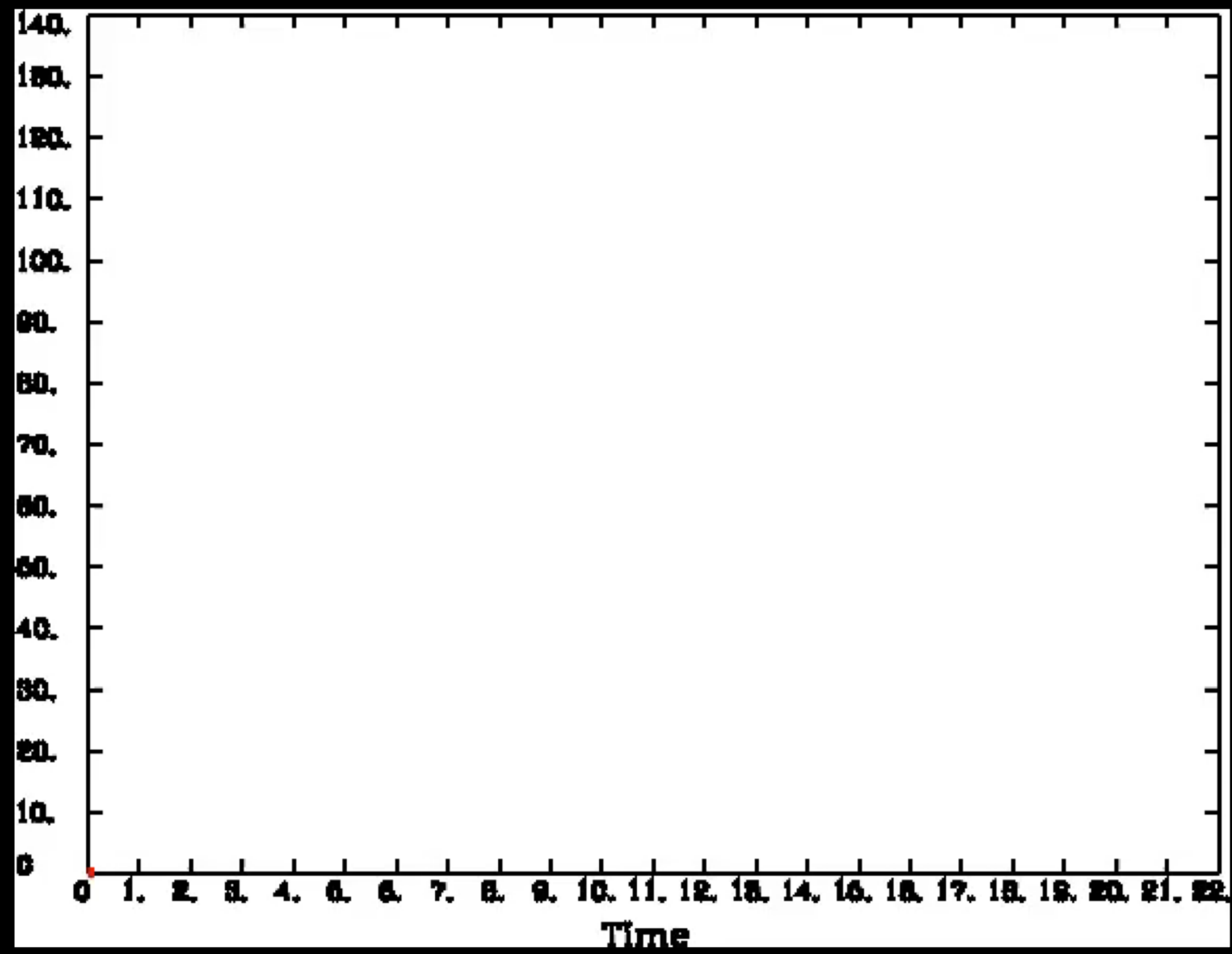
Review of fMRI



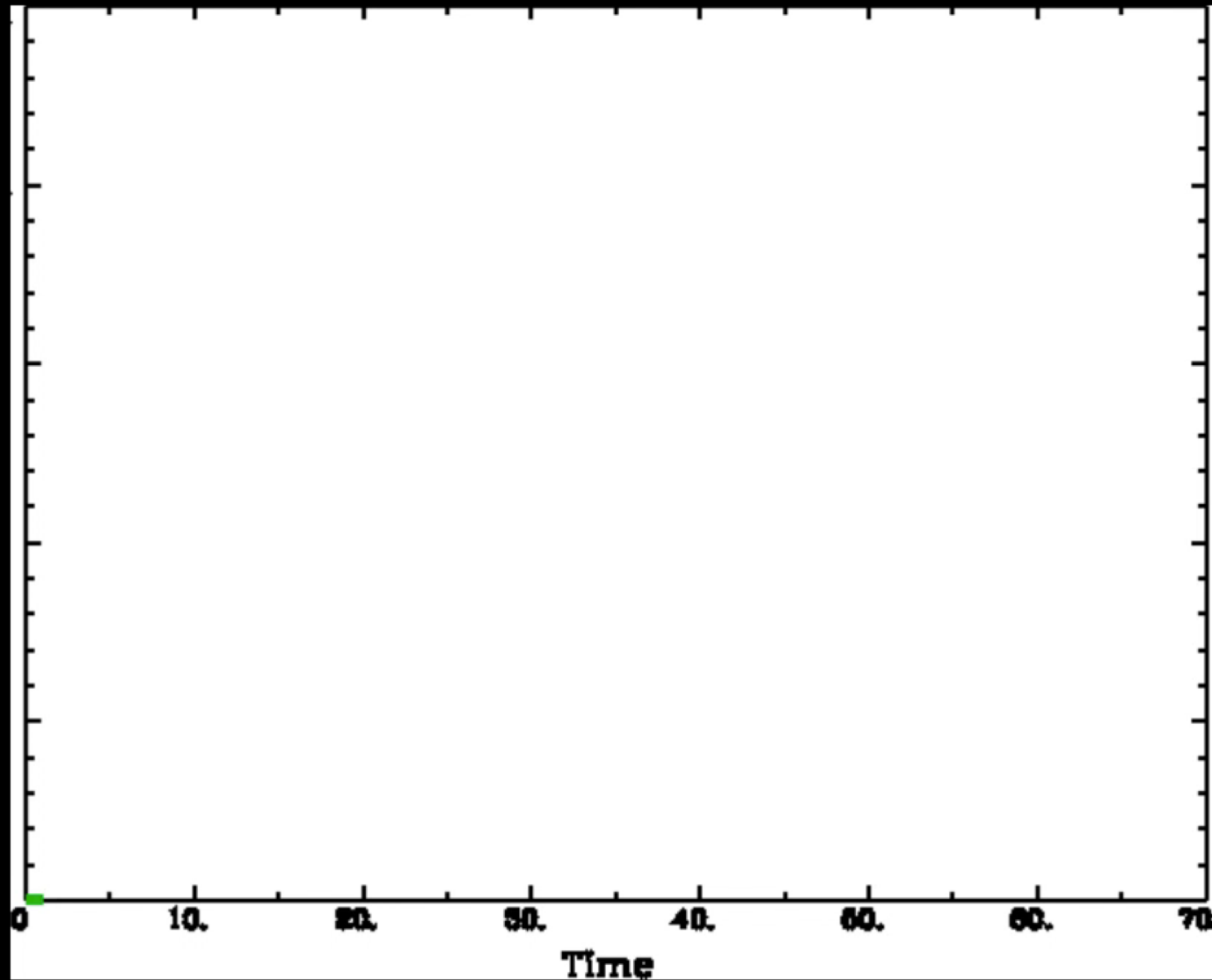
Kwong et al., 1992

Review of fMRI

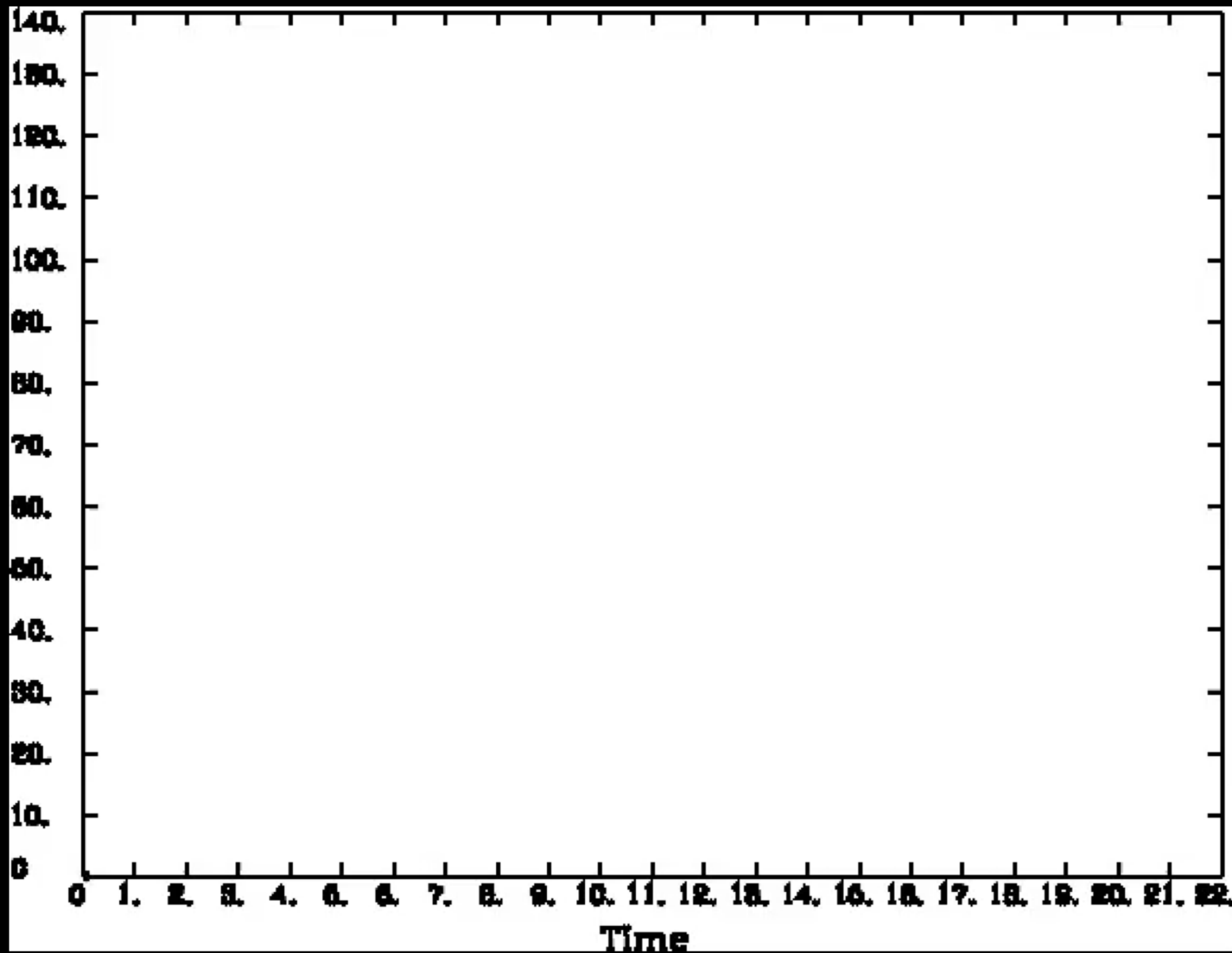
The BOLD Response



The BOLD Response: Duration



The BOLD Response: Convolution



Applet Demonstration of Convolution

<https://phiresky.github.io/convolution-demo/>

Interim Summary

1. Stimulus transduced into neural firing
2. More neural firing = more oxygen consumption
3. More oxygen consumption = more blood flow
4. More blood flow = greater measured signal

Observed signal is a few steps removed from actual neural activity

What We've Done So Far...

1. Overview of fMRI
2. Preprocessing the individual subject
3. Experimental Designs
4. Timing Files
5. Creating the general linear model (GLM)

Behavioral vs. fMRI Experiments

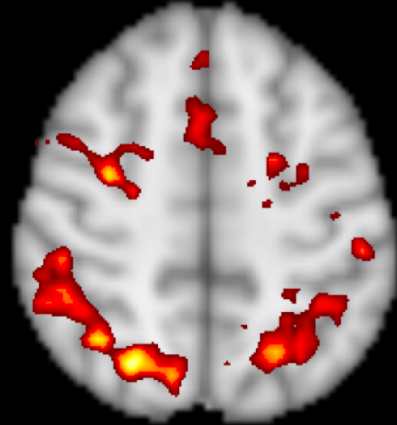
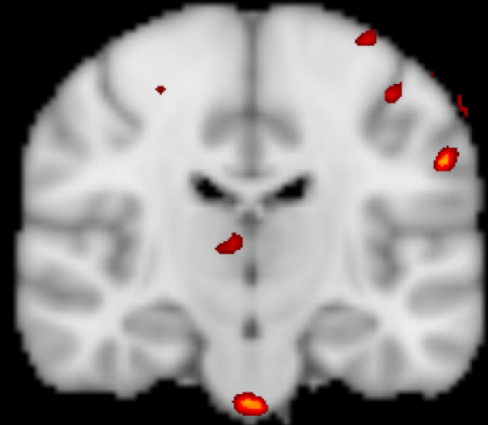
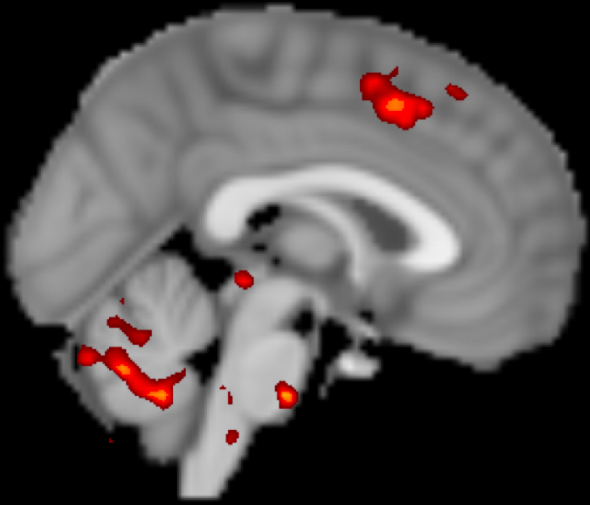
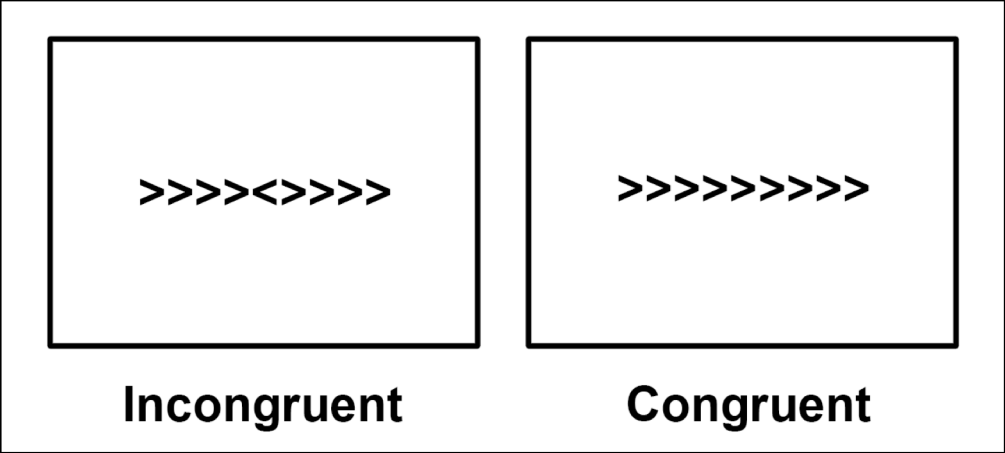
Flanker task: Behavioral task adapted for fMRI analysis

Behavioral

- * Dependent measure of interest is reaction time
- * Can have the same amount of time between trials

fMRI

- * Two dependent measures: reaction time & the BOLD response
- * Will need differing amounts of time between trials



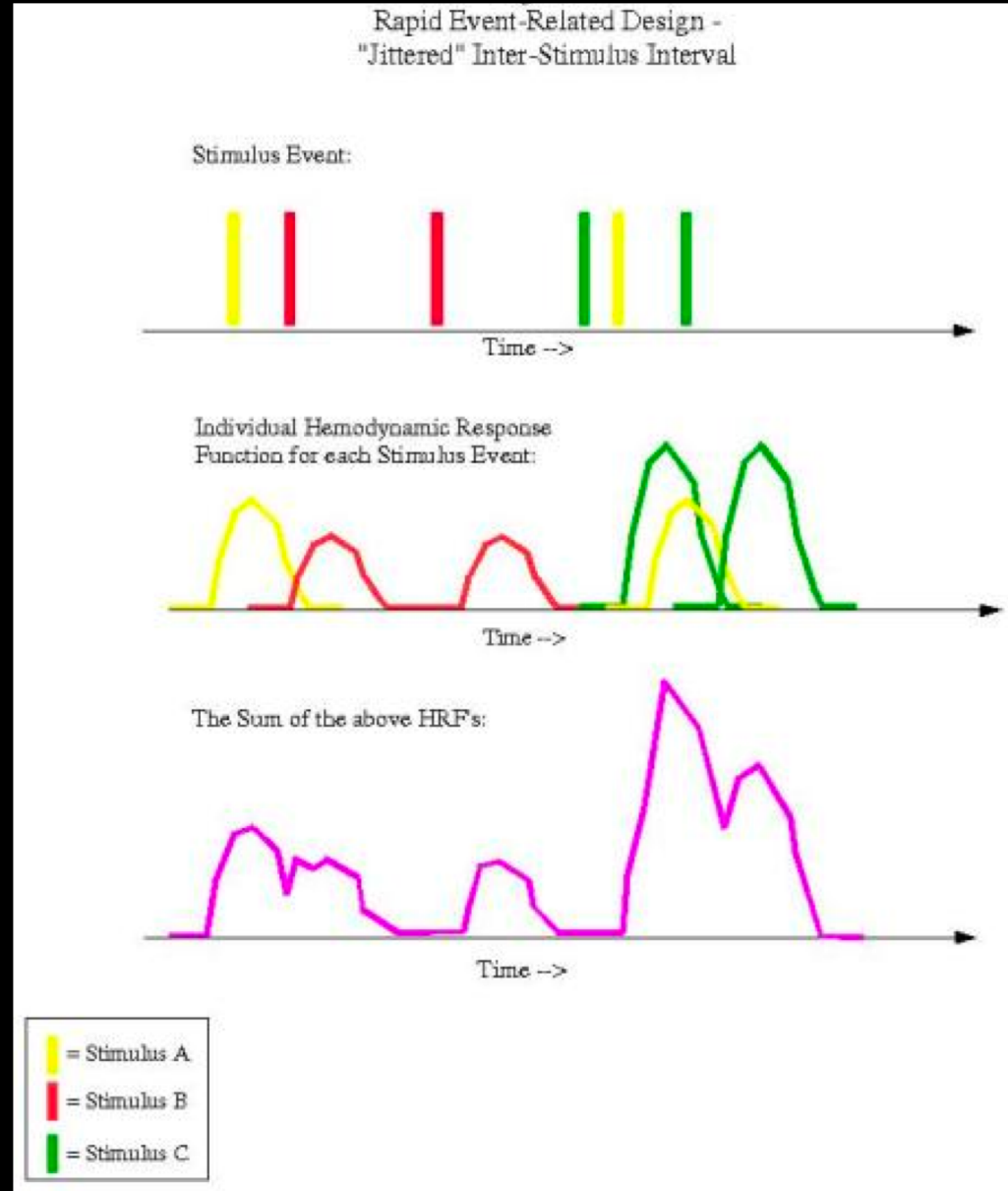
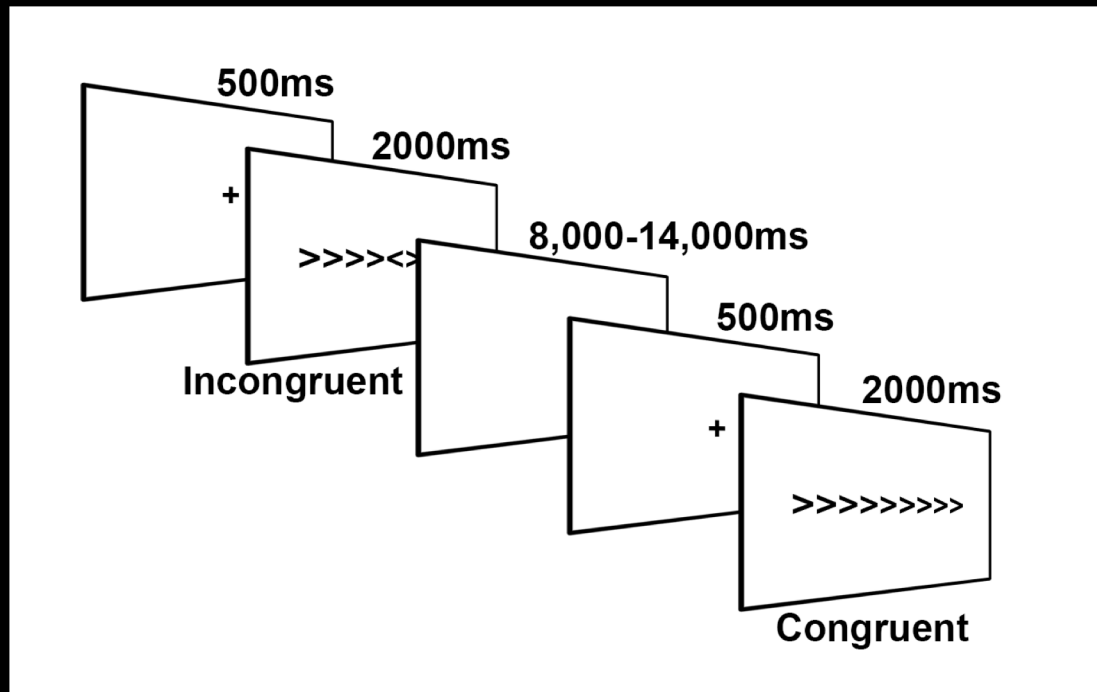
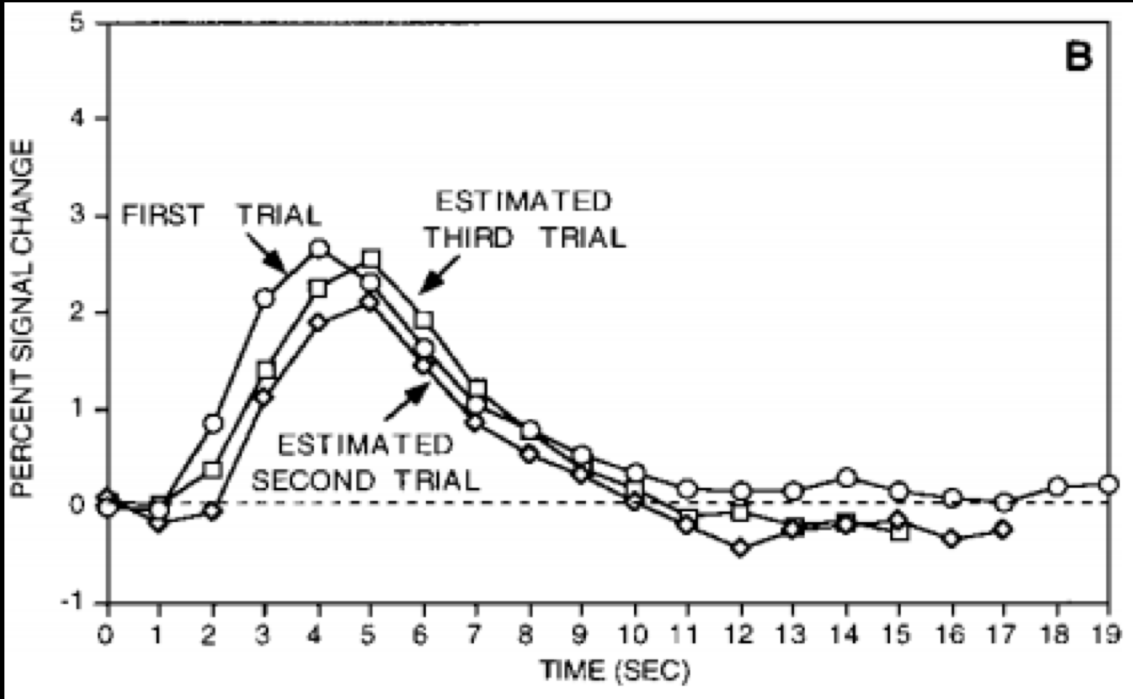
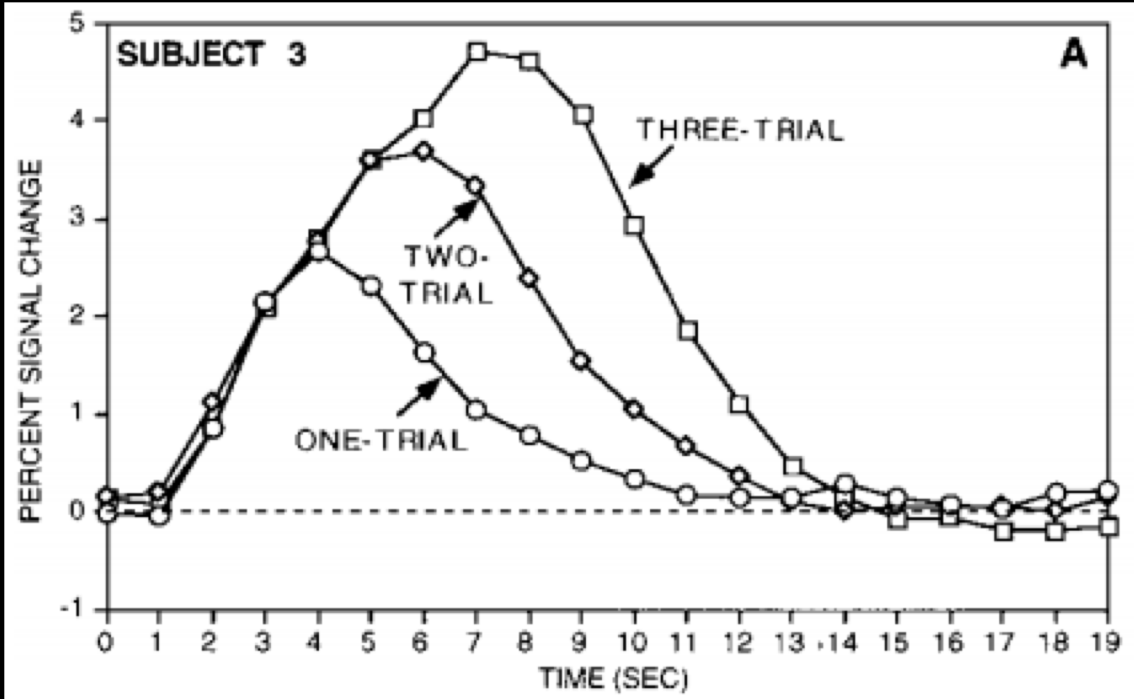


Image from Bob Cox

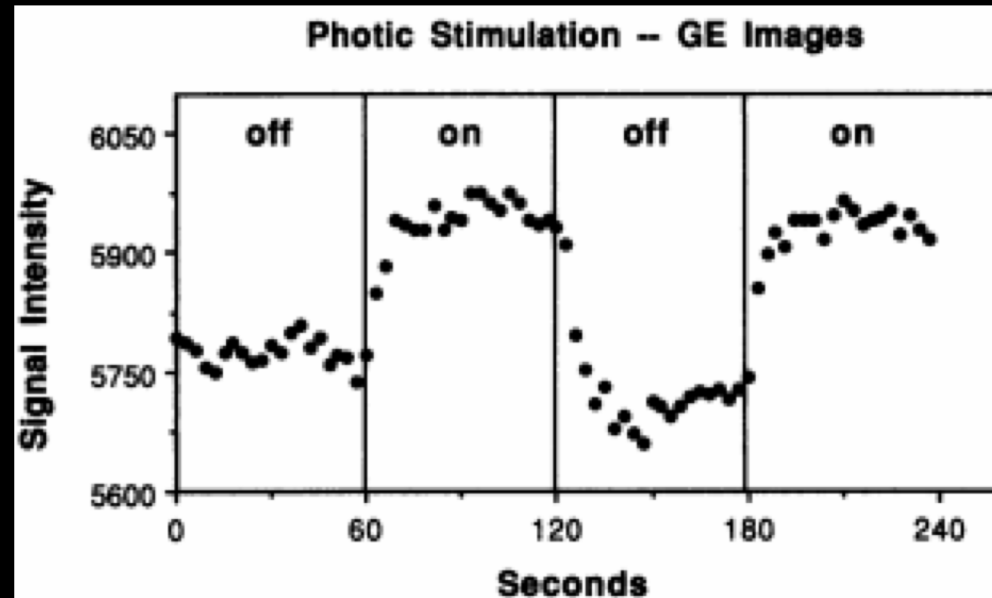
Experimental Designs

Linearity



Experimental Designs

1. Block design (e.g., Kwong et al., 1992)

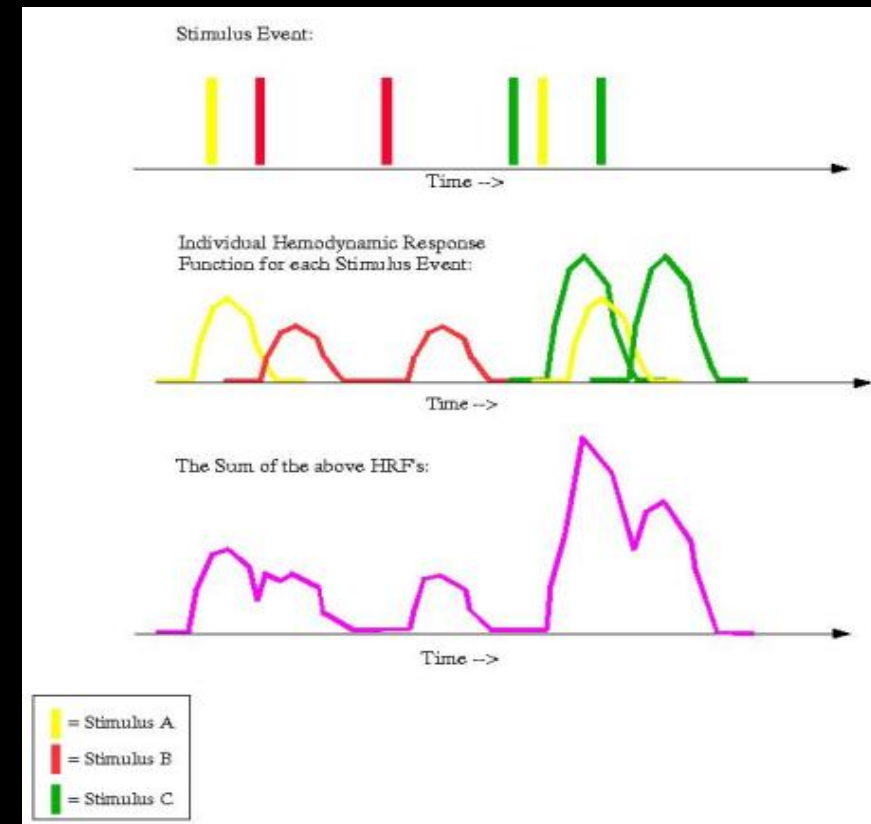
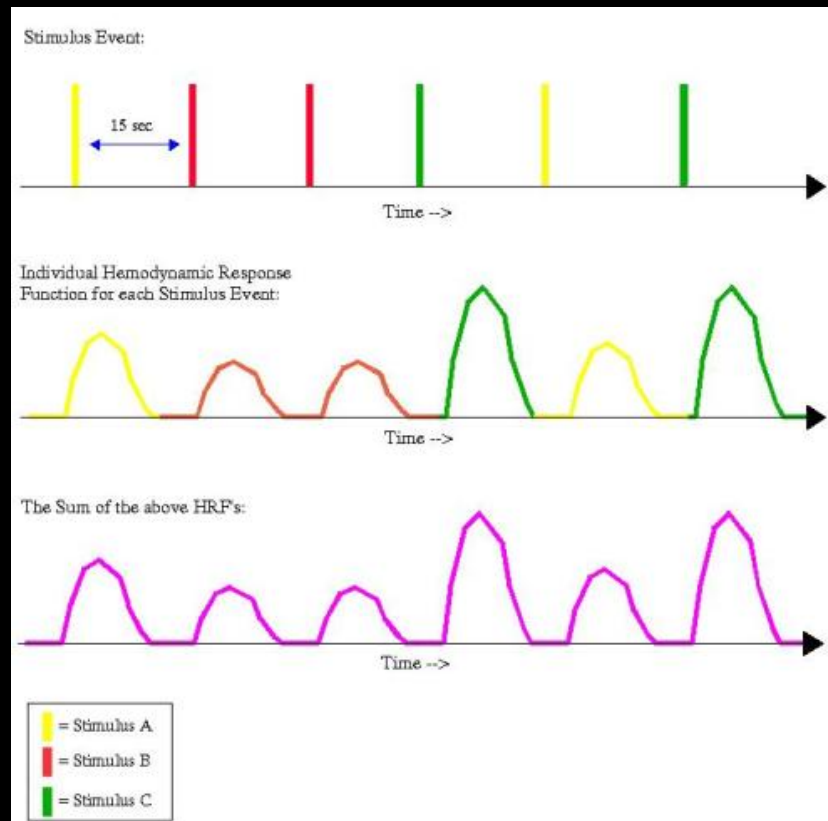


Advantages: Powerful, easy to design

Disadvantages: Boring, predictable, cannot use complex designs

Experimental Designs

2. Event-related designs

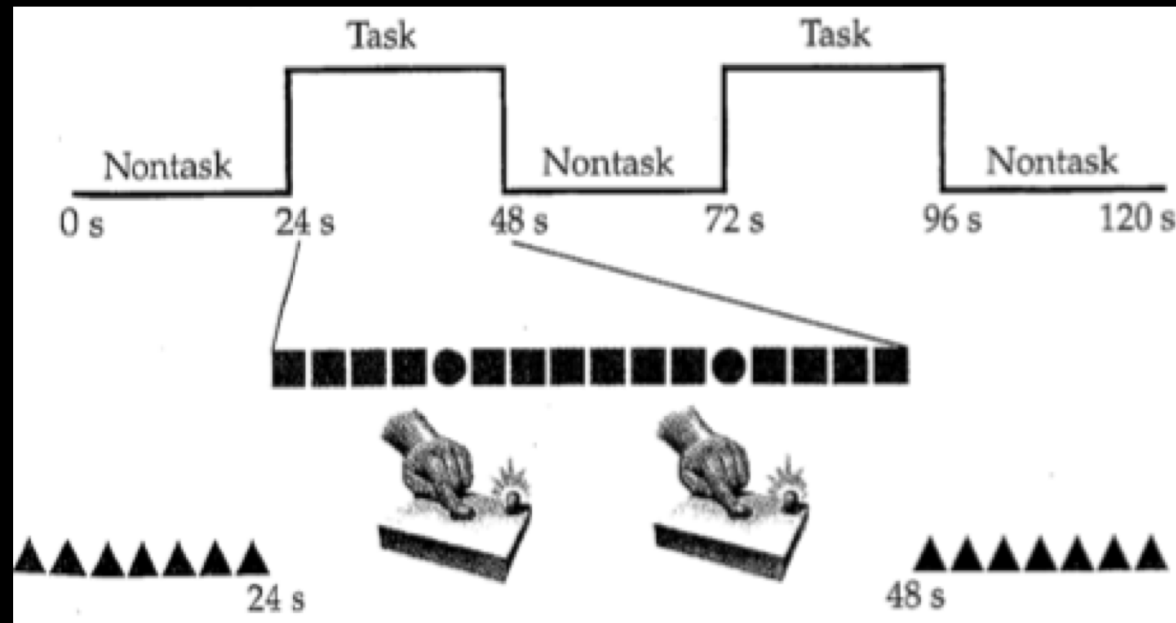


Advantages: More engaging, can use more complex designs

Disadvantages: Less power, susceptible to collinearity

Experimental Designs

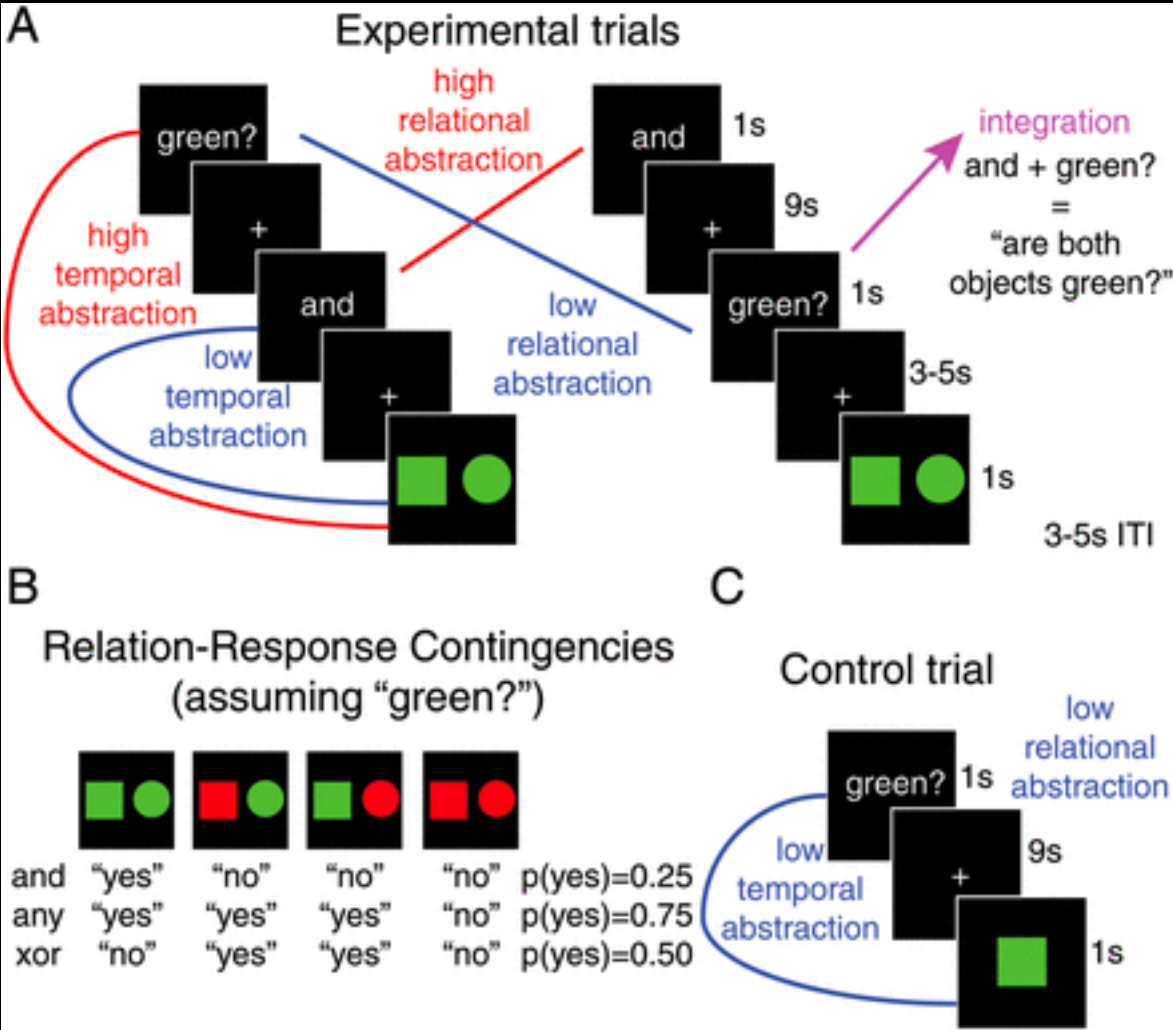
Mixed Designs



Block: State effects; trial: item-related effects

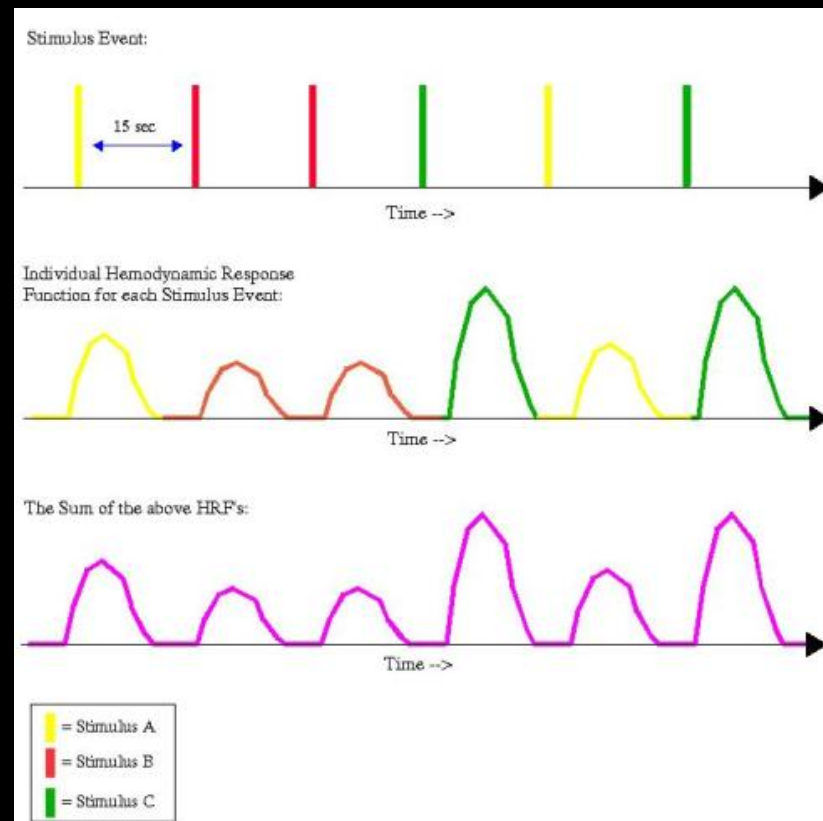
Disadvantages: Very sensitive to errors in HRF modeling

Experimental Designs



Behavioral vs. fMRI Experiments

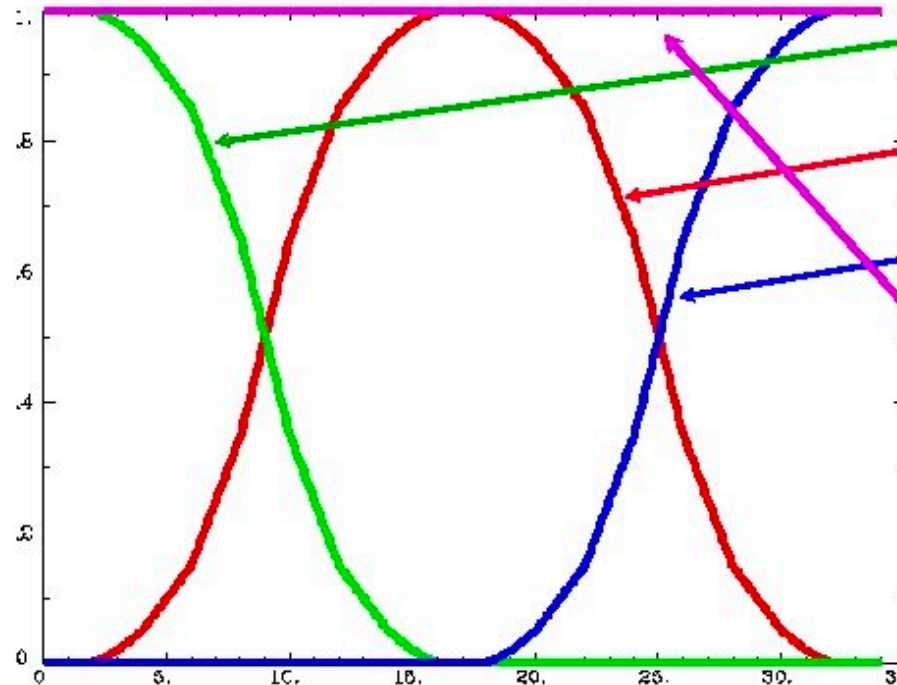
Differing amounts of time between trials (i.e., jitter)
are needed to avoid collinearity



Behavioral vs. fMRI Experiments

-29-

Multiple Regressors: Collinearity!!



Green curve = signal model for #1
Red curve = signal model for class #2
Blue curve = signal model for #3
Purple curve = #1 + #2 + #3 which is exactly = 1

- We cannot — *in principle or in practice* — distinguish sum of 3 signal models from constant baseline!!

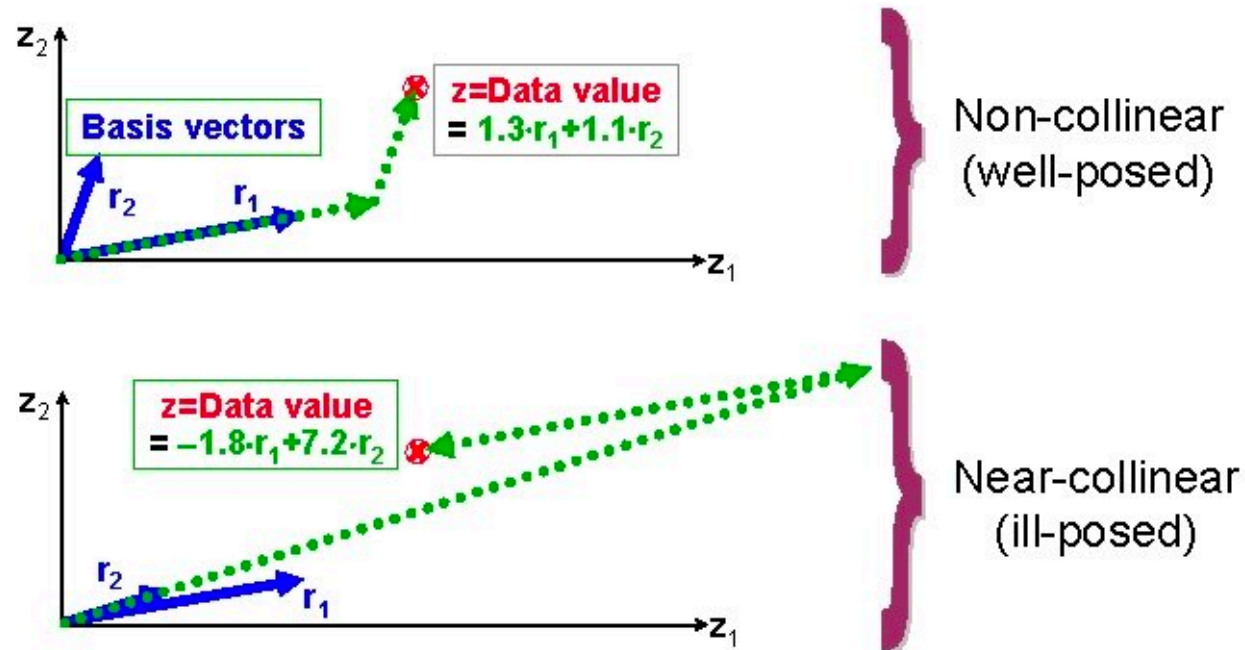
No analysis can distinguish the cases
 $Z(t) = 10 + 5 \cdot \#1$ and
 $Z(t) = 0 + 15 \cdot \#1 + 10 \cdot \#2 + 10 \cdot \#3$
and an infinity of other possibilities

Collinear designs are **bad bad bad!**

Behavioral vs. fMRI Experiments

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The Geometry of Collinearity - 1



- Trying to fit data as a sum of basis vectors that are nearly parallel doesn't work well: solutions can be huge
- Exactly parallel basis vectors would be impossible:
 - Determinant of matrix to invert would be zero

Questions?

Demonstration of viewing the time-series

Timing Files

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

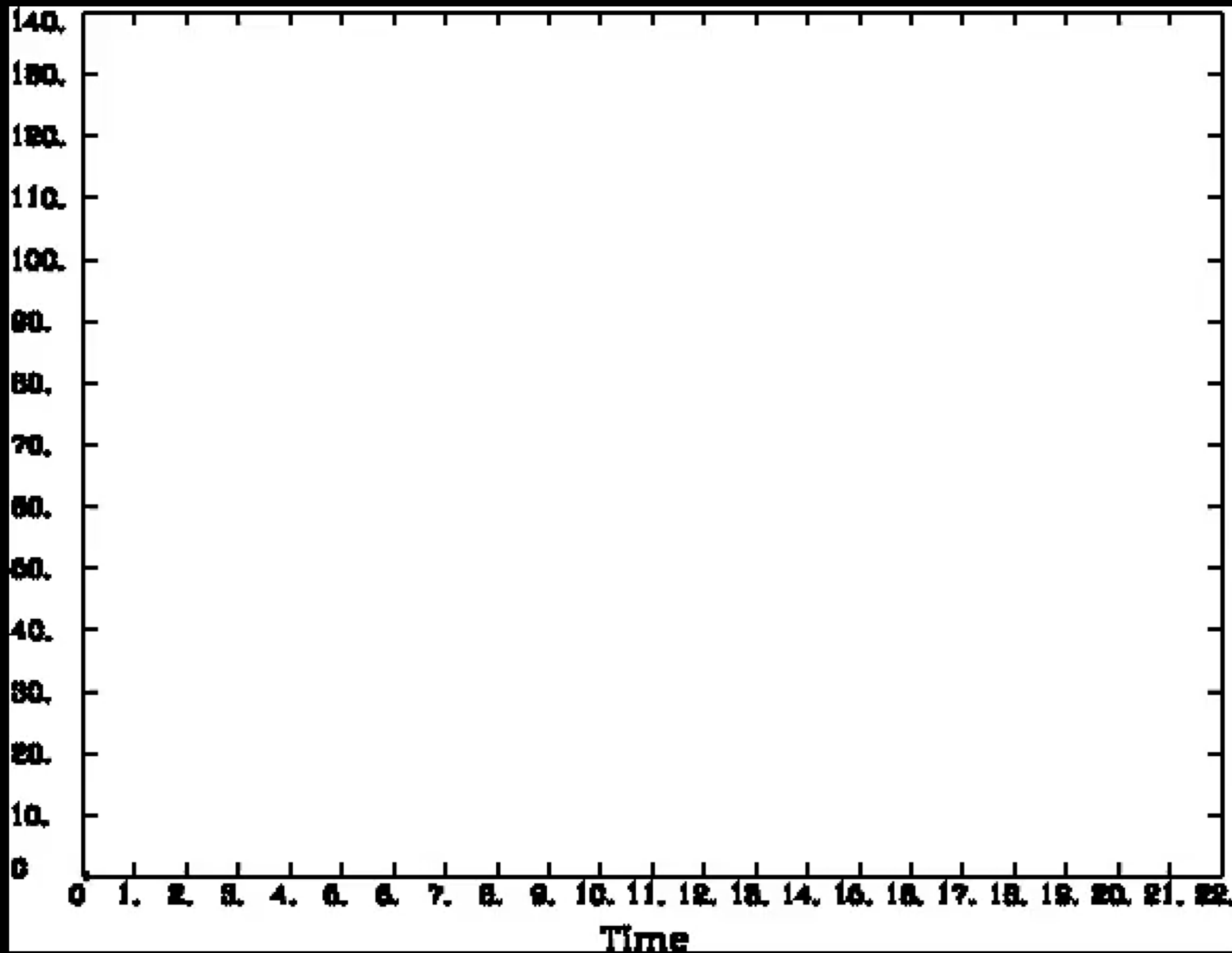


```
onset duration trial_type
0.0 2.0 incongruent_correct
10.0 2.0 incongruent_correct
20.0 2.0 incongruent_correct
32.0 2.0 congruent_correct
42.0 2.0 congruent_correct
52.0 2.0 incongruent_correct
64.0 2.0 congruent_correct
76.0 2.0 congruent_correct
88.0 2.0 incongruent_correct
102.0 2.0 congruent_correct
116.0 2.0 congruent_correct
```



The screenshot shows the 'Batch Editor' window with the 'MRI model specification' module selected. The 'Onsets' field is highlighted, and a 'Specify...' button is visible below it. The interface includes a menu bar (File, Edit, View, SPM, BasicIO) and a 'Module List' on the left. The main area displays various parameters for the MRI model, such as 'Directory', 'Timing parameters', 'Data & Design', and 'Onsets'. The 'Onsets' field is currently empty, and the 'Specify...' button is used to input the onset times from the table above.

The BOLD Response: Convolution



How to Write out Timings?

behav_sub01.xls [Compatibility Mode] Search Sheet

Home Insert Page Layout Formulas Data Review View Share

A3 fx 43.7179423237685

	A	B	C	D	E	F	G	H	I
1	WhyFace	WhyFace	WhyHand	WhyHand	HowFace	HowFace	HowHand	HowHand	
2	Onset (s)	Duration (s)	Onset (s)	Duration (s)	Onset (s)	Duration (s)	Onset (s)	Duration (s)	
3	43.72	8.28	21.23	9.02	61.59	7.49	2.27	10.58	
4	117.27	7.99	98.21	10.02	135.06	7.55	80.69	9.07	
5	152.59	7.54	206.98	7.50	171.38	6.75	189.44	7.07	
6	225.20	7.69	282.41	9.92	243.09	7.50	264.56	9.62	
7									
8									

2x2 Model Parametric Model +

Ready Average: 134.69 Count: 4 Sum: 538.77 150%

How to Write out Timings?

Depends on what stimulus presentation software you use

My advice: Write the timings in BIDS format (Onset, Duration, Trial Type, etc)

These can be easily edited and imported into any of the major packages

Early on in the experiment (here, in the "InitializeVariables" InLine object) create a timing file. Later on, after each trial add lines to the text file about the onset and duration of each condition.

```
InitializeVariables
3 trialIdx = 0
4 totalAcc = 0
5
6 'Create text file for writing timing info
7
8 If c.GetAttrib("Session") = 1 Then 'only open file for new session
9     Open "OnsetTimes_" & c.GetAttrib("Subject") & ".txt" For Output As #1
10    Print #1, "Run", "Event", "Onset", "Dur"
11    Close #1
12 End If

WriteTimingInfo
1 'Write timing info to text file
2
3 Open "OnsetTimes_" & c.GetAttrib("Subject") & ".txt" For Append As #1
4     Print #1, c.GetAttrib("Session"), c.GetAttrib("Condition"), _
5     CDb1(c.GetAttrib("ExpStroopSlide.OnsetTime") - StartTimestamp)/1000, _
6     c.GetAttrib("ExpStroopSlide.Duration")
7
8 'Also Log button presses
9     Print #1, c.GetAttrib("Session"), c.GetAttrib("Condition"), _
10    CDb1(c.GetAttrib("ExpStroopSlide.RTTime") - StartTimestamp)/1000, _
11    c.GetAttrib("ExpStroopSlide.RT")
12 Close #1
```

How to Write out Timings?

DS000102 - SUB-01 - FUNC - SUB-01_TASK-FLANKER_RUN-1_EVENTS.TSV

 [DOWNLOAD](#)

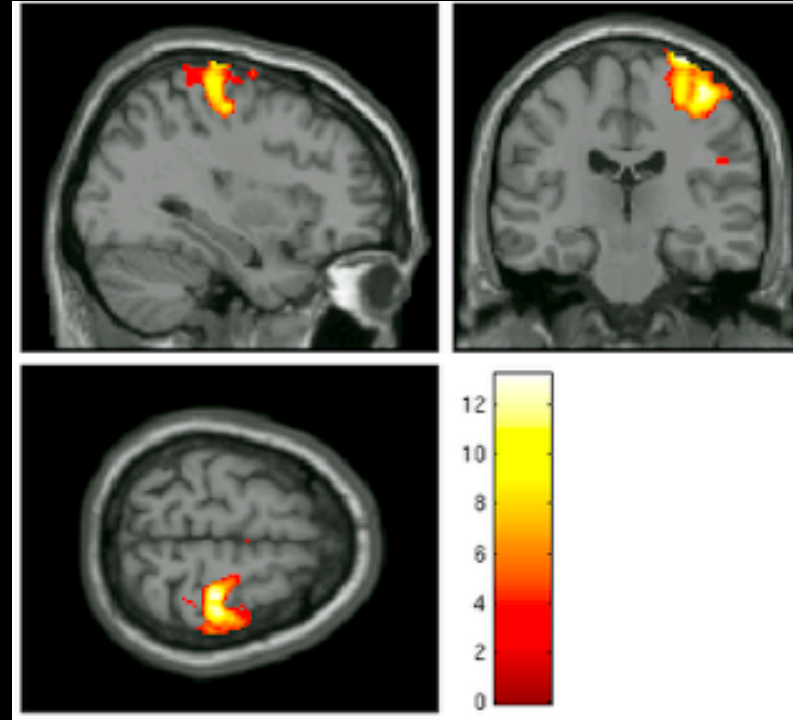
ONSET	DURATION	TRIAL_TYPE	RESPONSE_T...	CORRECTNESS	STIMVAR	RSPONSE	STIMULUS	COND
0.0	2.0	incongruen...	1.095	correct	2	1	incongruent	cond003
10.0	2.0	incongruen...	0.988	correct	2	1	incongruent	cond003
20.0	2.0	congruent_...	0.591	correct	1	1	congruent	cond001
30.0	2.0	congruent_...	0.499	correct	1	1	congruent	cond001
40.0	2.0	incongruen...	0.719	correct	2	1	incongruent	cond003
52.0	2.0	congruent_...	0.544	correct	1	1	congruent	cond001
64.0	2.0	congruent_...	0.436	correct	1	1	congruent	cond001
76.0	2.0	incongruen...	0.47	correct	2	1	incongruent	cond003
88.0	2.0	congruent_...	0.409	correct	1	1	congruent	cond001
102.0	2.0	incongruen...	0.563	correct	2	1	incongruent	cond003
116.0	2.0	congruent_...	0.493	correct	1	1	congruent	cond001
130.0	2.0	congruent_...	0.398	correct	1	1	congruent	cond001
140.0	2.0	congruent_...	0.466	correct	1	1	congruent	cond001
150.0	2.0	incongruen...	0.518	correct	2	1	incongruent	cond003
164.0	2.0	incongruen...	0.56	correct	2	1	incongruent	cond003
174.0	2.0	incongruen...	0.533	correct	2	1	incongruent	cond003
184.0	2.0	congruent_...	0.439	correct	1	1	congruent	cond001

Onset Times Recommendations

No matter how you choose to write them out, you need to verify them

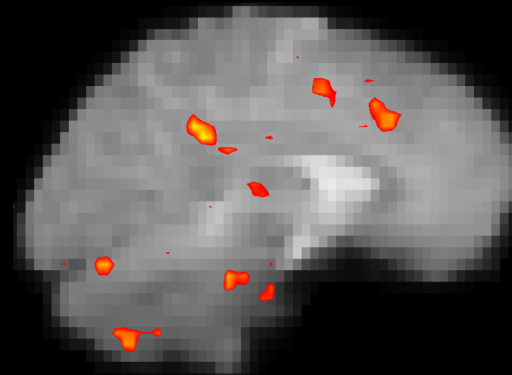
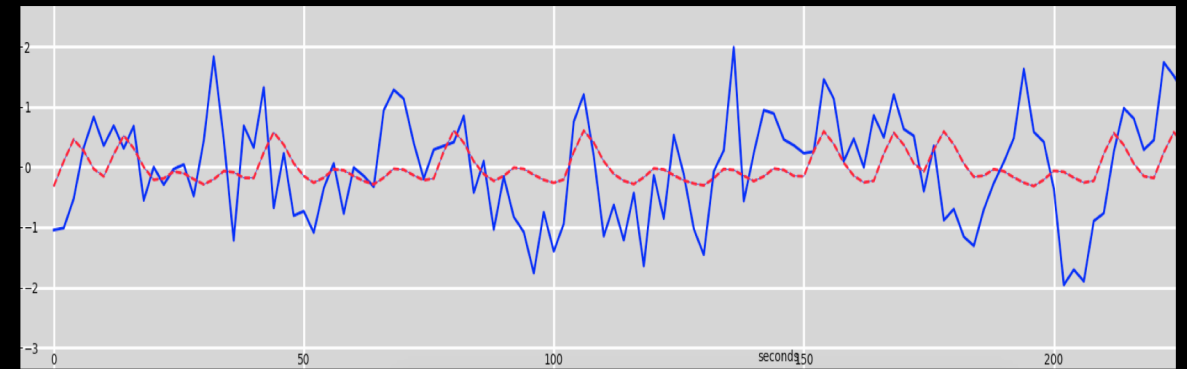
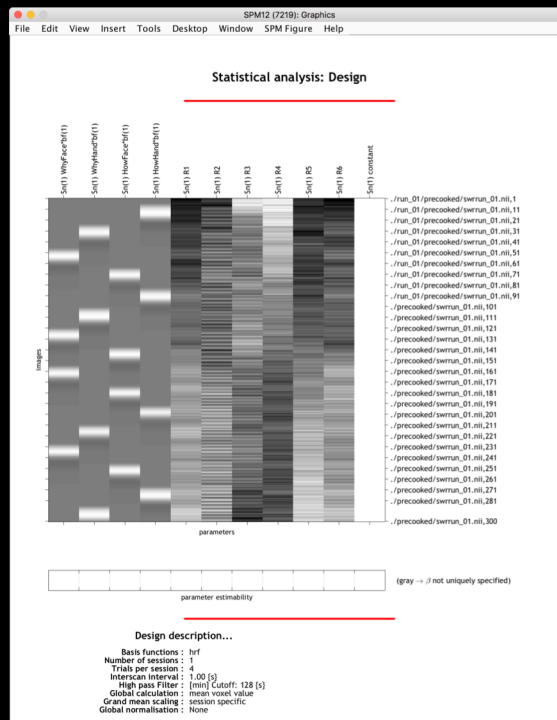
Some scanners acquire a few “dummy scans” at the beginning

If the experiment has a motor response, check that contrast first



Overview of model fitting

Fit the Model at each voxel (“mass univariate”)



The General Linear Model (GLM)

Uses one or more regressors (independent variables) to predict an outcome measure (dependent variable)

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon$$

Y = Outcome variable

β = Beta Weights (parameter estimates)

X = Regressor

ε = Residual

The General Linear Model (GLM)

$$Y = \beta_1 X_1 + \beta_2 X_2 + \beta_3 X_3 + \varepsilon$$

Assume that:

$$Y = \text{GPA}, X_1 = \text{IQ}, X_2 = \text{Drinks per week}, X_3 = \text{Height}$$



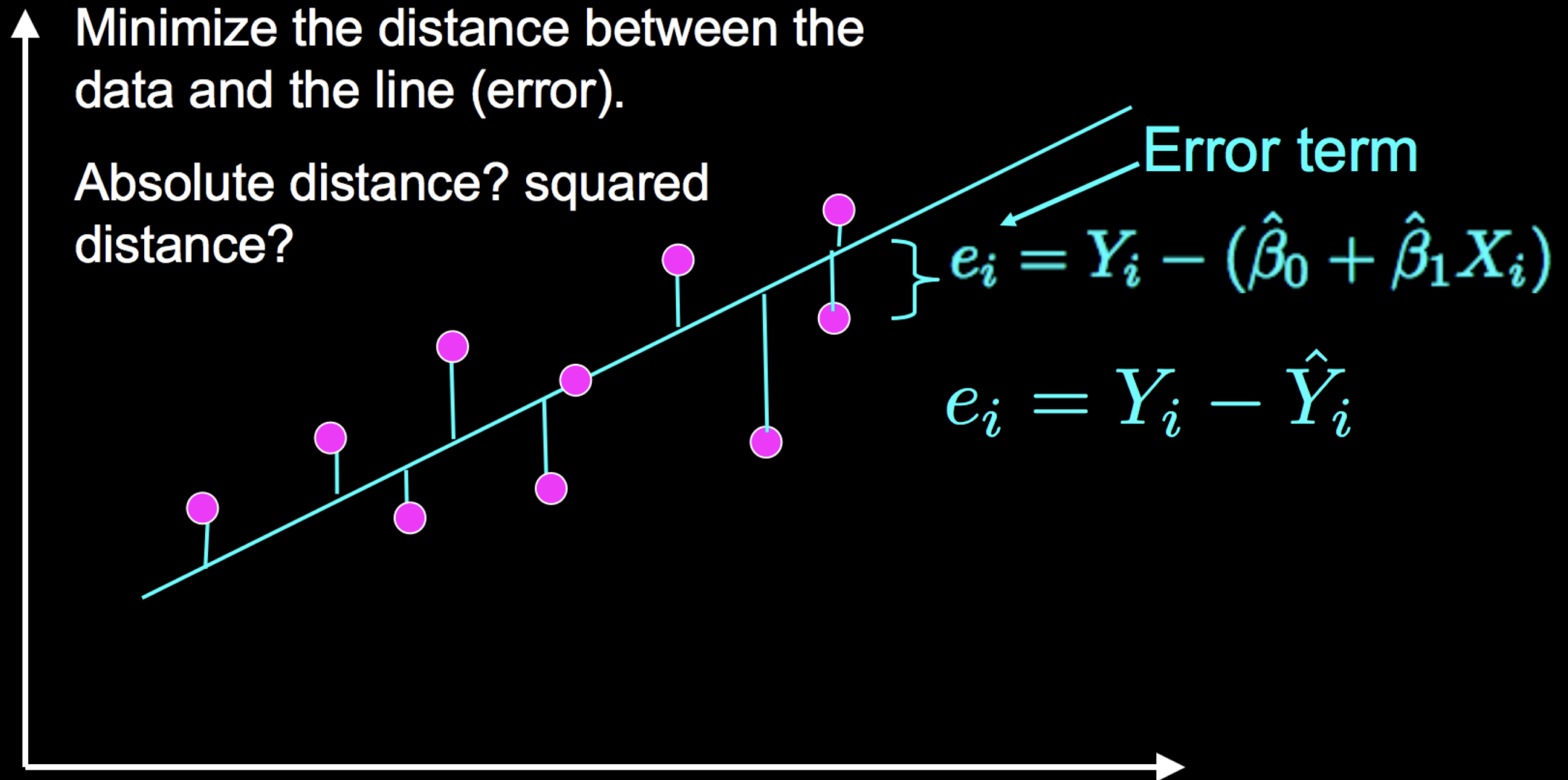
$$\text{GPA} = (\beta_1 * \text{IQ}) + (\beta_2 * \text{Drinks}) + (\beta_3 * \text{Height}) + \varepsilon$$



$$\beta_1 = 0.05^*, \beta_2 = -0.07^*, \beta_3 = 0.01 \text{ (not significant)}$$

IQ and drinks per week contribute to GPA; height doesn't

The General Linear Model (GLM)



The General Linear Model (GLM)

We can use these numbers to calculate the variance

$$SSE = \sum (Y_i - \hat{Y}_i)^2 = \sum e_i^2$$

$$s^2 = \frac{\sum e_i^2}{N - 2}$$

The General Linear Model (GLM)

Test statistic

$$t = (\bar{x} - \mu_0) / (s / \sqrt{n})$$

where:

- \bar{x} = the sample mean
- μ_0 = the hypothesized population mean
- s = the sample standard deviation
- n = the sample size

The General Linear Model (GLM)

Deriving a beta weight (β) can be calculated by using linear algebra:

$$Y = X\hat{\beta}$$

$$X'Y = (X'X)\hat{\beta}$$

$$(X'X)^{-1}X'Y = \hat{\beta}$$

$$\widehat{\text{Var}}[\hat{\beta}] = \hat{\sigma}^2(X'X)^{-1}$$

The General Linear Model (GLM)

t-statistics in fMRI are conceptually similar, but computed slightly differently:

$$t = \frac{c(X'X)^{-1}X'Y}{\sqrt{\hat{\sigma}^2 c(X'X)^{-1}c'}}$$

$$\hat{\sigma}^2 = \frac{e'e}{N-p}$$

where $e = Y - X\hat{\beta} = Y - \hat{Y}$

N = Number of time-points
p = Number of regressors

The General Linear Model (GLM)

Note: t-statistics are calculated at the 1st-level, but usually aren't carried into the 2nd-level analysis

In other words: Magnitude is carried to the group-level, not variance

This can be done in other programs, e.g. AFNI's 3dMEMA

Applying the GLM to fMRI Data

Applying the GLM to fMRI Data

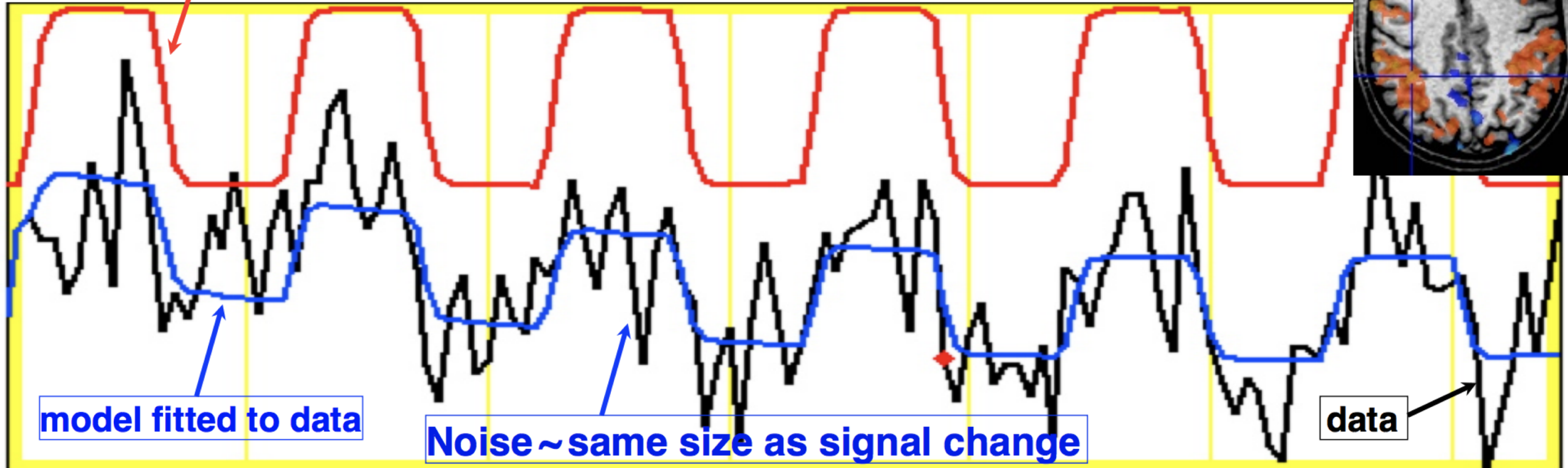
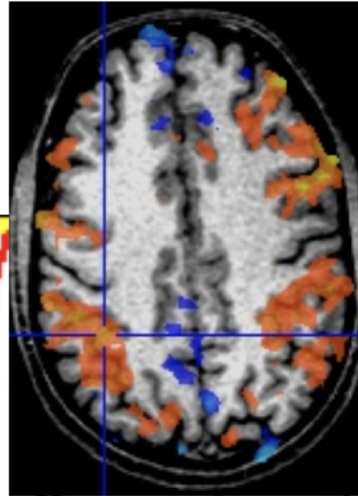
Block data of one run at a voxel

model regressor

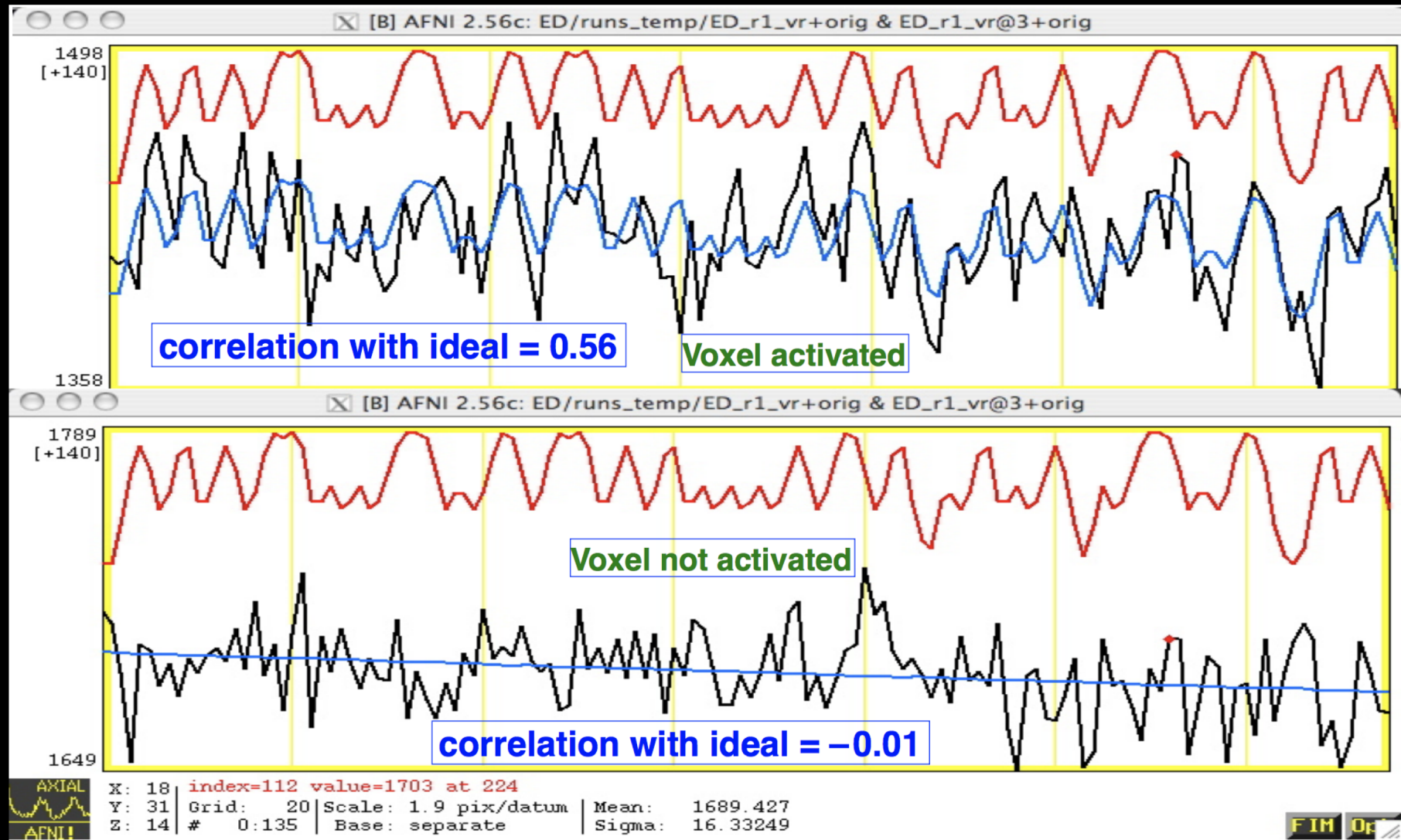
model fitted to data

Noise ~ same size as signal change

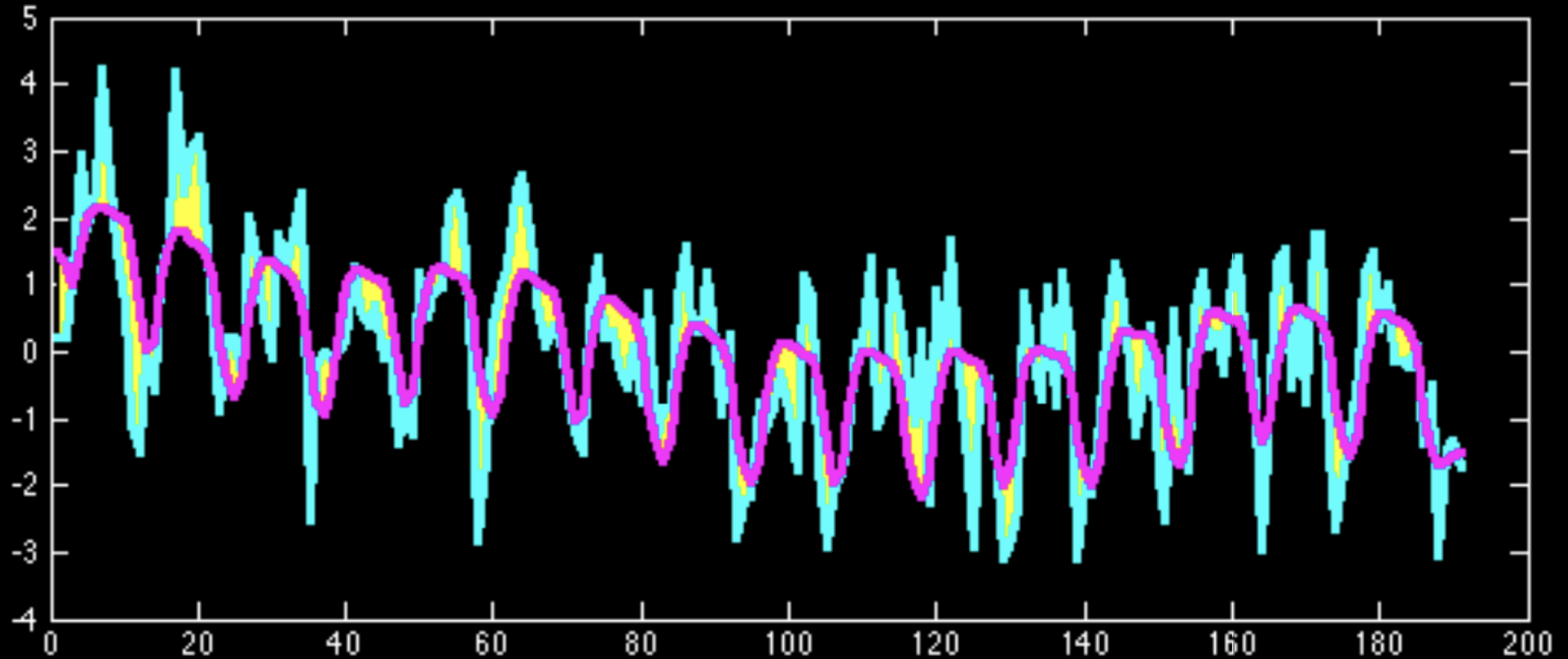
data



Applying the GLM to fMRI Data

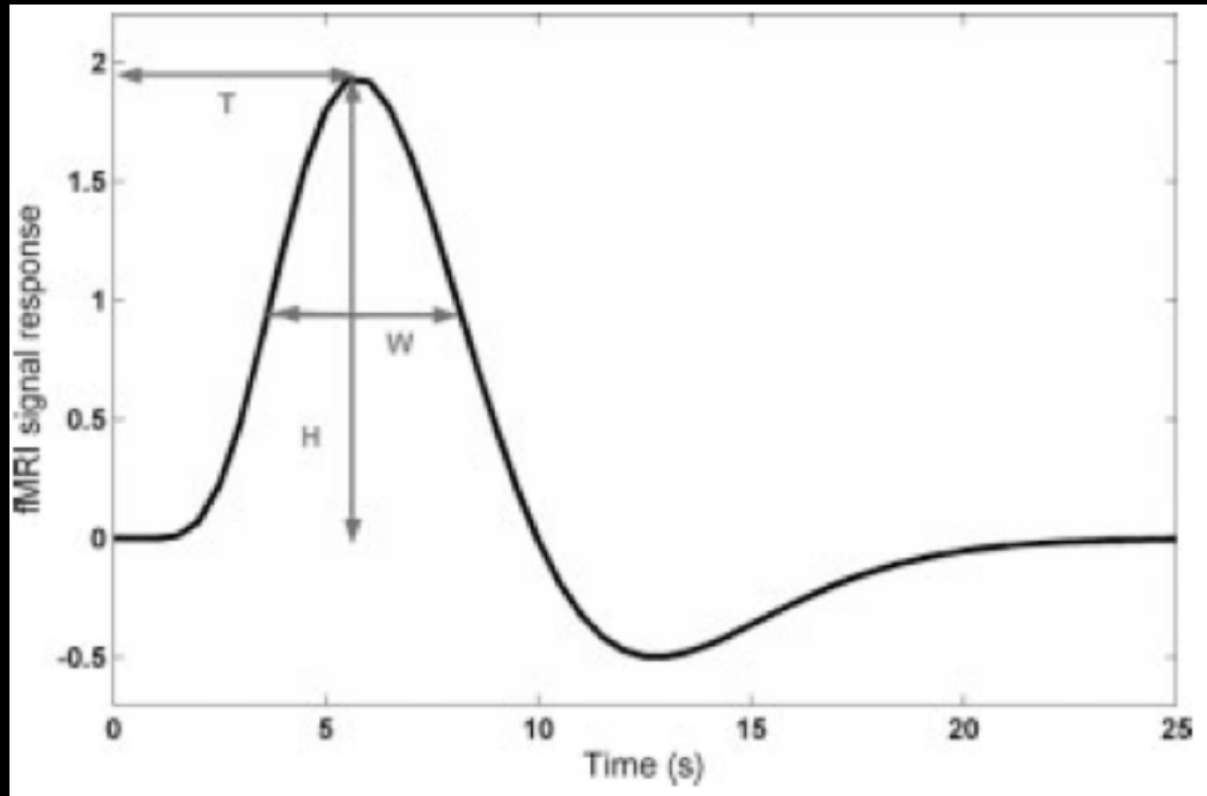


Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

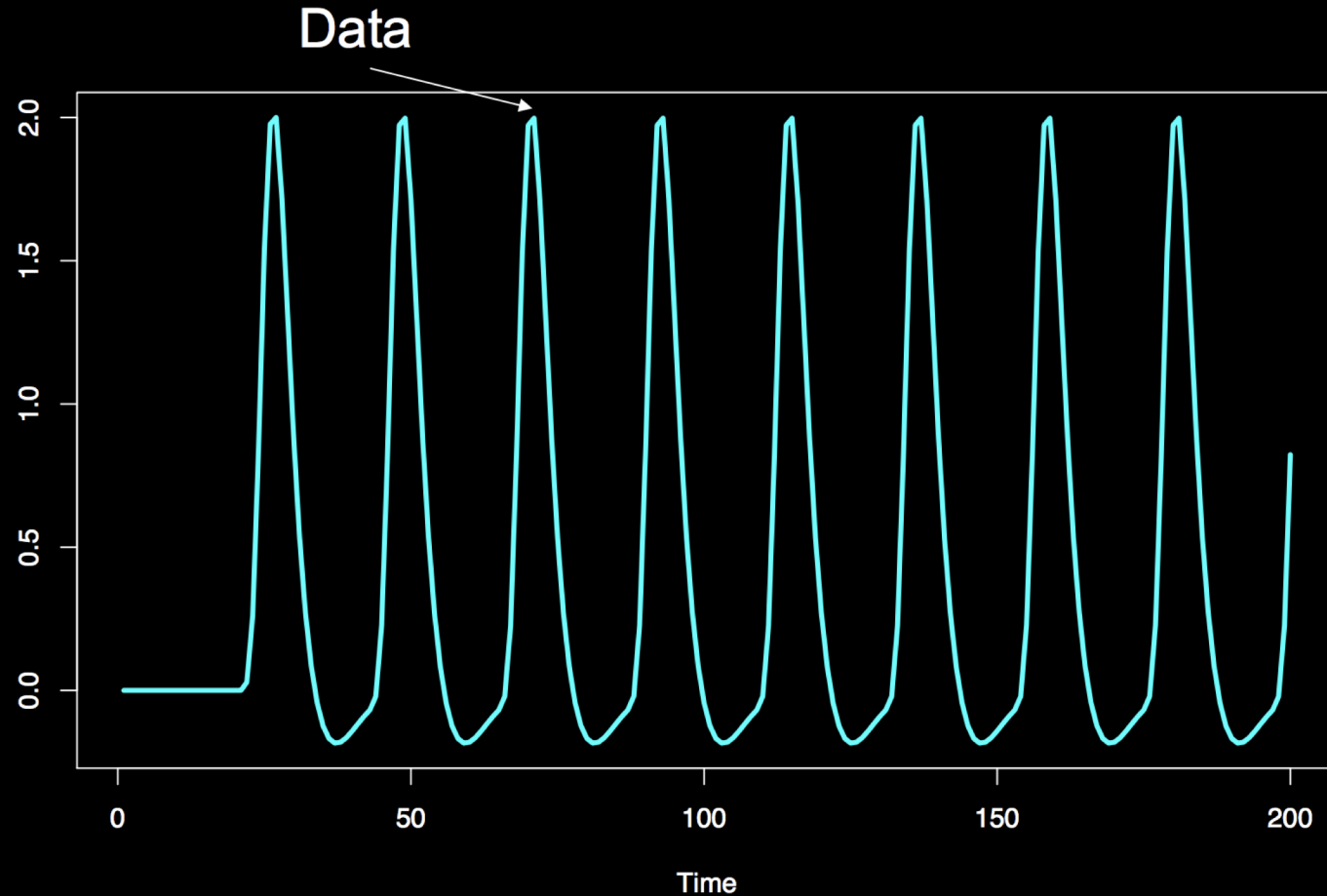
Revisiting the HRF



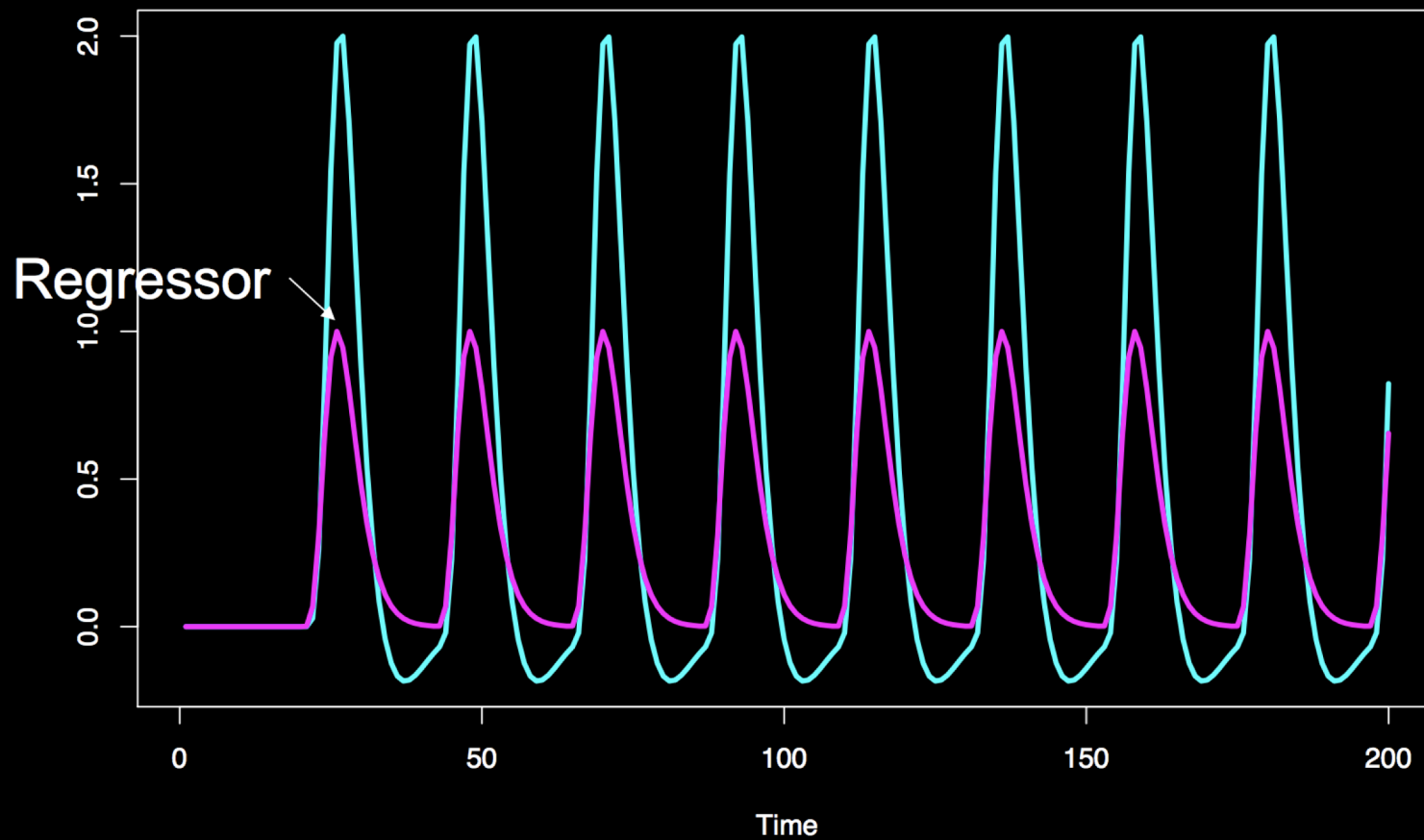
Canonical HRF: Width and delay are fixed, height is estimated as a beta

Applying the GLM to fMRI Data

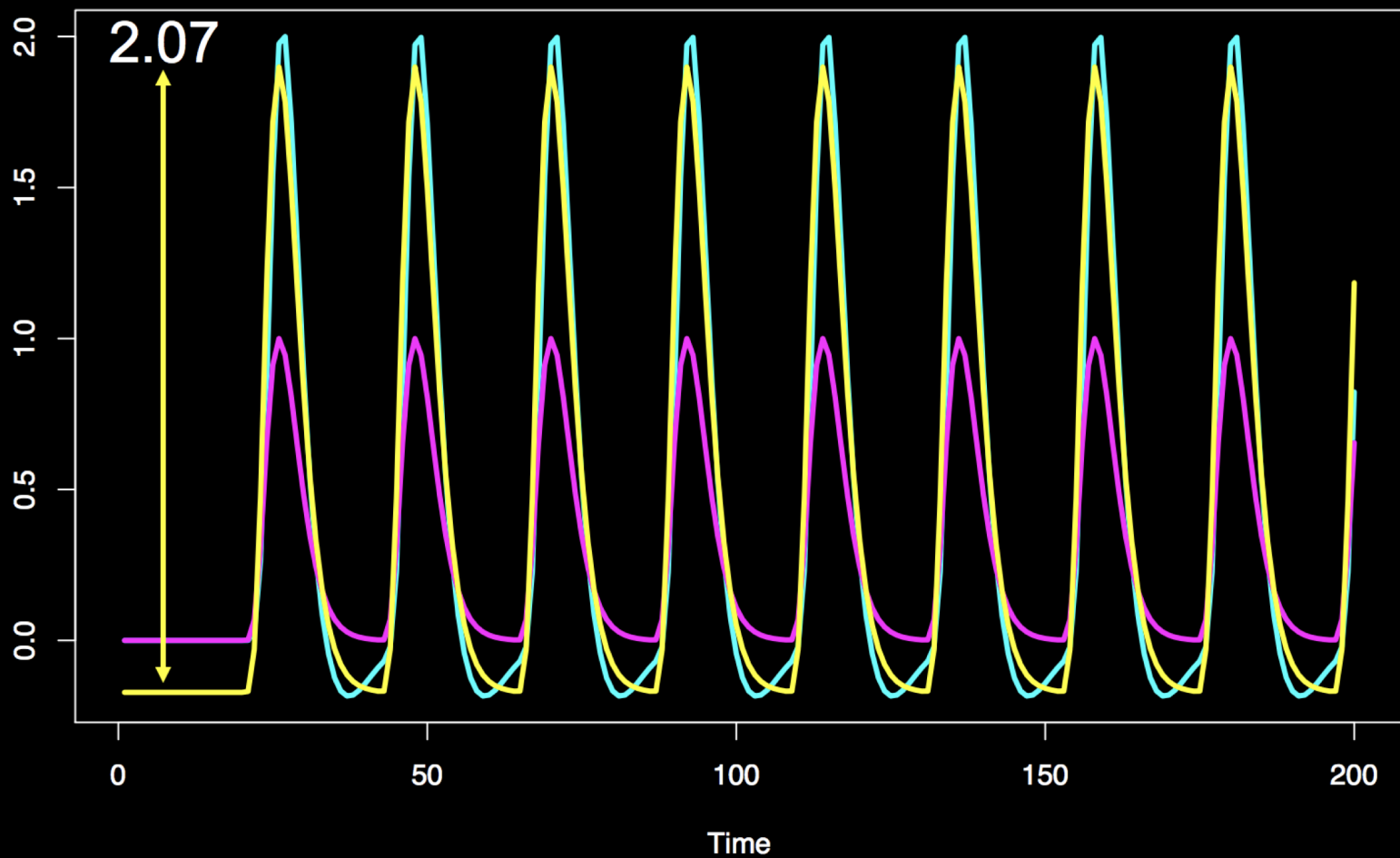
Why use a double-gamma (e.g., model the undershoot?)



Applying the GLM to fMRI Data



Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

SPM12 (7771): SPM{T}: Results

Design Contrasts Atlas

Event-related responses

which session (<=2) 1

Con

fitted response and adjusted data

plot controls

hold grid Box text attrib

p-values

whole brain current cluster small volume

Multivariate

eigenvariate CVA multivariate Bayes BMS p-value Hemodynamics

Display

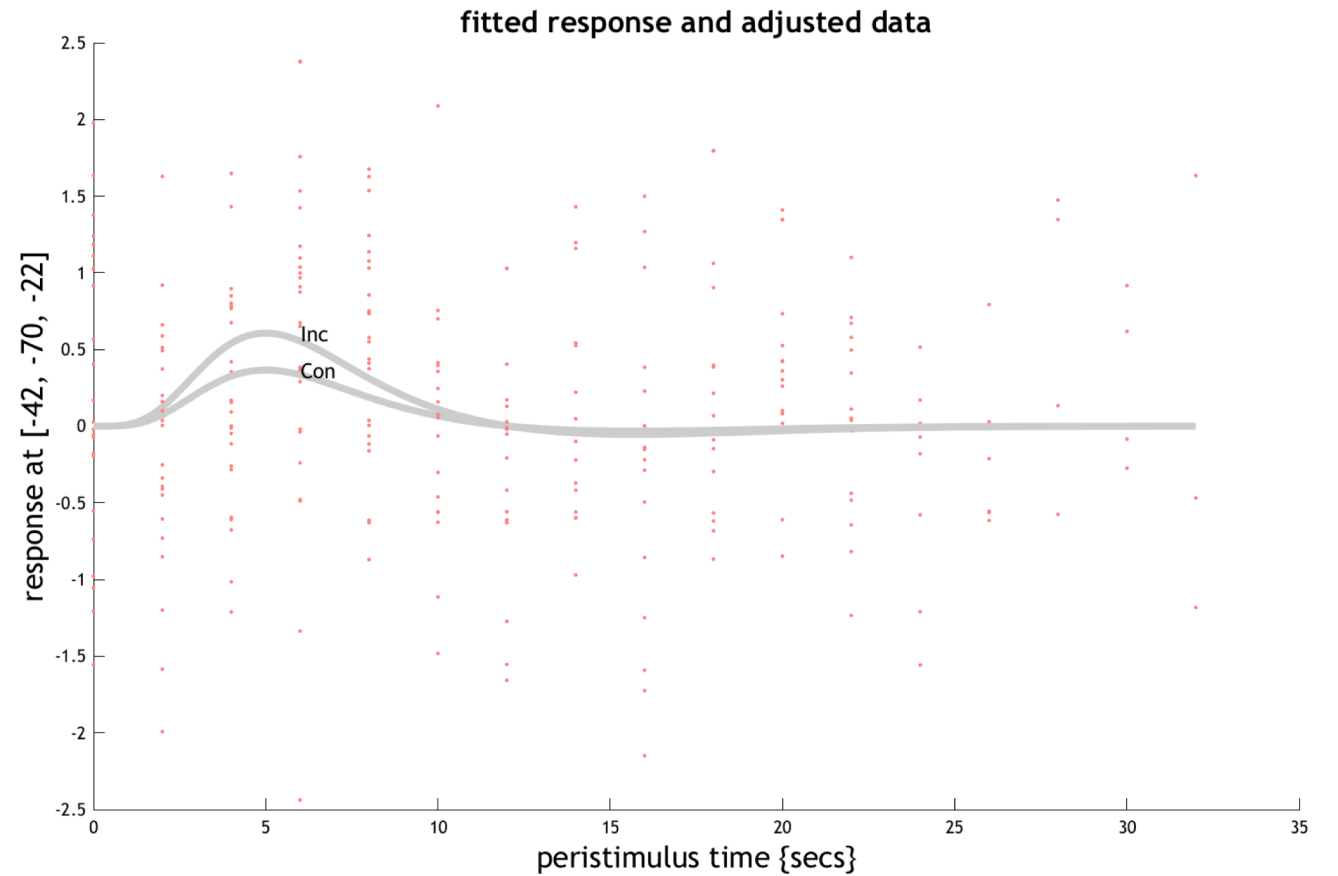
plot overlays... save... clear exit

co-ordinates

x = -42.00 y = -70.00 z = -22.00

statistic

3.58



Applying the GLM to fMRI Data

SPM12 (7771): SPM{T}: Results

Design Contrasts Atlas

Fitted responses

Inc-Con - All Sessions

predicted or adjusted response? adjusted

scan or time

plot controls

hold grid Box text attrib

p-values

whole brain

current cluster

small volume

Multivariate

eigenvariate CVA

multivariate Bayes

BMS p-value

Hemodynamics

Display

plot

overlays...

save...

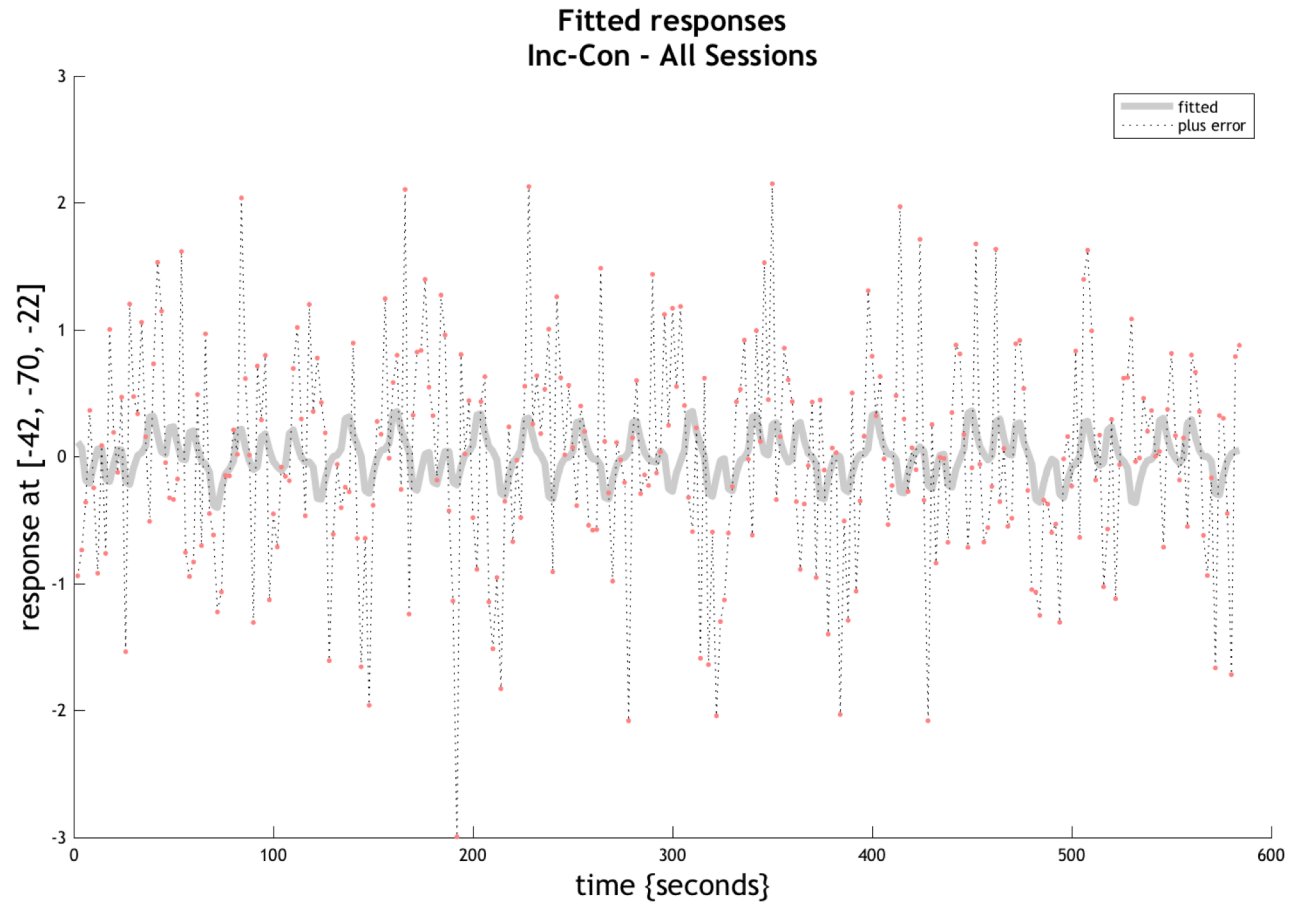
clear exit

co-ordinates

$x = -42.00$ $y = -70.00$ $z = -22.00$

statistic

3.58



Applying the GLM to fMRI Data

SPM12 (7771): SPM{T}: Results

Design Contrasts Atlas

Fitted responses

Inc-Con - All Sessions

predicted or adjusted response? adjusted

scan or time

plot controls

hold grid Box text attrib

p-values

whole brain

current cluster

small volume

Multivariate

eigenvariate CVA

multivariate Bayes

BMS p-value

Display

plot

overlays...

save...

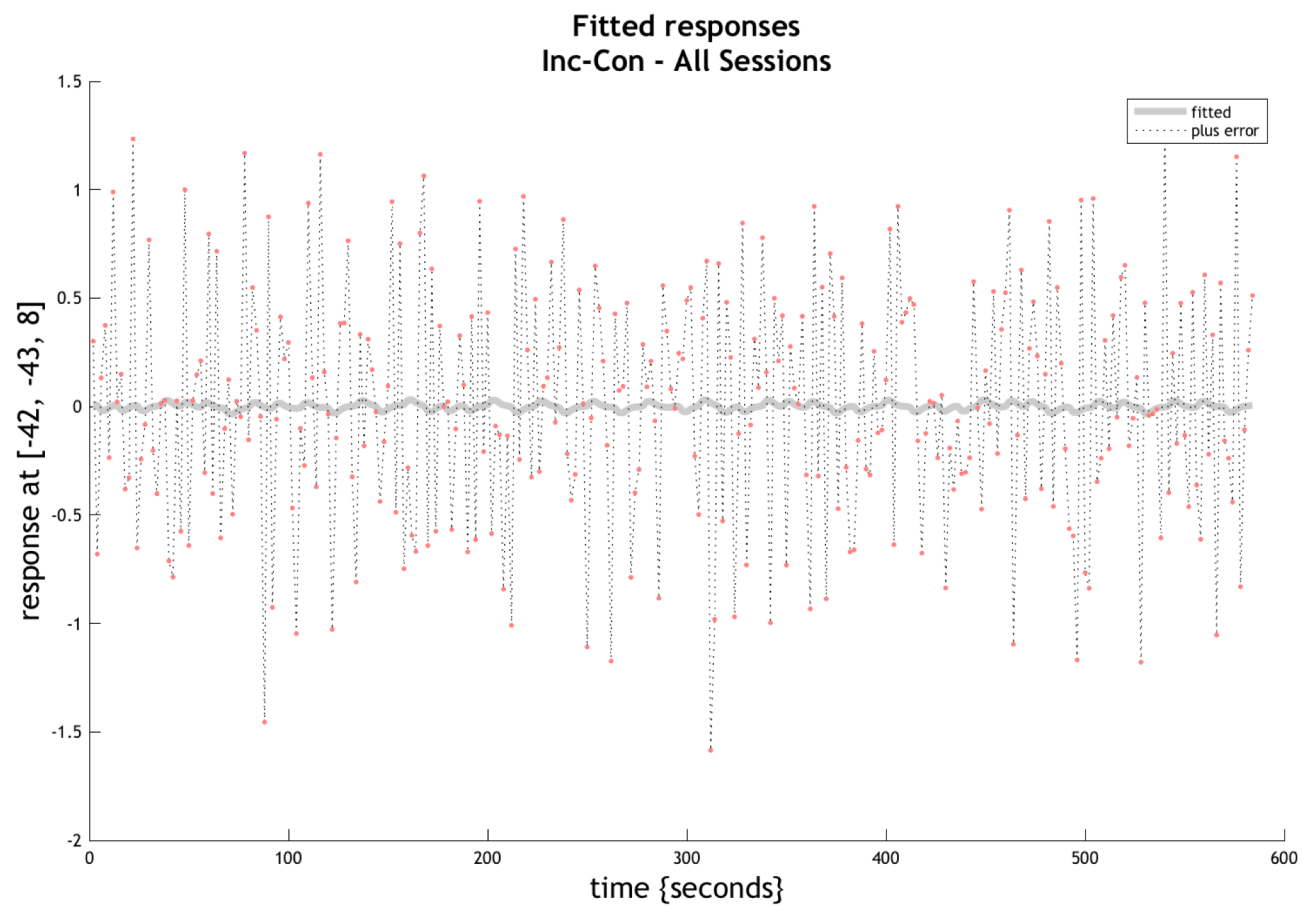
Hemodynamics

clear exit

co-ordinates

x = -42.00 y = -43.00 z = 8.00

statistic



SPM12 (7771): Menu

Realign (E... | Slice timing | Smooth

Coregiste... | Normalise... | Segment

Specify 1st-level | Review

Specify 2nd-level | Estimate

Results

Dynamic Causal Modelling

SPM for functional MRI

Display | Check Reg | Render... | FMRI

Toolbox: | PPIs | ImCalc | DICOM impo

Help | Utils... | Batch | Quit

SPM12 (7771): SPM{T}: Results

Design | Contrasts | Atlas

Contrast estimates and 90% C.I.

Inc-Con - All Sessions

plot controls

hold | grid | Box | text | attrib

p-values

whole brain | current cluster | small volume

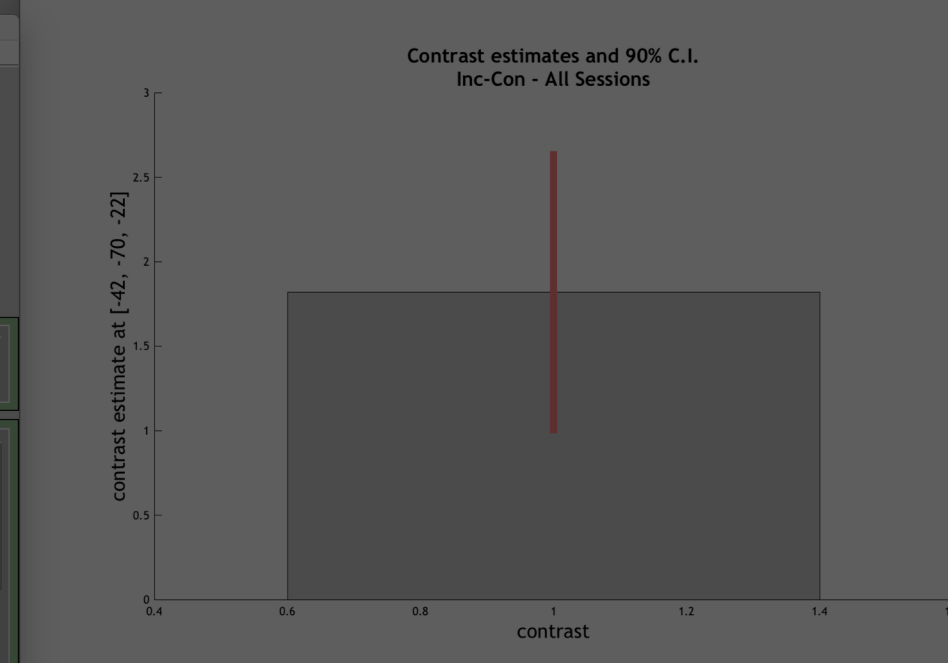
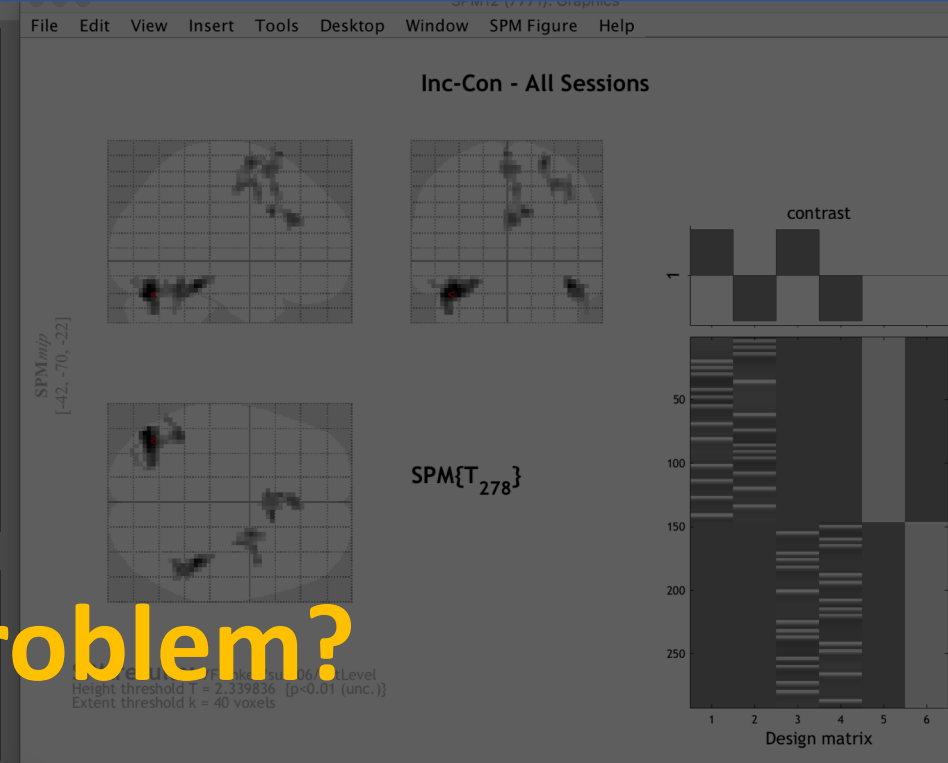
Multivariate

eigenvariate | CVA | multivariate Bayes | BMS | p-value

Display

plot | overlays... | save...

Hemodynamics | clear | exit



Problem?

Applying the GLM to fMRI Data

Other options

Grand mean scaling: Removes intersession variance, allows for combining data across subjects

Intensity normalization: Forces each volume to have the same mean (not recommended)

$$g_s = \frac{\sum_{n=1}^N g_{ns}}{N}$$

**Session-specific grand mean scaling:
Multiplies each volume in session s
by $100/g_s$**

Percent Signal Change

Some recommend reporting percent signal change instead of beta weights

**More accurate reflection of effect size, more comparable
between studies**

ROI tool like Marsbar will scale by the overall mean of the voxels in the region

Applying the GLM to fMRI Data

The screenshot shows the SPM Batch Editor window. The title bar reads "Batch Editor". The menu bar includes "File", "Edit", "View", "SPM", and "BasicIO". Below the menu bar are icons for file operations and a play button. The main area is divided into three sections:

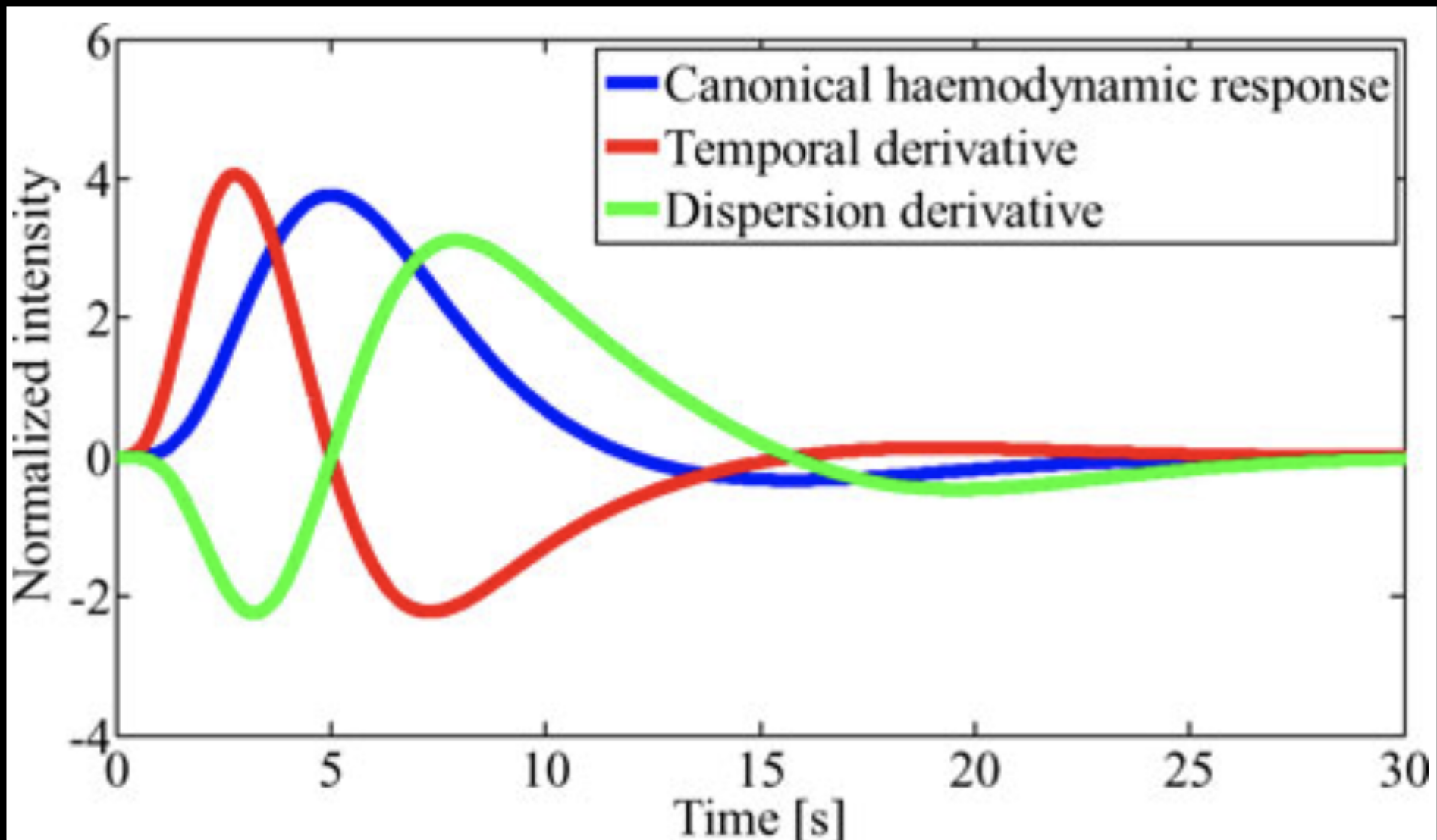
- Module List:** A list of modules with "fMRI model specification <-X" selected.
- Current Module: fMRI model specification:** A list of parameters and their values:

Help on: fMRI model specification	
Directory	<-X
Timing parameters	
. Units for design	<-X
. Interscan interval	<-X
. Microtime resolution	16
. Microtime onset	8
Data & Design	<-X
Factorial design	
Basis Functions	
. Canonical HRF	
. . Model derivatives	Time and Dispersion derivatives
Model Interactions (Volterra)	Do not model Interactions
Global normalisation	None
Masking threshold	0.8
Explicit mask	
Serial correlations	AR(1)
- Current Item: Model derivatives:** A list of options:
 - No derivatives
 - Time derivatives
 - *Time and Dispersion derivatives (selected)

Below the "Current Item" list is a "Specify..." button.

Model derivatives
Model HRF Derivatives. The canonical HRF combined with time and dispersion derivatives comprise an 'informed' basis set, as the shape of the canonical response conforms to the hemodynamic response that is commonly observed. The incorporation of the derivate terms allow for variations in subject-to-subject and voxel-to-voxel responses. The time derivative allows the peak response to vary by plus or minus a second and the dispersion derivative allows the width of the response to vary. The informed basis set requires an SPM{F} for inference. T-contrasts over just the canonical are perfectly valid but assume constant delay/dispersion. The informed basis set compares favourably with eg. FIR bases on many data sets. One of the following options must be selected:
* No derivatives

Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

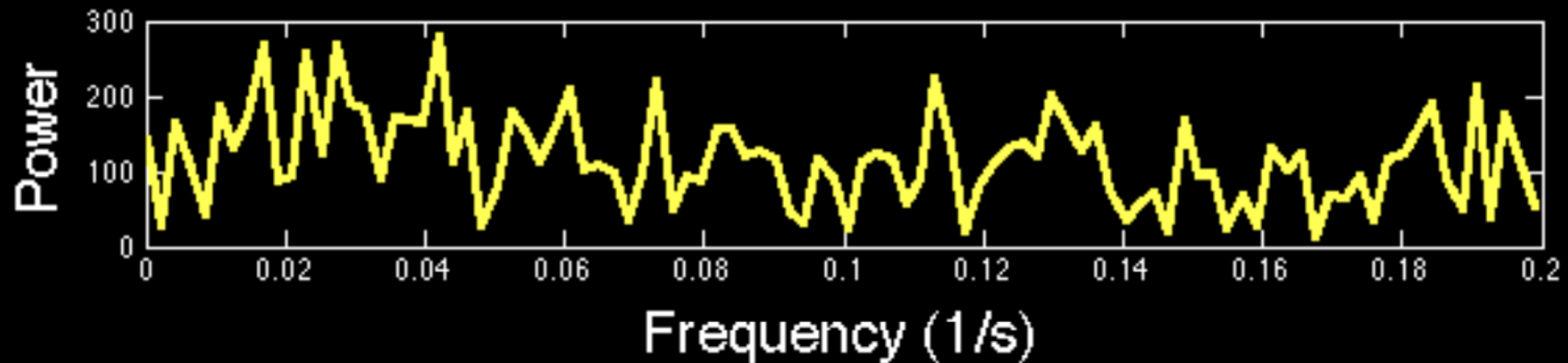
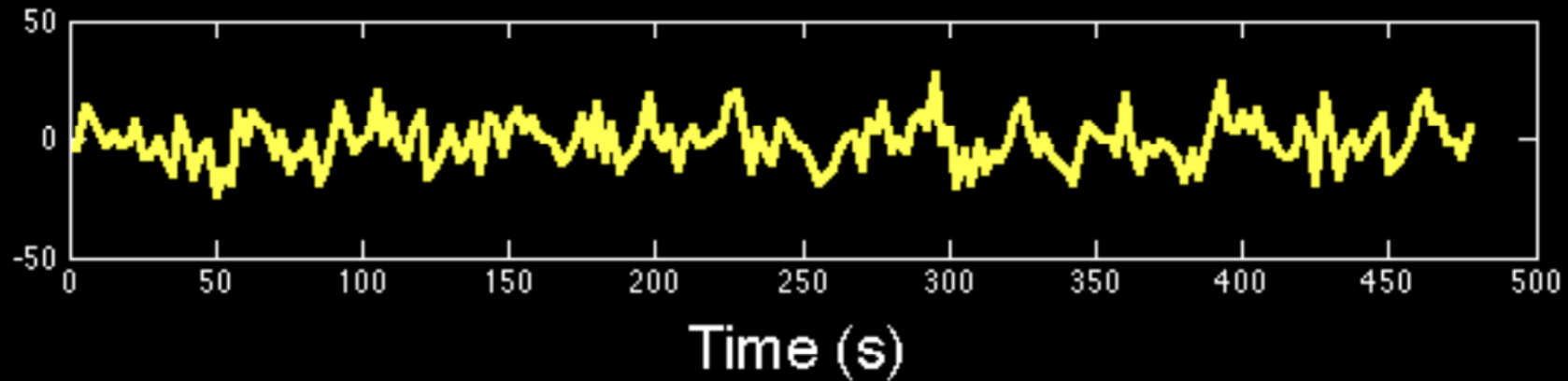
Benefits of time derivative

No interpolation of raw data, may capture variability in BOLD response

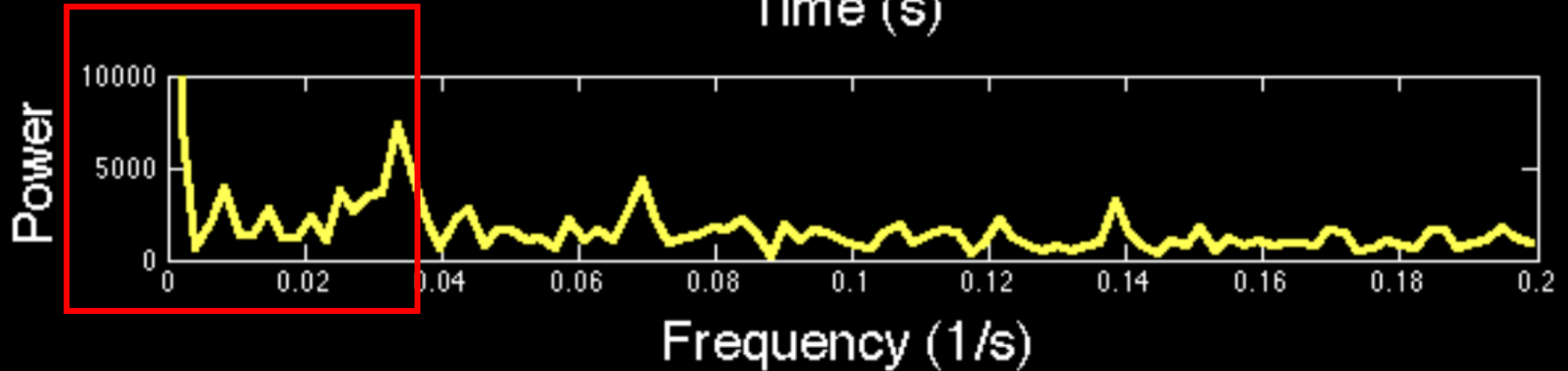
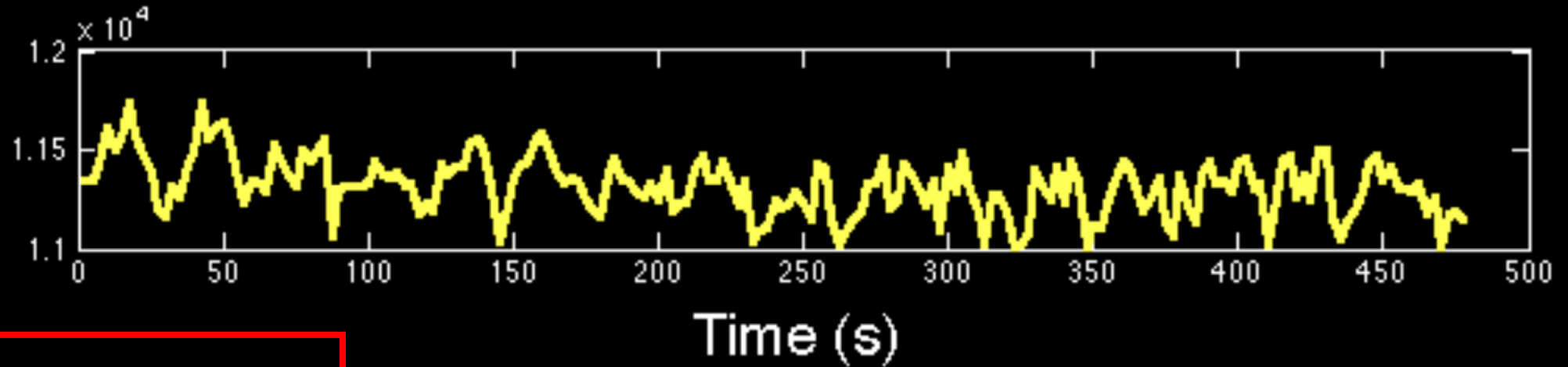
Cons: Requires an additional regressor in the model per condition

Applying the GLM to fMRI Data

Other options: Highpass filtering and prewhitening

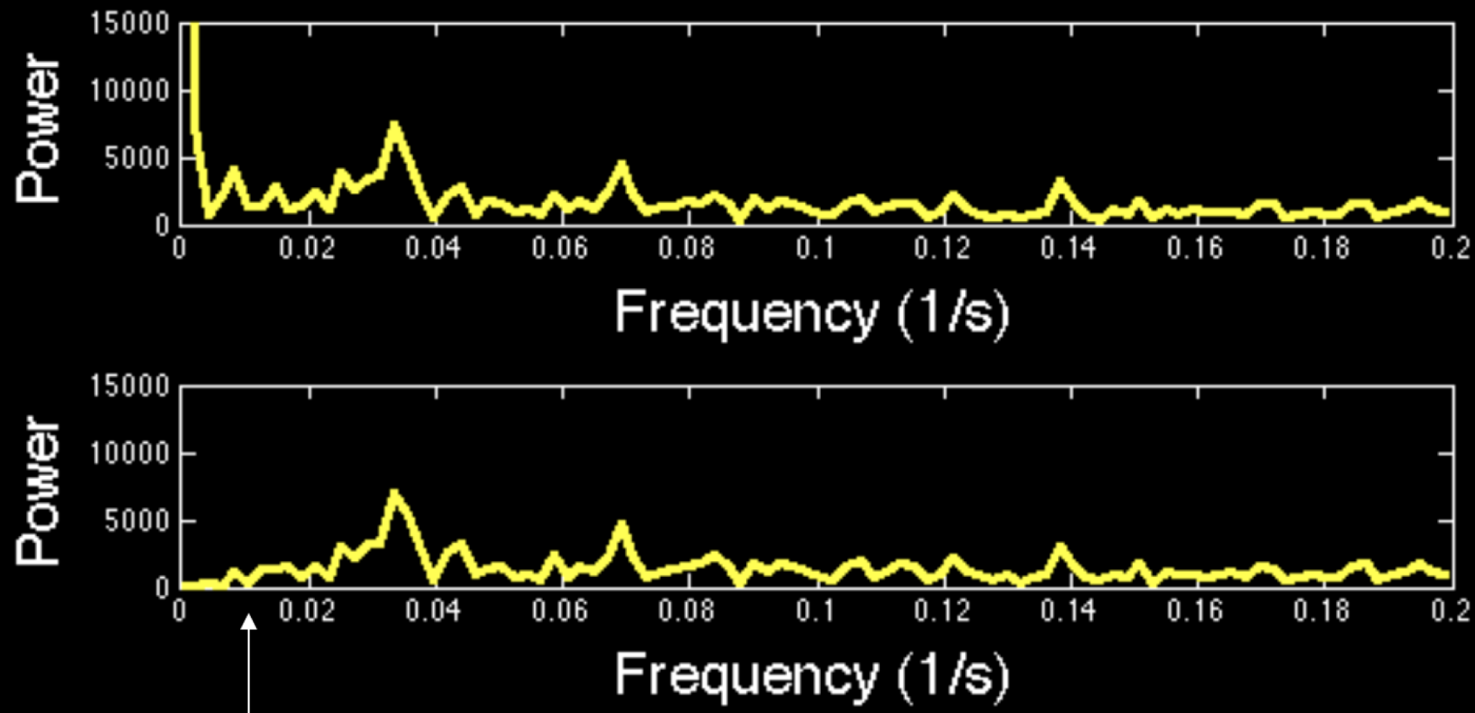


Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

Highpass filter removes frequencies below a certain threshold

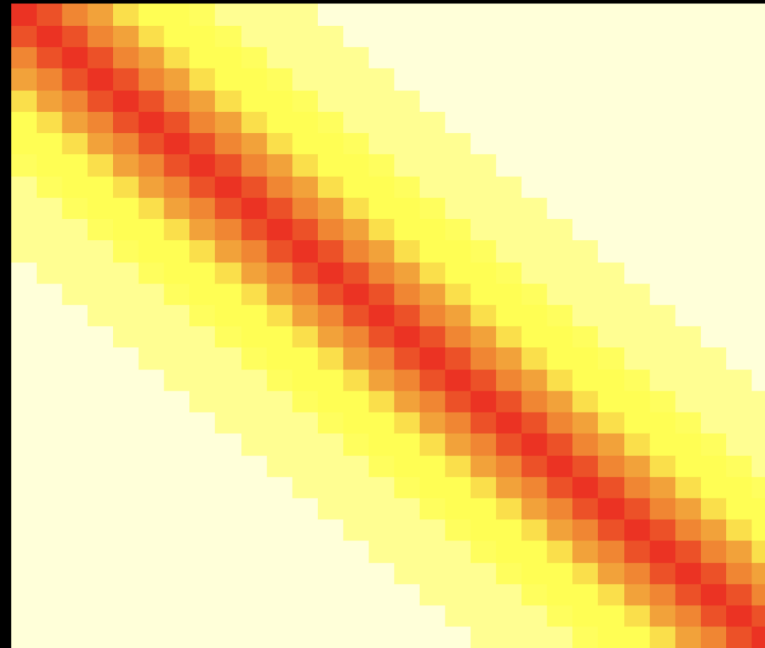


Filter below .01 Hz

Applying the GLM to fMRI Data

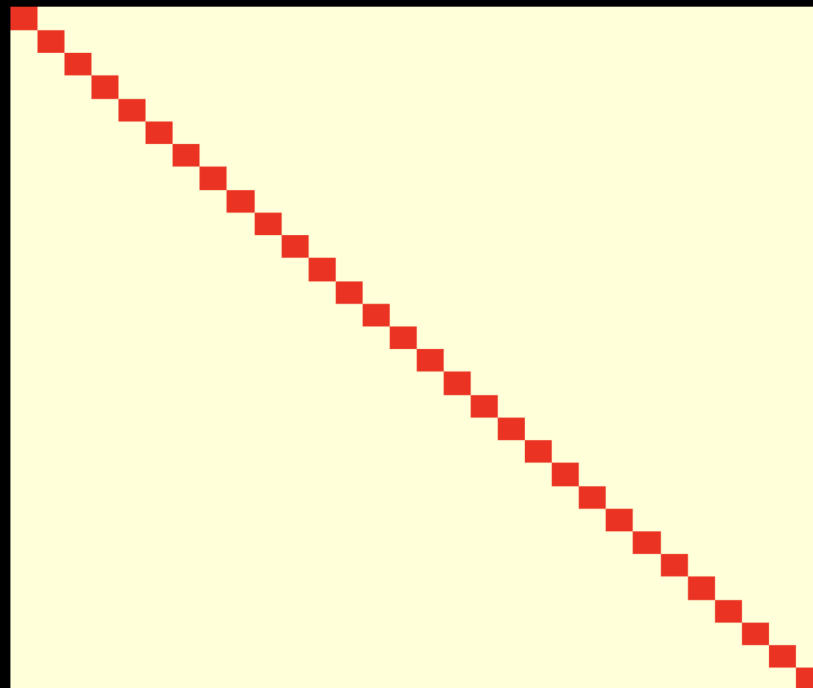
$$Y = X\beta + \epsilon$$

$$\text{Cov}(\epsilon) =$$



Applying the GLM to fMRI Data

$$\text{Cov}(K\epsilon) =$$



$$KY = KX\beta + K\epsilon$$

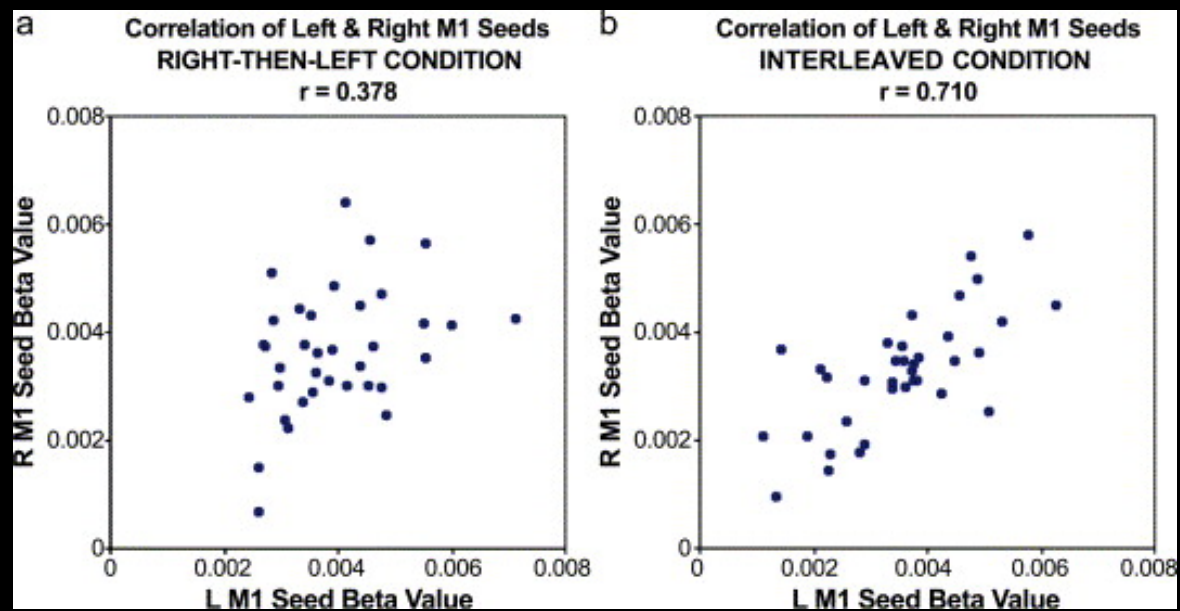
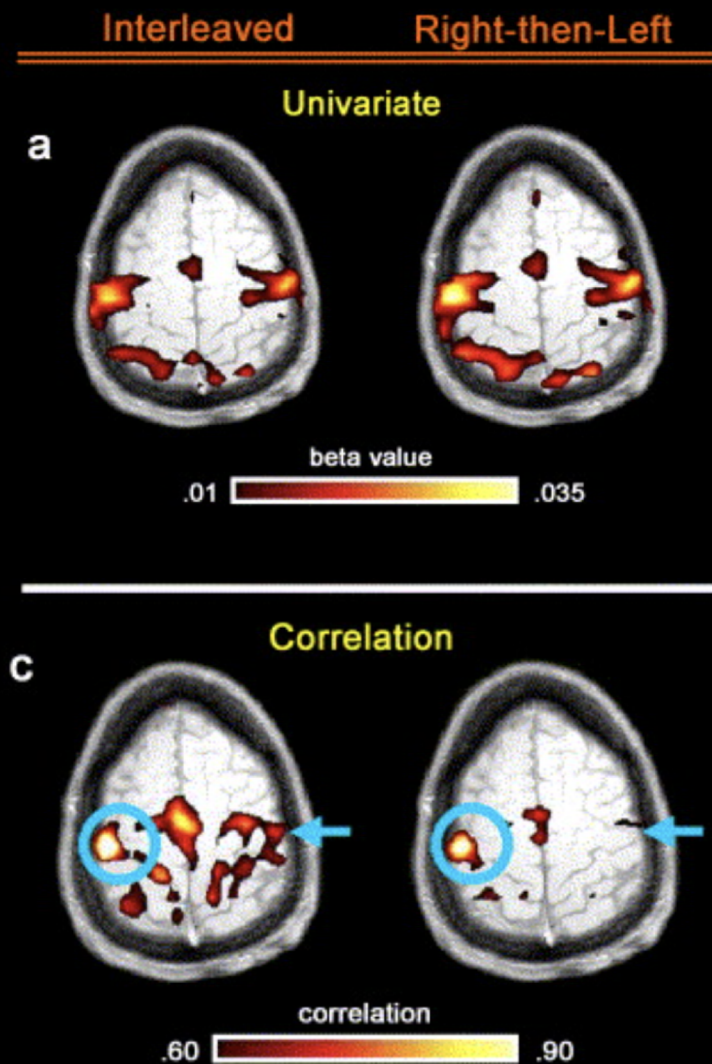
Applying the GLM to fMRI Data

Prewhitening

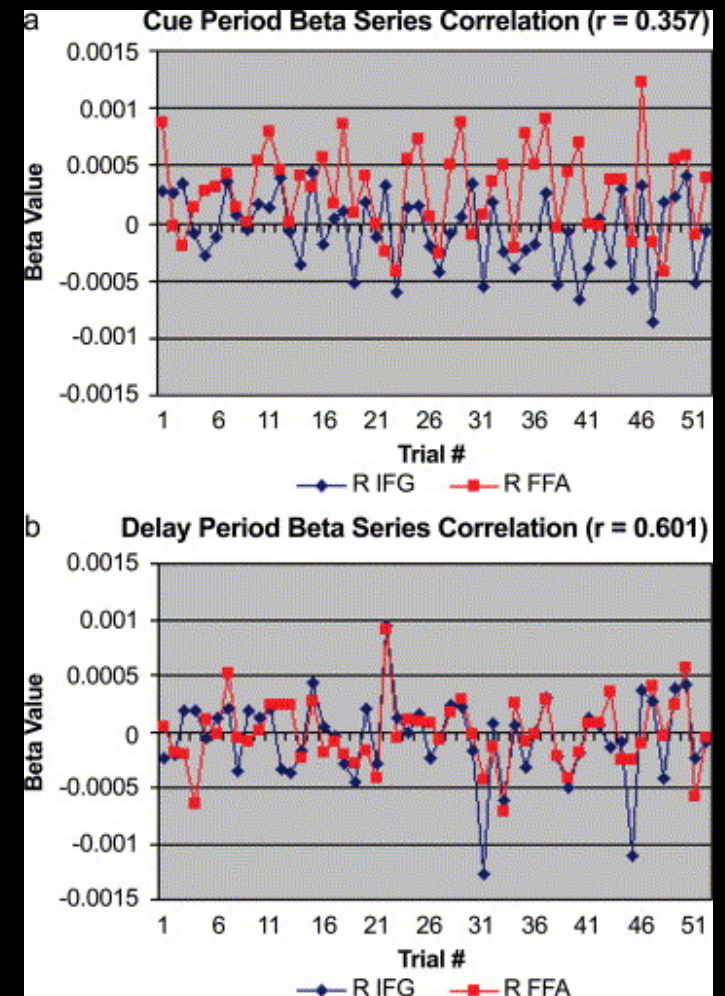
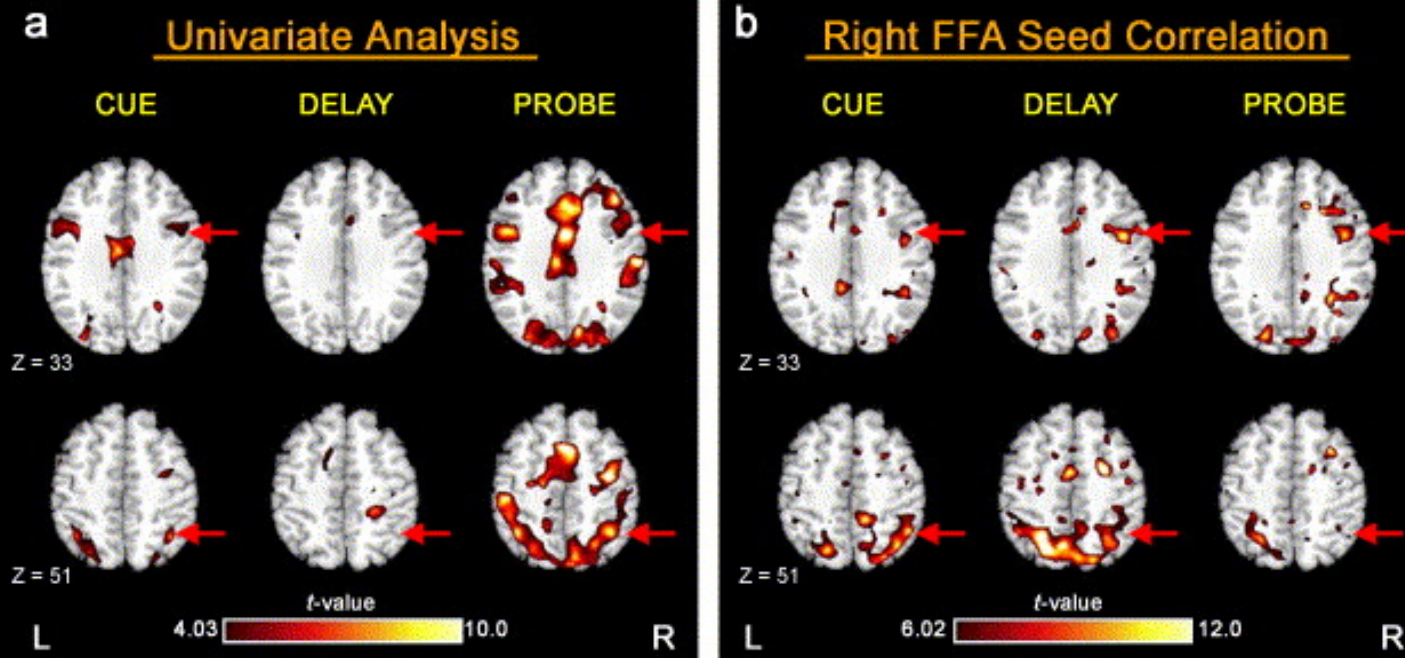
Gauss-Markov assumptions: Normally distributed errors, constant variance, and no temporal autocorrelation

Are fMRI data temporally autocorrelated?

Applying the GLM to fMRI Data



Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

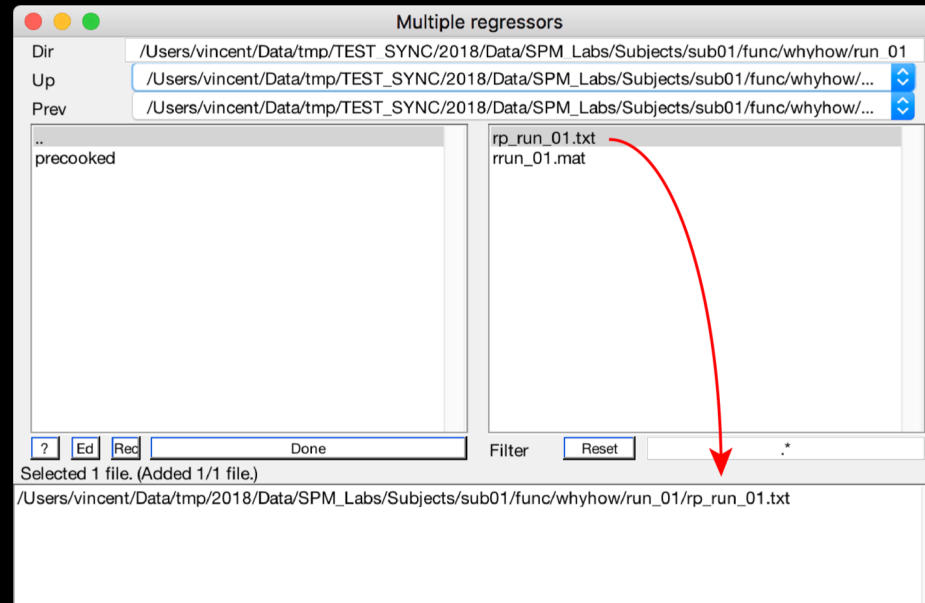
Drawback: Very tedious to implement without scripting!

For AFNI users: Can use 'IM' basis function in 3dDeconvolve

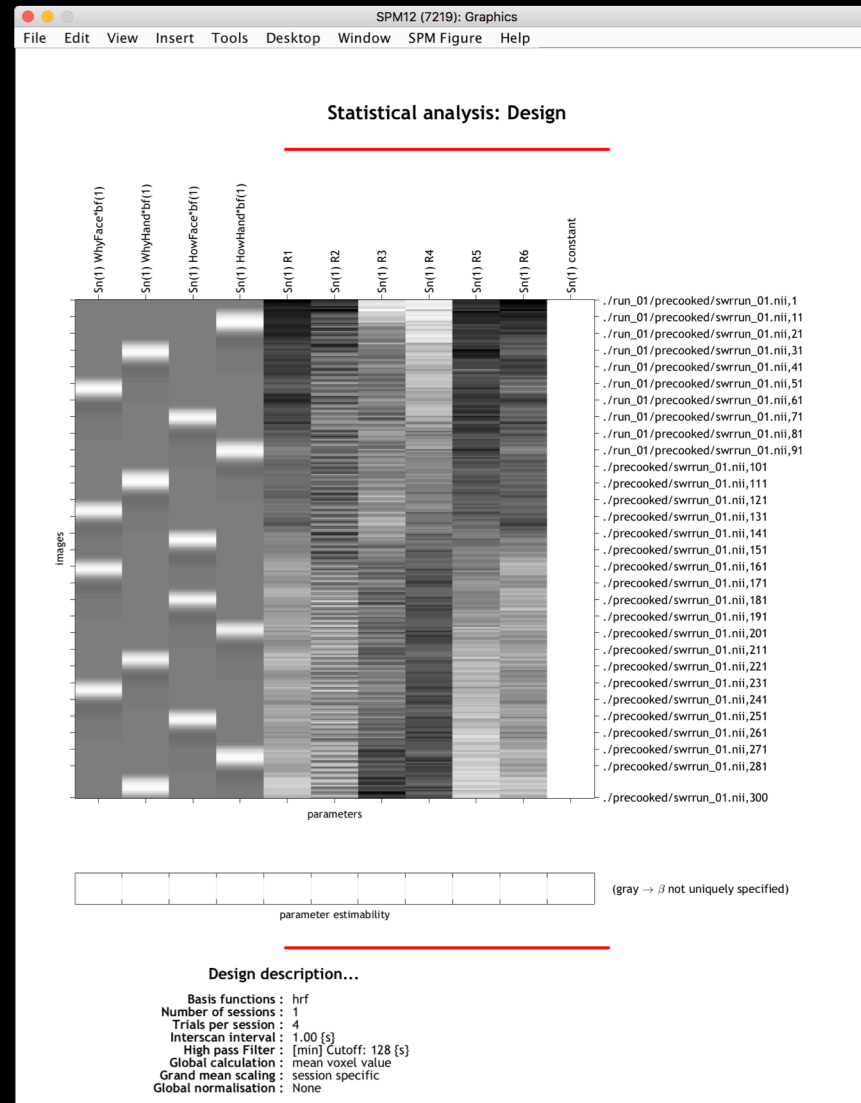
Applying the GLM to fMRI Data

What about nuisance regressors, such as motion?

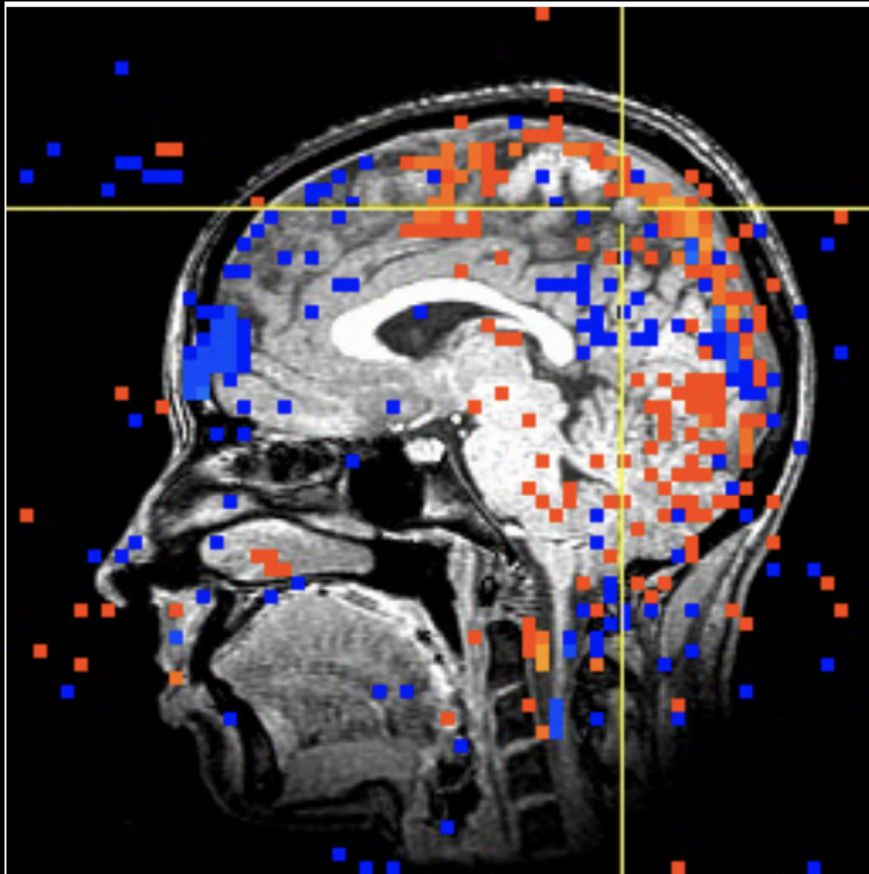
.. Multiple conditions	
.. Regressors	
.. Multiple regressors	
.. High-pass filter	128
Factorial design	
Basis Functions	



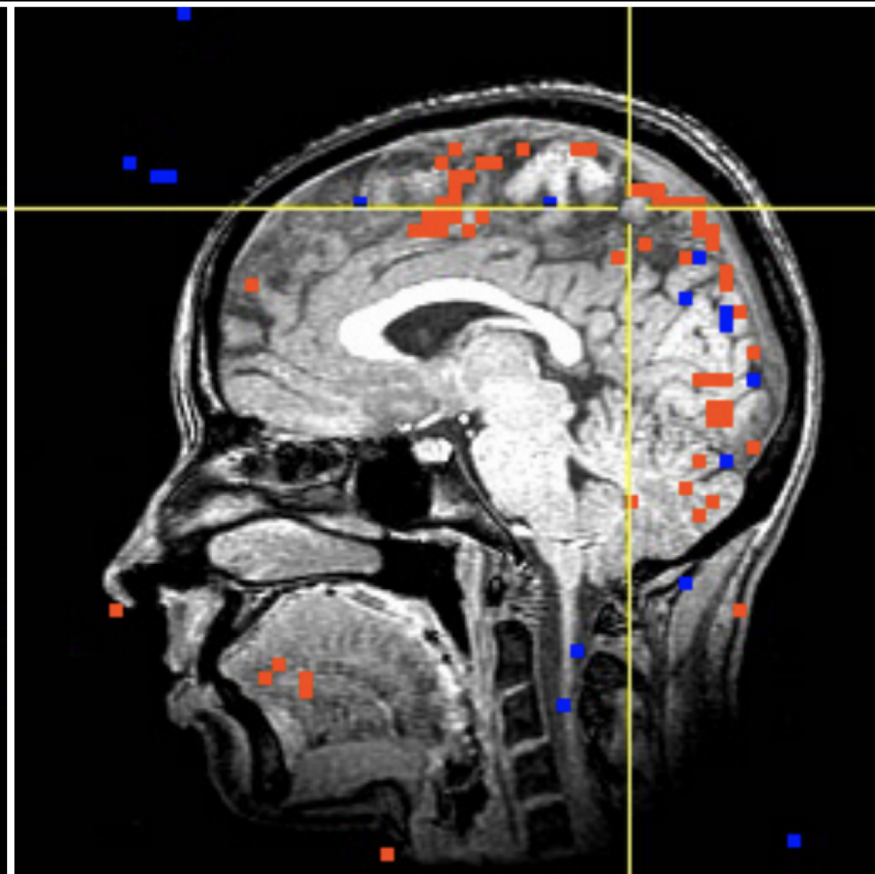
Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

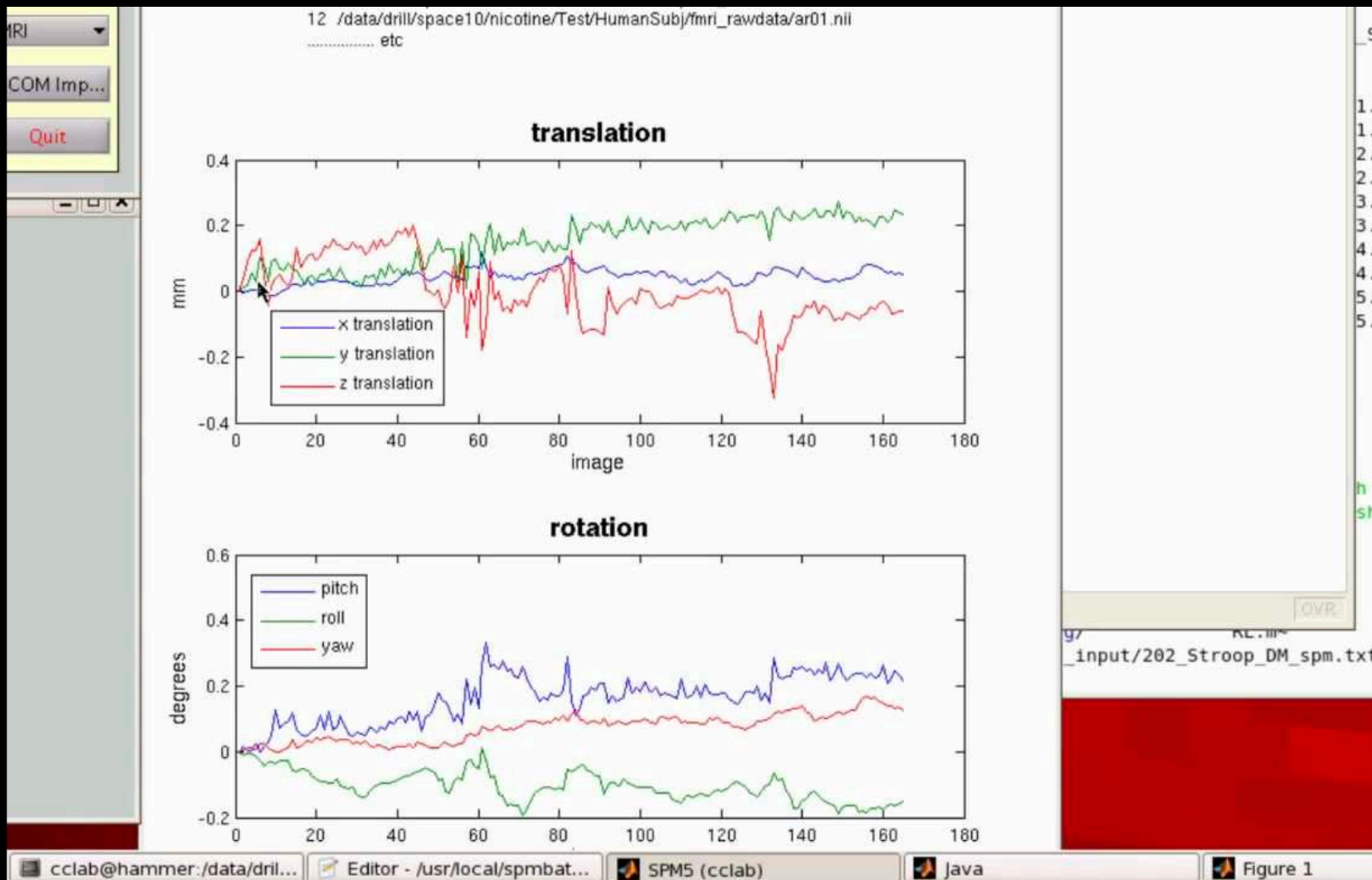


Activation map with image registration but *without* using movement estimates as regressors



Activation map when also using movement estimates as regressors

Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

Perennial Question: How much is too much?

Guideline from days of yore: >1 voxel over entire run, >0.5 voxel between volumes

More important: Does motion correlate with your task?

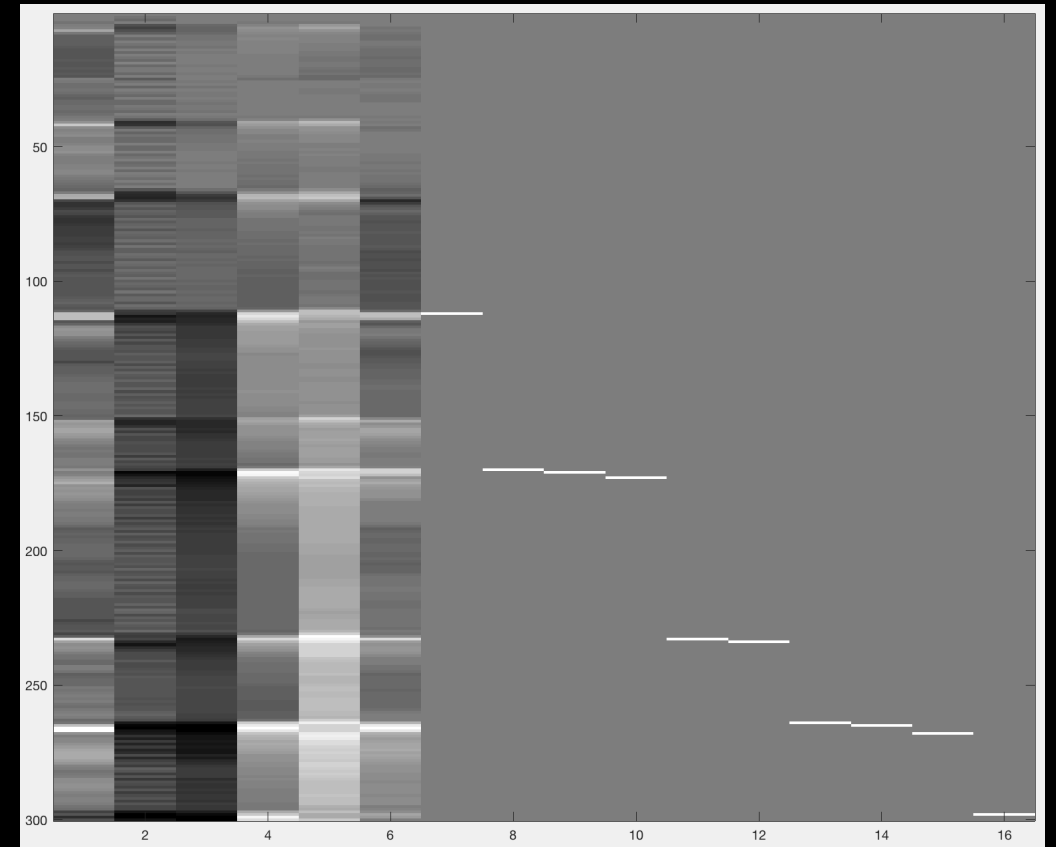
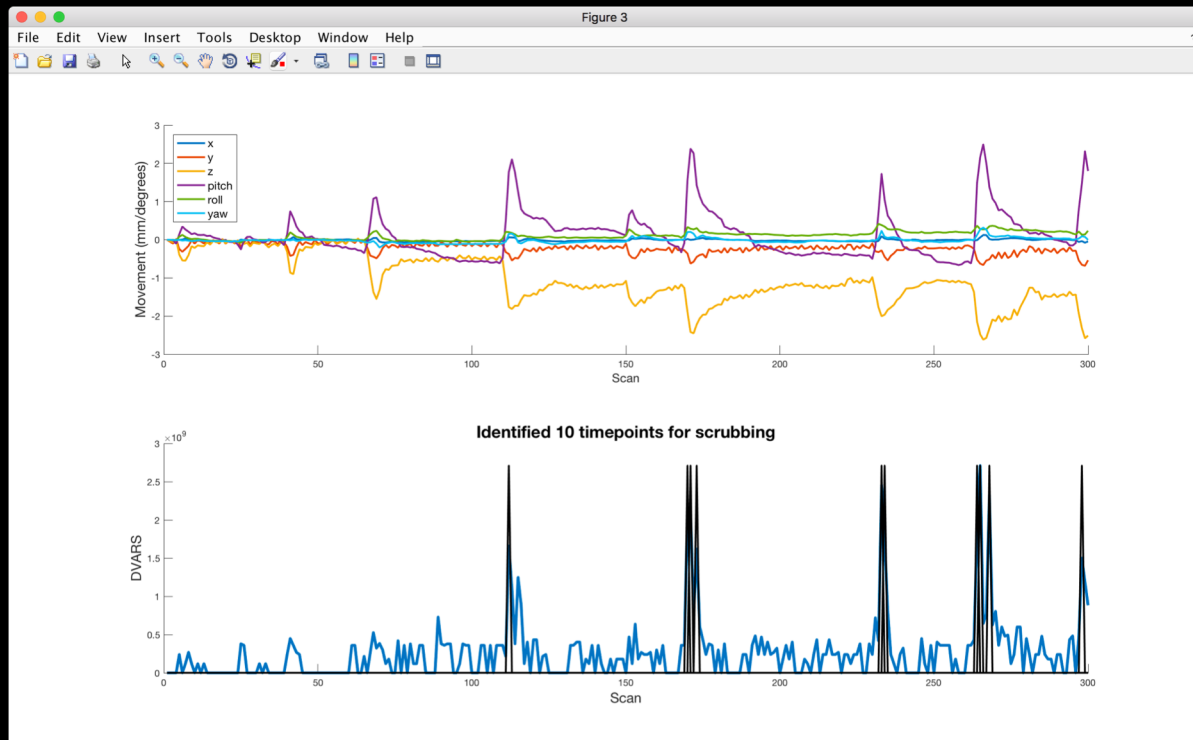
Applying the GLM to fMRI Data

Other nuisance regressors: DVARS, Framewise Displacement (FD)

Derivative Variance (DVARS) measures abrupt global signal changes from volume to volume (Power et al., 2011)

**Volumes that exceed a specified threshold are flagged for scrubbing:
Inserting that volume as a regressor into the GLM**

Applying the GLM to fMRI Data



Applying the GLM to fMRI Data

CGMN functional connectivity toolbox (20.0)

Project Tools Help **SETUP** DENOISING (1st-level) ANALYSES (1st-level) RESULTS (2nd-level)

All analyses

Basic

Structural

Functional

ROIs

Conditions

Covariates (1st-level)

Covariates (2nd-level)

Options

Preprocessing

QA plots

Done

First-level covariates / timeseries

Covariates	Subjects	Sessions	Covariate name
realignment	Subject 1	Session 1	scrubbing
QC timeseries	Subject 2		
scrubbing	Subject 3		
QC_FDconn	Subject 4		
	Subject 5		
	Subject 6		

rest

...

- DefaultMode.MPFC ROI.mat

nonparametricroi_pindex.mat

- covariate tools:

Step 4/4: Define/Edit second-level analyses

storage: 159.8Gb available (8%)

BU

Before we begin the Demo: SPM Terms for Analysis

1st-Level Analysis: Individual subject (all runs within the subject)

2nd-Level Analysis: Group-Level Analysis (all subjects within the experiment)

Also Before we begin: Contrasts and Contrast Weights

A contrast is simply one condition's beta weight subtracted from another

e.g., A-B

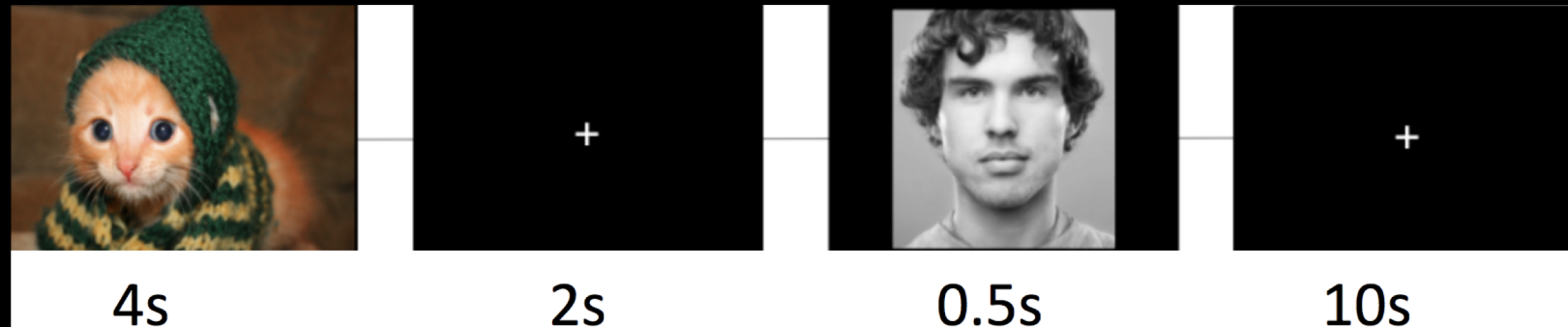
**General recommendations: Model everything that is related to the task,
and don't model any baseline events (e.g., implicit baseline)**

Also Before we begin: Contrasts and Contrast Weights

```
. Subject/Session
.. Scans 300 files
.. Conditions
... Condition
.... Name WhyFace
.... Onsets ...9169 117.2590563 152.5798844 225.1941691]
.... Durations ...9262 7.674989138 8.015399588 8.542317722]
.... Time Modulation No Time Modulation
.... Parametric Modulations
.... Orthogonalise modulations Yes
```

Also Before we begin: Contrasts and Contrast Weights

Example: Pos/Neg/Neu images



Onset time (s)	Duration (s)	Description
11	4	Negative
17	.5	Face
27.5	4	Neutral
33.5	.5	Face

Also Before we begin: Contrasts and Contrast Weights

Example: Where is Pos activation greater than Neg activation?

Contrast weights for each side should sum to +1 and -1

	Pos IAPS	Neg IAPS	Neu IAPS	Face after Pos	Face after Neg	Face after Neu
PosIAPS > NegIAPS	1	-1	0	0	0	0

Also Before we begin: Contrasts and Contrast Weights

Where is Pos activation greater than Neu activation?

	Pos IAPS	Neg IAPS	Neu IAPS	Face after Pos	Face after Neg	Face after Neu
PosIAPS > NegIAPS	1	-1	0	0	0	0

Also Before we begin: Contrasts and Contrast Weights

Where is both Pos and Neg activation greater than Neu activation?

	Pos IAPS	Neg IAPS	Neu IAPS	Face after Pos	Face after Neg	Face after Neu
PosIAPS > NegIAPS	1	-1	0	0	0	0

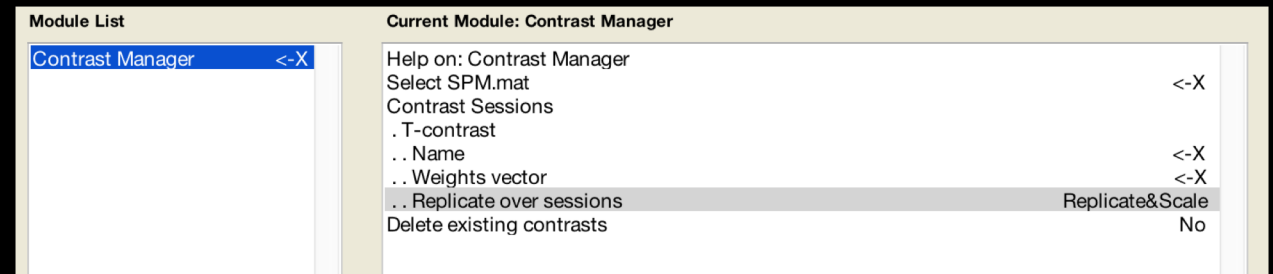
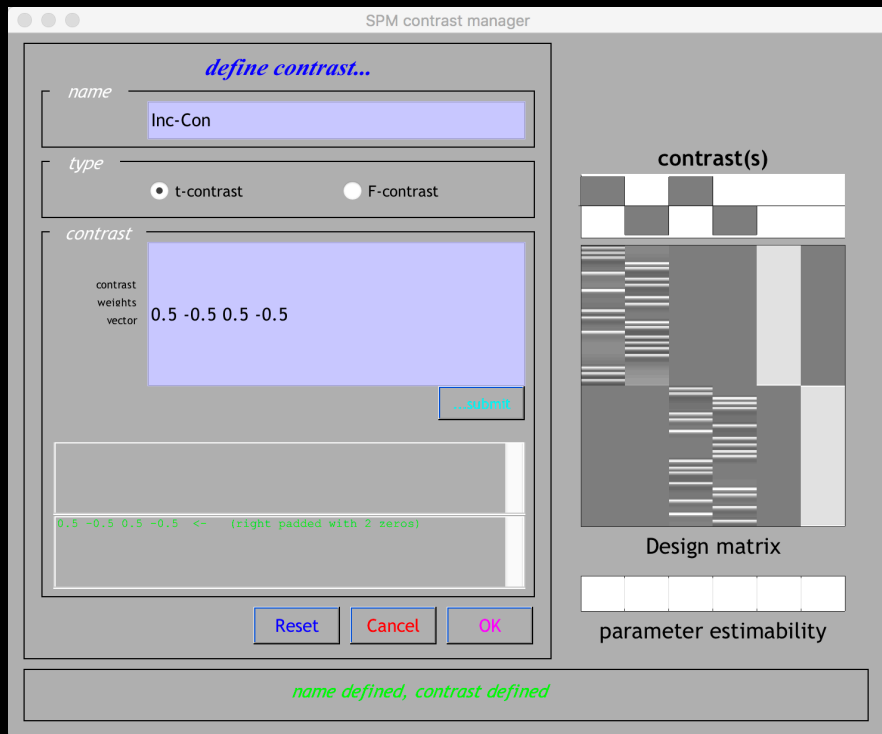
Also Before we begin: Contrasts and Contrast Weights

Where is average face activation greater than baseline?

	Pos IAPS	Neg IAPS	Neu IAPS	Face after Pos	Face after Neg	Face after Neu
PosIAPS > NegIAPS	1	-1	0	0	0	0

Also Before we begin: Contrasts and Contrast Weights

Contrast weights need to be weighted for number of runs as well



Also Before we begin: Contrasts and Contrast Weights

Module List

Named File Selector	
Realign: Estimate & Reslice	DEP
Slice Timing	DEP
Coregister: Estimate & Reslice	DEP
Segment	DEP
Normalise: Write	DEP
Smooth	DEP
File Set Split	DEP
fMRI model specification	DEP
Model estimation	DEP
Contrast Manager	DEP

Current Module: Contrast Manager

Help on: Contrast Manager

Select SPM.mat	DEP Model estimation: SPM.mat File
Contrast Sessions	
. T-contrast	
.. Name	Inc-Con
.. Weights vector	[1 -1]
.. Replicate over sessions	Replicate&Scale
. T-contrast	
.. Name	Con-Inc
.. Weights vector	[-1 1]
.. Replicate over sessions	Replicate&Scale
. T-contrast	
.. Name	Inc
.. Weights vector	[1 0]
.. Replicate over sessions	Replicate&Scale
. T-contrast	
.. Name	Con
.. Weights vector	[0 1]
.. Replicate over sessions	Replicate&Scale
Delete existing contrasts	No

1st-level setup: Demonstration

Other Experimental Modeling Options

Parametric Modulation

Finite Impulse Response (FIR)

Why do these types of analyses?

Parametric Modulation

Uses Auxiliary Behavioral Information (ABI)

Continuous (or several finely graded) ABI levels

Parametric modulators are estimated in addition
to the regressor they modulate

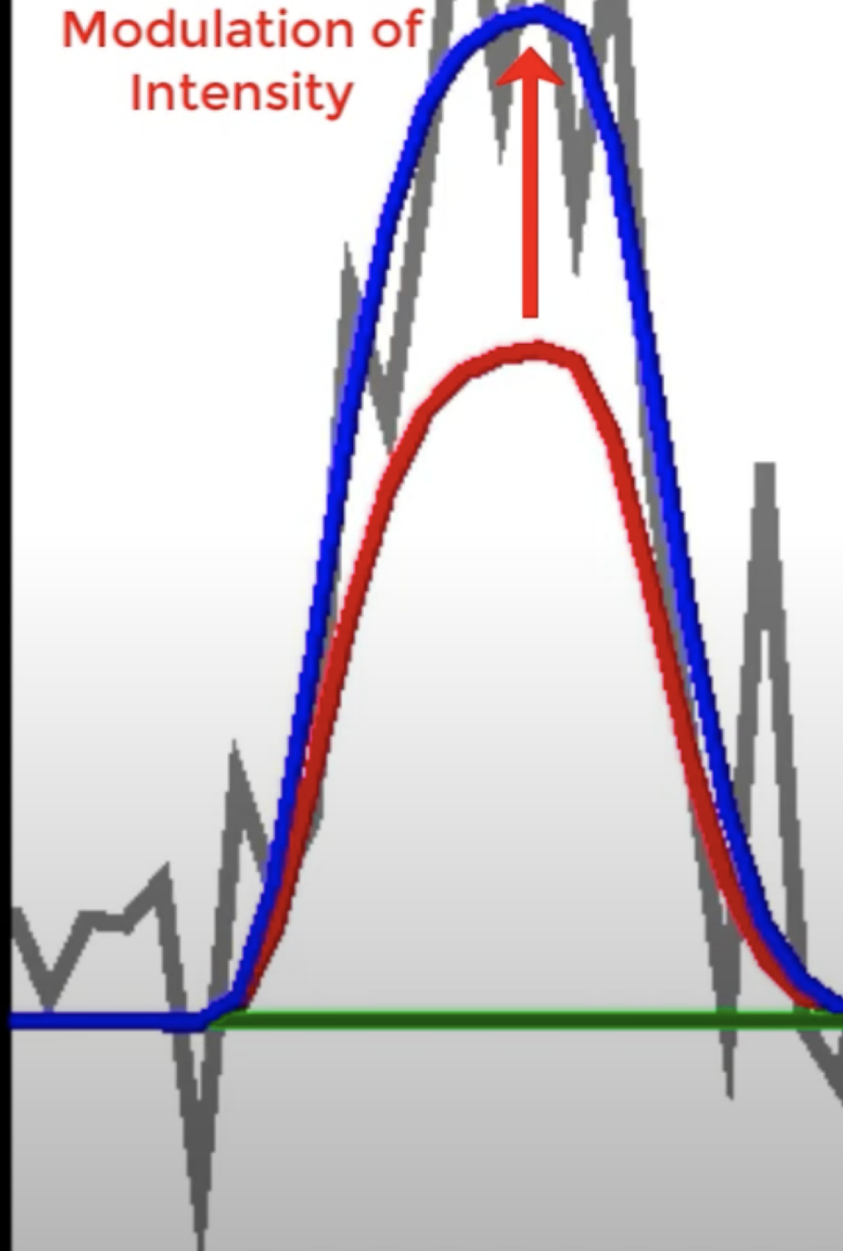
Parametric Modulation

Example: Light intensity

**Regressor for a “Light” trial, and also a regressor
for the intensity of the light**



Parametric
Modulation of
Intensity



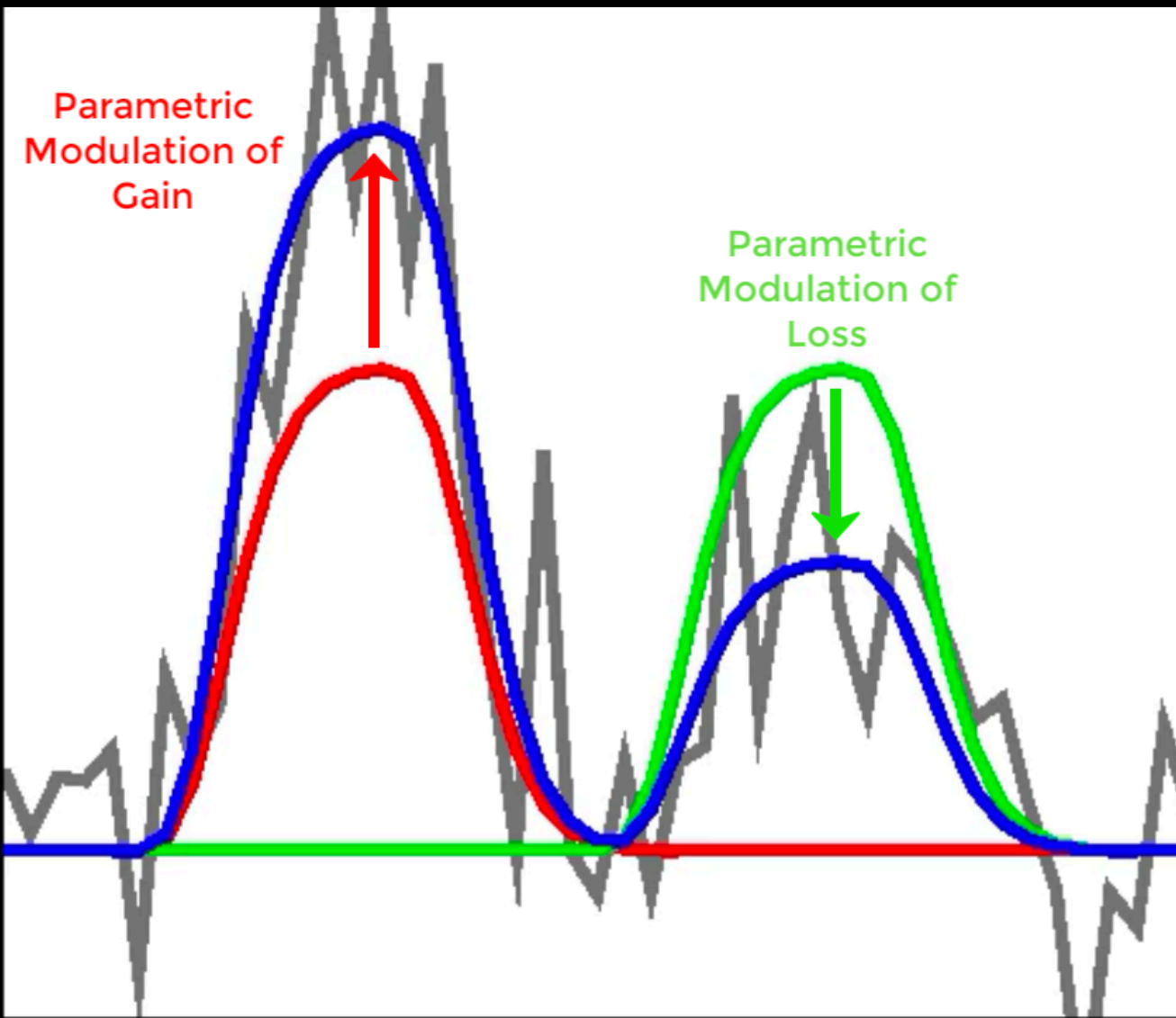
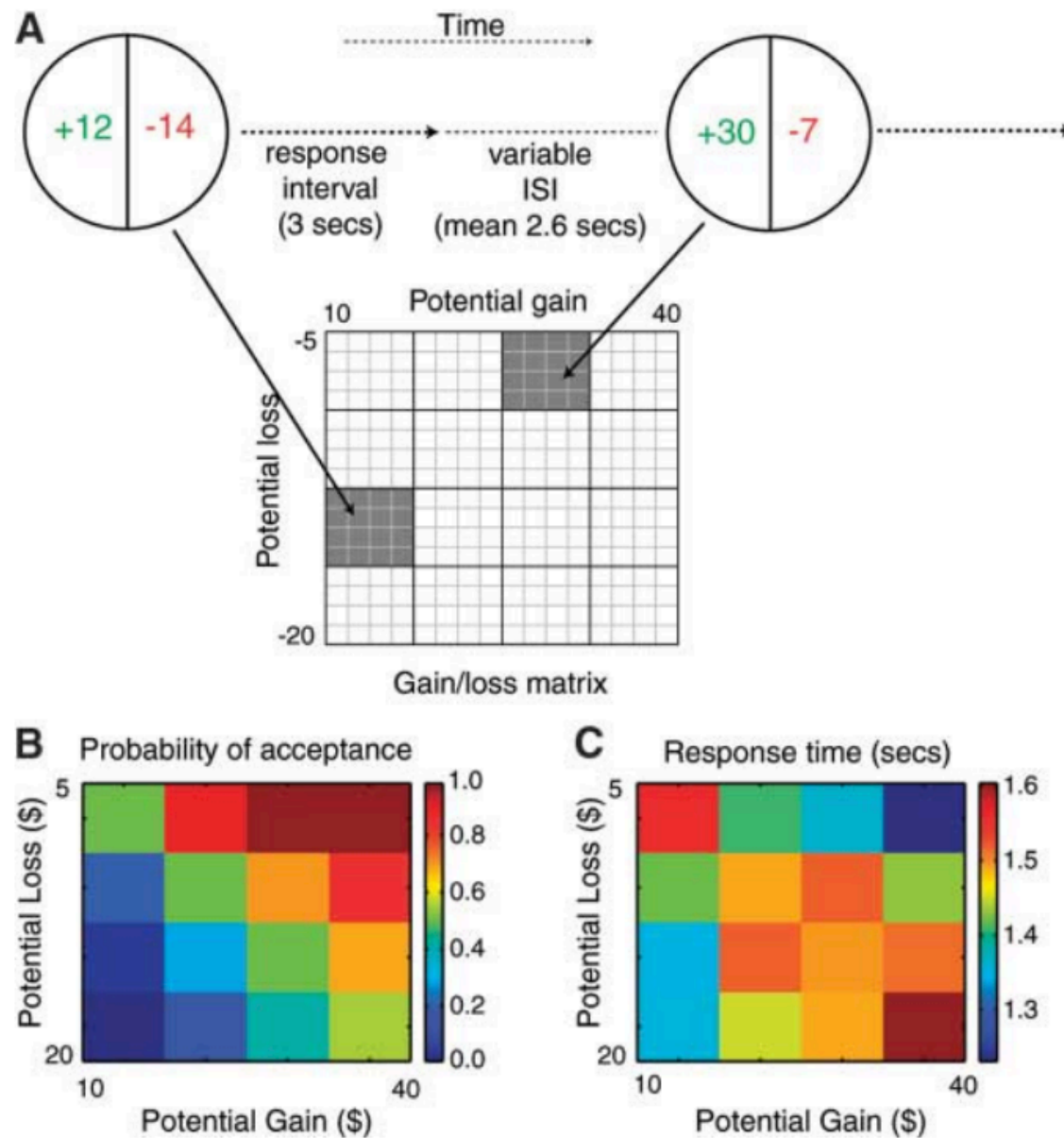


Fig. 1. (A) An illustration of the event-related task design. During each trial, the participant was presented for 3 s with a display showing the size of the potential gain (in green) and loss (in red). After the accept or reject response, a variable interval was presented to allow for optimal deconvolution of fMRI responses to each trial (27). Gambles were not resolved during scanning. The values of gain and loss for each trial were sampled from the gain/loss matrix, as shown here for two example gambles; a gamble from each cell in this 16×16 matrix was presented during scanning, but the data were collapsed into a 4×4 matrix for analysis. All combinations of gains and losses were presented. ISI, interstimulus interval. **(B)** Color-coded heatmap of probability of gamble acceptance at each level of gain/loss (red indicates high willingness to accept the gamble, and blue indicates low willingness to accept the gamble). **(C)** Color-coded heatmap of response times (red indicates slower response times, and blue indicates faster response times).



diminished physiological response to stimulation (22).

Examination of regions of interest in the striatum and VMPFC from the gain/loss conjunction analysis (Fig. 3) revealed that these

coefficient of loss aversion (i.e., the ratio of sensitivity to losses versus gains) is highly correlated across risky and riskless contexts (23). Therefore, we surmise that a similar mechanism may contribute to other manifestations of loss aversion.

Fig. 3. Conjunction analysis results. **(A)** Map showing regions with conjointly significant positive gain response and negative loss response ($P < 0.05$, whole-brain corrected, in each individual map) (see also table S1). Red pixels indicate regions showing significant conjunction; green circles highlight clusters included in the respective heatmaps to the right. L, left; R, right. **(B)** Heatmaps were created by averaging parameter estimates versus baseline within each cluster in the conjunction map for each of the 16 cells (of 16 gambles each) in the gain/loss matrix; color coding reflects strength of neural response for each condition, such that dark red represents the strongest activation and dark blue represents the strongest deactivation.

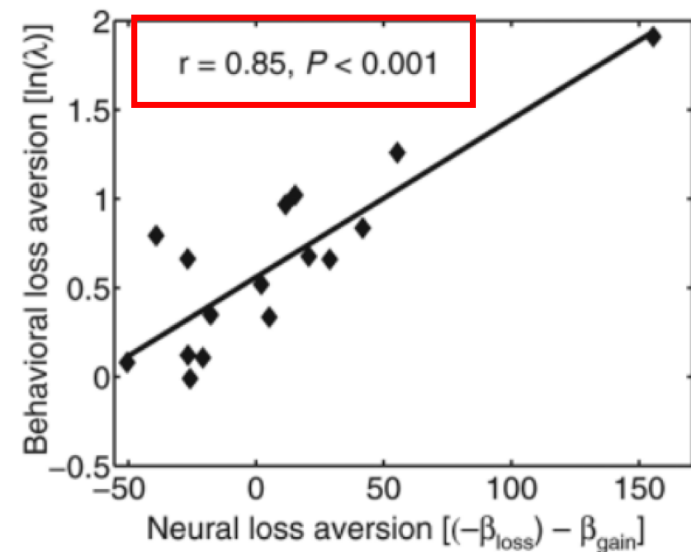
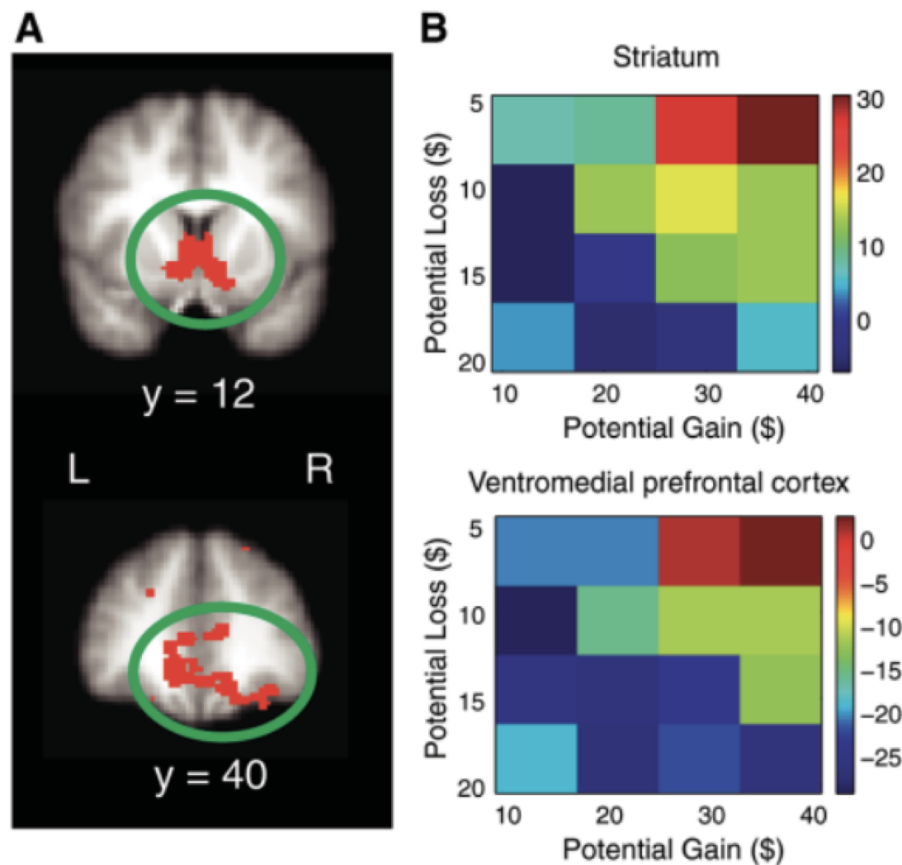
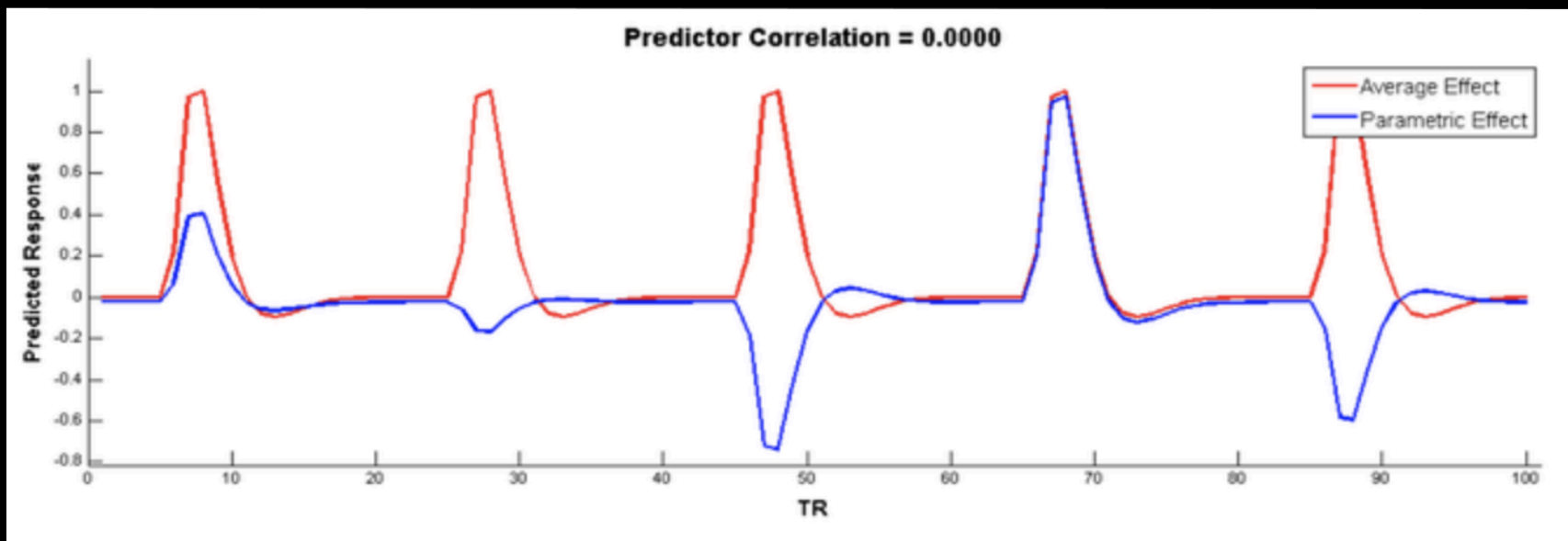
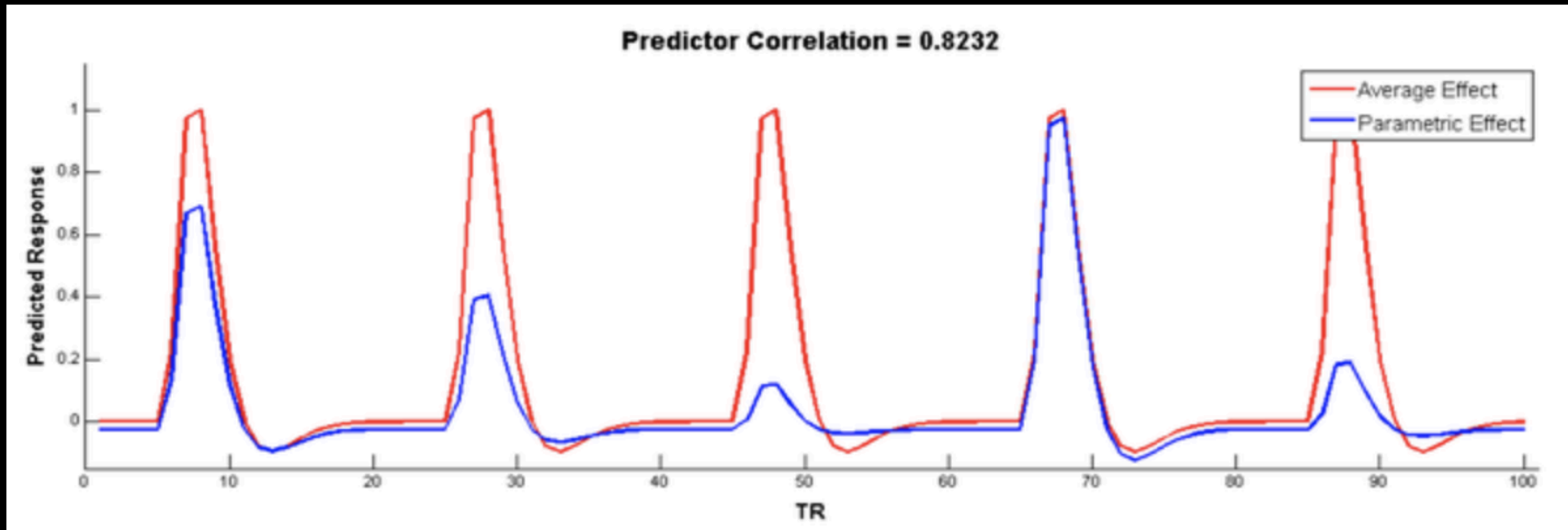


Fig. 4. Scatterplot of correspondence between neural loss aversion and behavioral loss aversion in ventral striatum [Montreal Neurological Institute coordinates (x, y, z): 3.6, 6.3, 3.9; center of gravity in millimeters]. Regression line and P value were computed with the use of robust regression by iteratively reweighted least squares to prevent the influence of outliers; however, this regression also remained highly significant ($P = 0.004$) when the extreme data point (top right-hand corner) was removed from the analysis. β_{loss} and β_{gain} are the unstandardized regression coefficients for the loss and gain variables, respectively.

Parametric Modulation: Mean Centering



Courtesy of
Bob Spunt

Parametric Modulation: Other Considerations

Orthogonalizing the regressors as part of the design

Orthogonalizing as part of the GLM



Module List

fMRI model specification <-X

Current Module: fMRI model specification

.... Time Modulation	No Time Modulation
.... Parametric Modulations	
..... Parameter	
..... Name	<-X
..... Values	<-X
..... Polynomial Expansion	<-X
..... Parameter	
..... Name	<-X
..... Values	<-X
..... Polynomial Expansion	<-X
.... Orthogonalise modulations	Yes
.. Multiple conditions	
.. Regressors	
.. Multiple regressors	
.. High-pass filter	128
Factorial design	
Basis Functions	
.. Canonical HRF	
.. Model derivatives	No derivatives
Model Interactions (Volterra)	Do not model Interactions
Global normalisation	None

Current Item: Orthogonalise modulations

 Yes
 No

Specify...

Orthogonalise modulations

Orthogonalise regressors within trial types.

One of the following options must be selected:

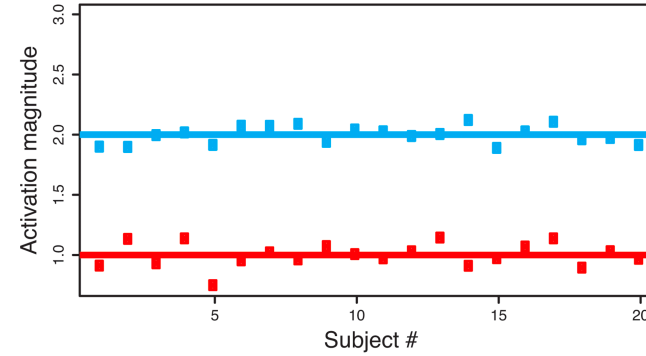
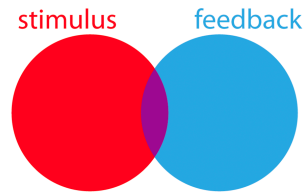
* Yes

* No

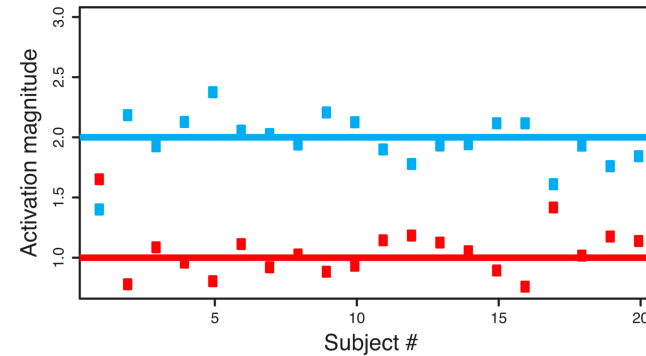
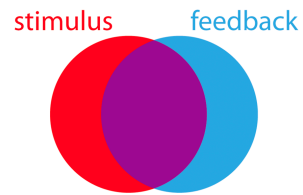
Should be set
to "No"

Why?

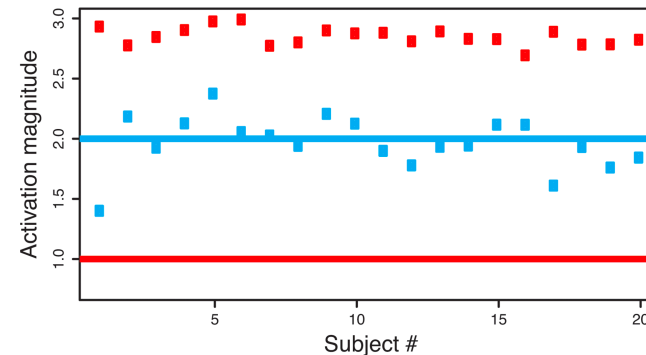
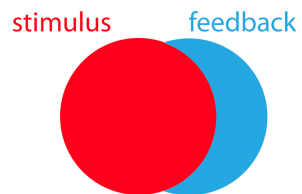
Low collinearity
ISI=3s



High collinearity
ISI=1s

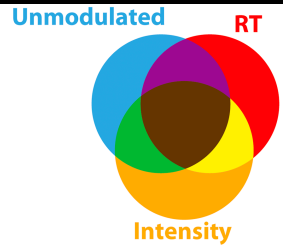


Feedback
orthogonalized
with respect to
Stimulus

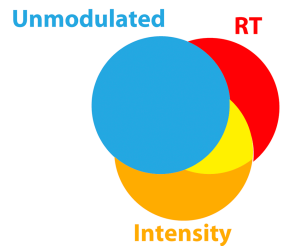


Why?

Regressors without orthogonalization

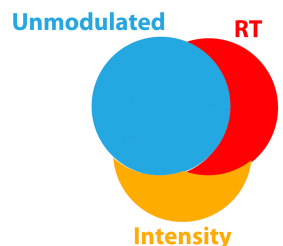


Correct orthogonalization for interpretable Unmodulated



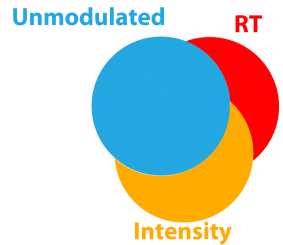
RT wrt Unmod
Intensity wrt Unmod

SPM
RT first
Intensity second



RT wrt Unmod
Intensity wrt Unmod and RT

SPM
Intensity first
RT second



RT wrt Unmod and Intensity
Intensity wrt Unmod

Demonstration of Parametric Modeling Setup

Other Experimental Modeling Options

Parametric Modulation

Finite Impulse Response (FIR)

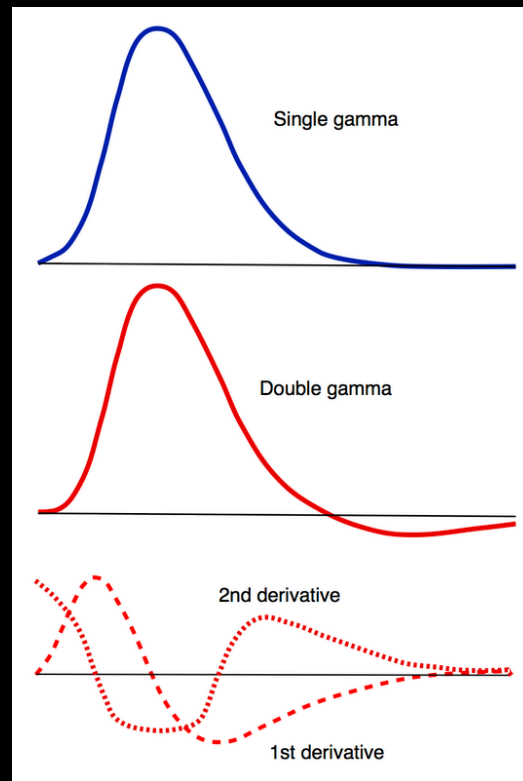
Other Experimental Modeling Options

Parametric Modulation

Finite Impulse Response (FIR)

Finite Impulse Response (FIR)

Basis functions such as the HRF assume a stereotypical shape



Source: mri-q.com

Finite Impulse Response (FIR)

But what if we don't want to assume a shape?

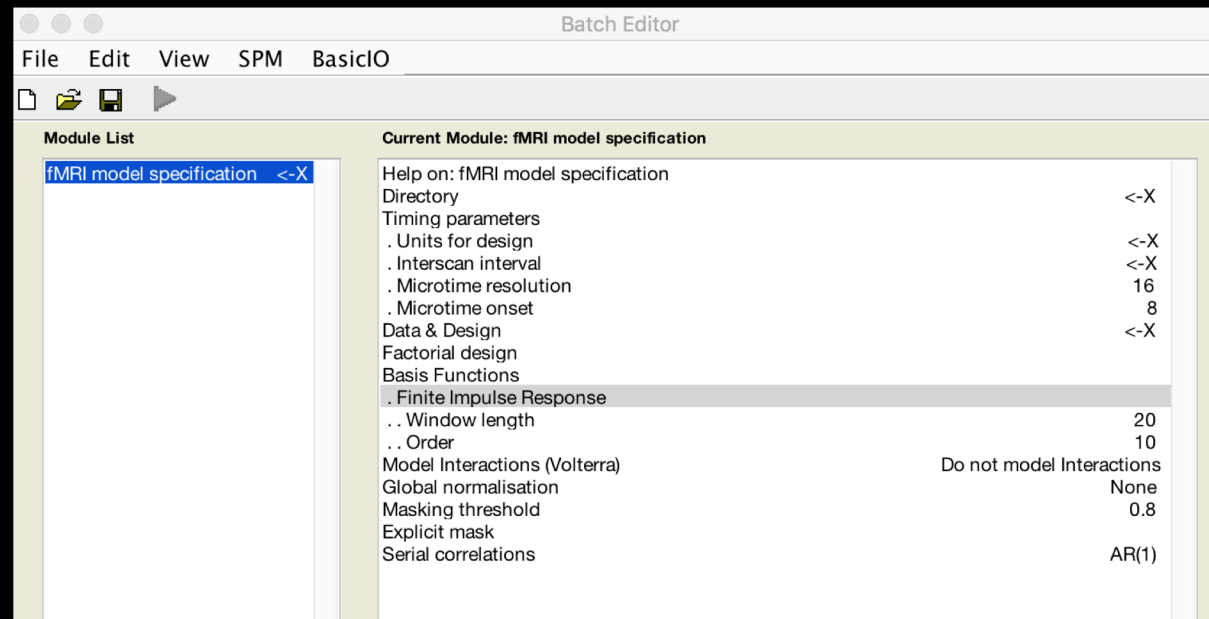
Example: You want to see whether the peak for condition A is later than the peak for condition B

Another example: You think the overall shape of the BOLD response is different between patients and controls, even though the amplitude is the same

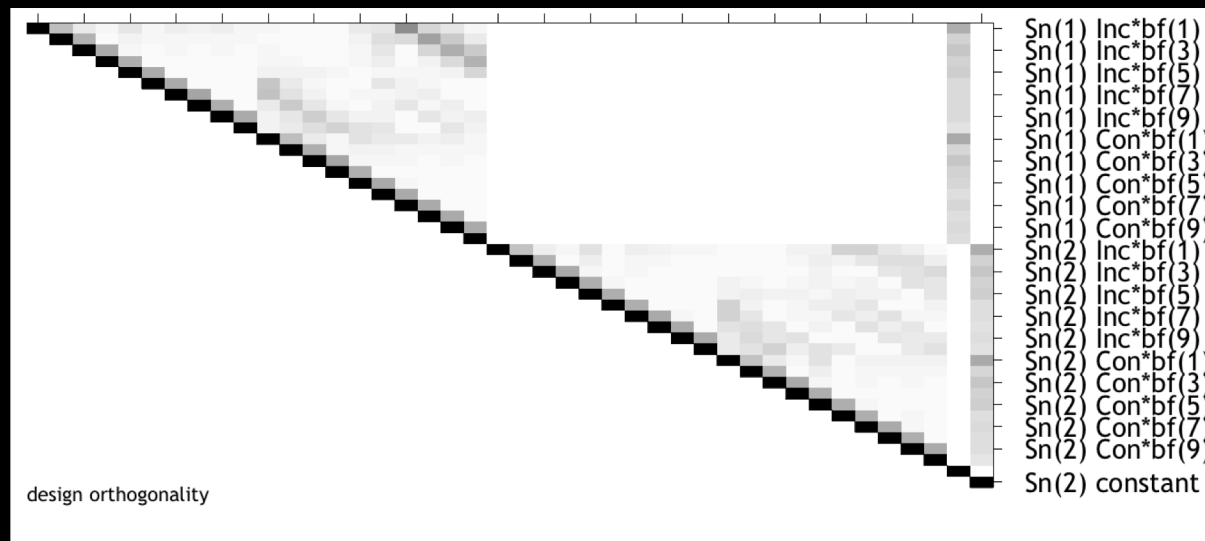
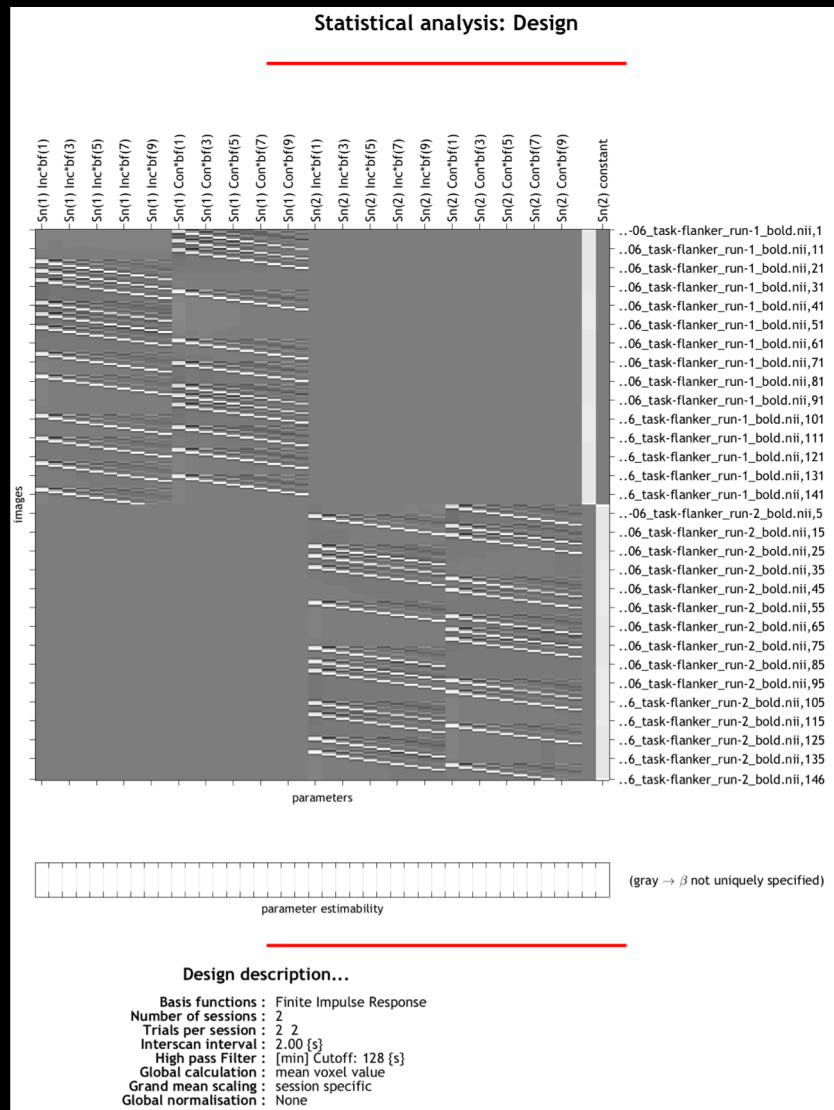
Finite Impulse Response (FIR)

You specify the window length and number of timepoints

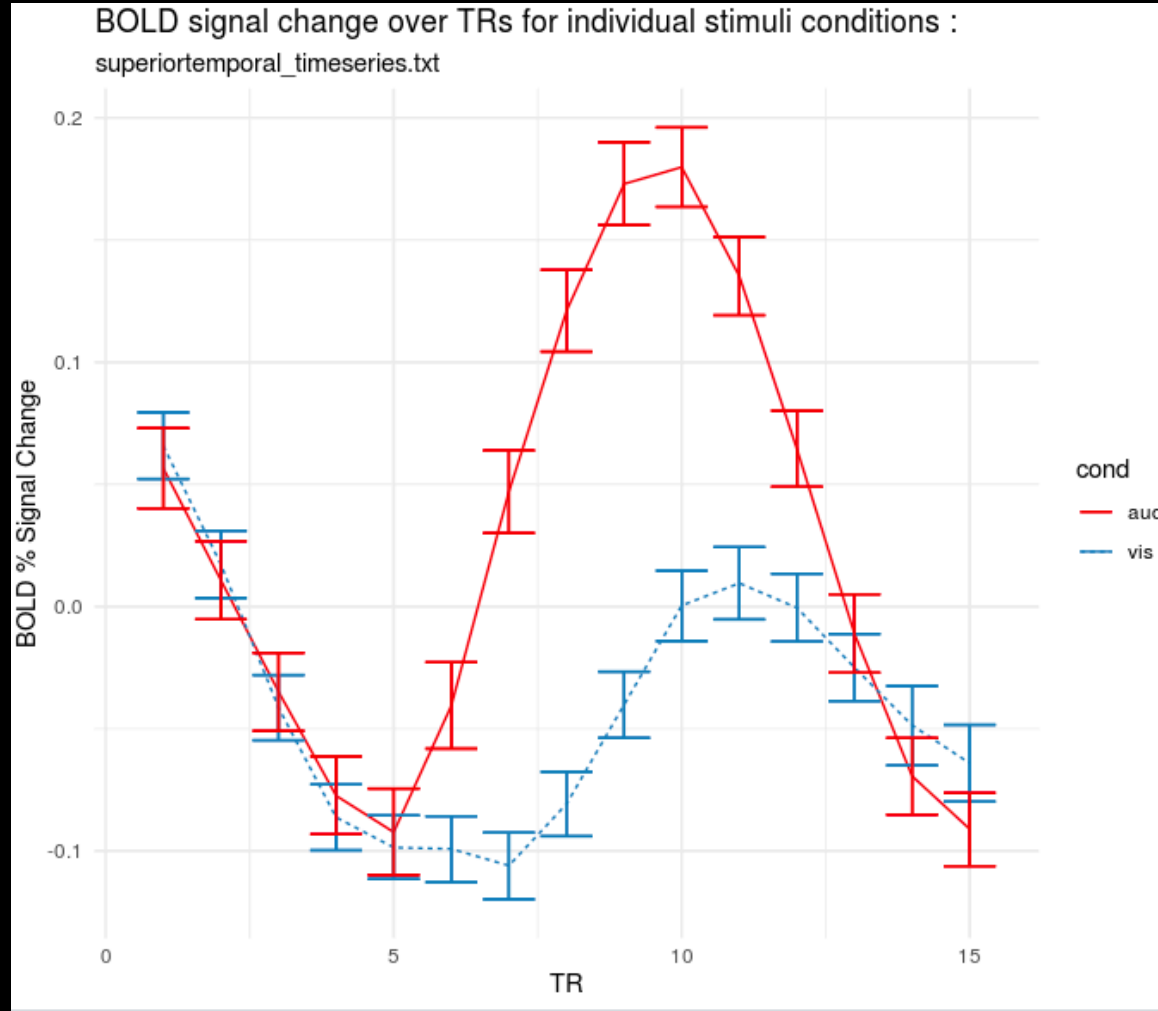
e.g.: 20s window, 10 timepoints



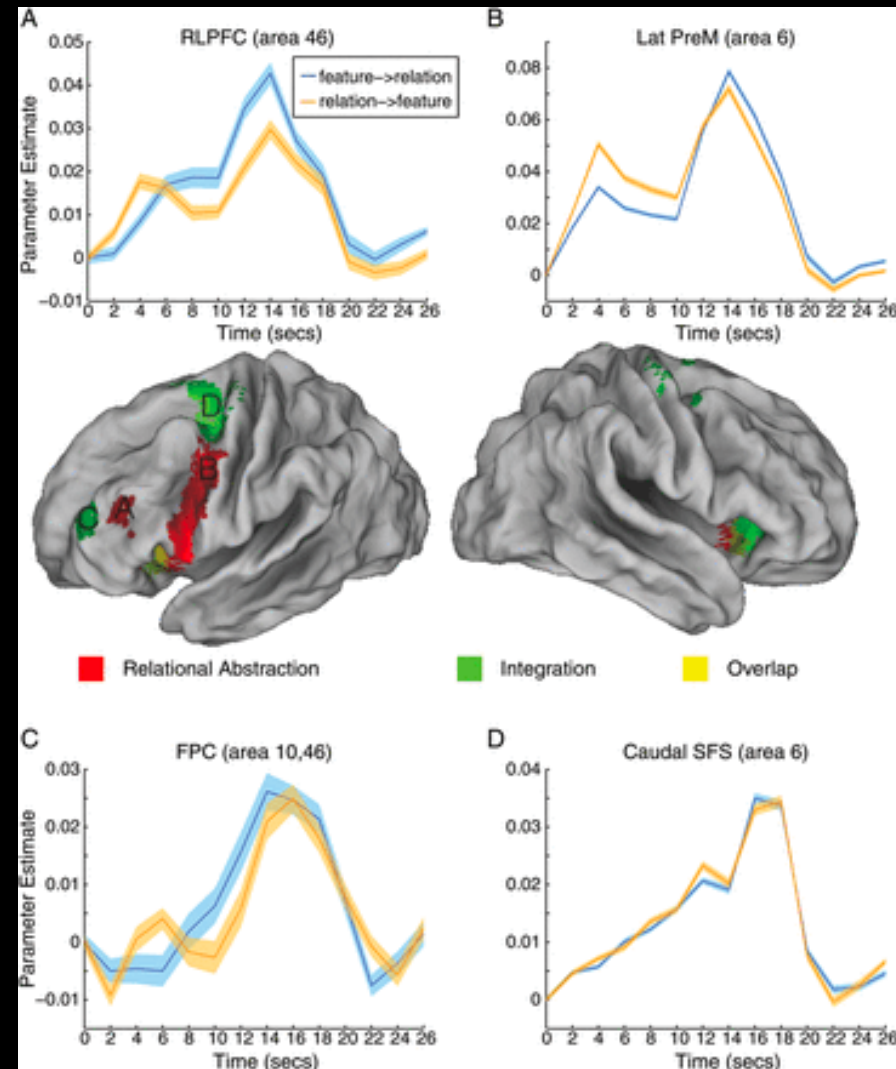
Finite Impulse Response (FIR)



Finite Impulse Response (FIR)



Finite Impulse Response (FIR)



Demonstration of FIR Modeling Setup

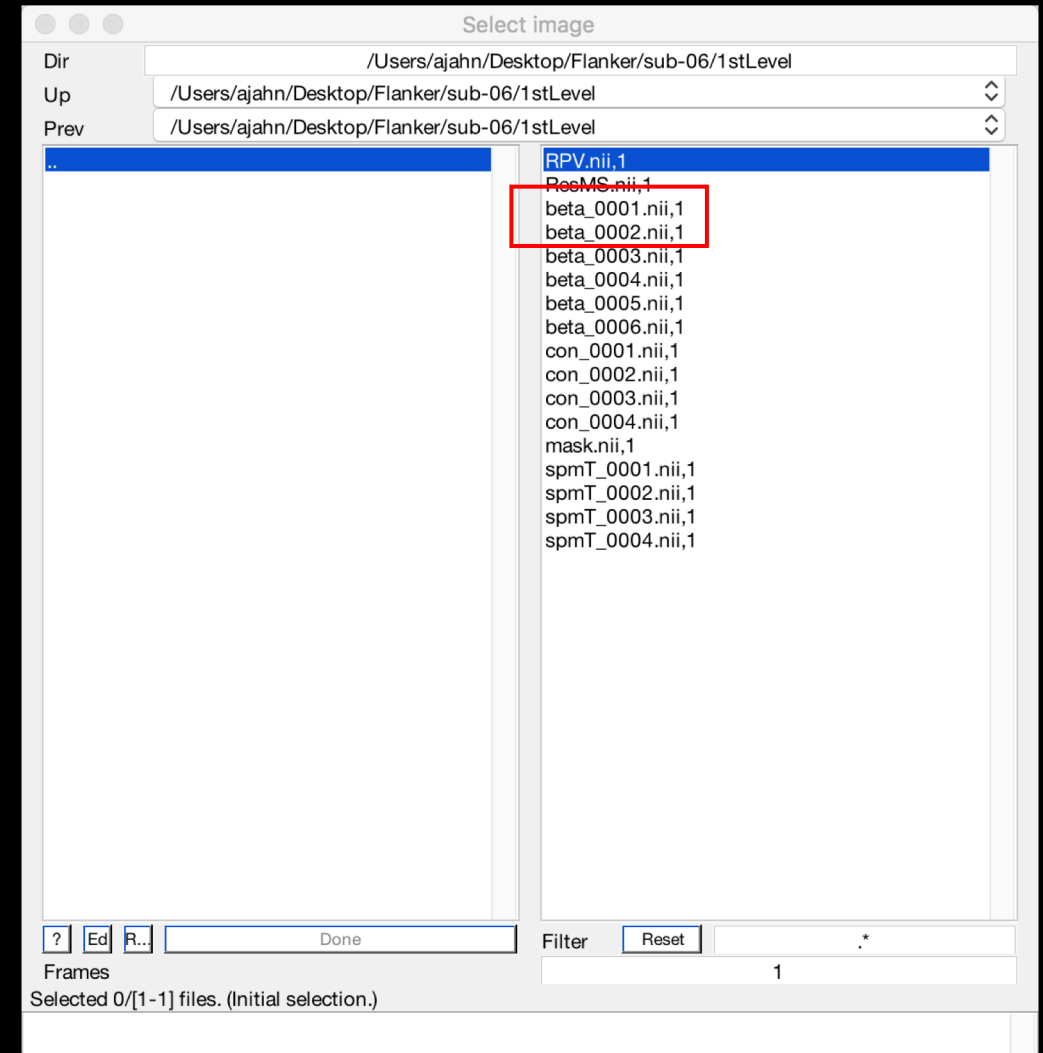
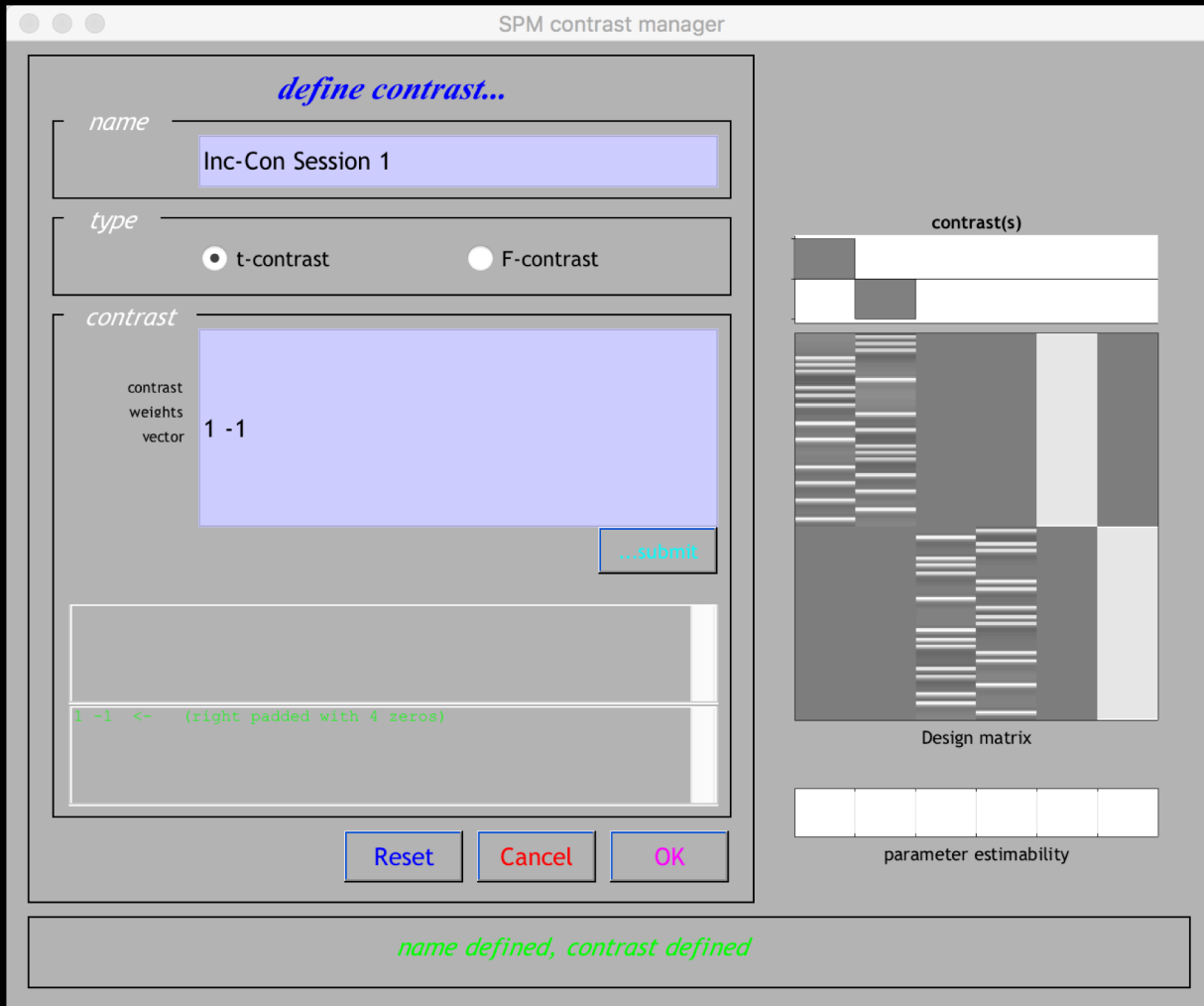
ImCalc: The Image Calculator

One of the most versatile tools is the image calculator

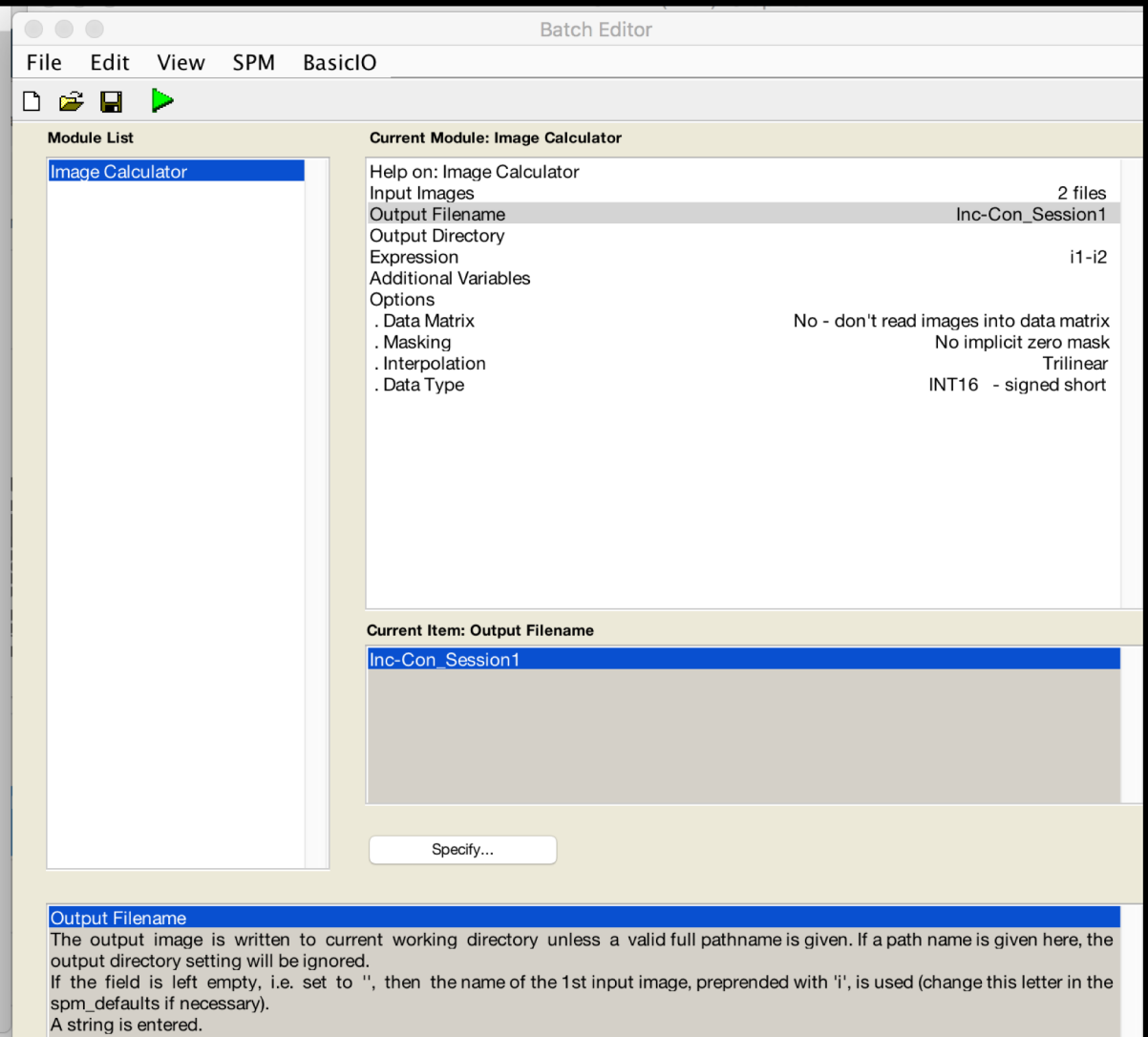
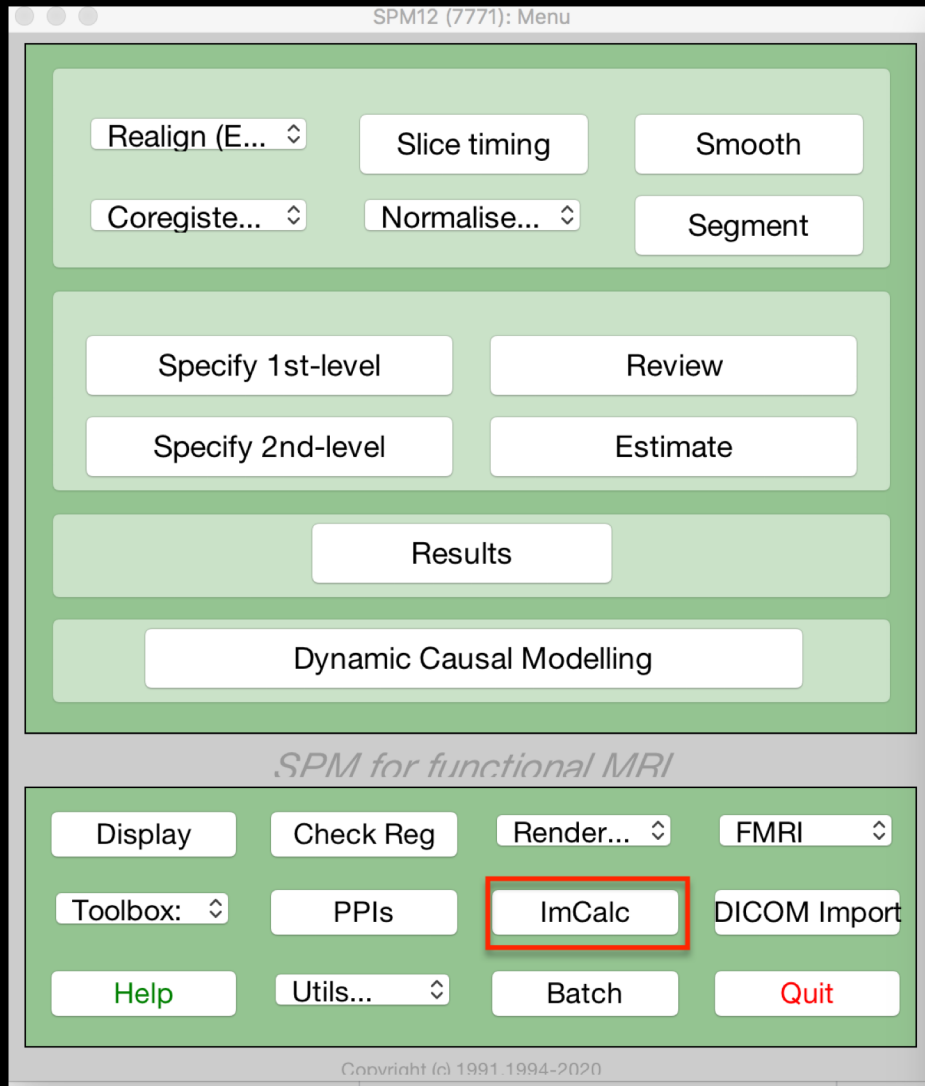
Every package has one (AFNI, FSL, MRtrix, etc.)

Simple to do basic arithmetic on a 3D image

ImCalc: The Image Calculator



ImCalc: The Image Calculator



ImCalc: The Image Calculator

SPM12 (7771): Graphics
File Edit View Insert Tools Desktop Window SPM Figure Help

mm: 0.0 30.0 30.0
vx: 27.0 48.3 34.3
Intensity: 0.000696186

File: **./1stLevel/beta_0001.nii**
Dimensions: 53 x 63 x 52
Datatype: float32
Intensity: Y = 1 X
spm_spm:beta (0001) - Sn(1) Inc*bf(1)

Vox size: -3 x 3 x 3
Origin: 27 38.3 24.3
Dir Cos: 1.000 0.000 0.000
0.000 1.000 0.000
0.000 0.000 1.000

Full Volume Hide Crosshair
World Space Trilinear interp.
Auto Window Add Overlay...

right {mm}	0
forward {mm}	0
up {mm}	0
pitch {rad}	0
roll {rad}	0
yaw {rad}	0
resize {x}	1
resize {y}	1
resize {z}	1

Set Origin Reorient...

SPM12 (7771): Graphics
File Edit View Insert Tools Desktop Window SPM Figure Help

mm: 0.0 30.0 30.0
vx: 27.0 48.3 34.3
Intensity: -0.37464

File: **./1stLevel/beta_0002.nii**
Dimensions: 53 x 63 x 52
Datatype: float32
Intensity: Y = 1 X
spm_spm:beta (0002) - Sn(1) Con*bf(1)

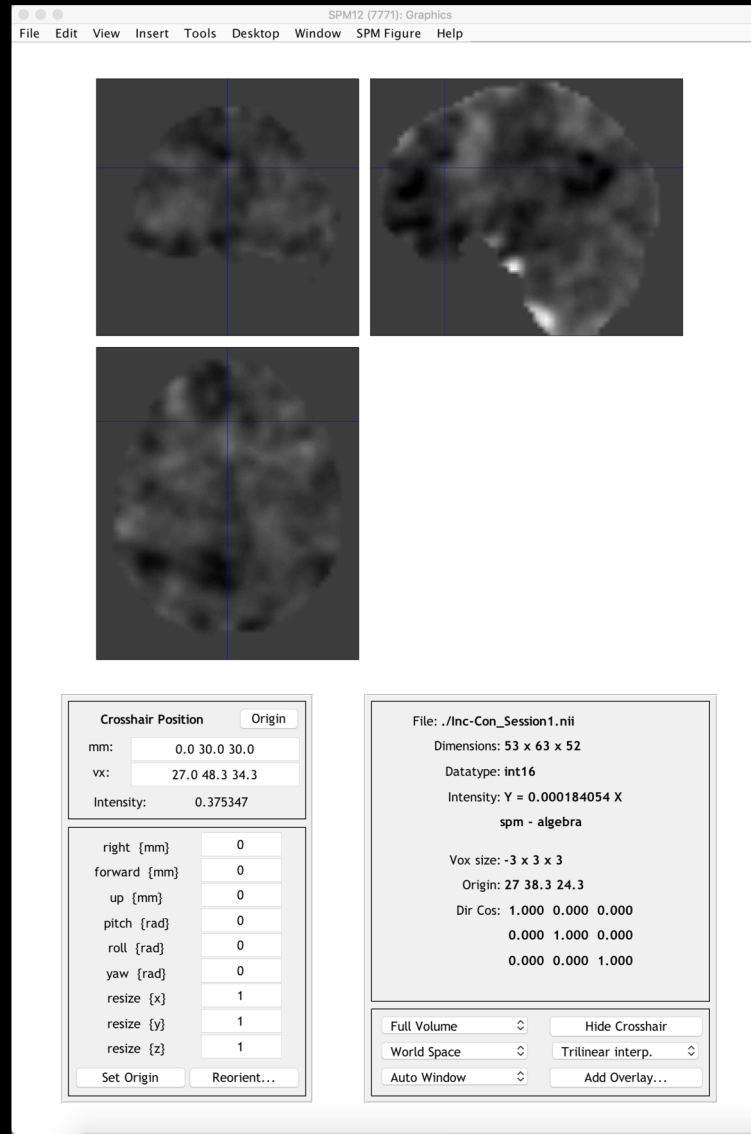
Vox size: -3 x 3 x 3
Origin: 27 38.3 24.3
Dir Cos: 1.000 0.000 0.000
0.000 1.000 0.000
0.000 0.000 1.000

Full Volume Hide Crosshair
World Space Trilinear interp.
Auto Window Add Overlay...

right {mm}	0
forward {mm}	0
up {mm}	0
pitch {rad}	0
roll {rad}	0
yaw {rad}	0
resize {x}	1
resize {y}	1
resize {z}	1

Set Origin Reorient...





ImCalc: The Image Calculator



Demonstration

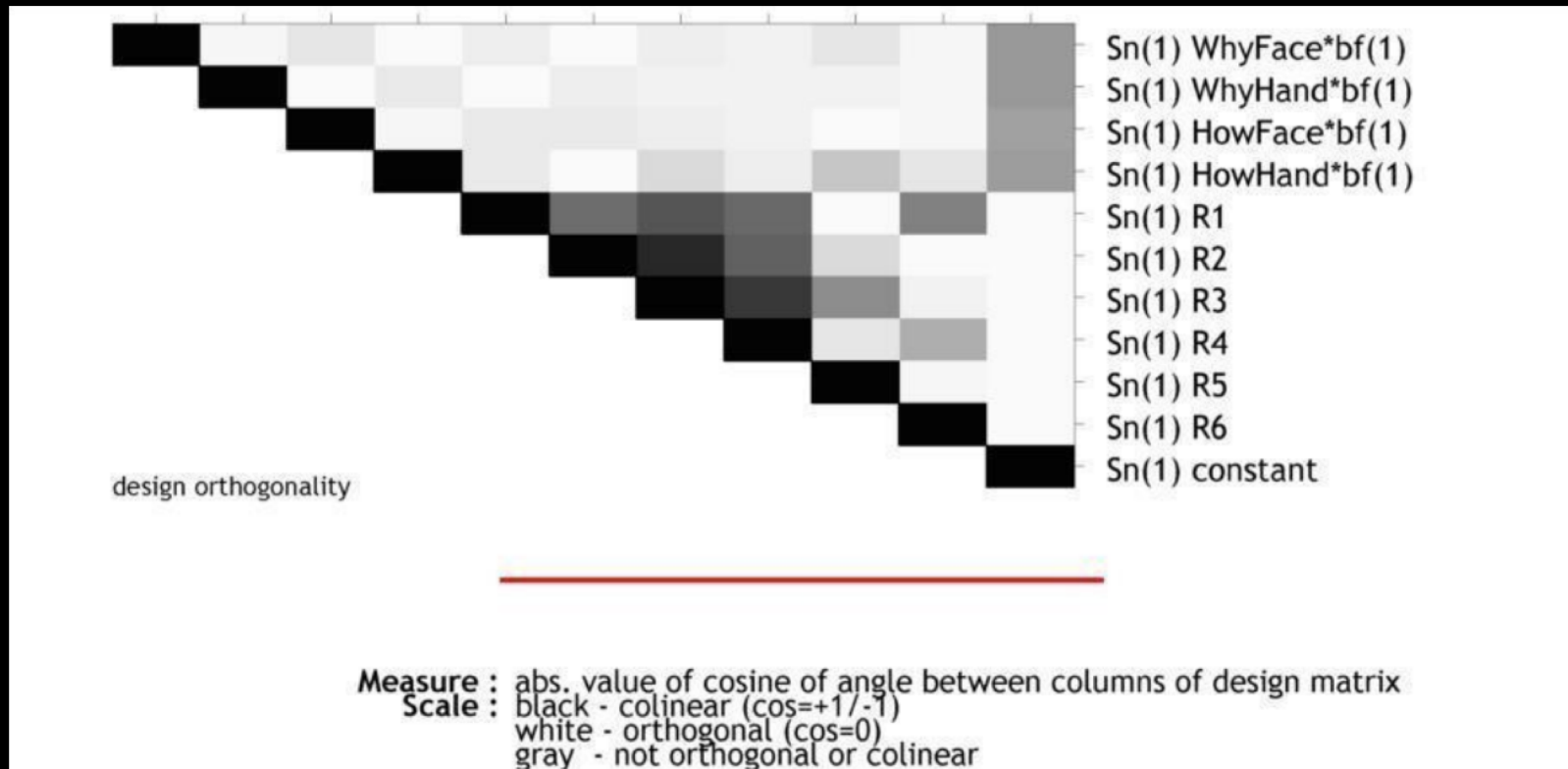
Preview of Today's Lab

Dataset collected by Emily Falk; 2x2 factorial design

		QUESTION	
		Why	How
STIMULUS	Face	<p>Is the person expressing self-doubt?</p> 	<p>Is the person looking to their side?</p> 
	Hand	<p>Is the person helping someone?</p> 	<p>Is the person using both hands?</p> 

Preview of Today's Lab

Block design



Preview of Today's Lab

Current module: Mini-model specification

```
.... Name                                     HowFace
.... Onsets                                  ...284 135.0593544 171.3800147 243.0883199]
.... Durations                               ...4532 10.7859291 8.894711134 9.210554915]
.... Time Modulation                         No Time Modulation
.... Parametric Modulations
.... Orthogonalise modulations               Yes
... Condition
.... Name                                     HowHand
.... Onsets                                  ...6296 80.6916593 189.4403629 264.5608179]
.... Durations                               ...313 10.45648544 9.137848595 10.19211621]
.... Time Modulation                         No Time Modulation
.... Parametric Modulations
.... Orthogonalise modulations               Yes
.. Multiple conditions
.. Regressors
.. Multiple regressors                       ...eLab/sub05/func/whyhow/run_01/rp_run_01.txt
.. High-pass filter                          128
Factorial design
Basis Functions
. Canonical HRF
.. Model derivatives                          No derivatives
Model Interactions (Volterra)                Do not model Interactions
Global normalisation                          None
Masking threshold                            0.8
Explicit mask
Serial correlations                           AR(1)
```

Current Item: Directory

Questions?