Multivariate analyses & decoding

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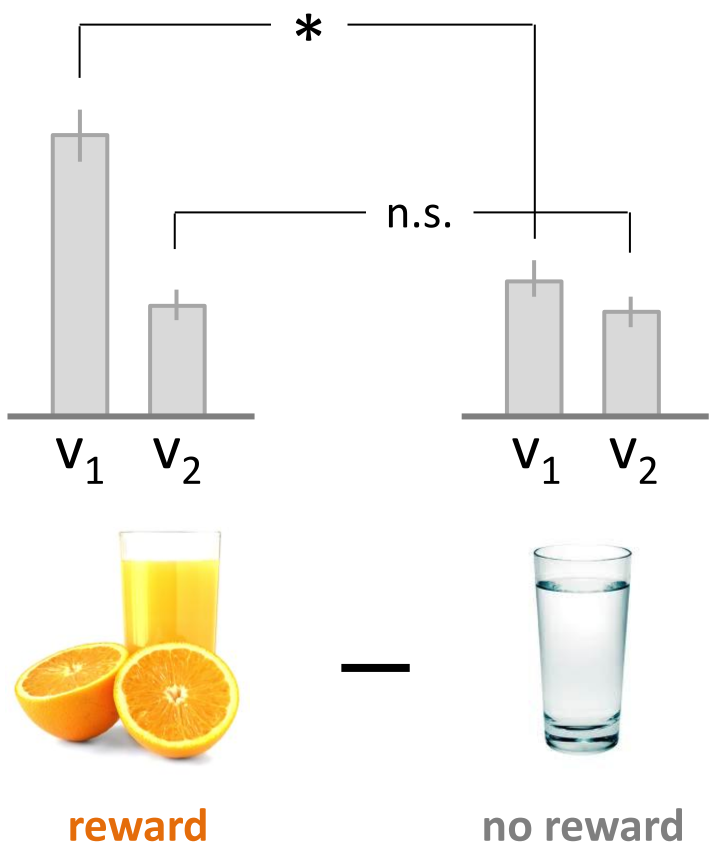
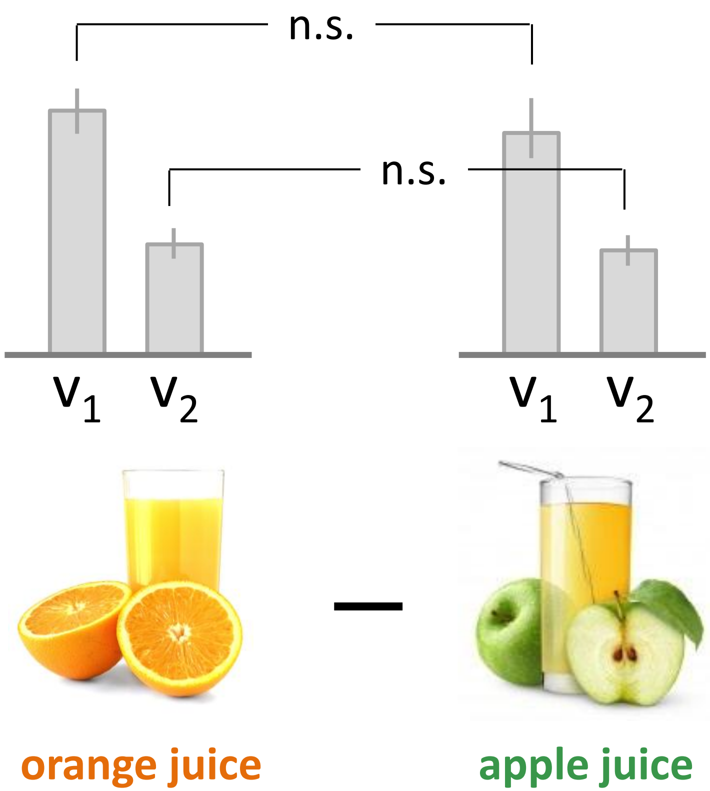
Why multivariate?

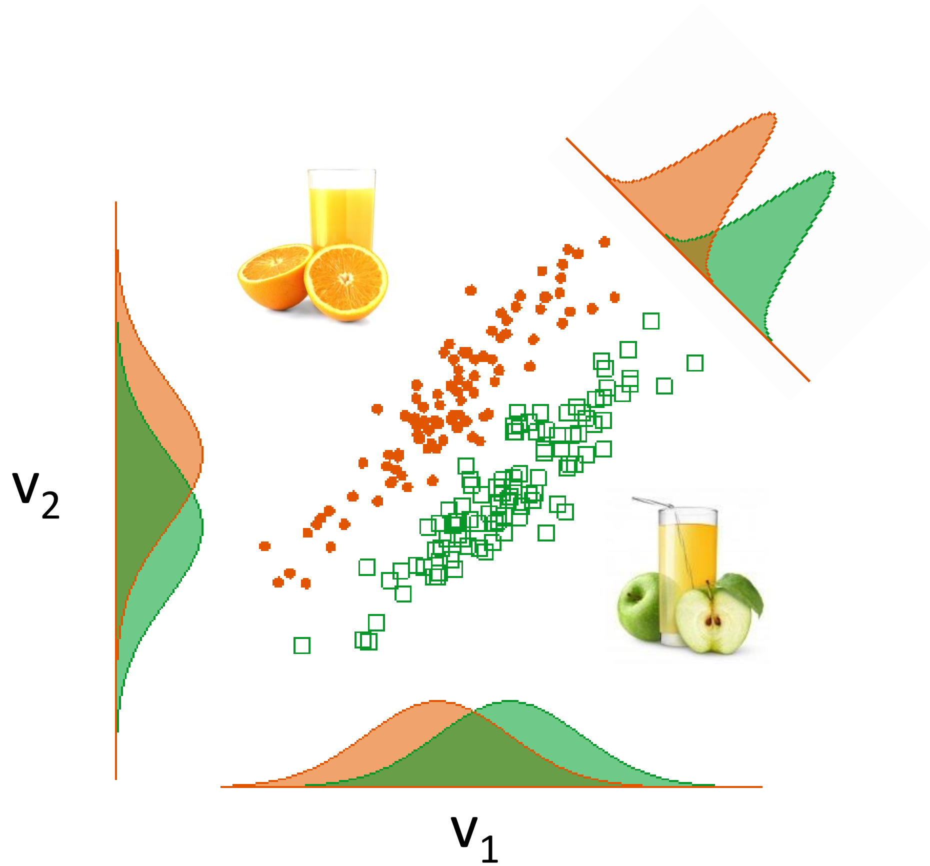
Univariate approaches are excellent for localizing activations in individual voxels.



Why multivariate?

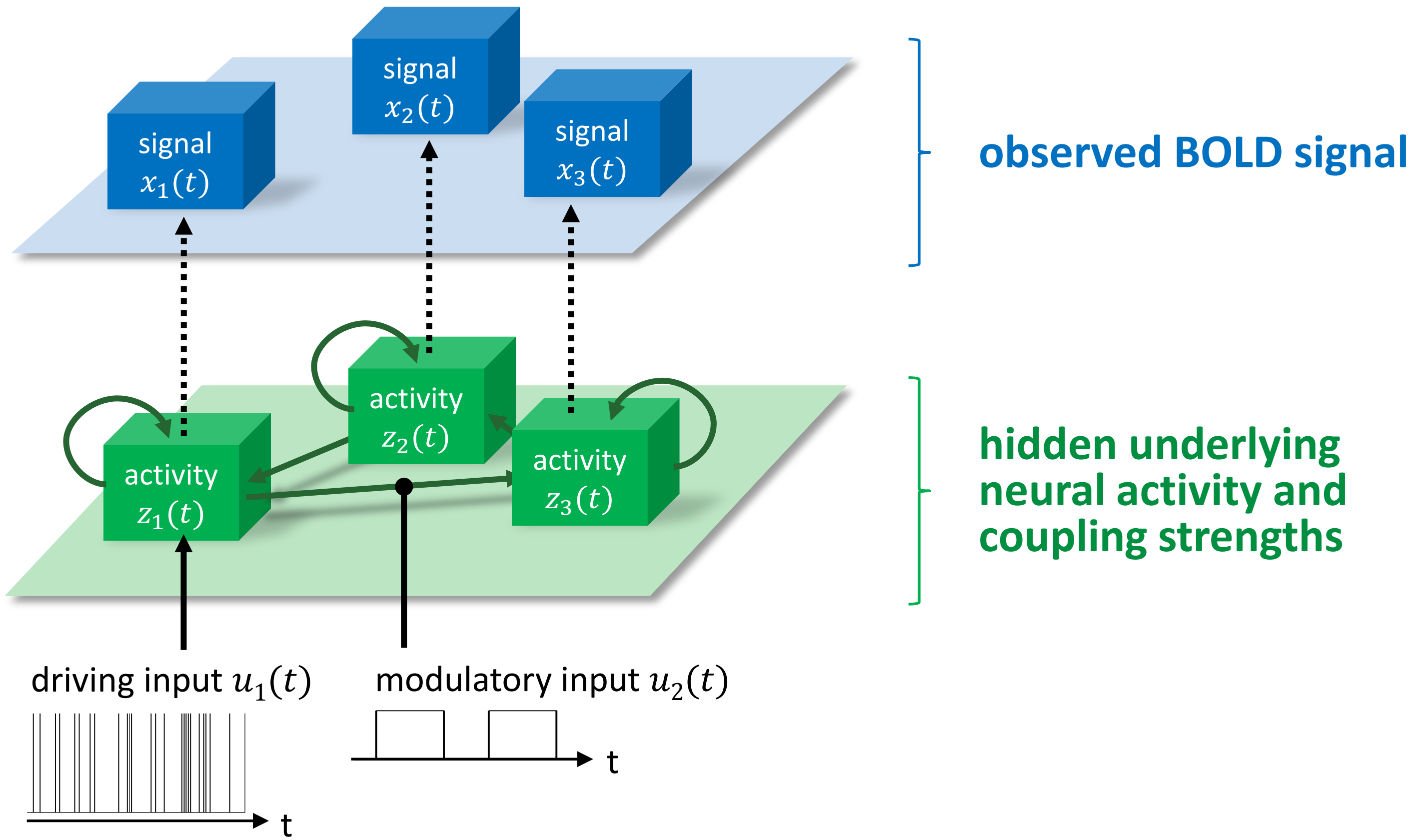
Multivariate approaches can be used to examine responses that are jointly encoded in multiple voxels.





Why multivariate?

Multivariate approaches can utilize 'hidden' quantities such as coupling strengths.



Friston, Harrison & Penny (2003) *NeuroImage;* Stephan & Friston (2007) *Handbook of Brain Connectivity;* Stephan et al. (2008) *NeuroImage*

Overview

Overview

Encoding vs. decoding

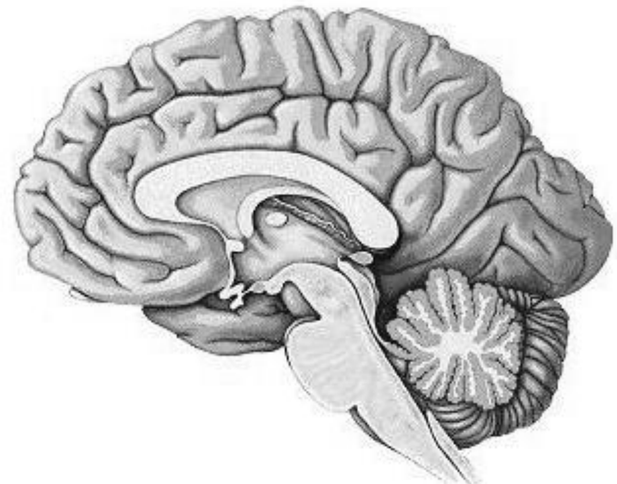
condition
stimulus
response
prediction error

encoding model

$g: X_t \rightarrow Y_t$

decoding model

$h: Y_t \rightarrow X_t$



context (cause or consequence)

$X_t \in \mathbb{R}^d$

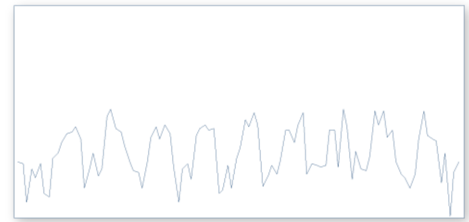
BOLD signal

$Y_t \in \mathbb{R}^v$

Regression vs. classification

Regression model

independent variables (regressors) → f → **continuous** dependent variable



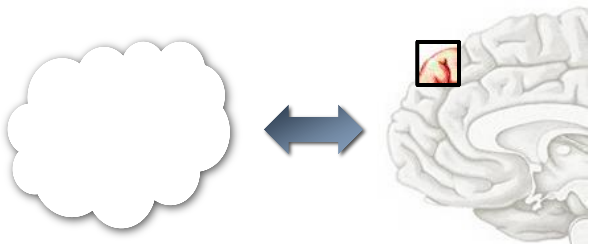
Classification model

independent variables (features) → f → **categorical** dependent variable (label)

vs.

Univariate vs. multivariate models

A univariate model considers a single voxel at a time.

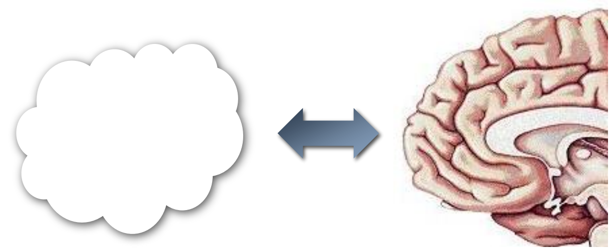


context
$X_t \in \mathbb{R}^d$

BOLD signal
$Y_t \in \mathbb{R}$

Spatial dependencies between voxels are only introduced afterwards, through random field theory.

A multivariate model considers many voxels at once.



context
$X_t \in \mathbb{R}^d$

BOLD signal
$Y_t \in \mathbb{R}^v, \ \mathrm{v} \gg 1$

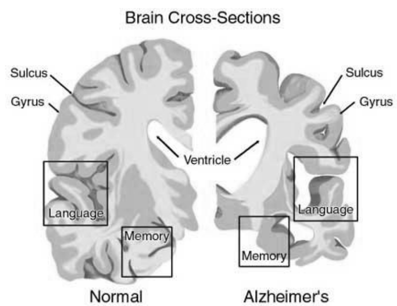
Multivariate models enable inferences on distributed responses without requiring focal activations.

Prediction vs. inference

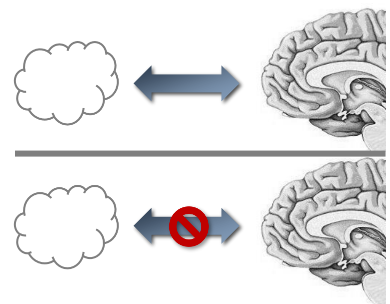
The goal of **prediction** is to find a highly accurate encoding or decoding function.

The goal of **inference** is to decide between competing hypotheses.

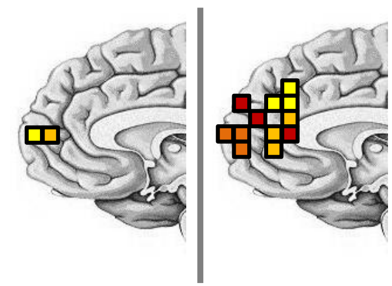
predicting a cognitive state using a brain-machine interface



predicting a subject-specific diagnostic status



comparing a model that links distributed neuronal activity to a cognitive state with a model that does not



weighing the evidence for sparse vs. distributed coding

predictive density

$$p(X_{new}|Y_{new}, X, Y) = \int p(X_{new}|Y_{new}, \theta) p(\theta|X, Y) d\theta$$

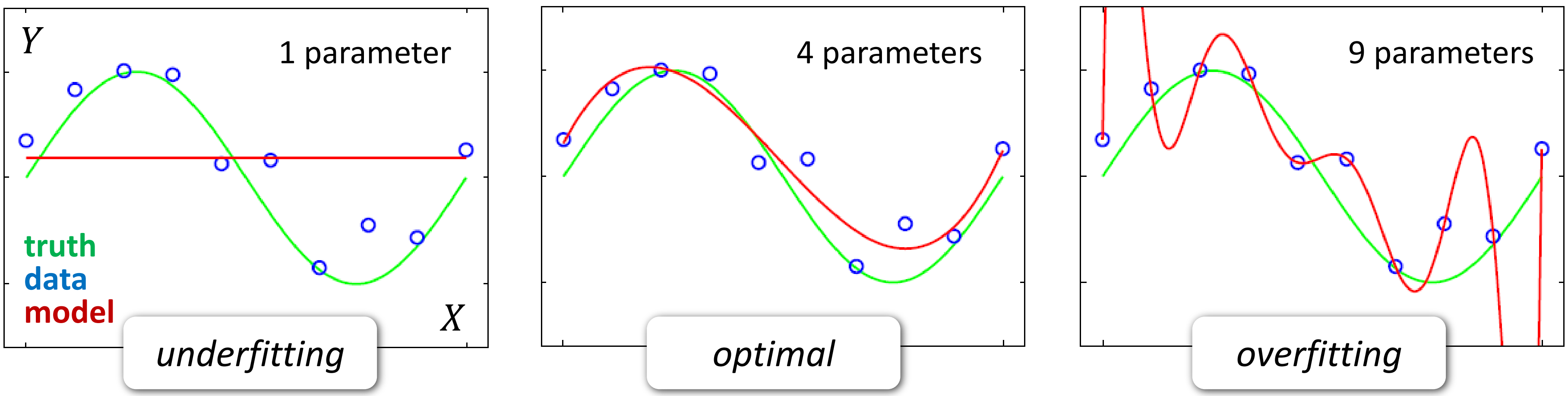
marginal likelihood (model evidence)

$$p(X|Y) = \int p(X|Y, \theta) p(\theta) d\theta$$

Goodness of fit vs. complexity

Goodness of fit is the degree to which a model explains observed data.

Complexity is the flexibility of a model (including, but not limited to, its number of parameters).



We wish to find the model that optimally trades off goodness of fit and complexity.

Bishop (2007) *PRML*

Summary of modelling terminology

General Linear Model (GLM)

- mass-univariate encoding model
- to regress context onto brain activity and find clusters of similar effects

Dynamic Causal Modelling (DCM)

- multivariate encoding model
- to evaluate connectivity hypotheses

Classification

- multivariate decoding model
- to predict a categorical context label from brain activity

Multivariate Bayes (MVB)

- multivariate decoding model
- to evaluate anatomical and coding hypotheses

Overview

1 Introduction

2 Classification

3 Multivariate Bayes

4 Model-based analyses

Constructing a classifier

A principled way of designing a classifier would be to adopt a probabilistic approach:

$Y_t \xrightarrow{\;f\;}$ that k which maximizes $p(X_t = k | Y_t, X, Y)$

In practice, classifiers differ in terms of how strictly they implement this principle.

Generative classifiers

use Bayes' rule to estimate $p(X_t|Y_t) \propto p(Y_t|X_t)p(X_t)$

- *Gaussian Naïve Bayes*
- *Linear Discriminant Analysis*

Discriminative classifiers

estimate $p(X_t|Y_t)$ directly without Bayes' theorem

- *Logistic regression*
- *Relevance Vector Machine*

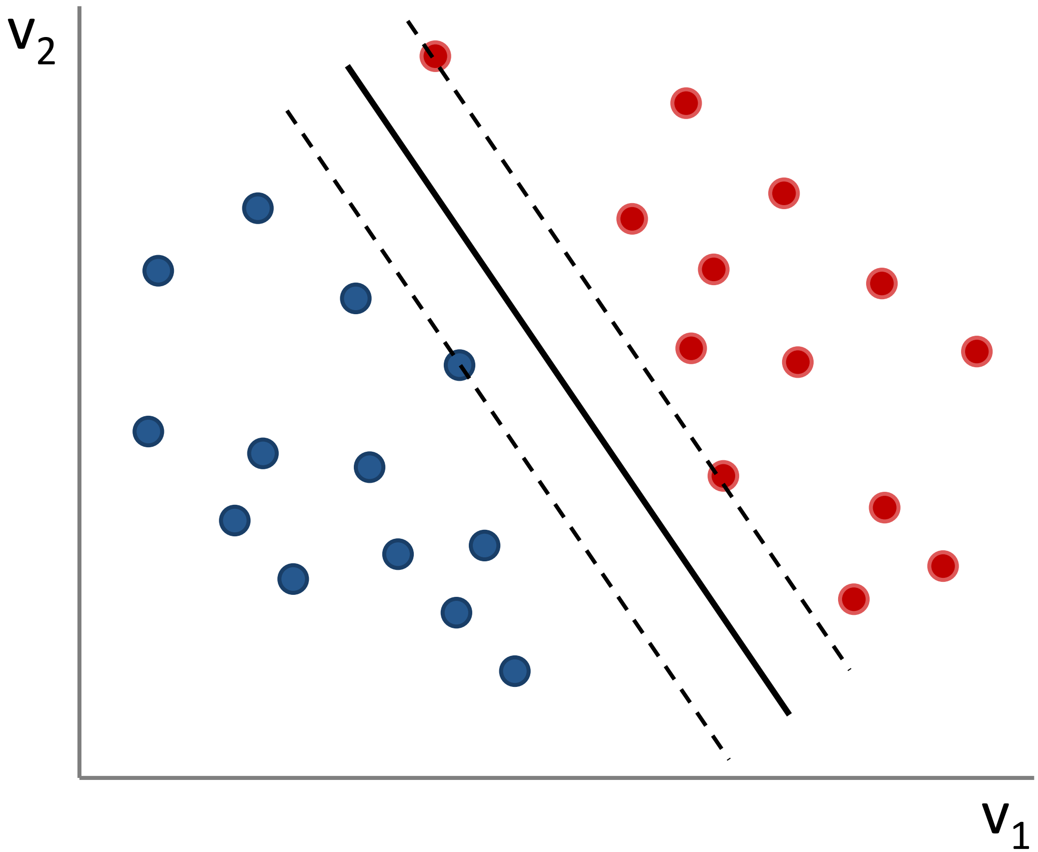
Discriminant classifiers

estimate $f(Y_t)$ directly

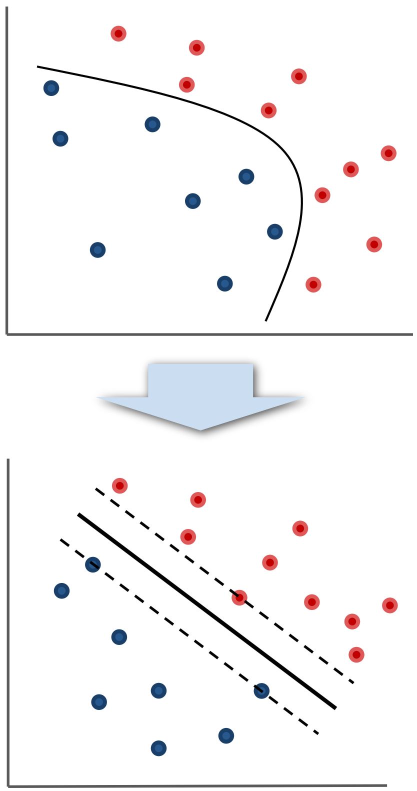
- *Fisher's Linear Discriminant*
- *Support Vector Machine*

Support vector machine (SVM)

Linear SVM

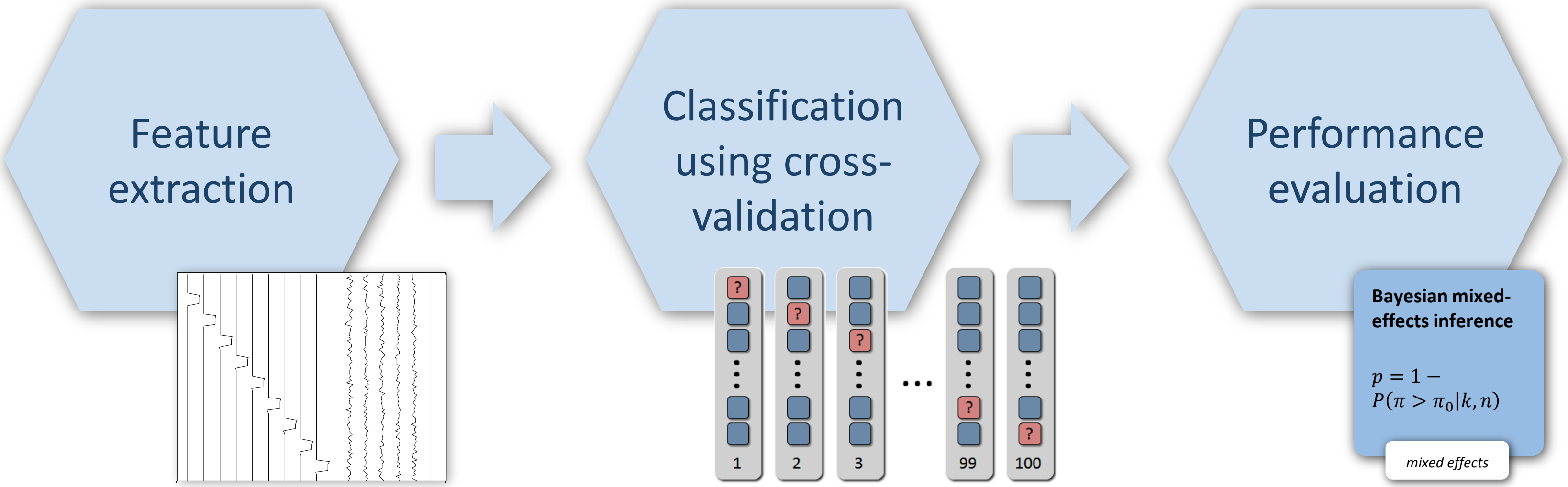


Nonlinear SVM



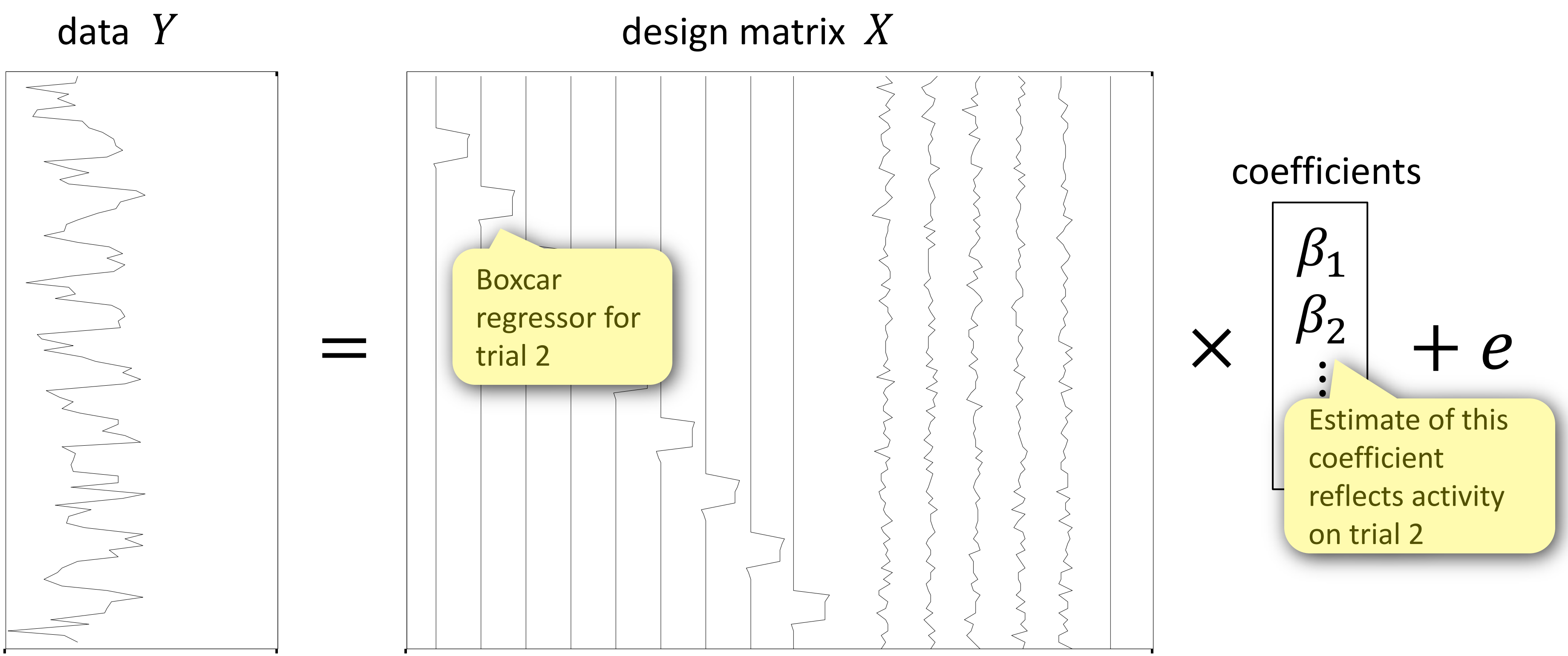
Vapnik (1999) Springer; Schölkopf et al. (2002) MIT Press

Stages in a classification analysis



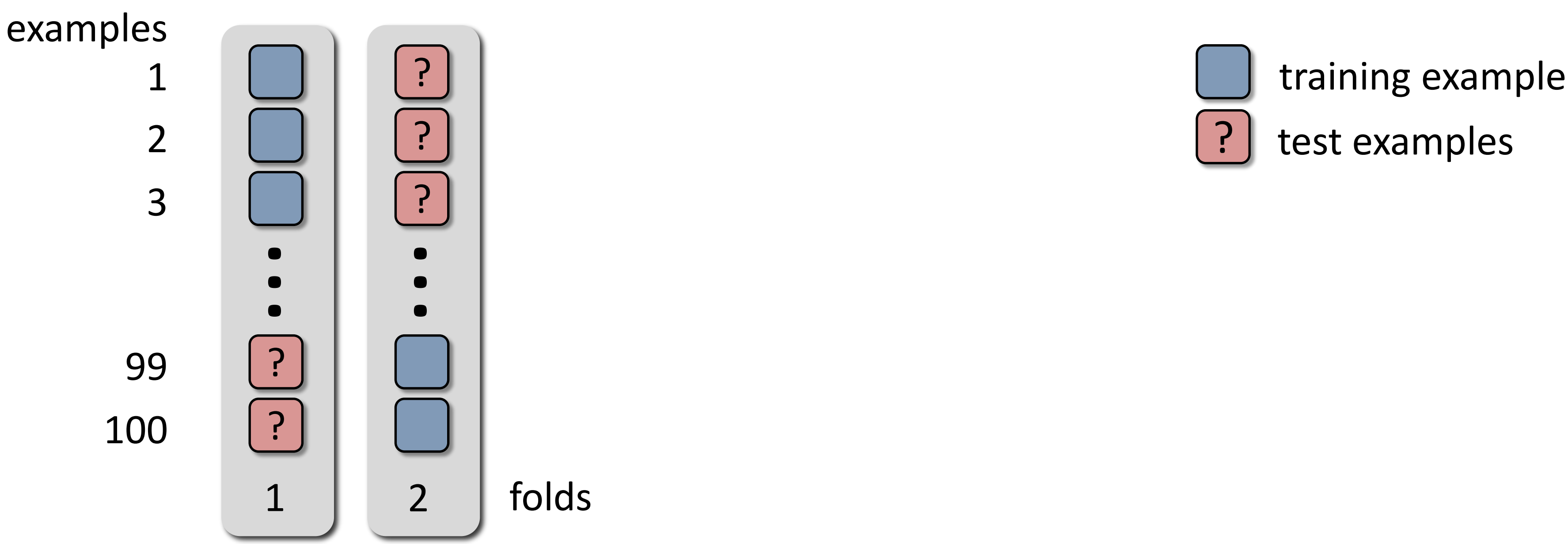
Feature extraction for trial-by-trial classification

We can obtain trial-wise estimates of neural activity by filtering the data with a GLM.



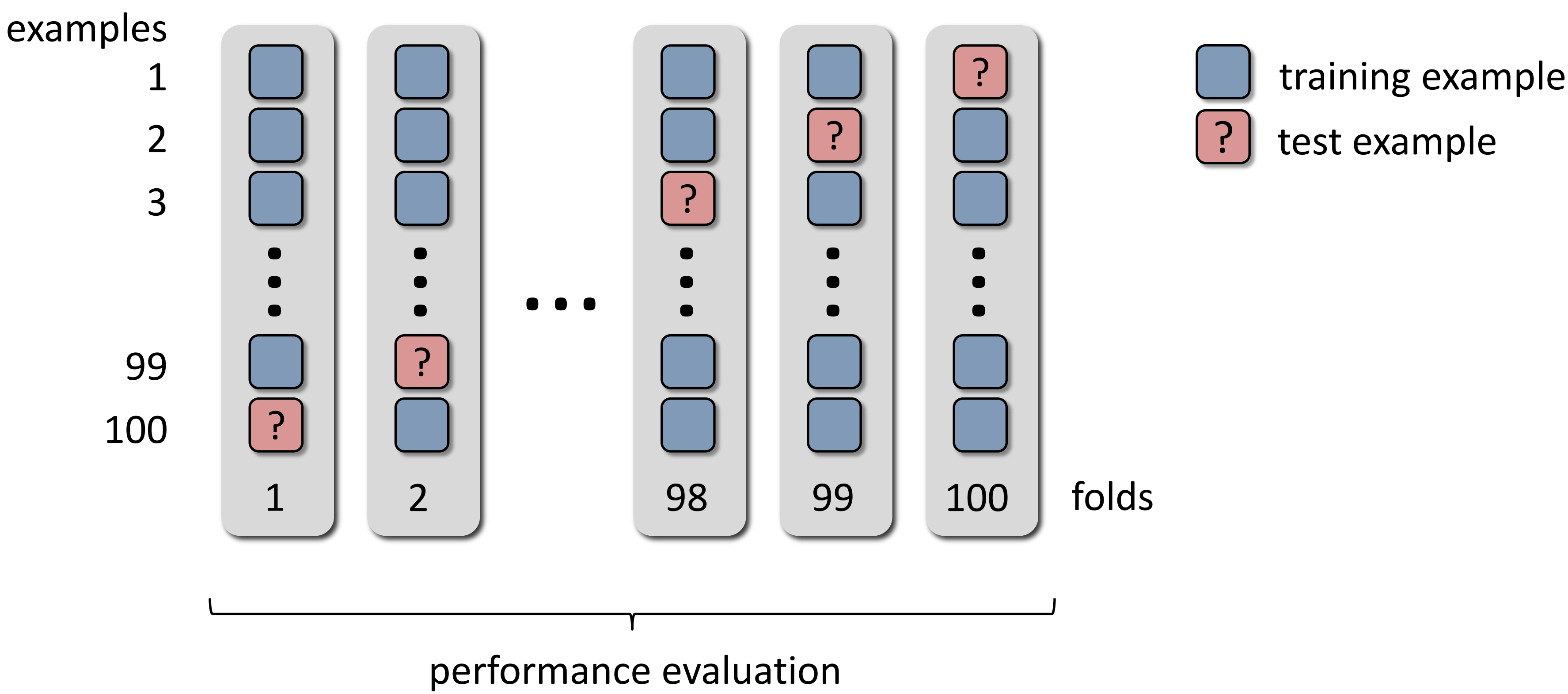
Cross-validation

The generalization ability of a classifier can be estimated using a resampling procedure known as *cross-validation*. One example is 2-fold cross-validation:



Cross-validation

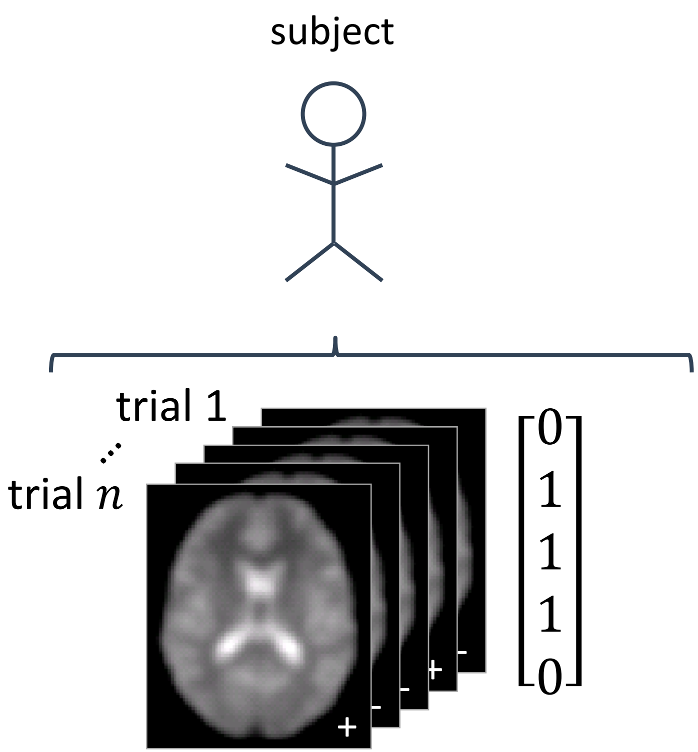
A more commonly used variant is *leave-one-out* cross-validation.



Performance evaluation

Single-subject study with n trials

The most common approach is to assess how likely the obtained number of correctly classified trials could have occurred by chance.



Binomial test

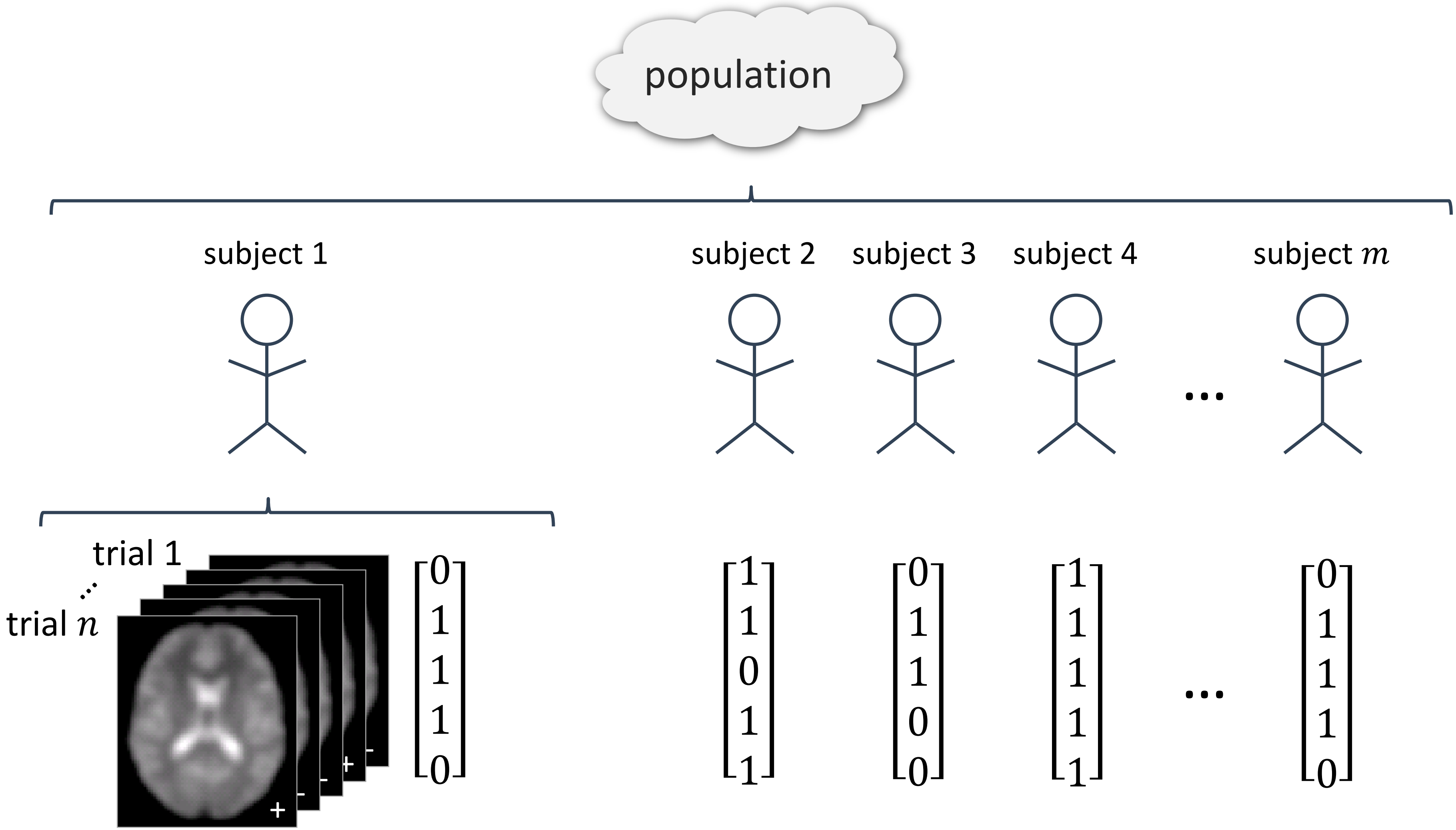
$$p = P(X \geq k|H_0) = 1 - B(k|n, \pi_0)$$

In MATLAB:

```
p = 1 - binocdf(k,n,pi_0)
```

k	number of correctly classified trials
n	total number of trials
π_0	chance level (typically 0.5)
B	binomial cumulative density function

Performance evaluation



Performance evaluation

Group study with m subjects, n trials each

In a group setting, we must account for both within-subjects (fixed-effects) and between-subjects (random-effects) variance components.

available for download soon

~~Binomial test on concatenated data~~

$$\cancel{p = 1 - B\left(\sum k \middle| \sum n, \pi_0\right)}$$

fixed effects

~~Binomial test on averaged data~~

$$\cancel{p = 1 - B\left(\frac{1}{m}\sum k \middle| \frac{1}{m}\sum n, \pi_0\right)}$$

fixed effects

t-test on summary statistics

$$t = \sqrt{m}\,\frac{\bar{\pi} - \pi_0}{\hat{\sigma}_{m-1}}$$

$$p = 1 - t_{m-1}(t)$$

random effects

Bayesian mixed-effects inference

$$p = 1 - P(\pi > \pi_0 | k, n)$$

mixed effects

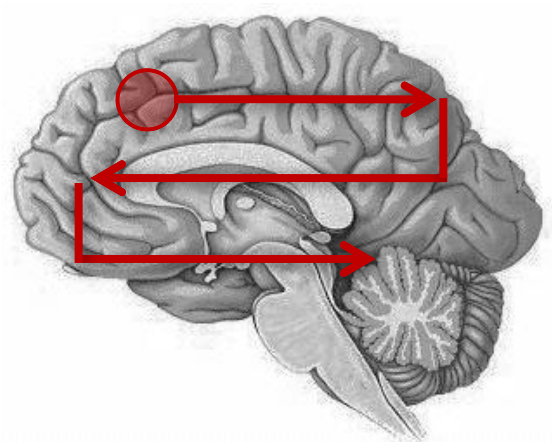
$\bar{\pi}$	sample mean of sample accuracies	π_0	chance level (typically 0.5)
$\hat{\sigma}_{m-1}$	sample standard deviation	t_{m-1}	cumulative Student's t-distribution

Brodersen, Mathys, Chumbley, Daunizeau, Ong, Buhmann, Stephan *(under review)*

Spatial deployment of informative regions

Which brain regions are jointly informative of a cognitive state of interest?

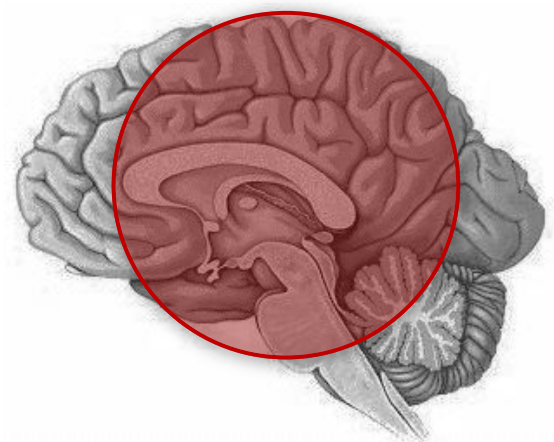
Searchlight approach



A sphere is passed across the brain. At each location, the classifier is evaluated using only the voxels in the current sphere → map of t-scores.

Nandy & Cordes (2003) *MRM*
Kriegeskorte et al. (2006) *PNAS*

Whole-brain approach

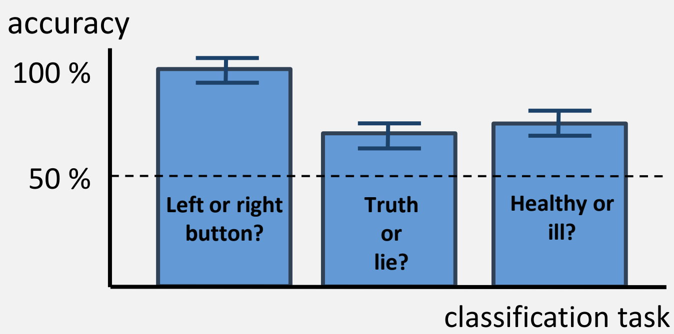


A constrained classifier is trained on whole-brain data. Its voxel weights are related to their empirical null distributions using a permutation test → map of t-scores.

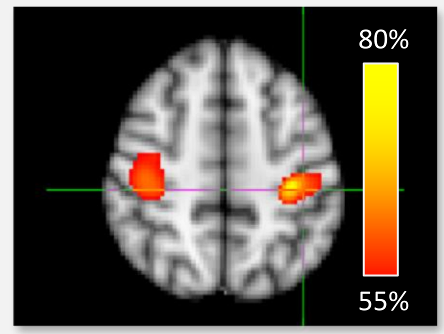
Mourao-Miranda et al. (2005) *NeuroImage*
Lomakina et al. *(in preparation)*

Summary: research questions for classification

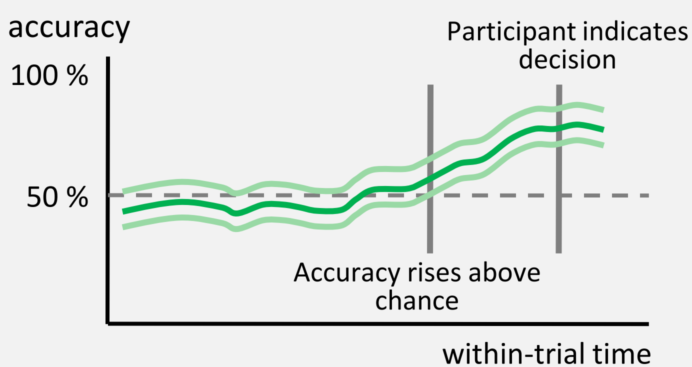
Overall classification accuracy



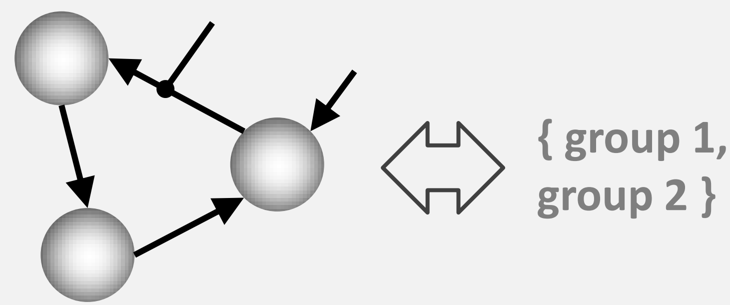
Spatial deployment of discriminative regions



Temporal evolution of discriminability



Model-based classification

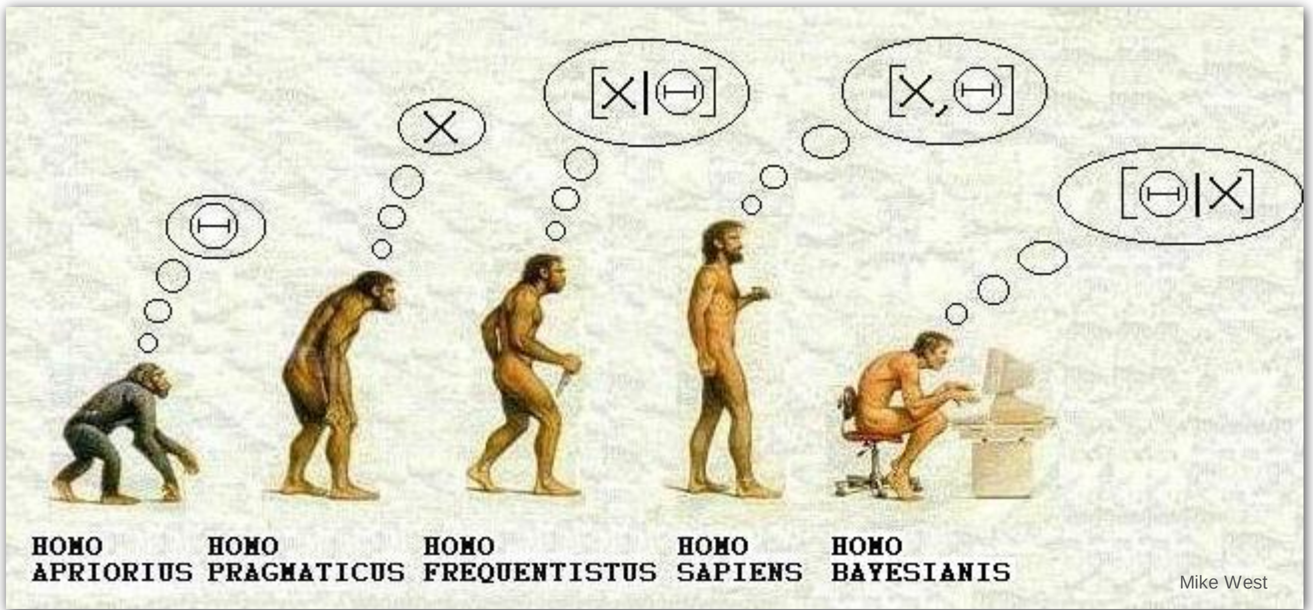


Pereira et al. (2009) *NeuroImage*, Brodersen et al. (2009) *The New Collection*

Overview

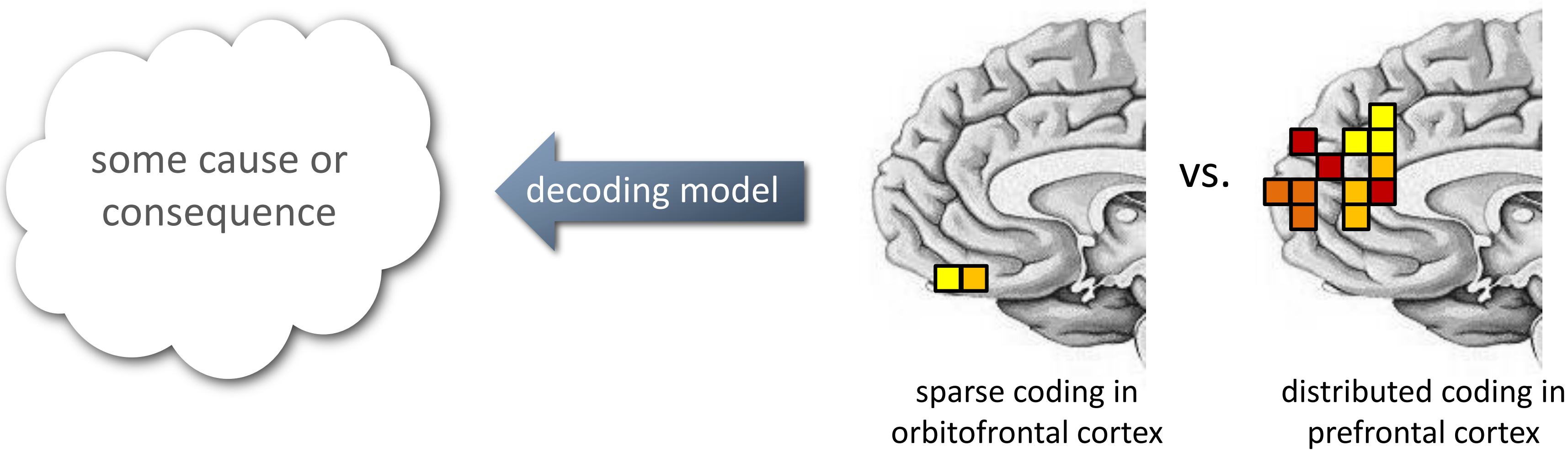
Multivariate Bayes

SPM brings multivariate analyses into the conventional inference framework of Bayesian hierarchical models and their inversion.



Multivariate Bayes

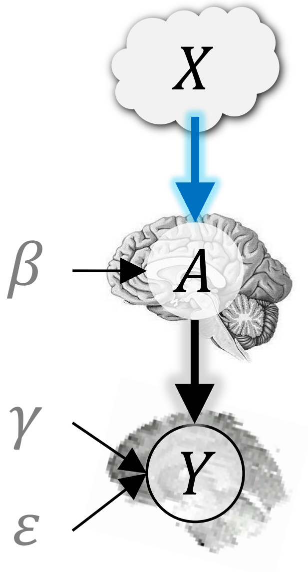
Multivariate analyses in SPM rest on the central tenet that inferences about how the brain represents things reduce to model comparison.



To make the ill-posed regression problem tractable, MVB uses a prior on voxel weights. Different priors reflect different coding hypotheses.

From encoding to decoding

Encoding model: GLM



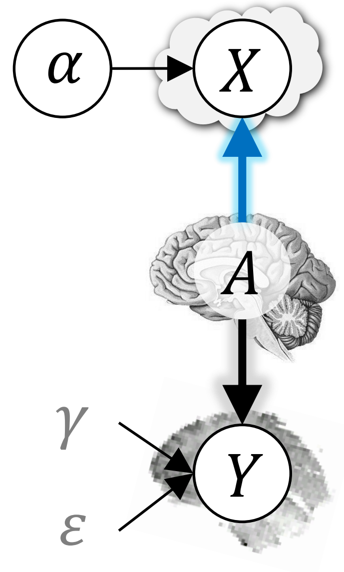
$$= X\beta$$

$$= TA + G\gamma + \varepsilon$$

In summary:

$$Y = TX\beta + G\gamma + \varepsilon$$

Decoding model: MVB



$$= A\alpha$$

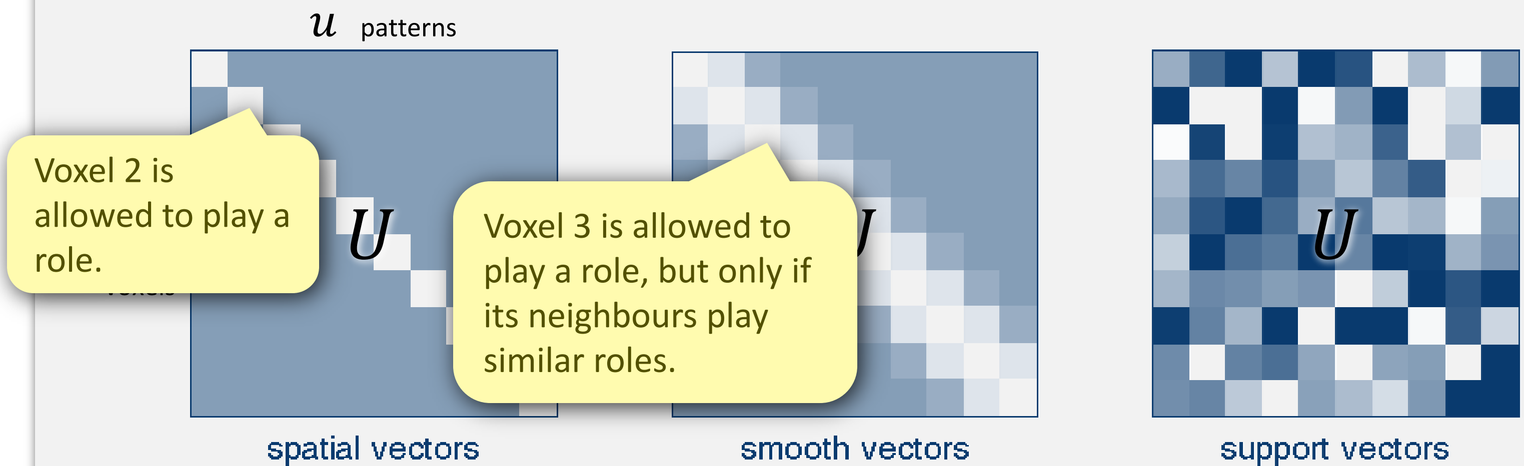
$$= TA + G\gamma + \varepsilon$$

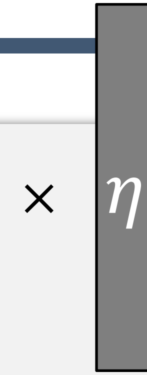
In summary:

$$TX = Y\alpha - G\gamma\alpha - \varepsilon\alpha$$

Specifying the prior for MVB

1st level – spatial coding hypothesis U





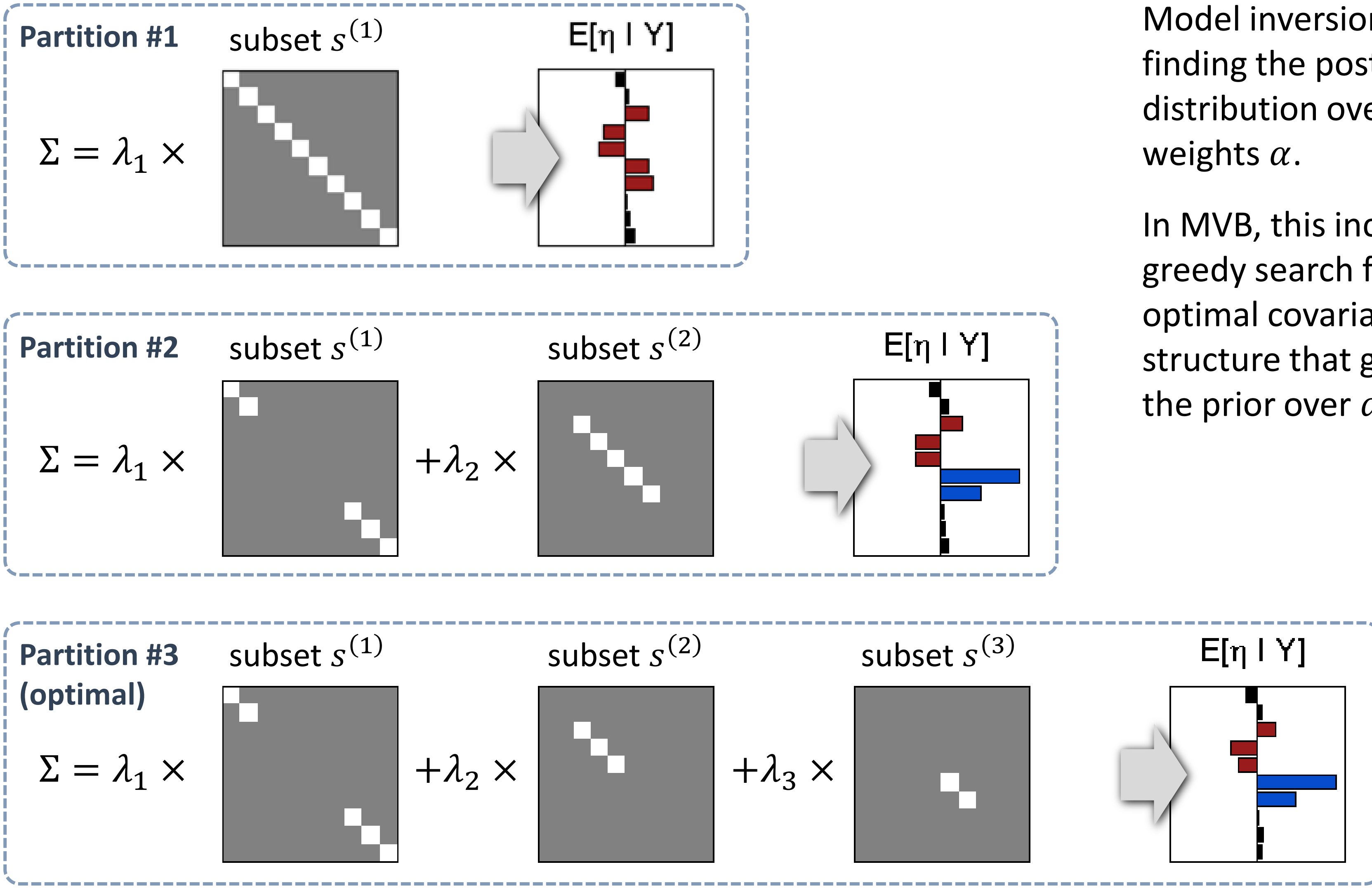
2nd level – pattern covariance structure Σ

$$p(\eta) = \mathcal{N}(\eta|0, \Sigma)$$

$$\Sigma = \sum_i \lambda_i s^{(i)}$$

Thus: $p(\alpha|\lambda) = \mathcal{N}_n(\alpha|0, U\Sigma U^T)$ and $p(\lambda) = \mathcal{N}(\lambda|\pi, \Pi^{-1})$

Inverting the model



Model inversion involves finding the posterior distribution over voxel weights α.

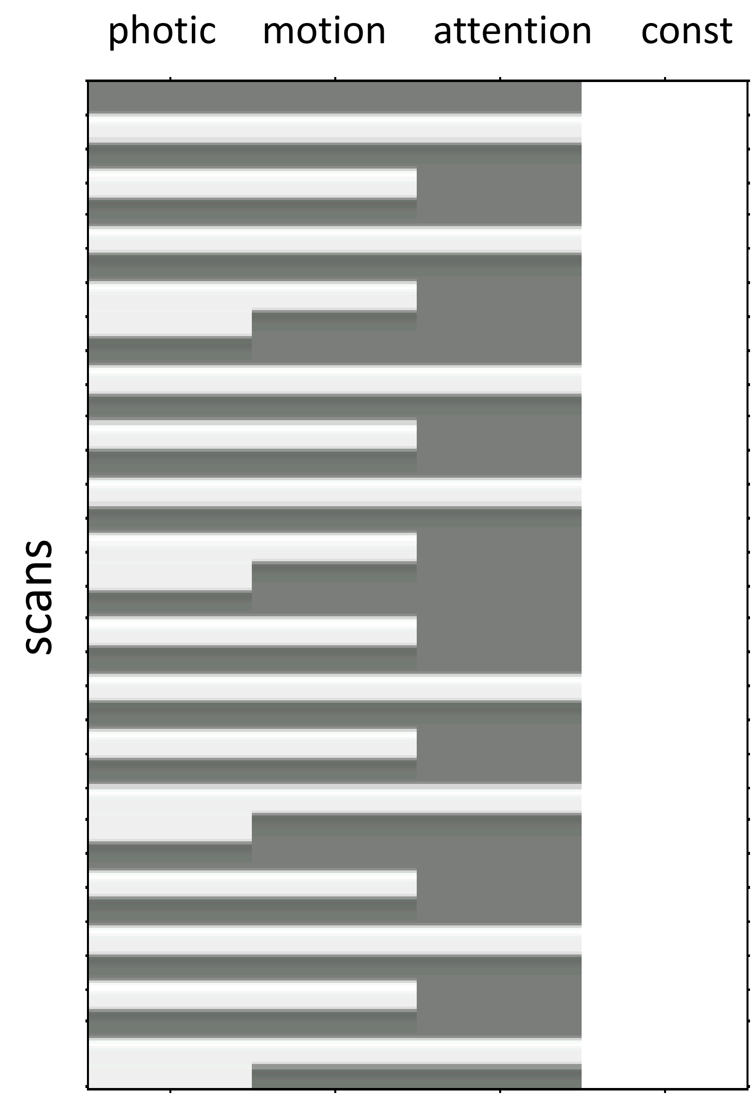
In MVB, this includes a greedy search for the optimal covariance structure that governs the prior over α.

Example: decoding motion from visual cortex

MVB can be illustrated using SPM's attention-to-motion example dataset.

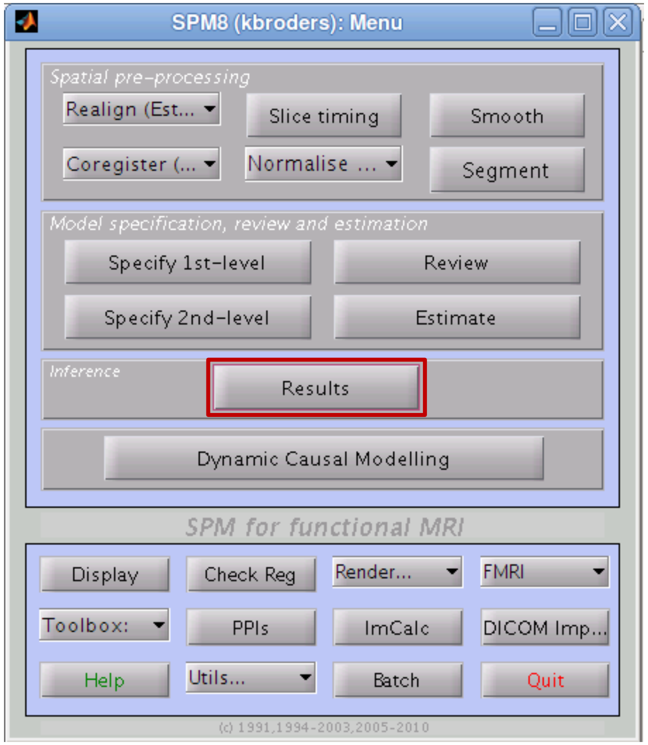
This dataset is based on a simple block design. There are three experimental factors:

- **photic** – display shows random dots
- **motion** – dots are moving
- **attention** – subjects asked to pay attention

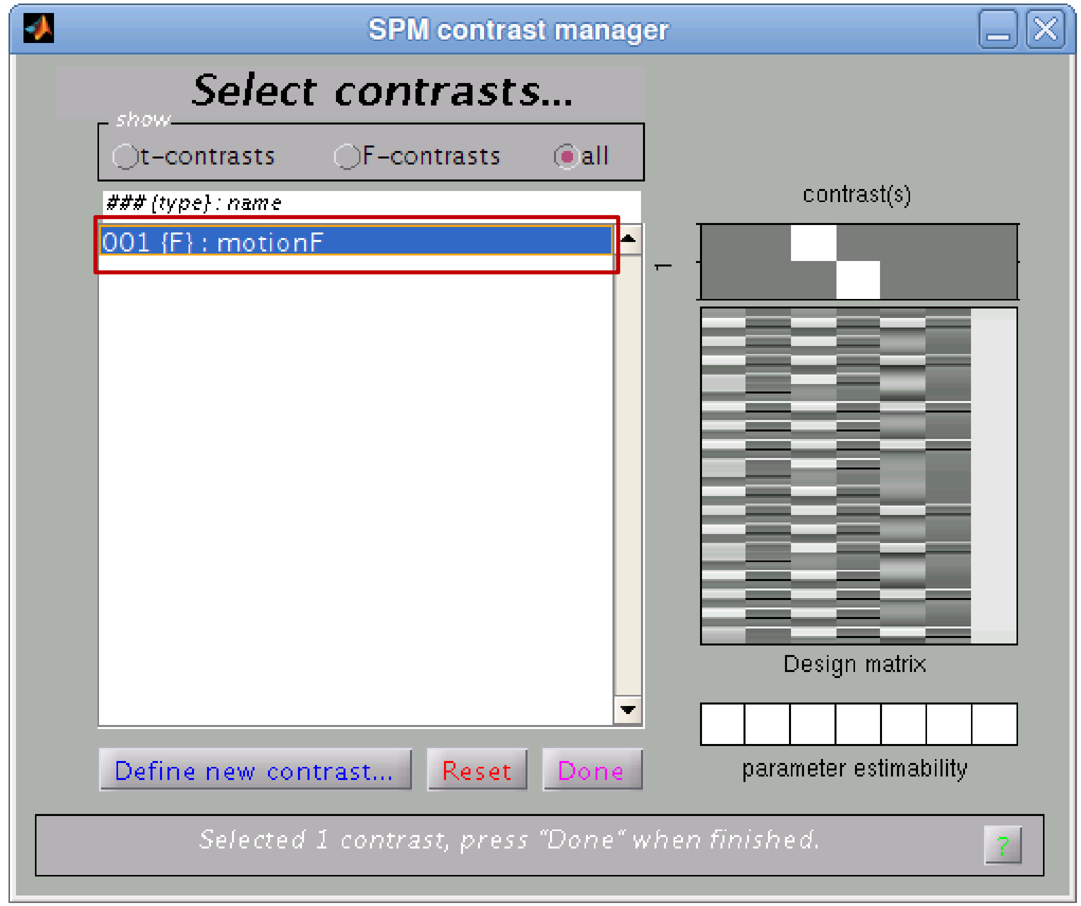


Buechel & Friston 1999 *Cerebral Cortex*
Friston et al. 2008 *NeuroImage*

Multivariate Bayes in SPM

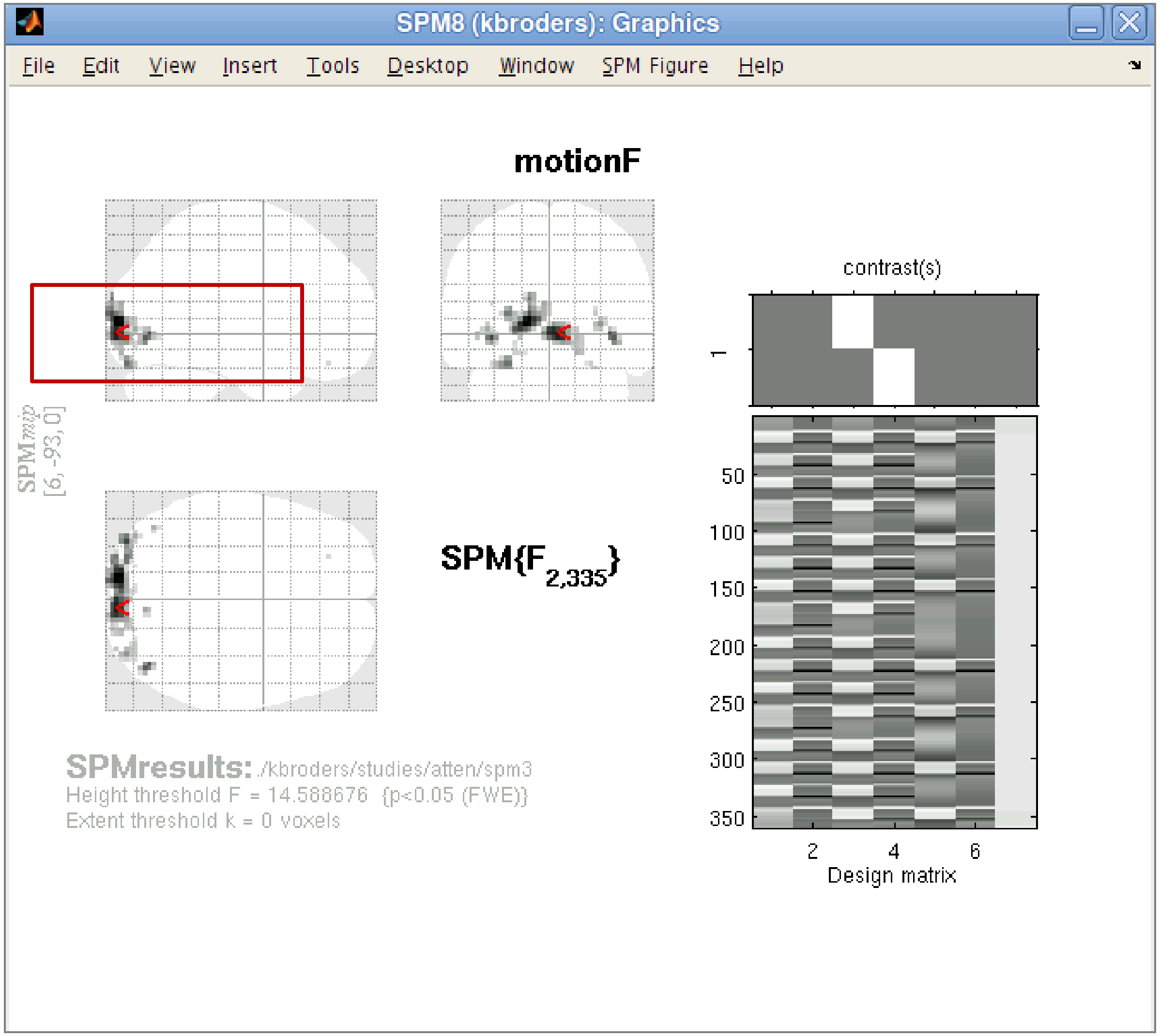


Step 1
After having specified and estimated a model, use the *Results* button.



Step 2
Select the contrast to be decoded.

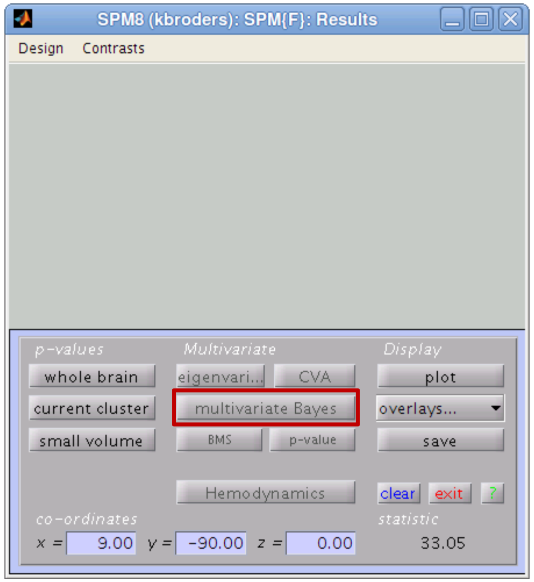
Multivariate Bayes in SPM



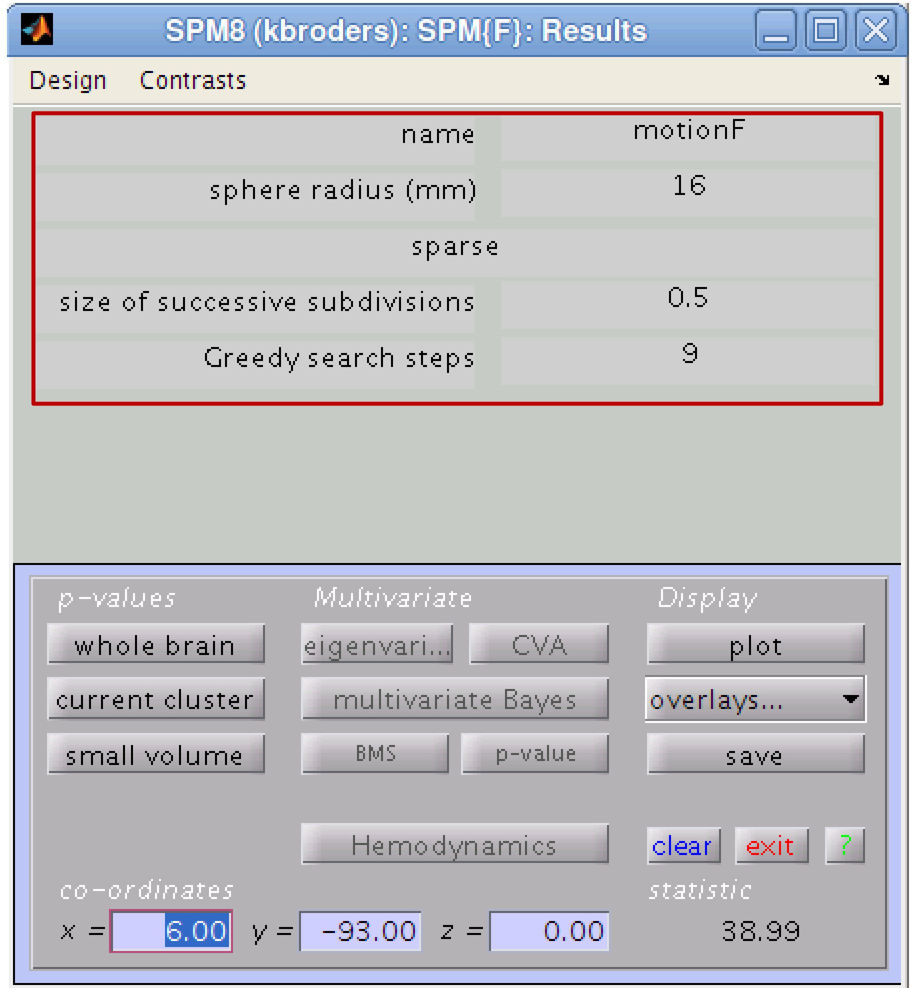
Step 3

Pick a region of interest.

Multivariate Bayes in SPM

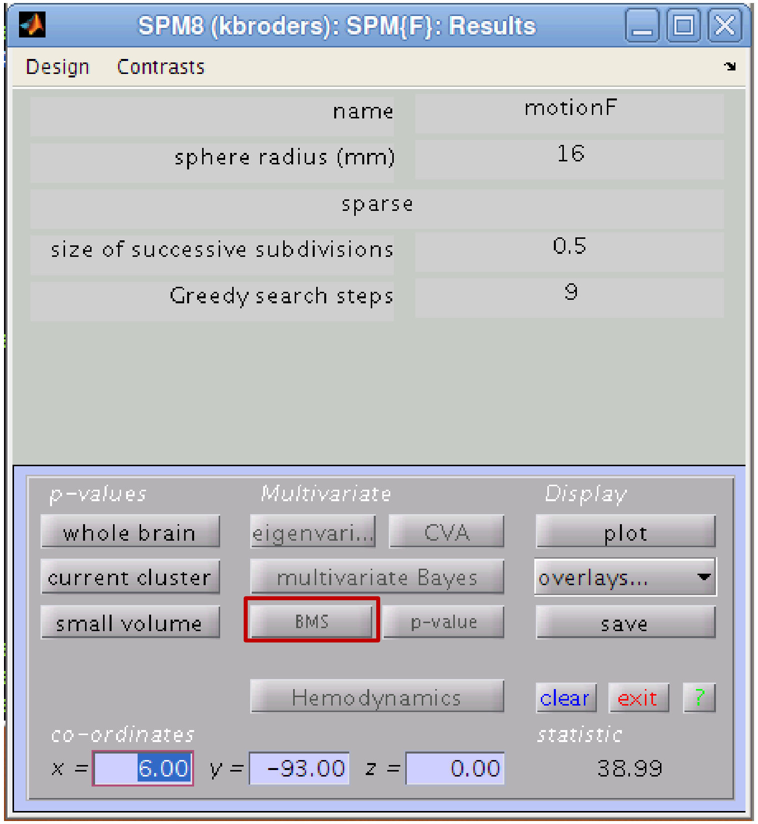


Step 4
Multivariate Bayes can be invoked from within the Multivariate section.

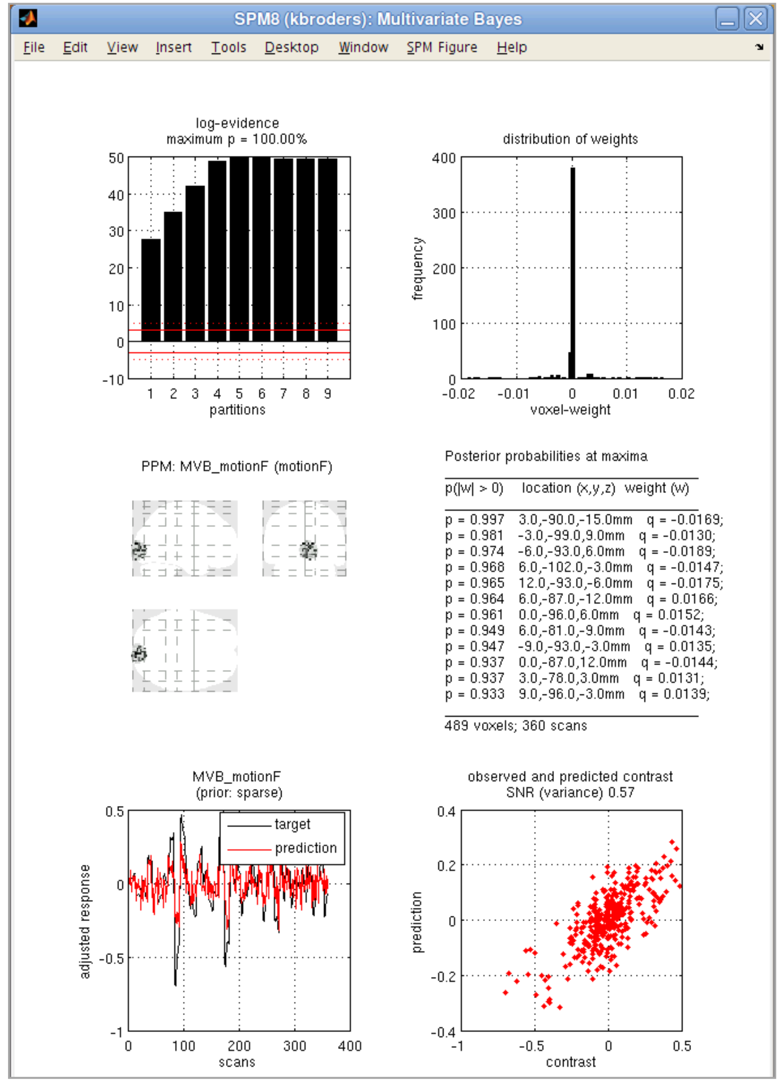


Step 5
Here, the region of interest is specified as a sphere around the cursor. The spatial prior implements a *sparse* coding hypothesis.

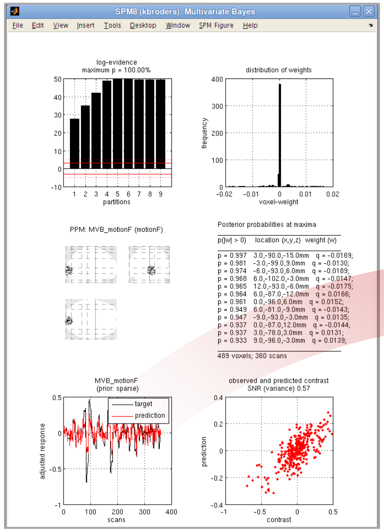
Multivariate Bayes in SPM

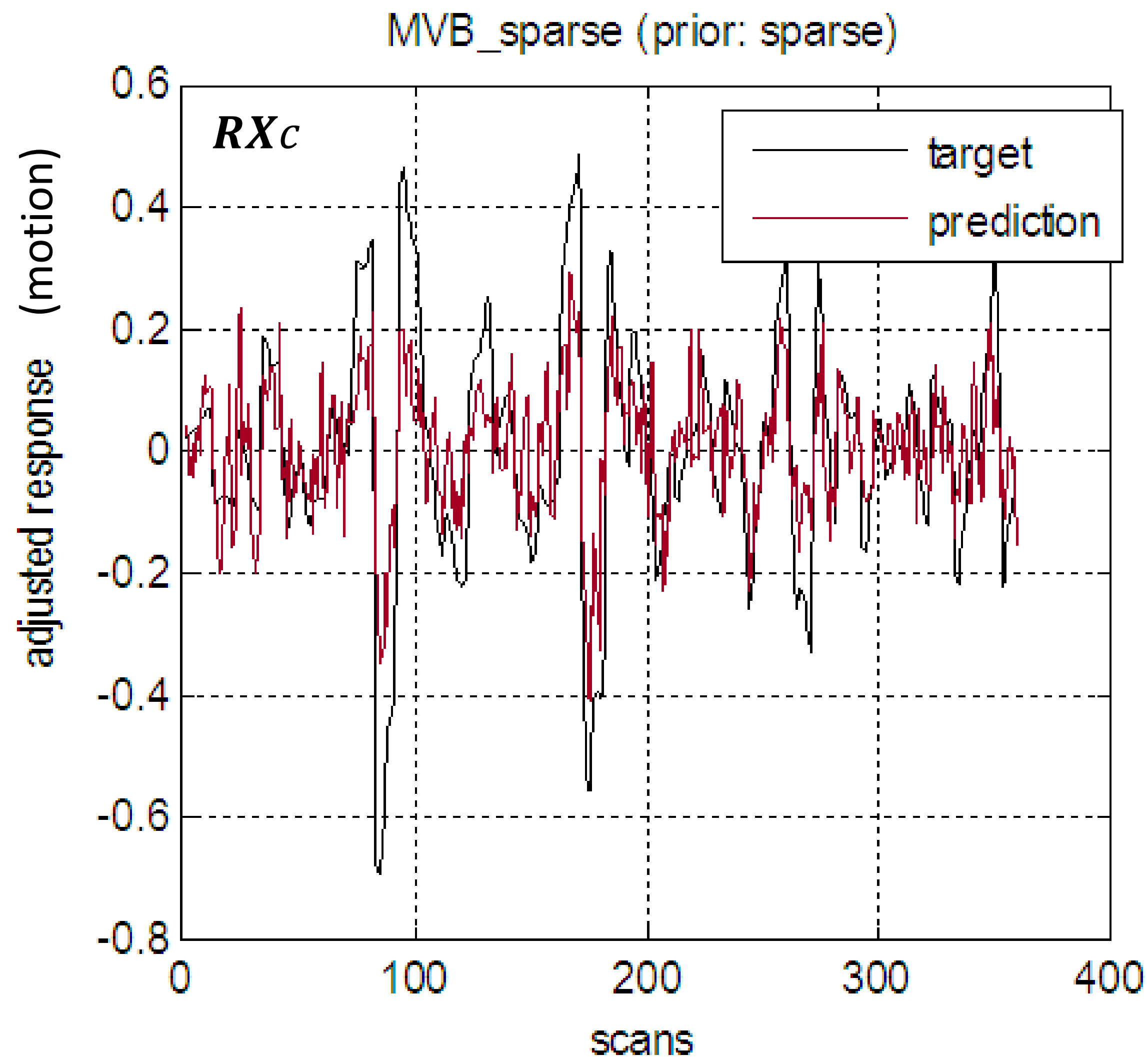


Step 6
Results can be displayed using the BMS button.

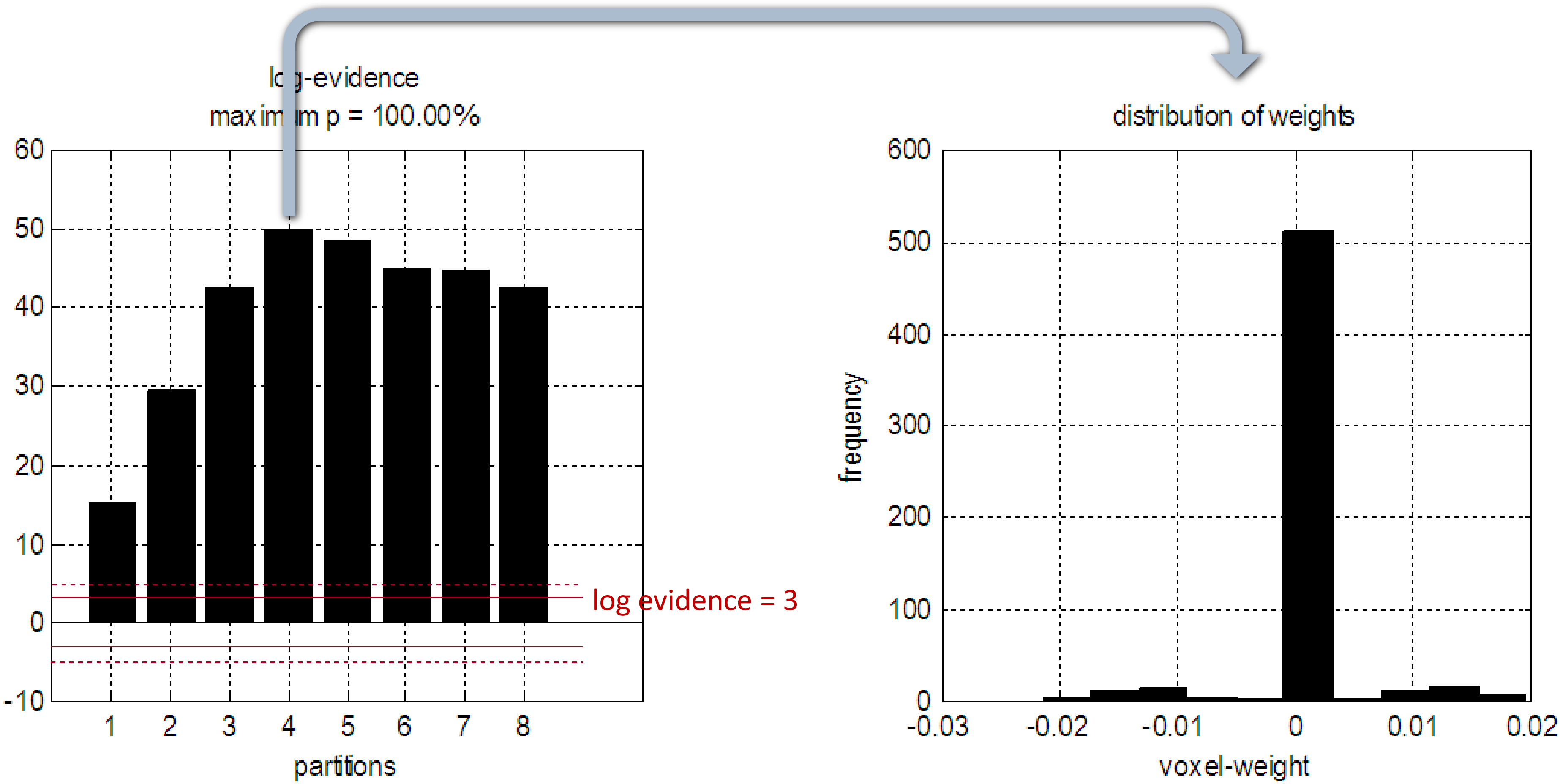


Observations vs. predictions

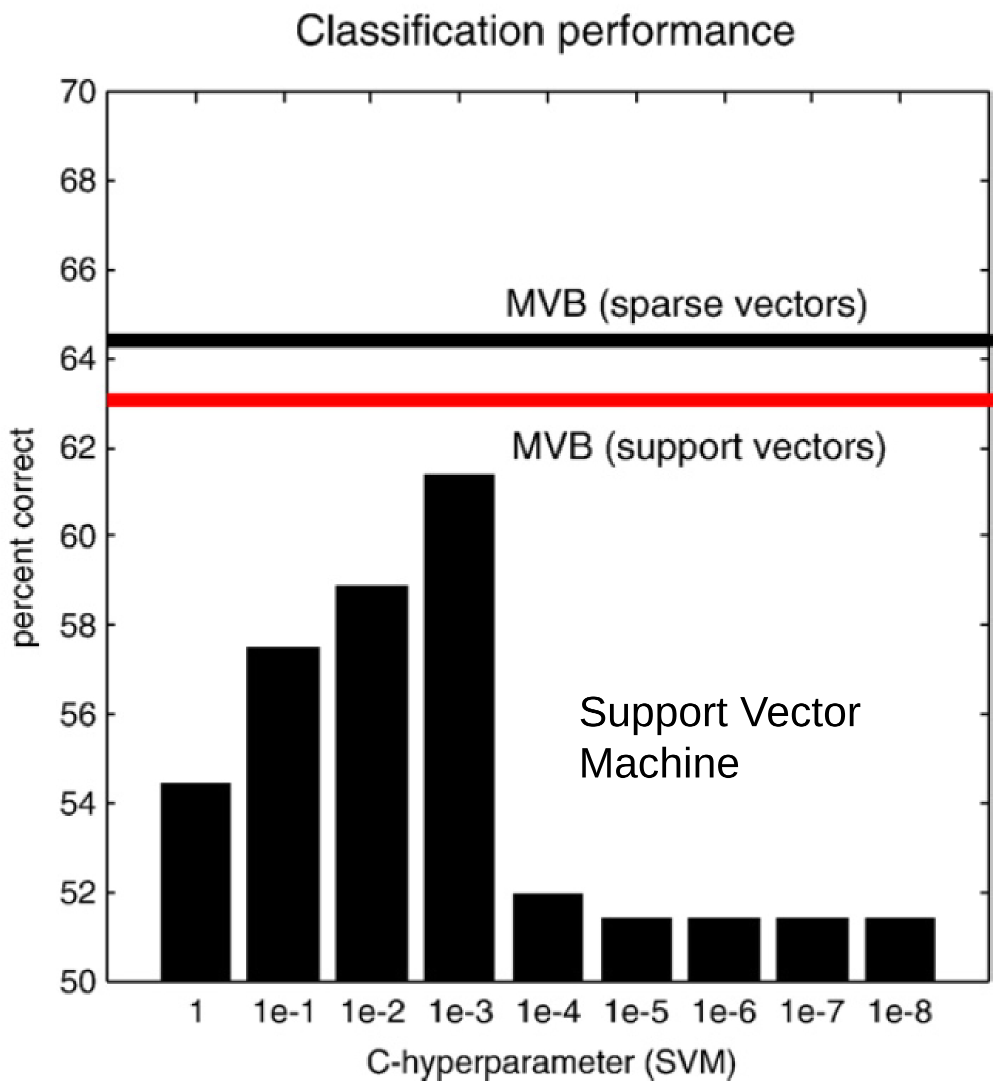




Model evidence and voxel weights



Using MVB for point classification

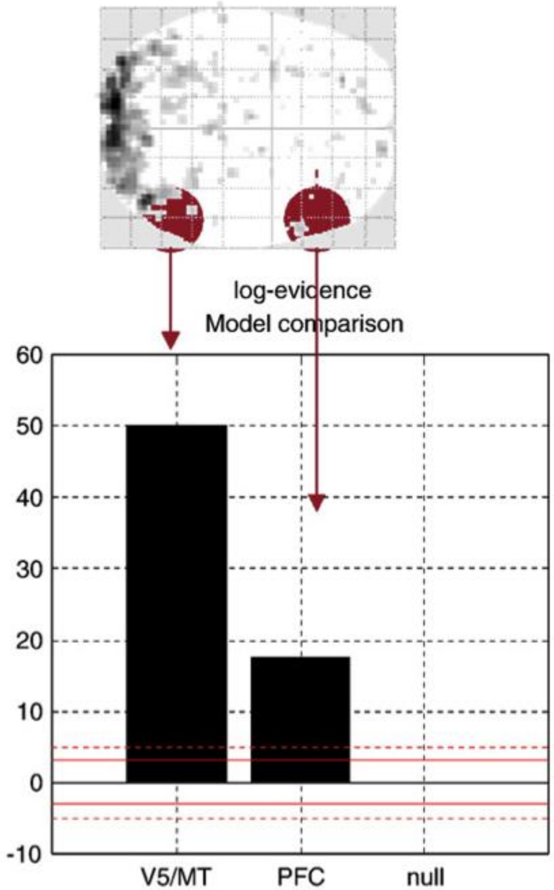


MVB may outperform conventional point classifiers when using a more appropriate coding hypothesis.

Summary: research questions for MVB

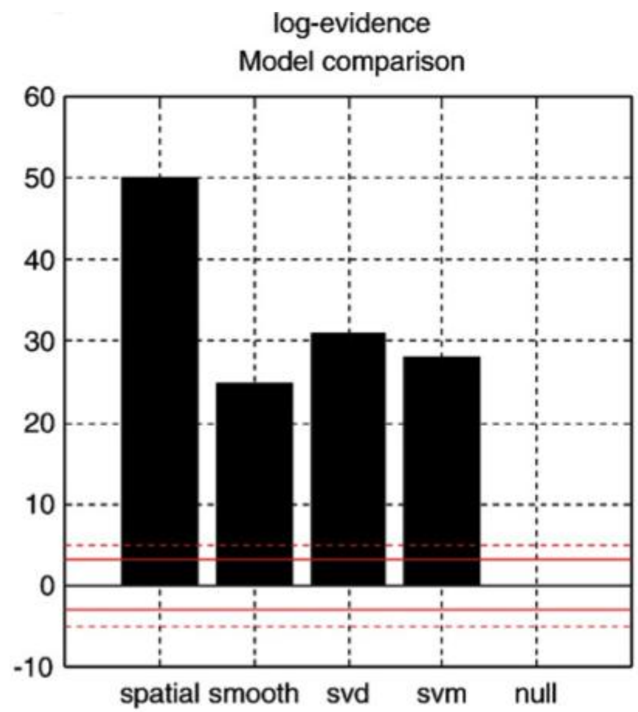
Where does the brain represent things?

Evaluating competing anatomical hypotheses



How does the brain represent things?

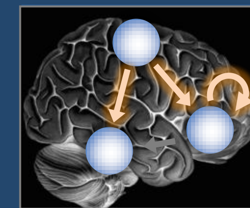
Evaluating competing coding hypotheses



Overview

Classification approaches by data representation

Model-based classification



How do patterns of hidden quantities (e.g., connectivity among brain regions) differ between groups?

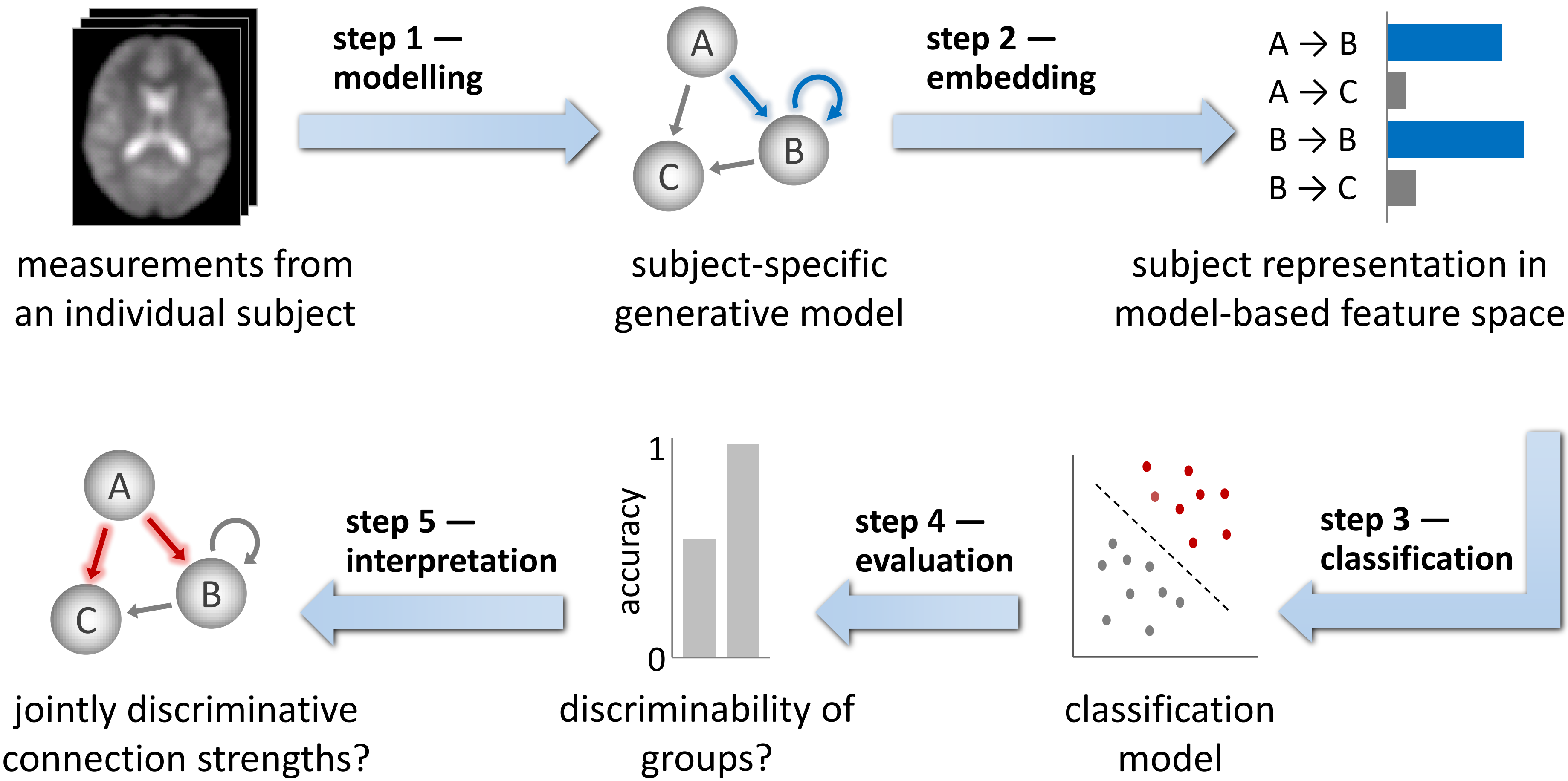
Activation-based classification

Which functional differences allow us to separate groups?

Structure-based classification

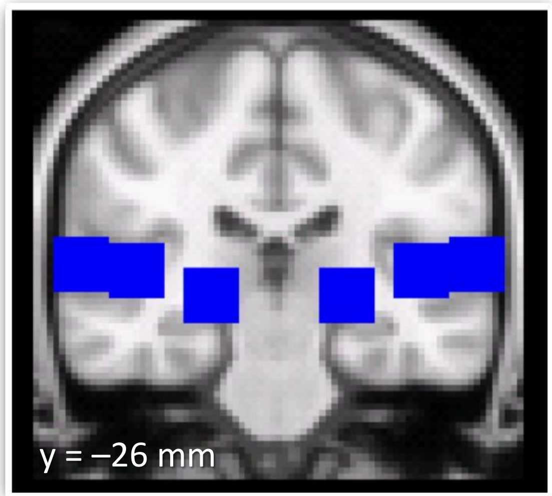
Which anatomical structures allow us to separate patients and healthy controls?

Generative embedding for model-based classification



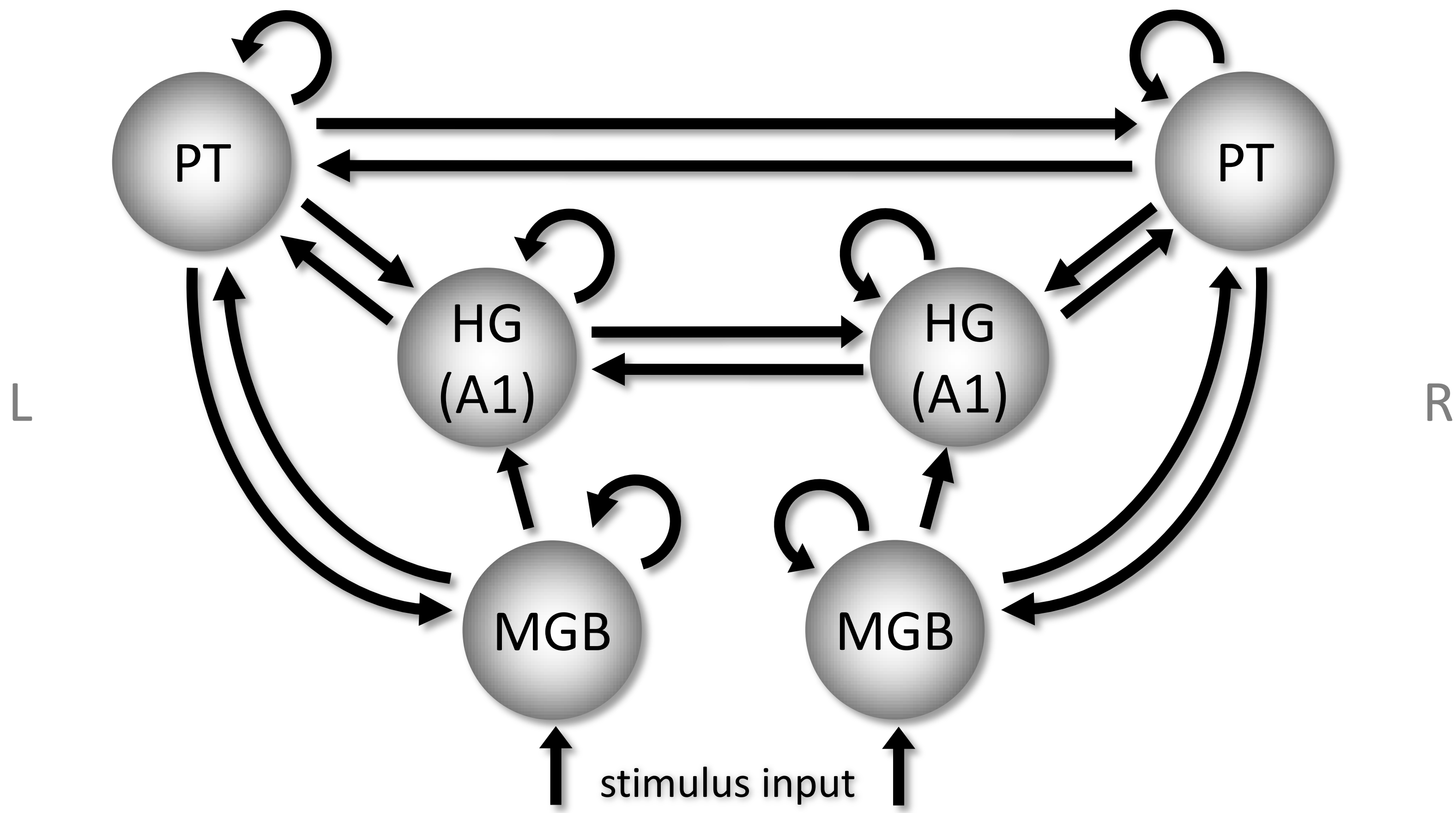
Brodersen, Haiss, Ong, Jung, Tittgemeyer, Buhmann, Weber, Stephan (2011) *NeuroImage*
Brodersen, Schofield, Leff, Ong, Lomakina, Buhmann, Stephan (2011) *PLoS Comput Biol*

Example: diagnosing stroke patients

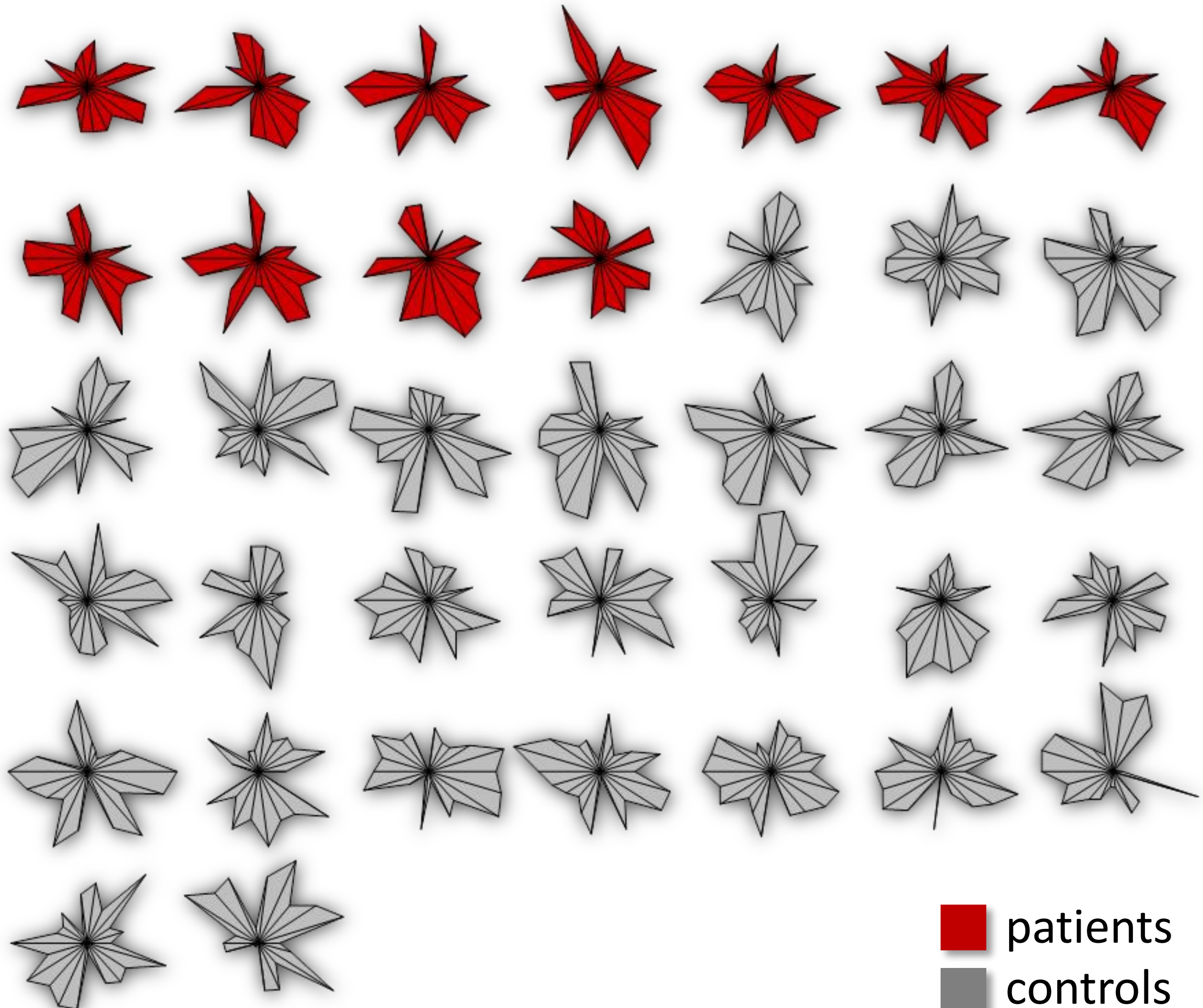


anatomical regions of interest

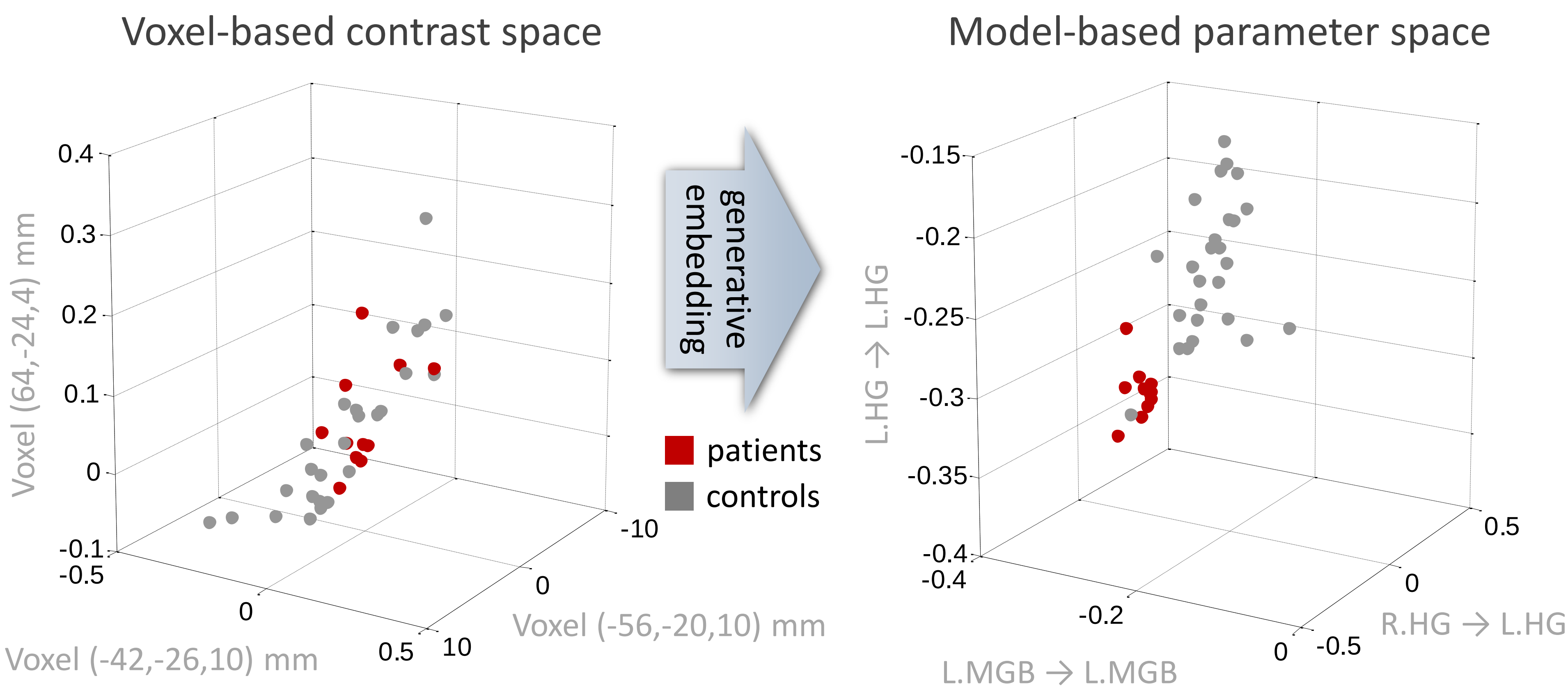
Example: diagnosing stroke patients



Multivariate analysis: connectional fingerprints



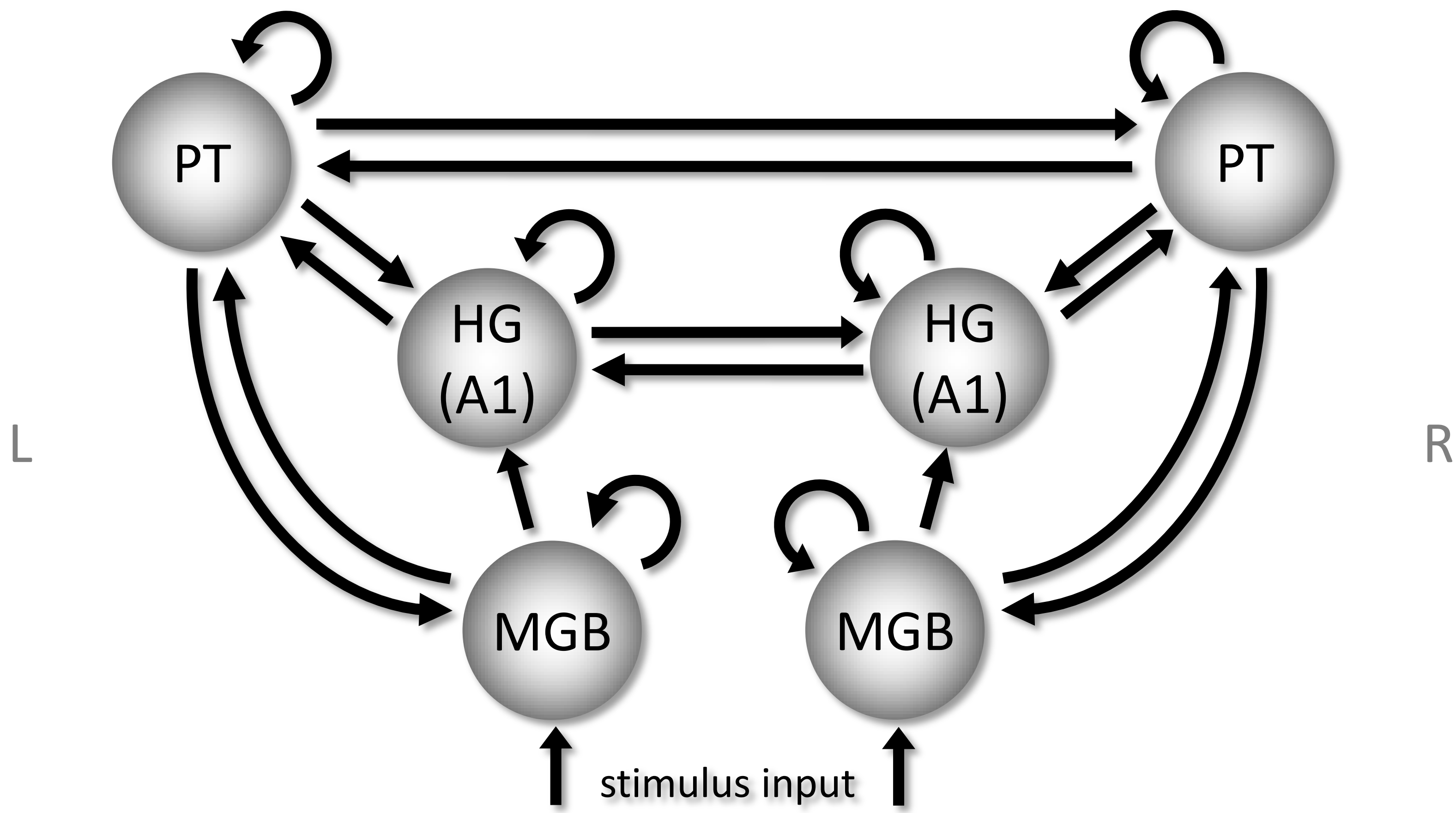
Dissecting diseases into physiologically distinct subgroups



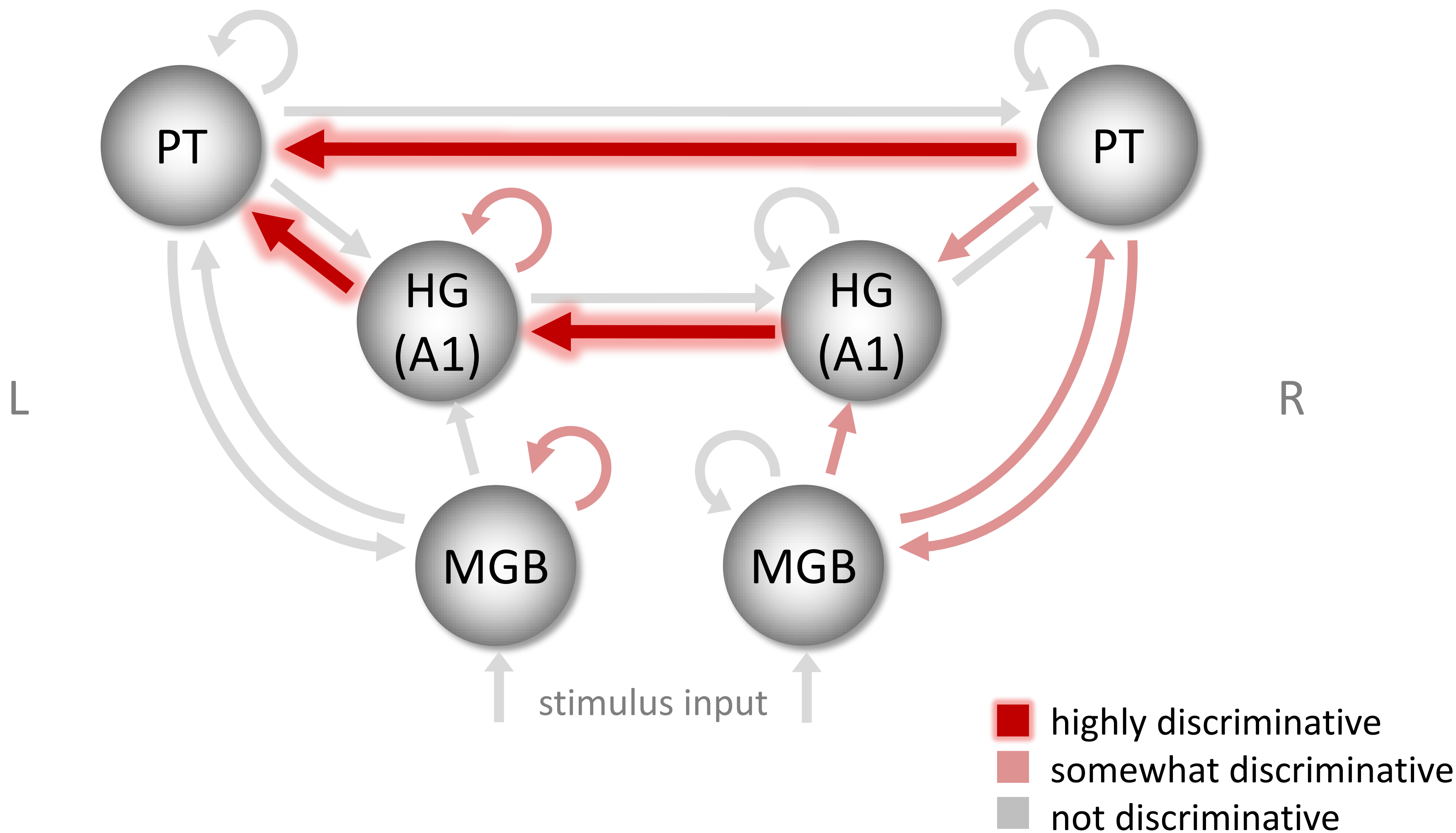
classification accuracy
(using all voxels in the regions of interest)
75%

classification accuracy
(using all 23 model parameters)
98%

Discriminative features in model space



Discriminative features in model space

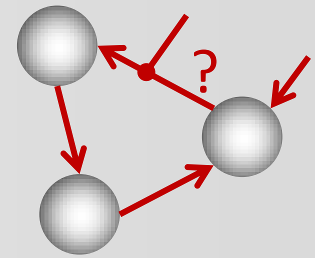


Generative embedding and DCM

Question 1 – What do the data tell us about hidden processes in the brain?

⇨ compute the posterior

$$p(\theta|y,m) = \frac{p(y|\theta,m)p(\theta|m)}{p(y|m)}$$

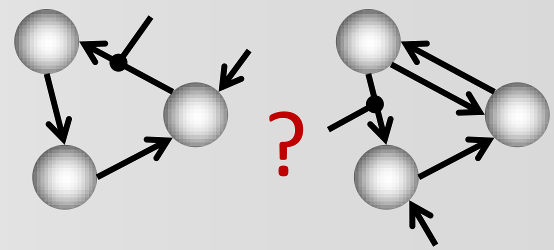


Question 2 – Which model is best w.r.t. the observed fMRI data?

⇨ compute the model evidence

$$p(m|y) \propto p(y|m)p(m)$$

$$= \int p(y|\theta,m)p(\theta|m)d\theta$$

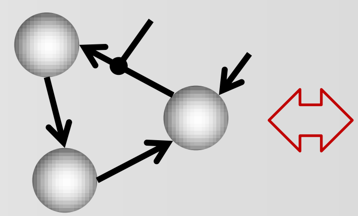


Question 3 – Which model is best w.r.t. an external criterion?

⇨ compute the classification accuracy

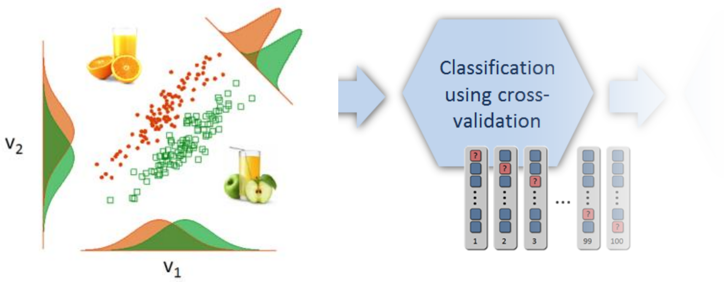
$$p(h(y) = x|y)$$

$$= \iiint p\big(h(y) = x\big|y, y_{\text{train}}, x_{\text{train}}\big)\, p(y)\, p\big(y_{\text{train}}\big)\, p\big(x_{\text{train}}\big)\; dy\; dy_{\text{train}}\; x_{\text{train}}$$



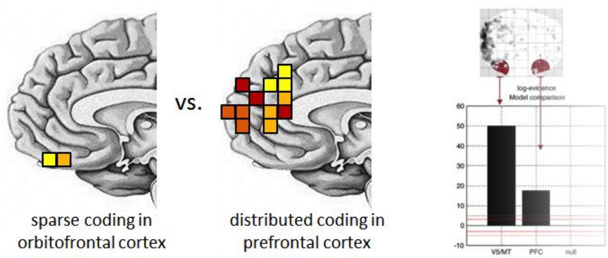
{ patient, control }

Summary



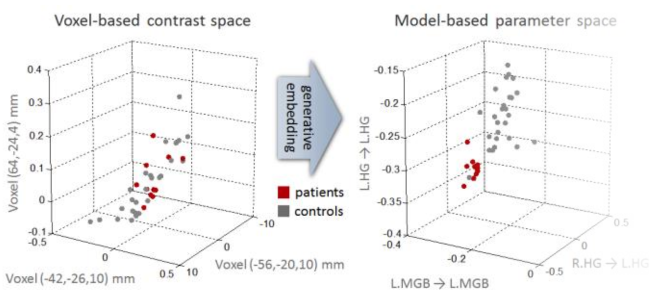
Classification

- to assess whether a cognitive state is linked to patterns of activity
- to assess the spatial deployment of discriminative activity



Multivariate Bayes

- to evaluate competing anatomical hypotheses
- to evaluate competing coding hypotheses



Model-based analyses

- to assess whether groups differ in terms of patterns of connectivity
- to generate new grouping hypotheses