

# fMRI 2: single participant GLM

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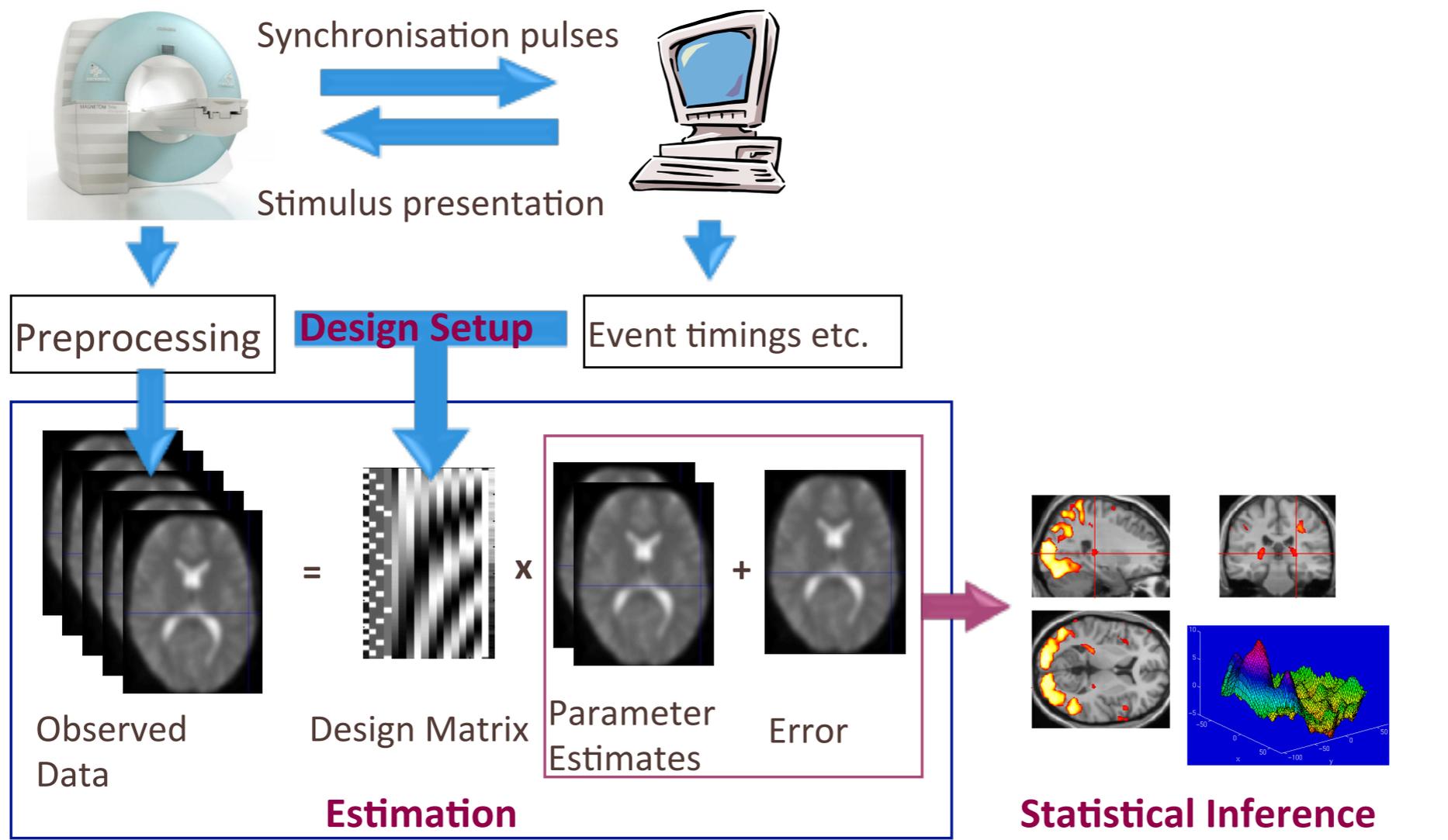
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Acknowledgment: Tibor Auer, Kendrick Kay



# Today

- How to fit fMRI responses with a general linear model
- Workshop: Building an fMRI model by hand in Matlab
- Implications for experimental design

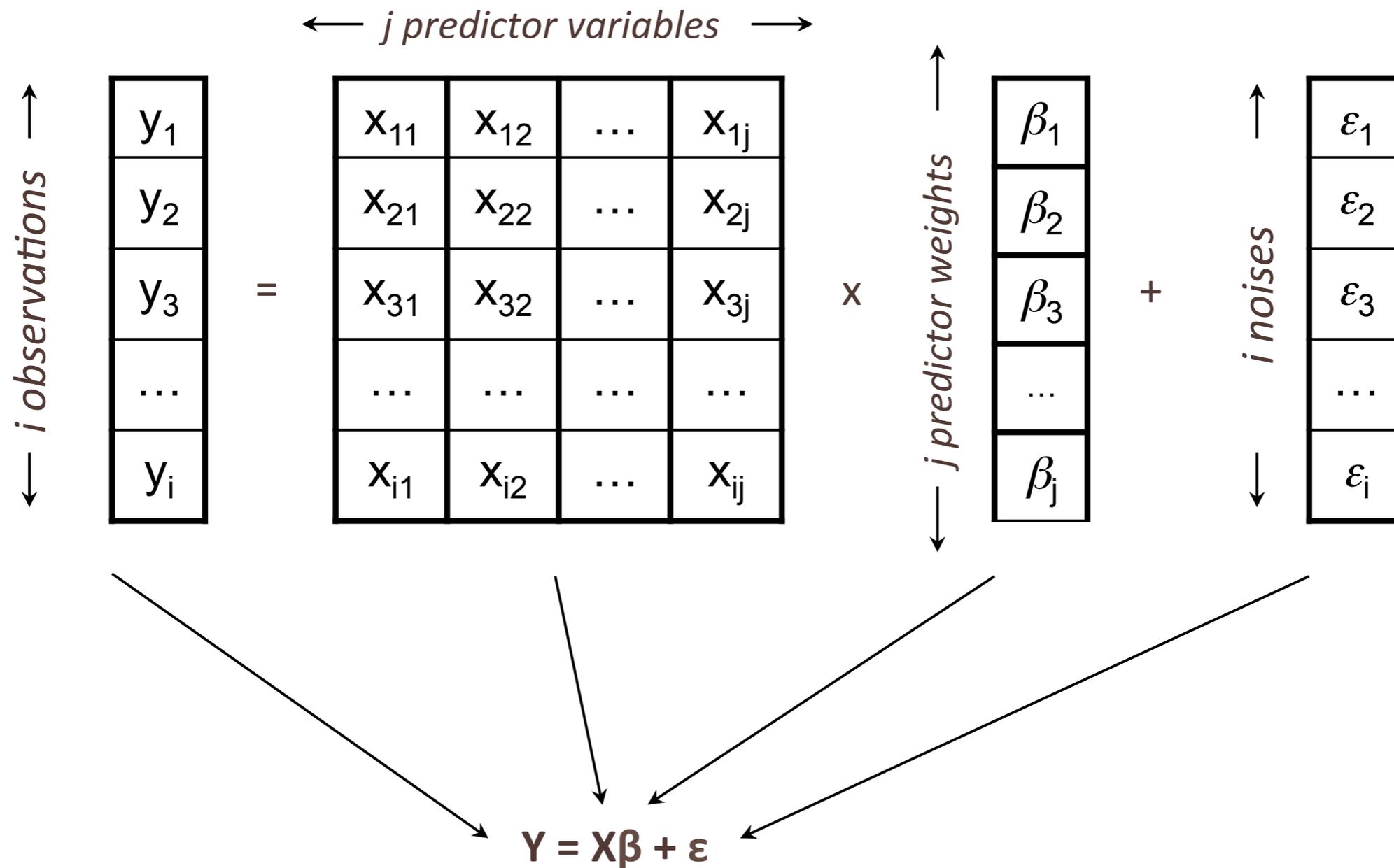


last session

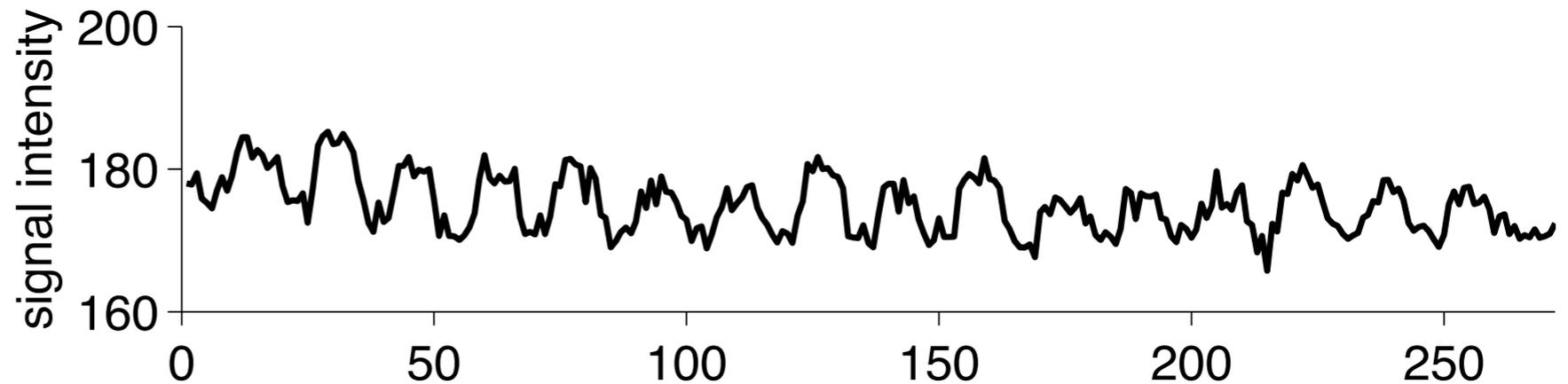
today

next session

# The general linear model



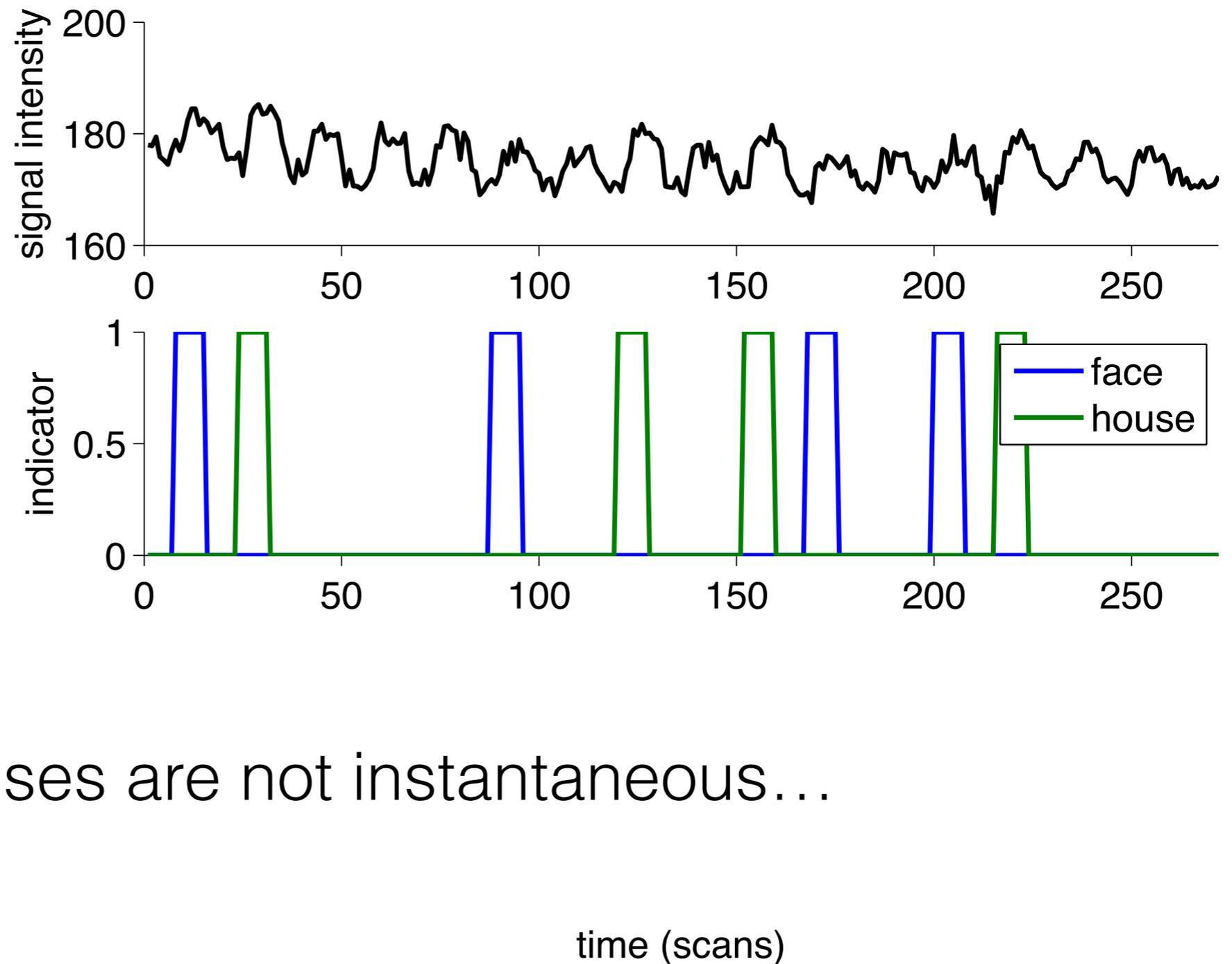
# A typical fMRI task



- Face blocks appeared at volumes 8, 88, 168, 200
- House blocks at volumes 24, 120, 152, 216
- All blocks lasted 8 volumes

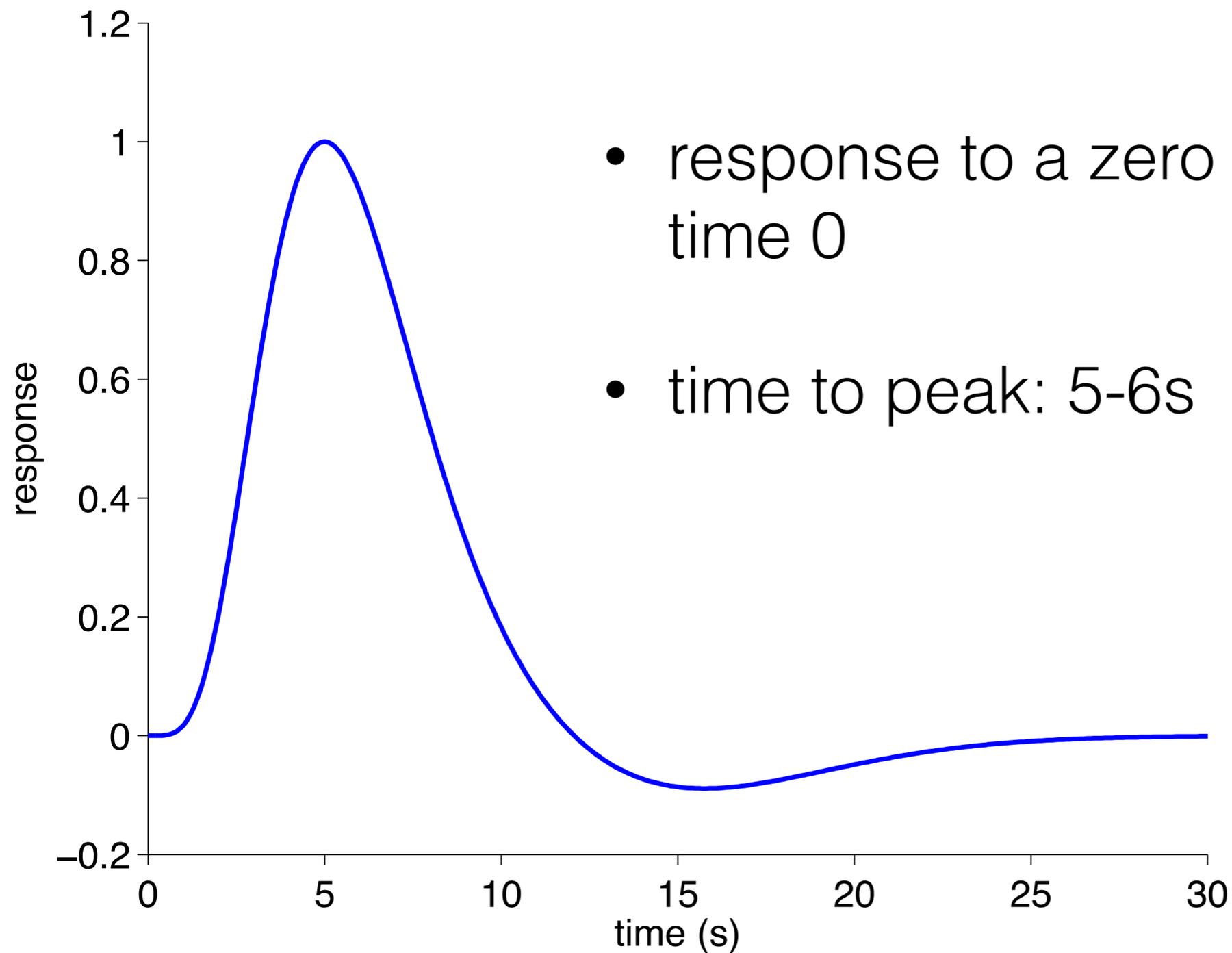
time (scans)

# A typical fMRI task

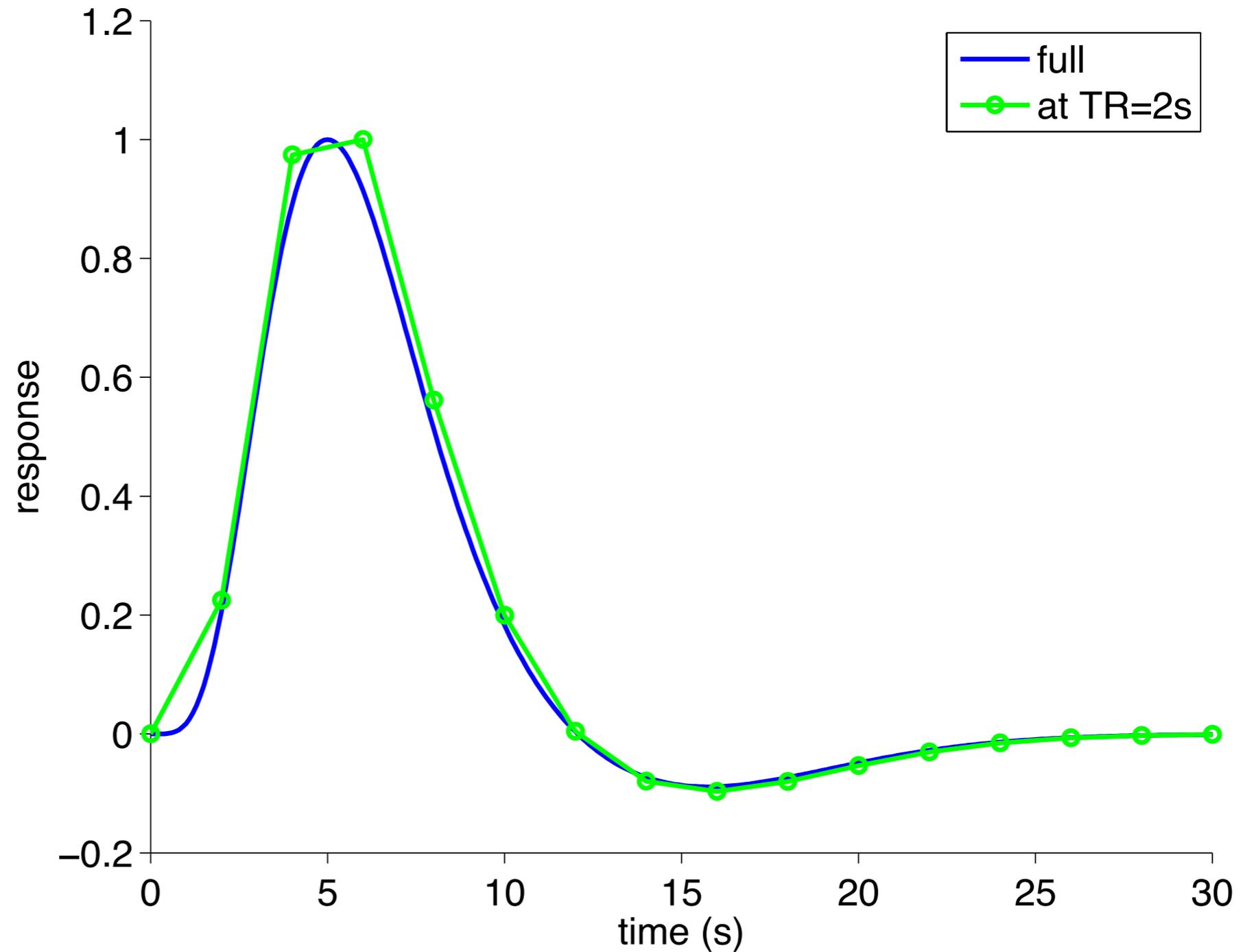


But fMRI responses are not instantaneous...

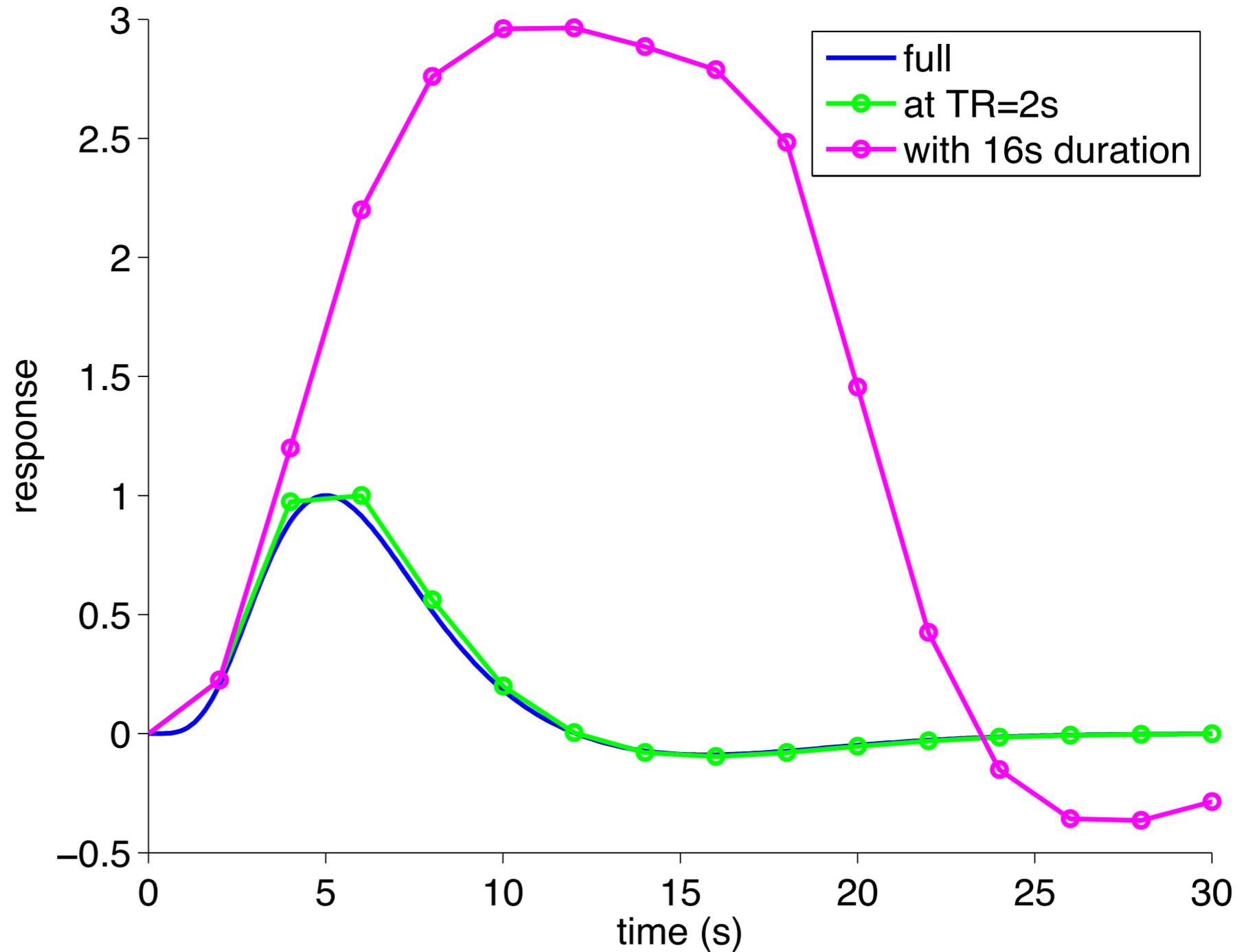
# The canonical SPM HRF



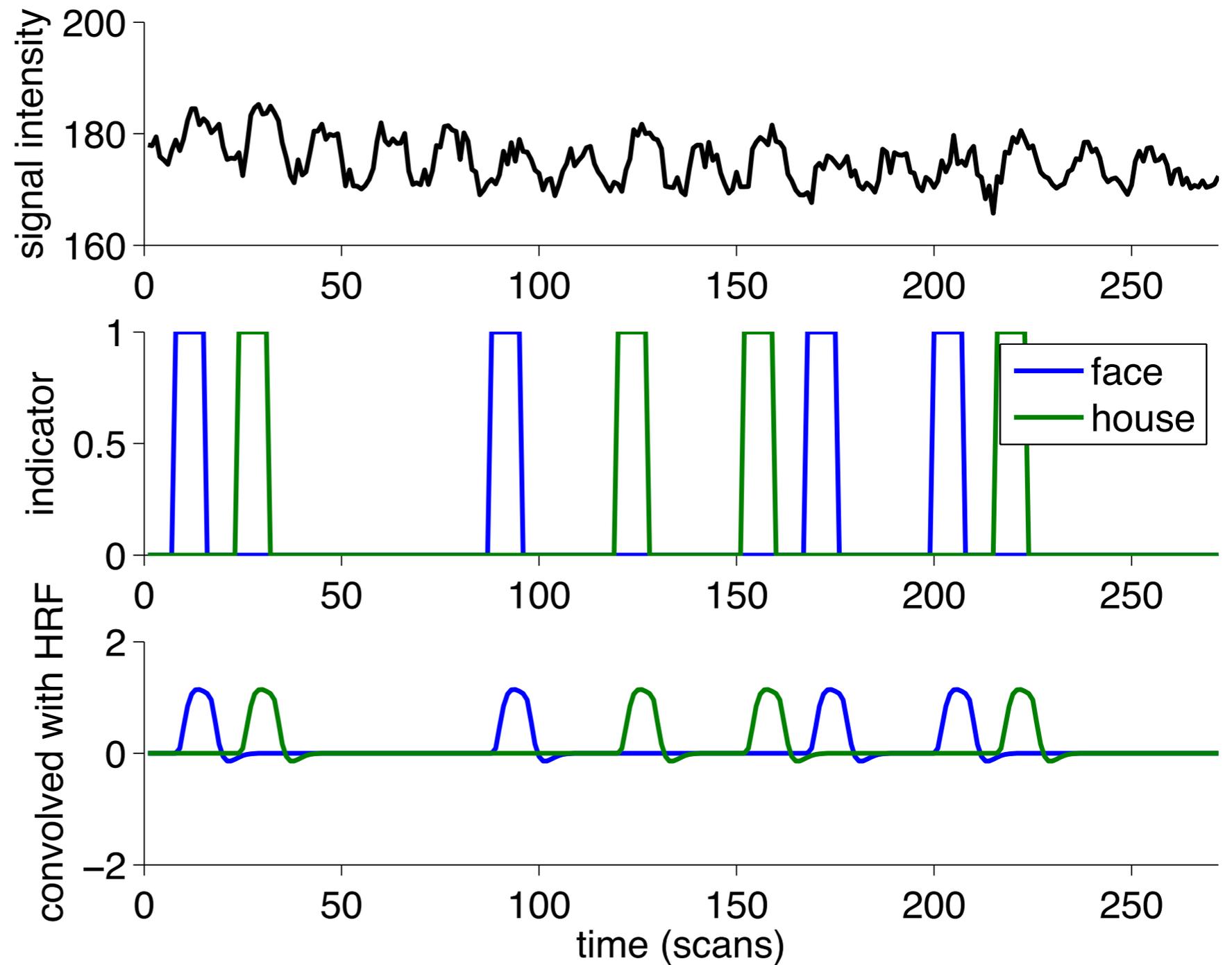
# The canonical SPM HRF



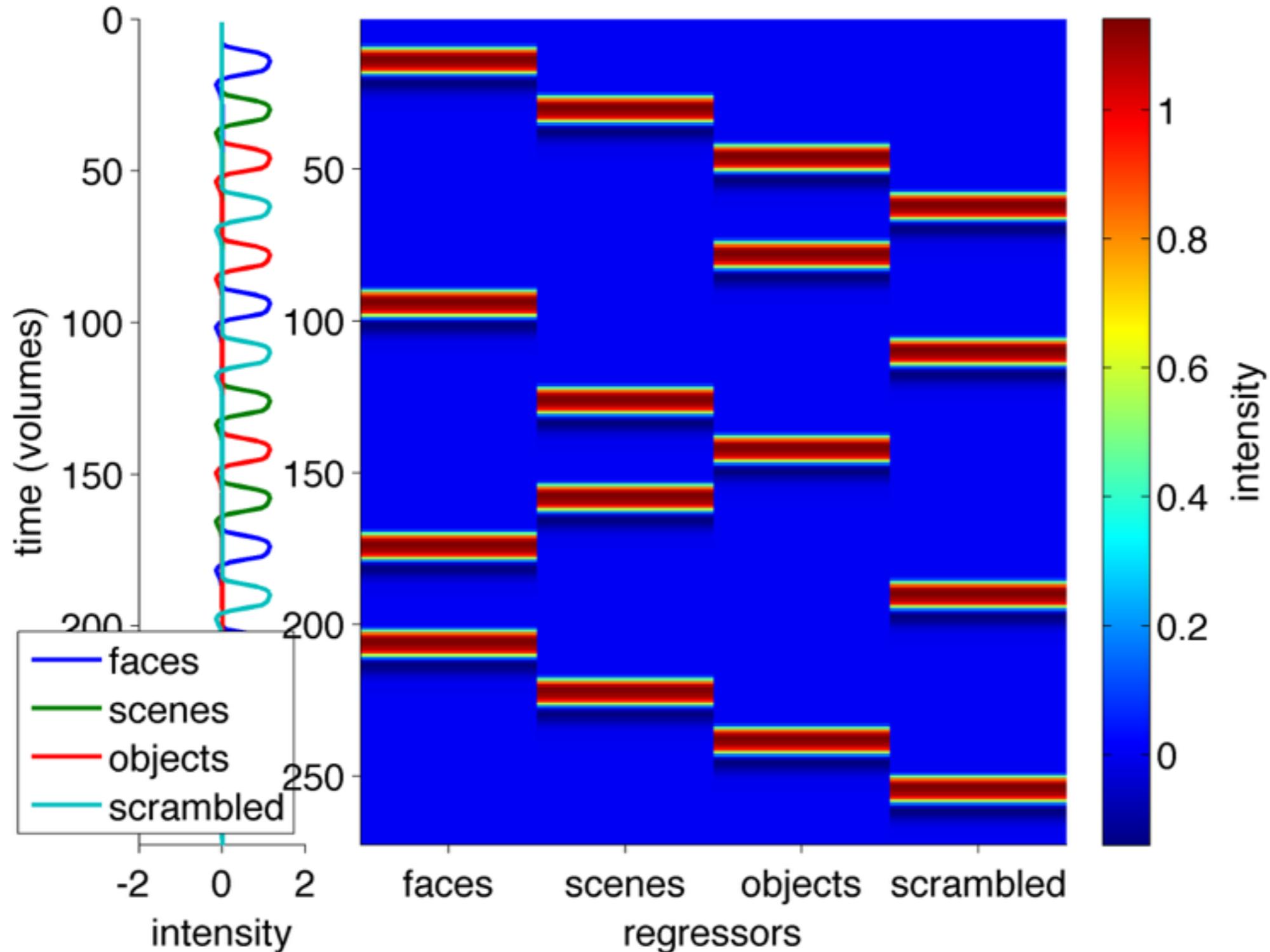
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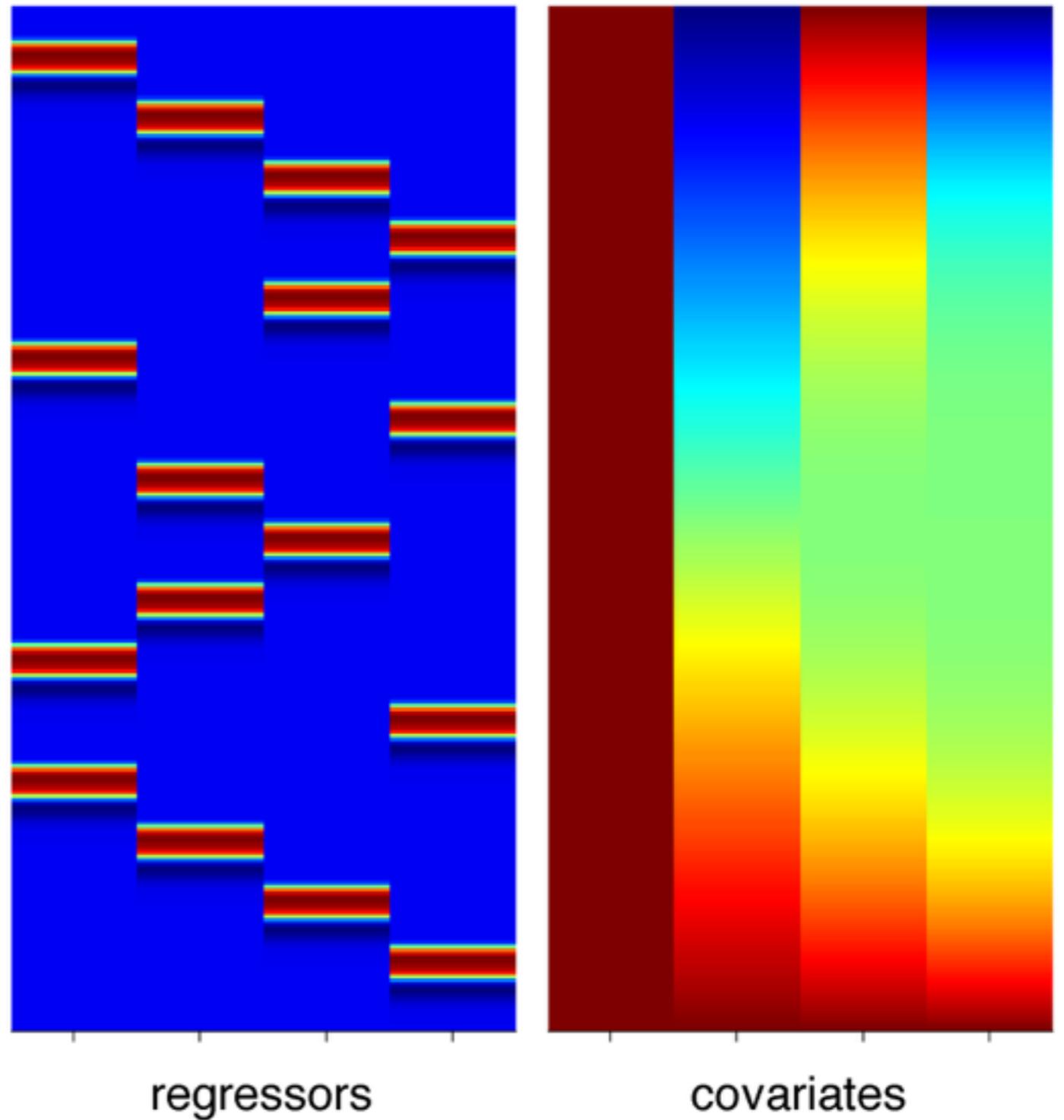
# A typical fMRI task



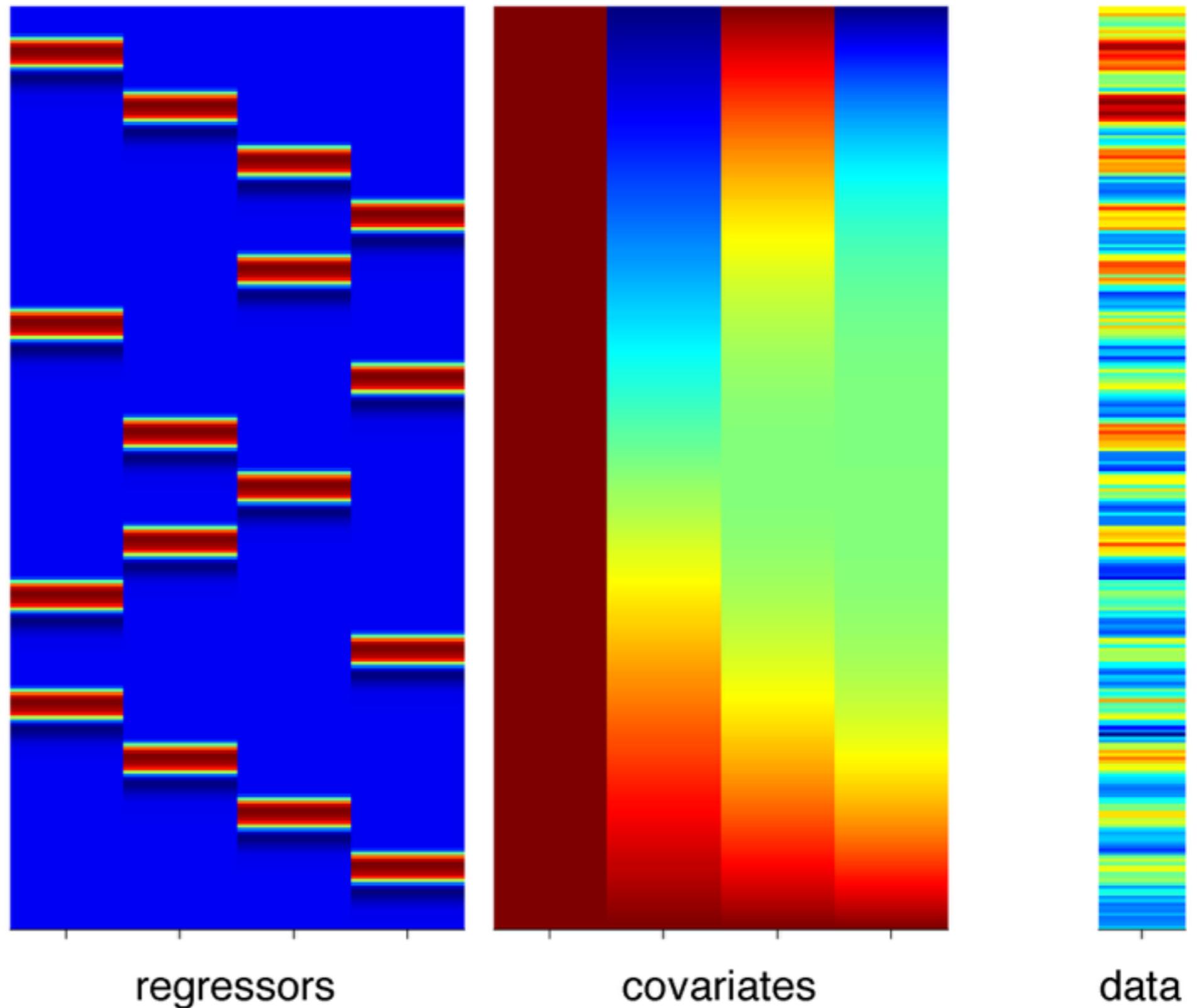
# The convolved design matrix

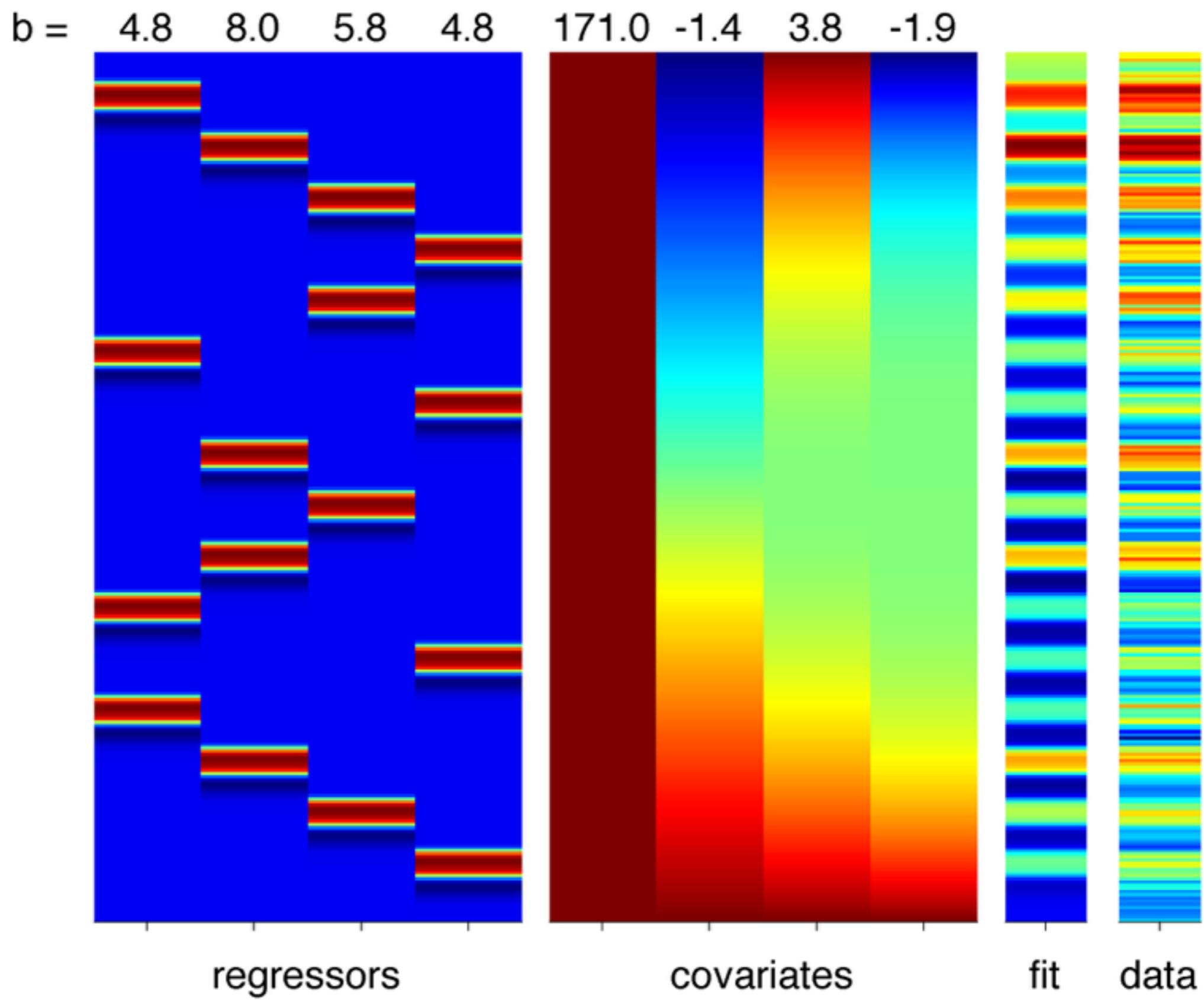


# Trend removal



What weights should we use to obtain a fitted timecourse that is as close as possible to the data (ie, smallest squared deviation)?

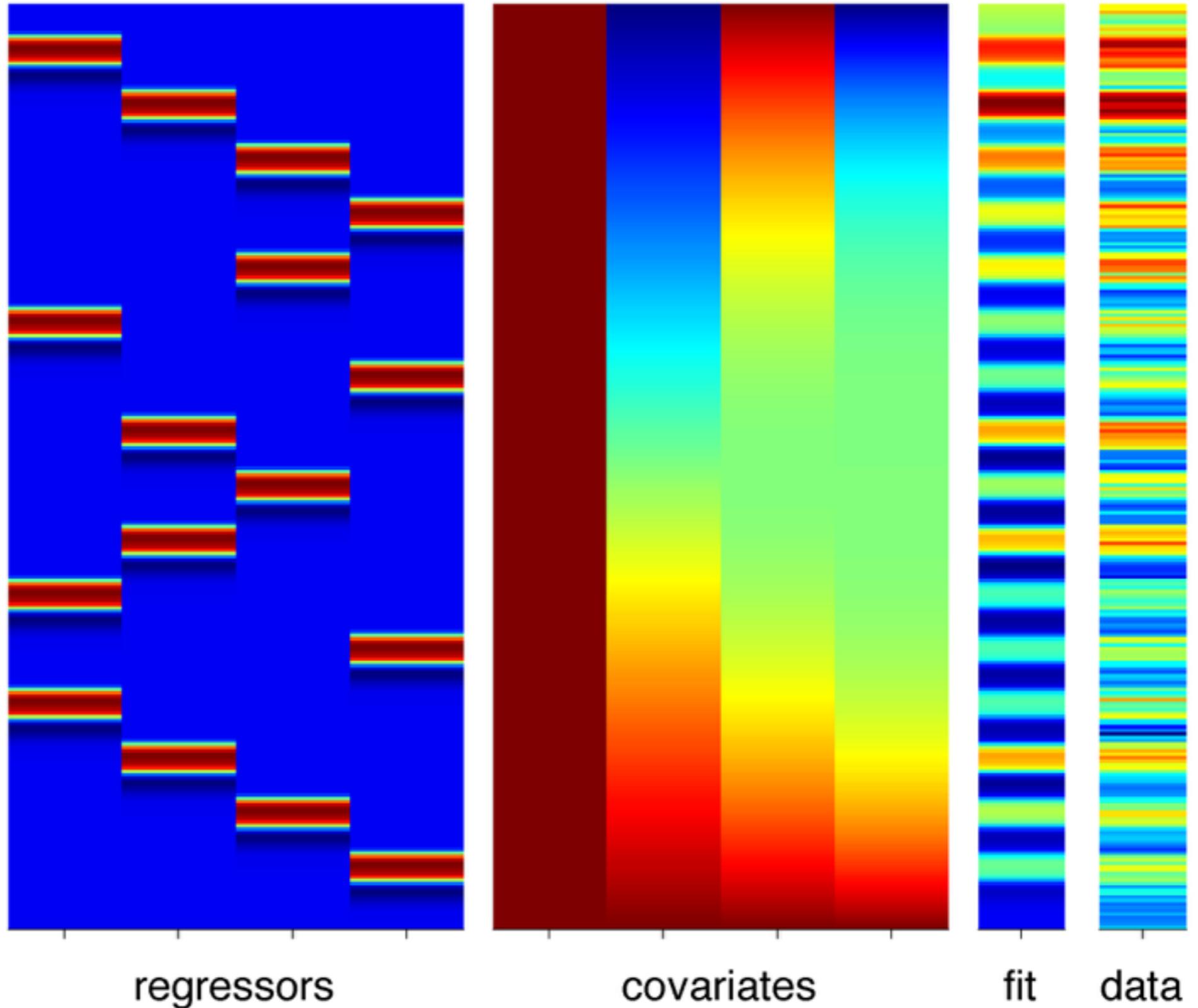




$$b * [-1 \ 1 \ 0 \ 0 \ 0 \ 0 \ 0 \ 0]' = 3.2 = 8.0 - 4.8$$

$$b * [.25 \ .25 \ .25 \ .25 \ 0 \ 0 \ 0 \ 0]' = 5.8 = \text{mean}(b_{\text{regressors}})$$

b = 4.8 8.0 5.8 4.8 171.0 -1.4 3.8 -1.9

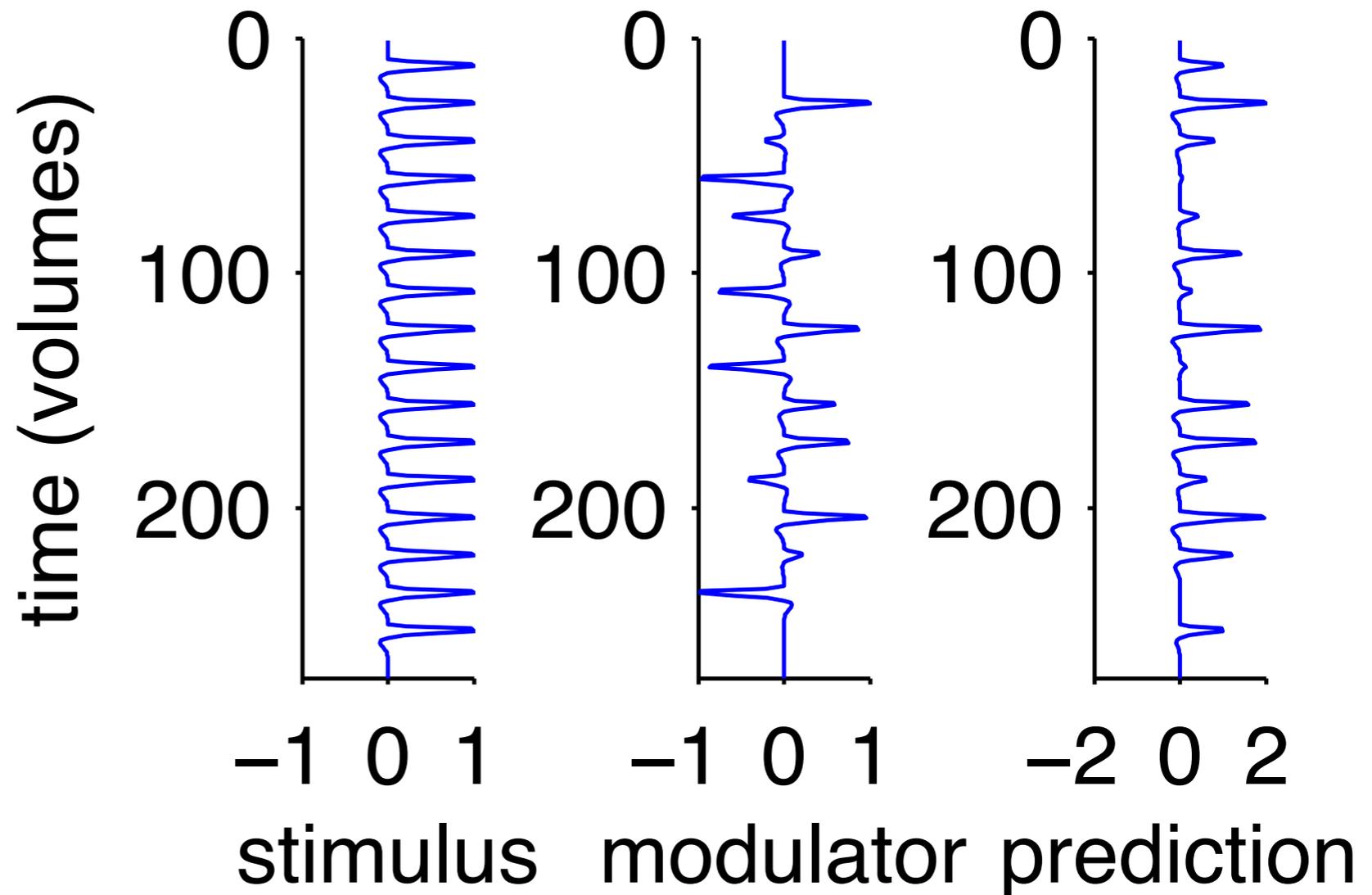


Contrast vectors are basically just a convenient way to average or subtract parameter estimates

# Serial autocorrelation

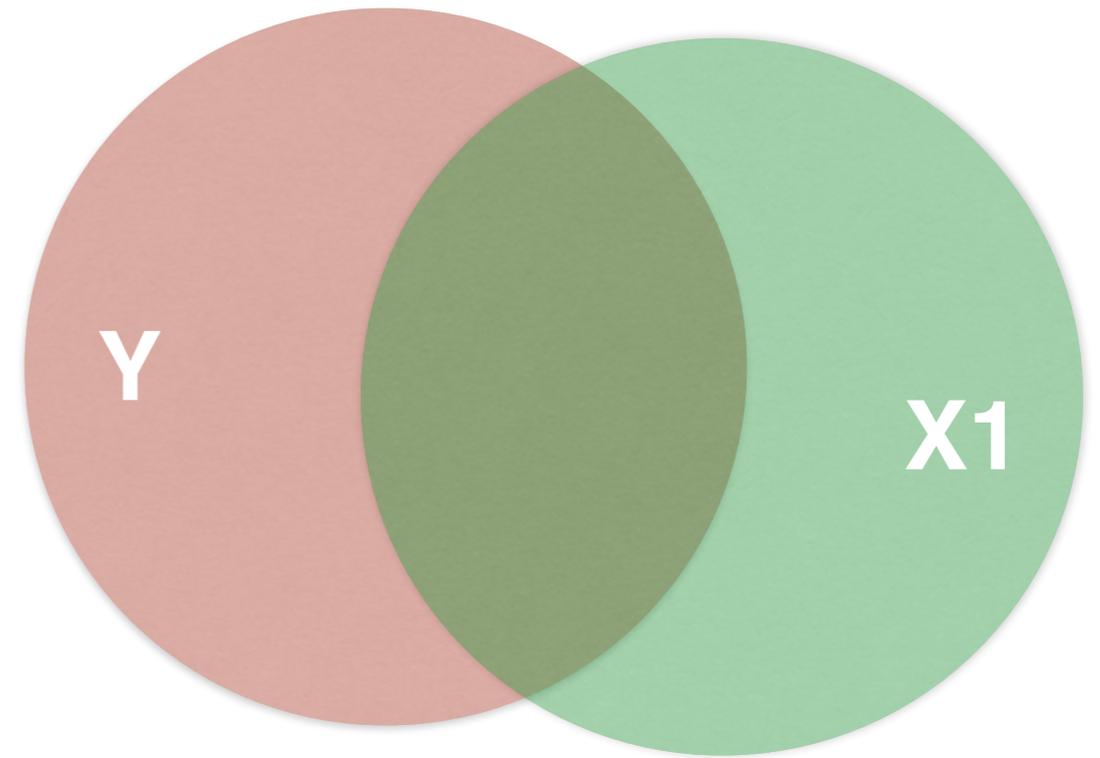
- fMRI data residuals are not independent and identically distributed (iid)
- Why not? Breathing, heartbeat cycle, unmodeled neuronal activity (remember, the BOLD response is temporally smooth)
- This invalidates the error term, which is used for parametric stats inference (T tests, standard errors etc, p values)
- SPM attempts to correct this by estimating (1st-order) autocorrelation and whitening data and design by this
- This works to some extent, but not perfectly (Eklund et al., 2012, NeuroImage) - if your analysis depends on single-participant parametric p values you may want to read this ref and consider alternative (permutation test) approaches
- But for the typical group analysis case, problems with AR modelling are not going to bias your inferences (more on this next time)

# Parametric modulators

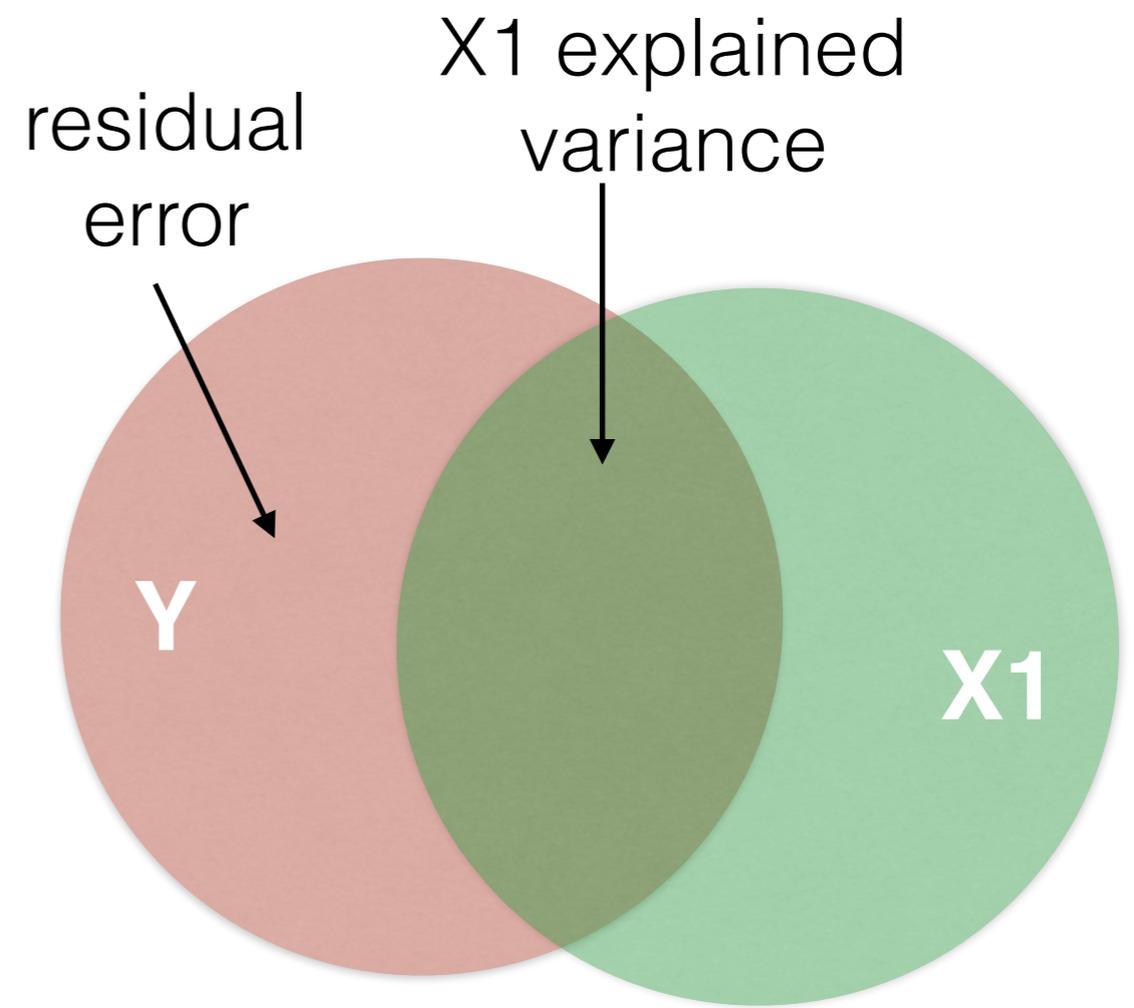


- Encode modulations of stimulus responses by continuous variables
- SPM solution is one regressor for the stimulus effect and another mean-centered regressor for each modulator on that response
- Why not just the modulator? Because we don't want to assume zero response when modulator=0
- Typical applications: Reinforcement learning (Dolan, O'Doherty), visual coding (Huth/Gallant, Kay), 'carry-over' fMRI adaptation (Aguirre), fancy grid cell stuff (Behrens)

# Orthogonalisation

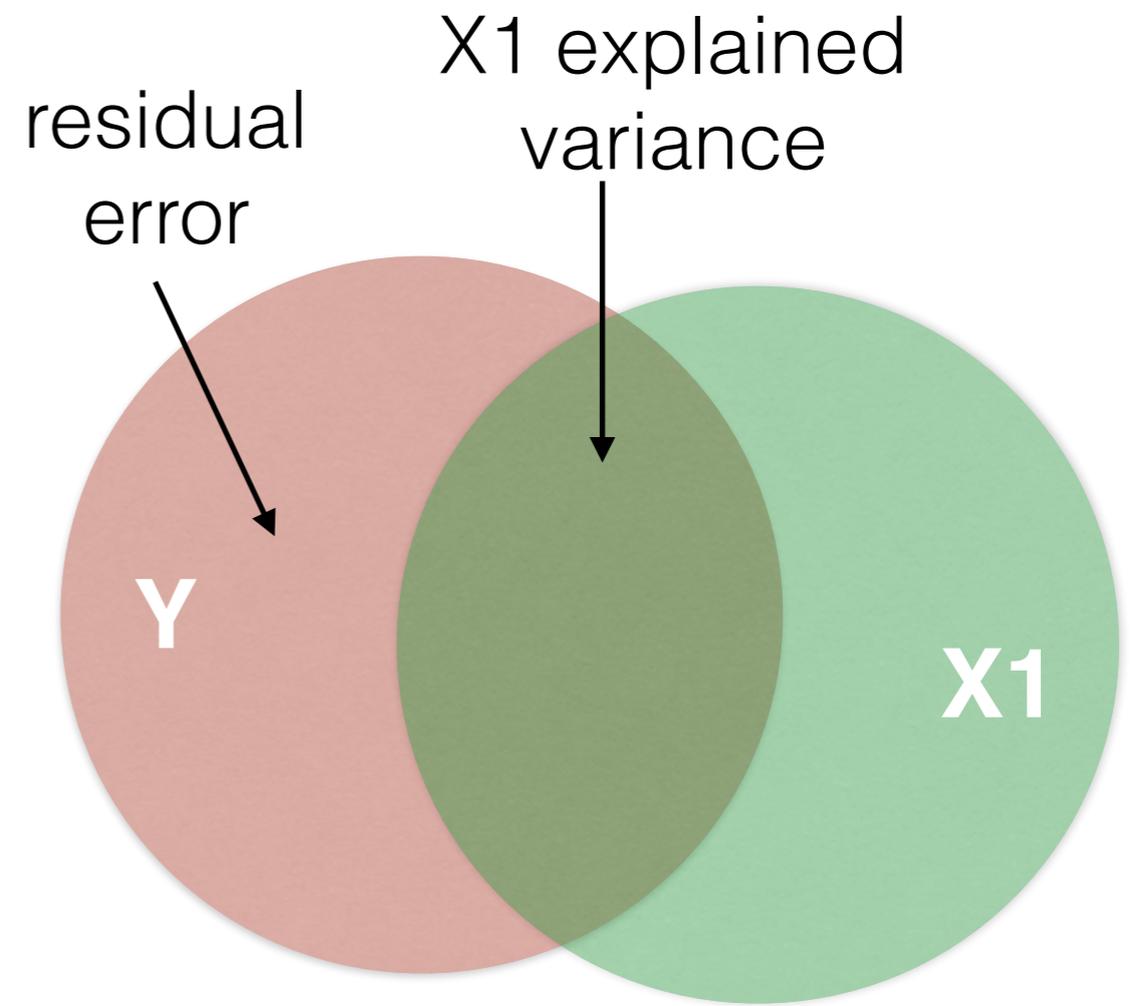


# Orthogonalisation



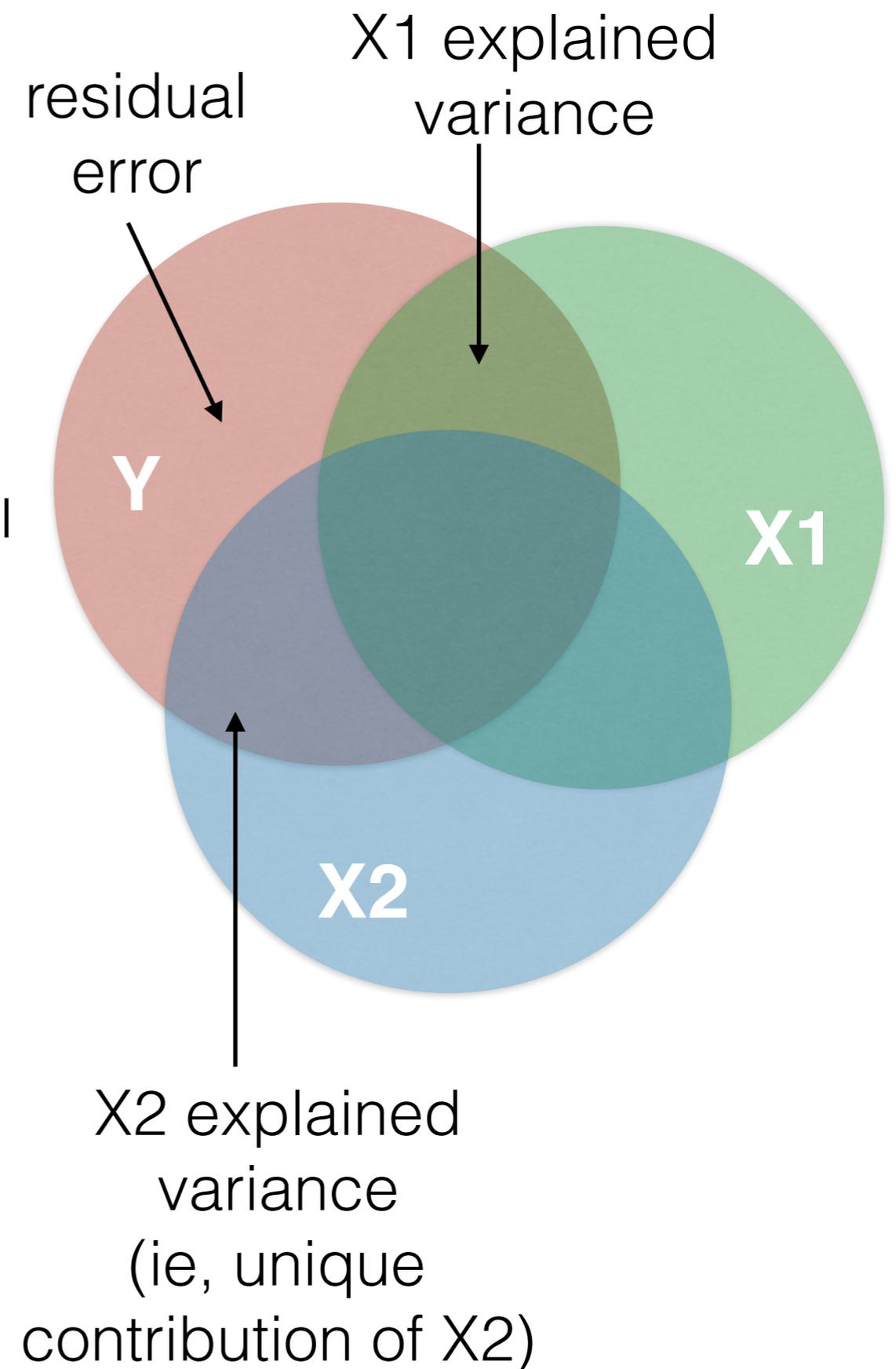
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- If we compare the models  $Y = X1$  and  $Y = X1 + X2$ , the  $\beta(X1)$  will explain more variance when it is the only predictor in the model



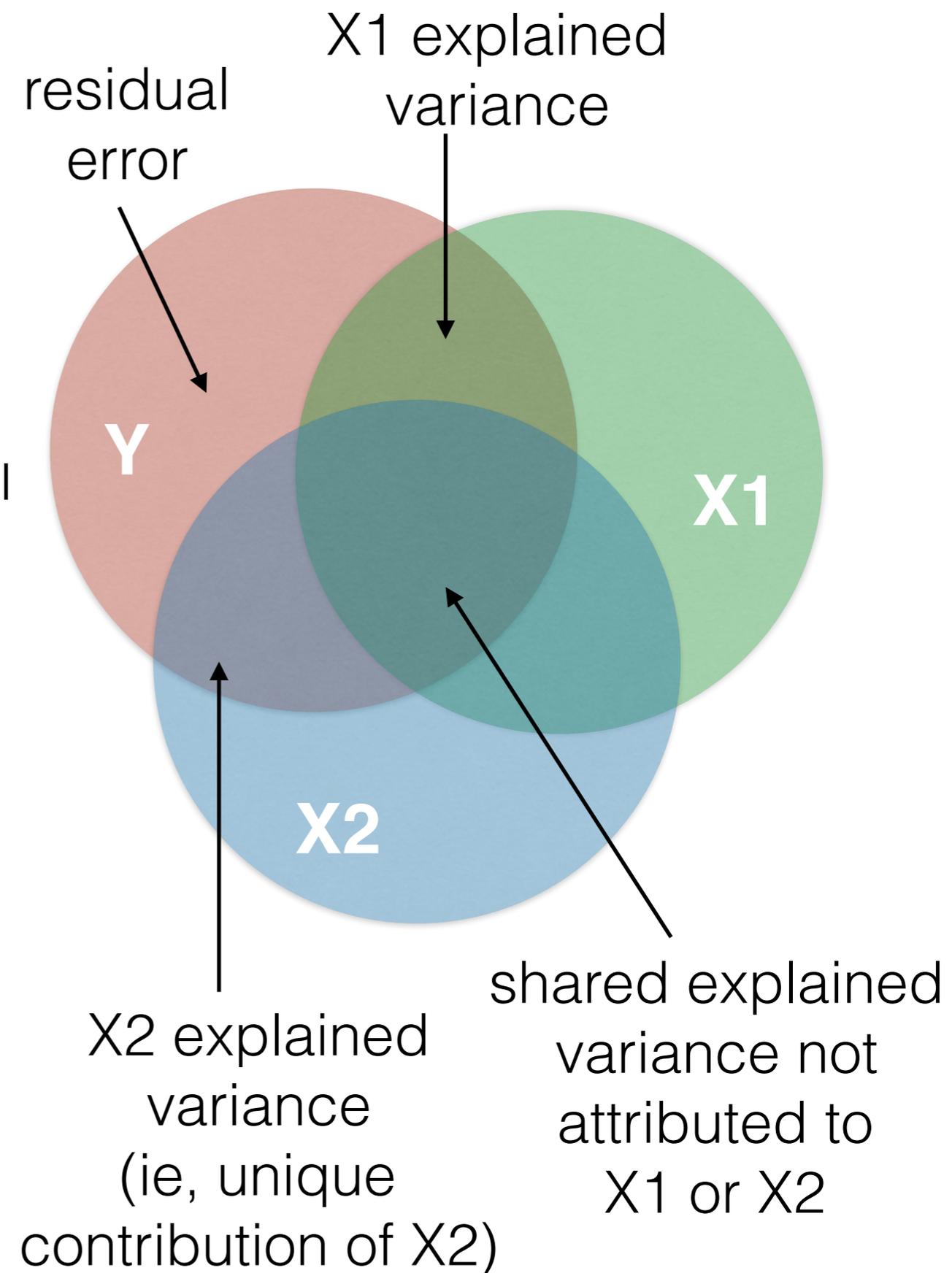
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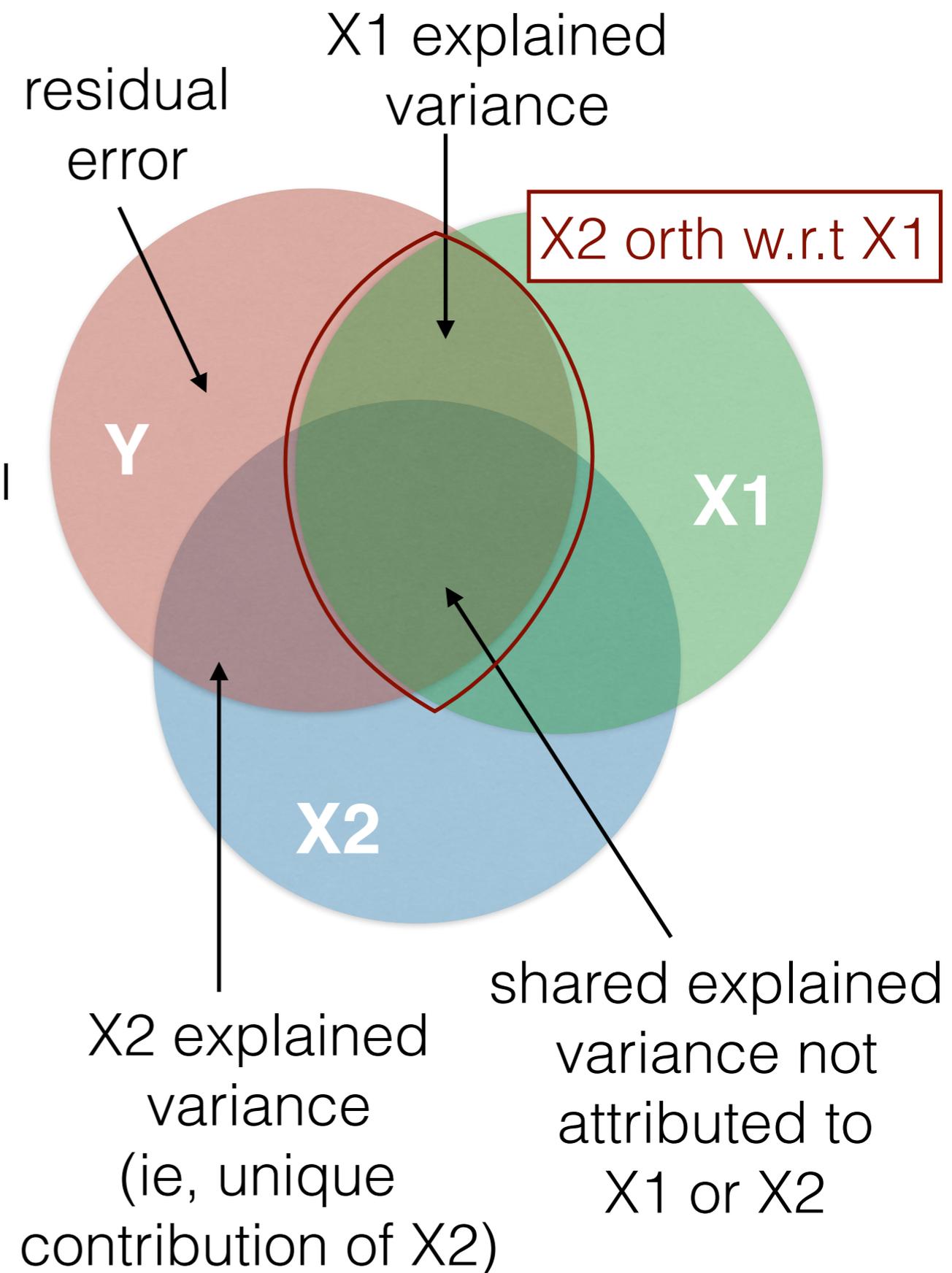
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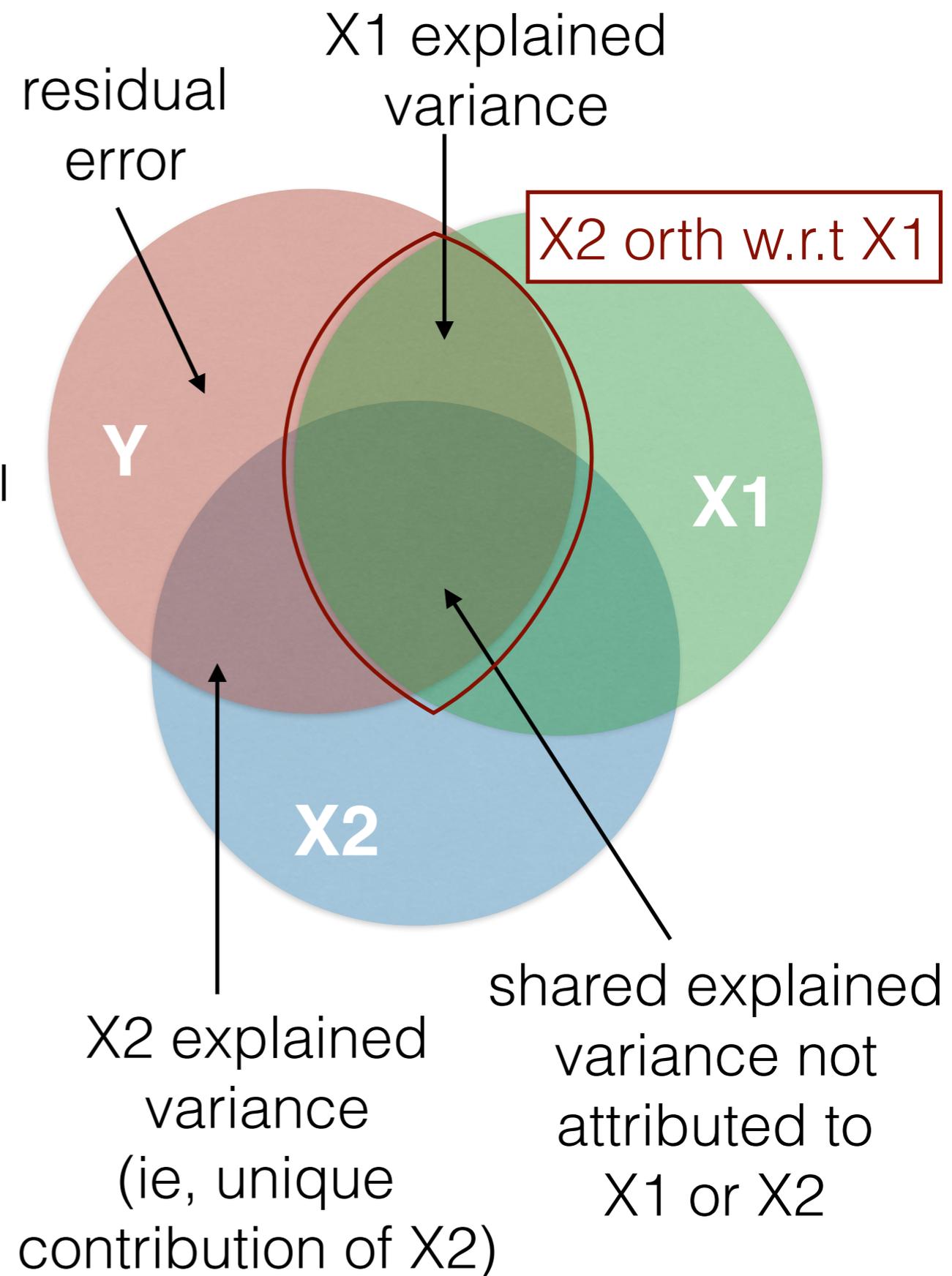
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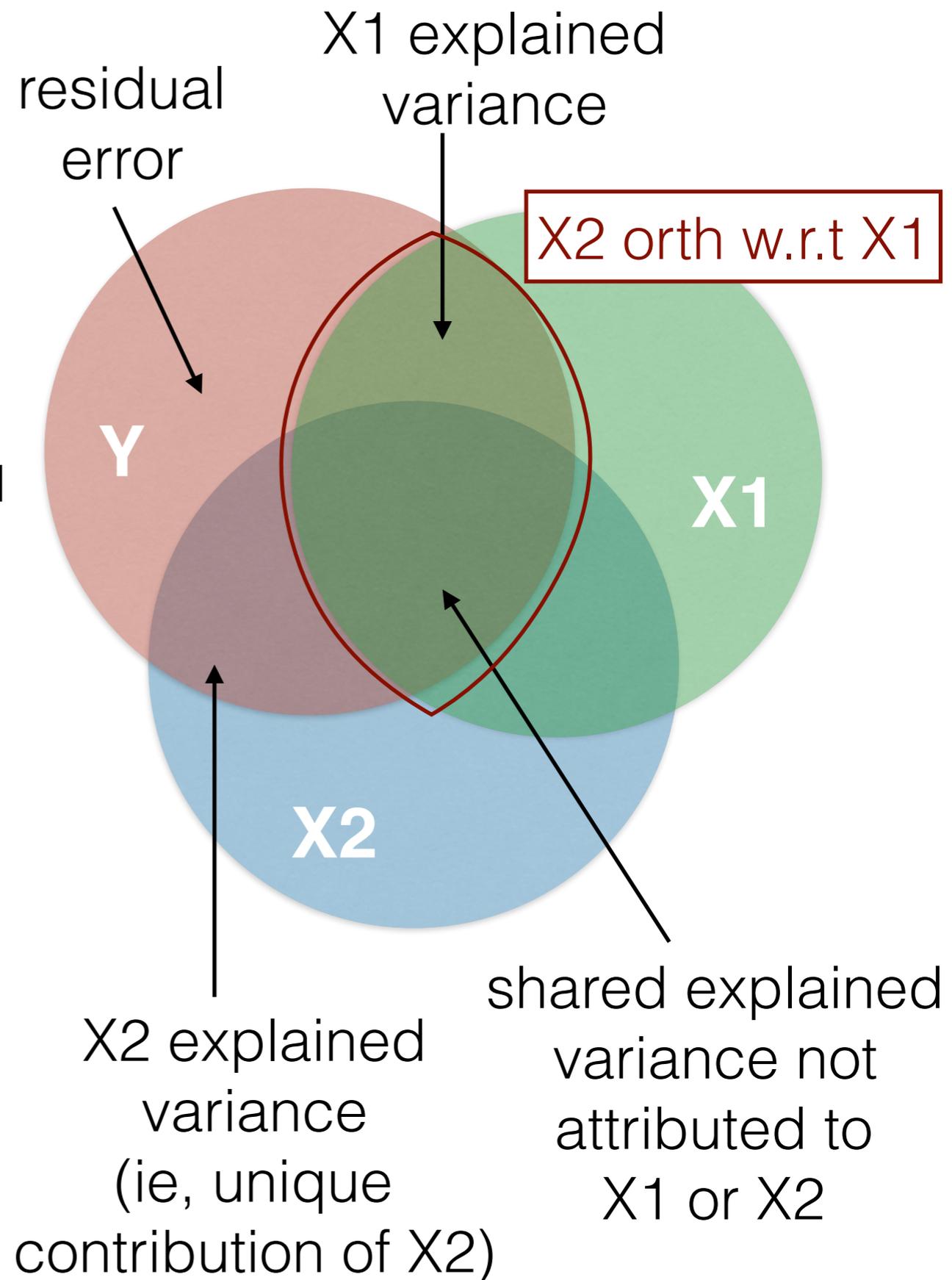
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  - The  $X2$  predictor will change - *but  $\beta(X2)$  will stay exactly the same* (counterintuitive but true!)
  - The  $X1$  predictor stays the same - *but  $\beta(X1)$  will change*, because all the shared variance now goes to  $X1$



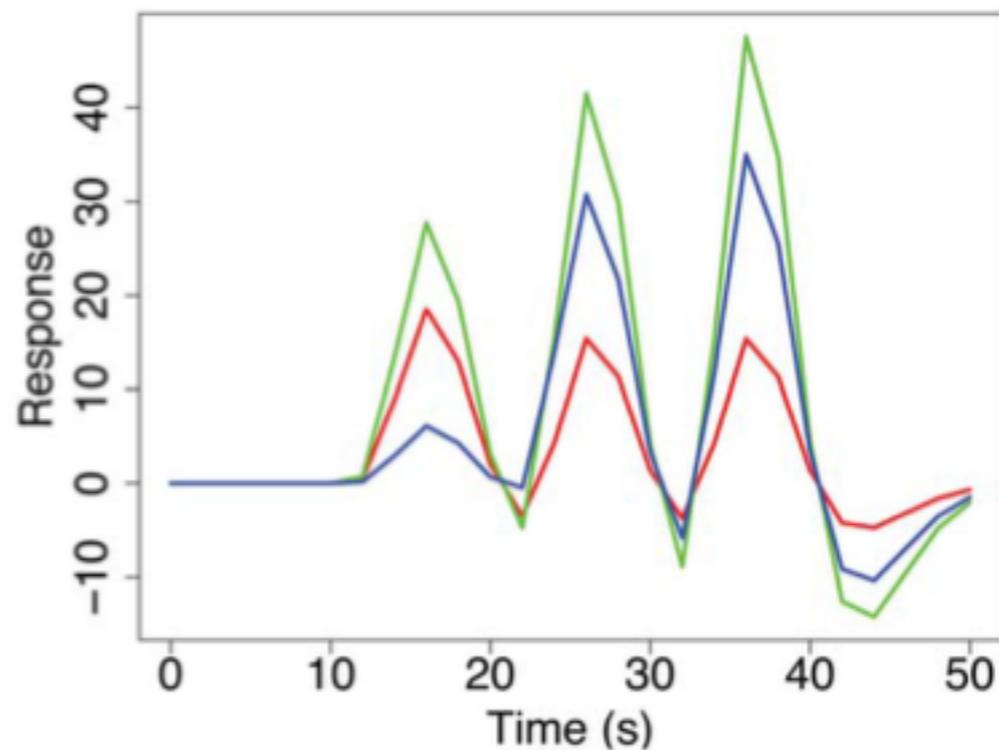
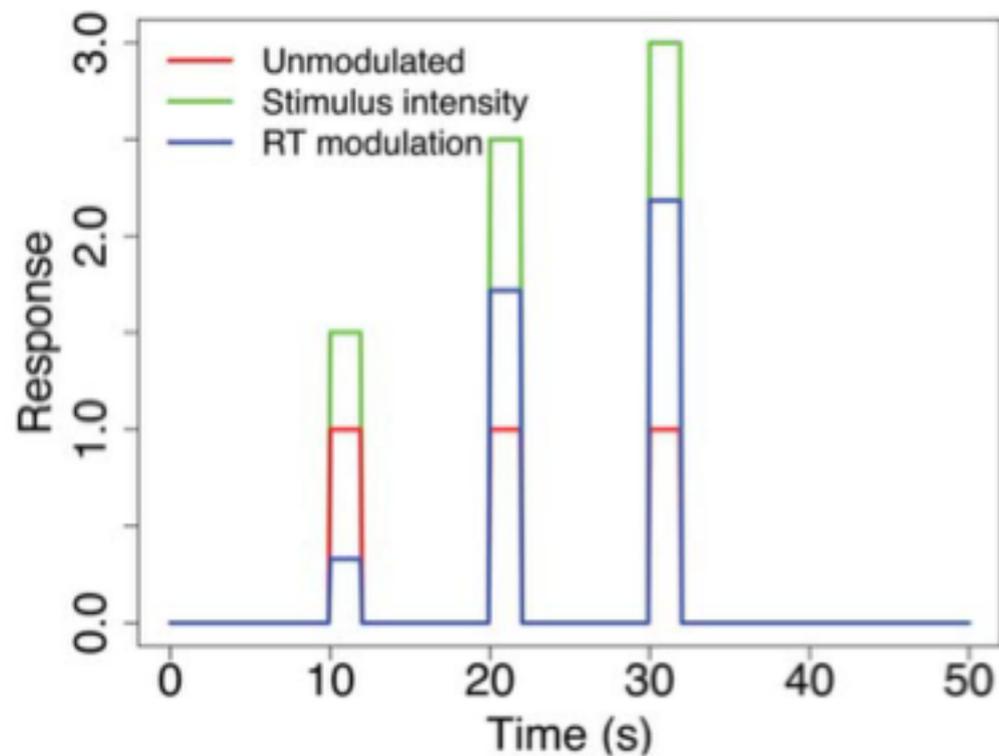
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  - The  $X1$  predictor stays the same - *but  $\beta(X1)$  will change*, because all the shared variance now goes to  $X1$
- In effect,  $\beta(X1)$  from the model  $Y = X1 + X2(\text{orth}(X1))$  will be similar to the model  $Y = X1$ , but with less residual error
  - Same beta but less error = 'better' stats



# When orthogonalisation makes sense

- We want the main regressor to reflect the mean response to the stimulus, and the modulators to reflect deviations from that mean
- Solution: orthogonalize the two modulators ('intensity', 'RT') with respect to the main task regressor ('unmodulated'). Changes 'unmodulated' estimates, but not the modulator estimates
- What happens if we don't do this? unmodulated response is response when intensity=0, RT=0. Hard to interpret.

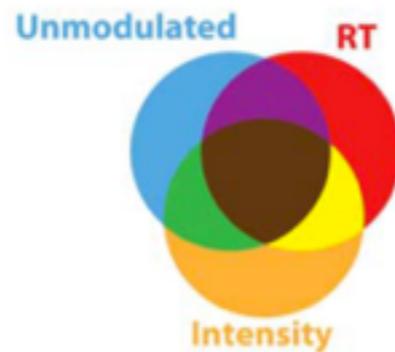


# When orthogonalisation make sense

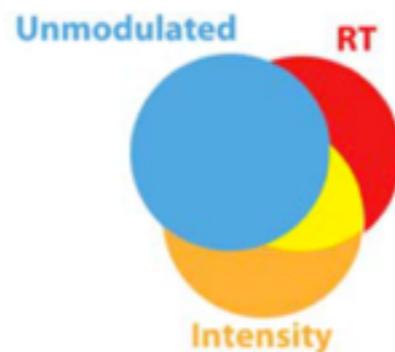
Careful - colour scheme changes!

- If you want the 'correct' case in SPM you will have to hand code the modulators (with appropriate orth) and add them (disabling SPM's own orth - only available in SPM12).
- Or fit the model twice, taking the second modulator each time
- Or switch to FSL...

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**

Workshop time

# Setup (if running in your own time)

- Open a terminal:
  - `cd /imaging/[yourusername]`
  - `scp -r /imaging/jc01/practicals/firstlevelmodel ./`
  - `cd firstlevelmodel`
  - `matlab_r2012b`
- In Matlab:
  - `edit firstlevelpractical`
  - other code to explore: `visualisedesign.m`, `loadfmridata.m`, `firstlevelpractical_exampleanswer.m`

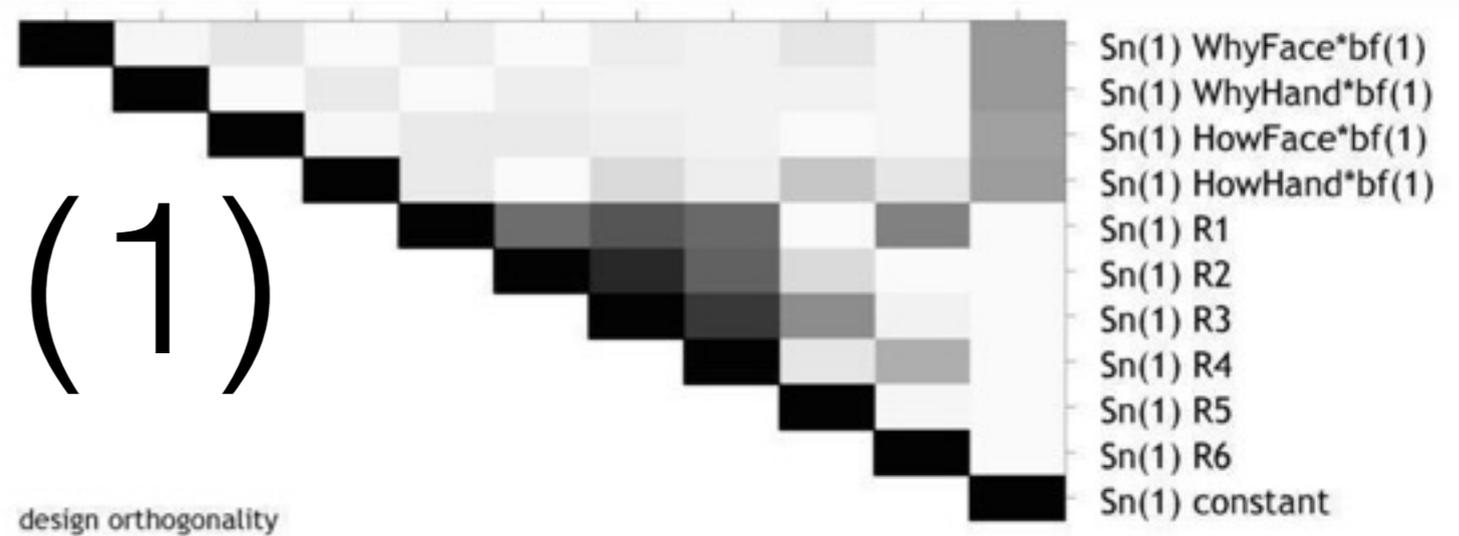
Break

# Designing fMRI experiments

Given what we now know about the assumed HRF shape and the noise model, what kind of design is most efficient for detecting the hypothesised effect?

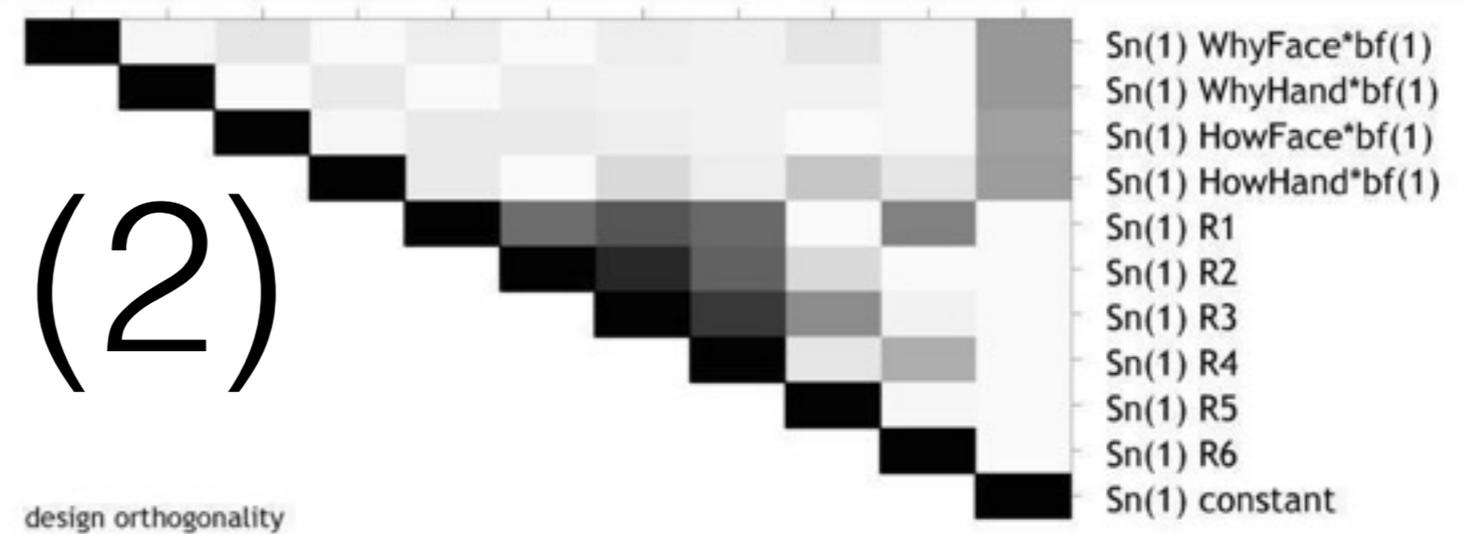
Experimental design has a *huge* effect on detection power in fMRI — this can make or break your study

# Collinearity (1)



- Dependencies between convolved regressors increases the variance of parameter estimates
  - NB, does *not* bias the fit - but can make it almost impossible to detect effects (e.g. the single-participant betas that go into group analysis will be highly variable)
- Big problem in fMRI, since convolution with HRF introduces dependencies between neighbouring events (e.g., encoding and recall phase in memory experiment)
- SPM outputs collinearity estimates (see above - basically predictor correlation matrix). Useful for finding pairs of dependent conditions. But a bit late to find this out at model fit stage!

# Collinearity (2)

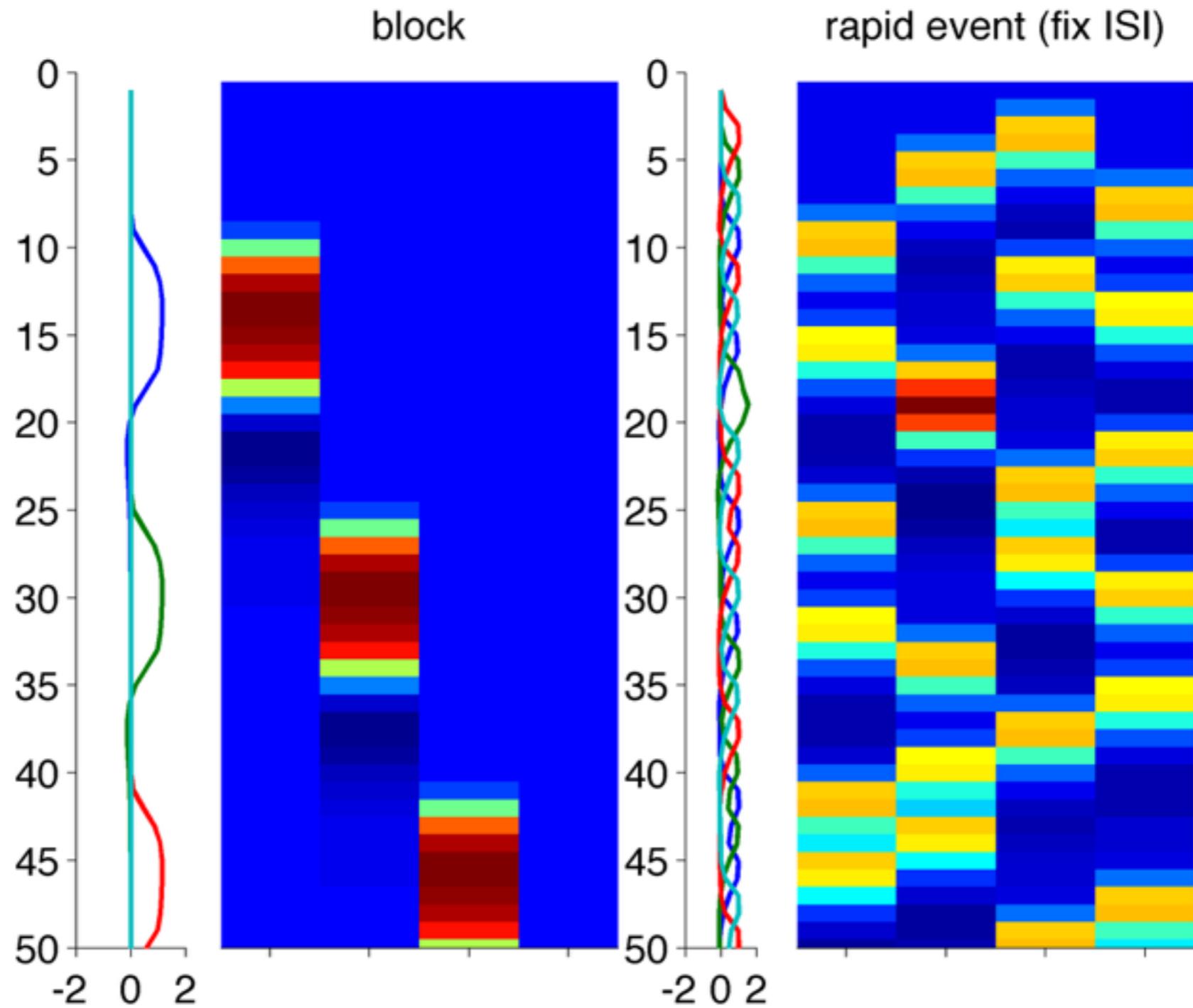


- Collinearity can also arise over sets of regressors - consider using variance inflation factor (VIF) to test for this *at experimental design stage*
- $VIF = 1 / (1 - R^2)$  where  $R^2$  comes from using all regressors but one to predict the final regressor
- Typical values:
  - $VIF = 1$  for completely orthogonal designs (zero correlation between prediction and left-out regressor)
  - $VIF = \text{Inf}$  for rank deficient designs (perfect correlation between prediction and left-out regressor)
  - By convention,  $VIF > 5$  indicates a problem (but lower is better, always)

... Can we fix collinearity by orthogonalizing regressors?

- No.

# Typical fMRI designs



Very efficient

Very inefficient

# Rules of thumb for fMRI design

1. Randomise trial order for each run to minimise collinearity
2. Cluster trials (pseudorandom event-related design or just block) to keep signal in low frequency band (the HRF convolution basically *low-pass filters* the regressor)
3. Don't put conditions you want to compare too far apart (>60s) (the de-trend *high-pass filters* the regressor)
4. Keep the number of conditions as small as possible to make the above easier (and to enable shorter runs)
5. For differential effects (ie, what you usually care about), fixed ISI works best
6. For much more on this, see Rik's SPM lectures, or CBU imaging wiki entry on design efficiency

# Useful references

- Rik's design efficiency wiki: <http://imaging.mrc-cbu.cam.ac.uk/imaging/DesignEfficiency>
- Jeanette Mumford's brain stats blog: [mumfordbrainstats.tumblr.com](http://mumfordbrainstats.tumblr.com) (see also facebook group)
- The SPM mailing list: <https://www.jiscmail.ac.uk/lists/SPM.html> (vast searchable archive)
- Kendrick Kay's course on Statistics and Data Analysis in MATLAB: <http://kendrickkay.net/psych5007/> (if you want to roll your own GLM)