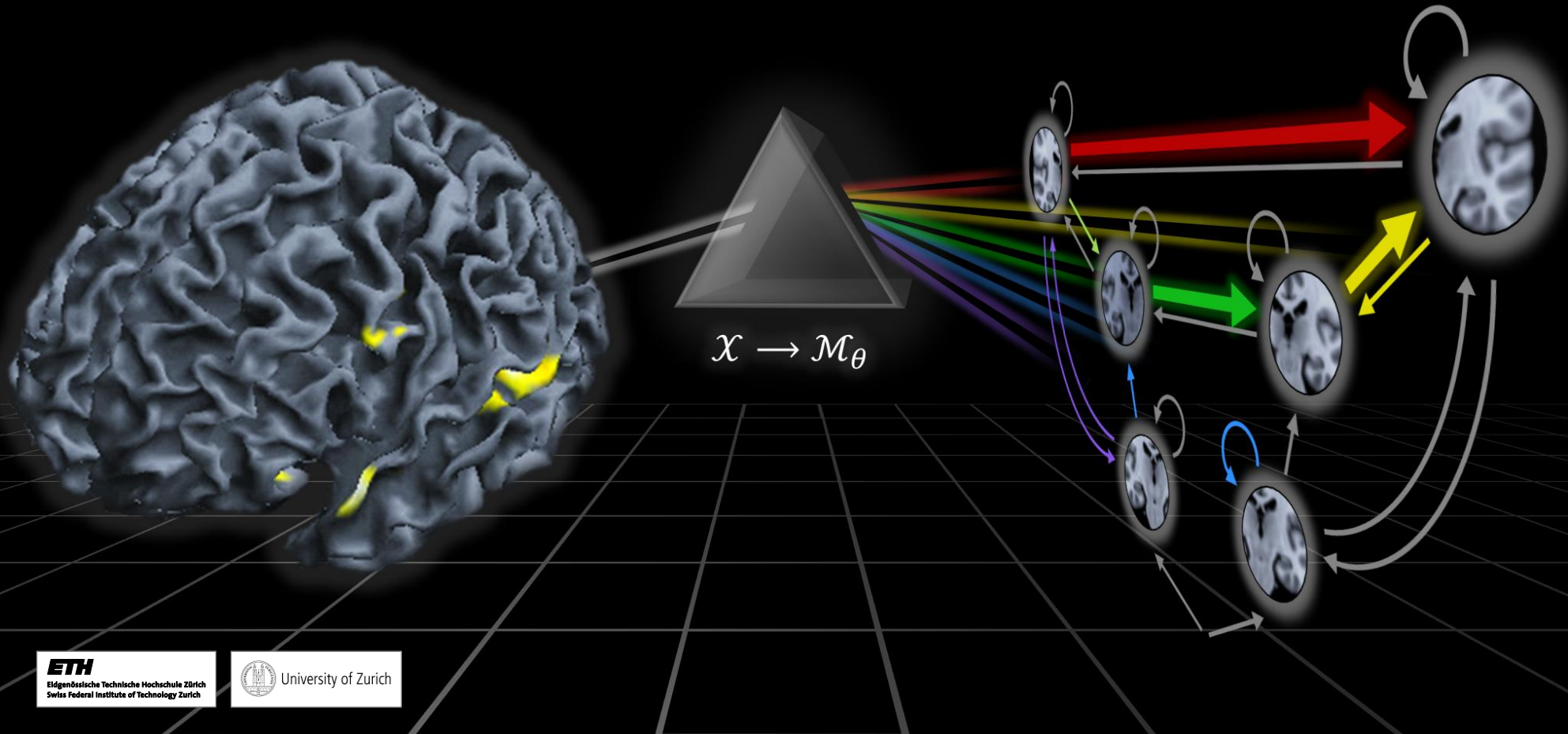


# Generative embedding and model-based classification

Kay H. Brodersen<sup>1,2</sup>

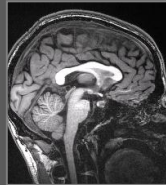
<sup>1</sup> Department of Computer Science, ETH Zurich, Switzerland

<sup>2</sup> Department of Economics, University of Zurich, Switzerland



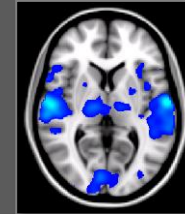
# Classification approaches by data representation

## Structure-based classification



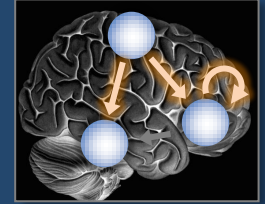
Which anatomical structures allow us to separate patients and healthy controls?

## Activation-based classification



Which functional differences allow us to separate groups?

## Model-based classification



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

# Colleagues & collaborators



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ETH Zurich



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**Joachim M Buhmann**  
ETH Zurich



**Alexander Leff**  
University College London

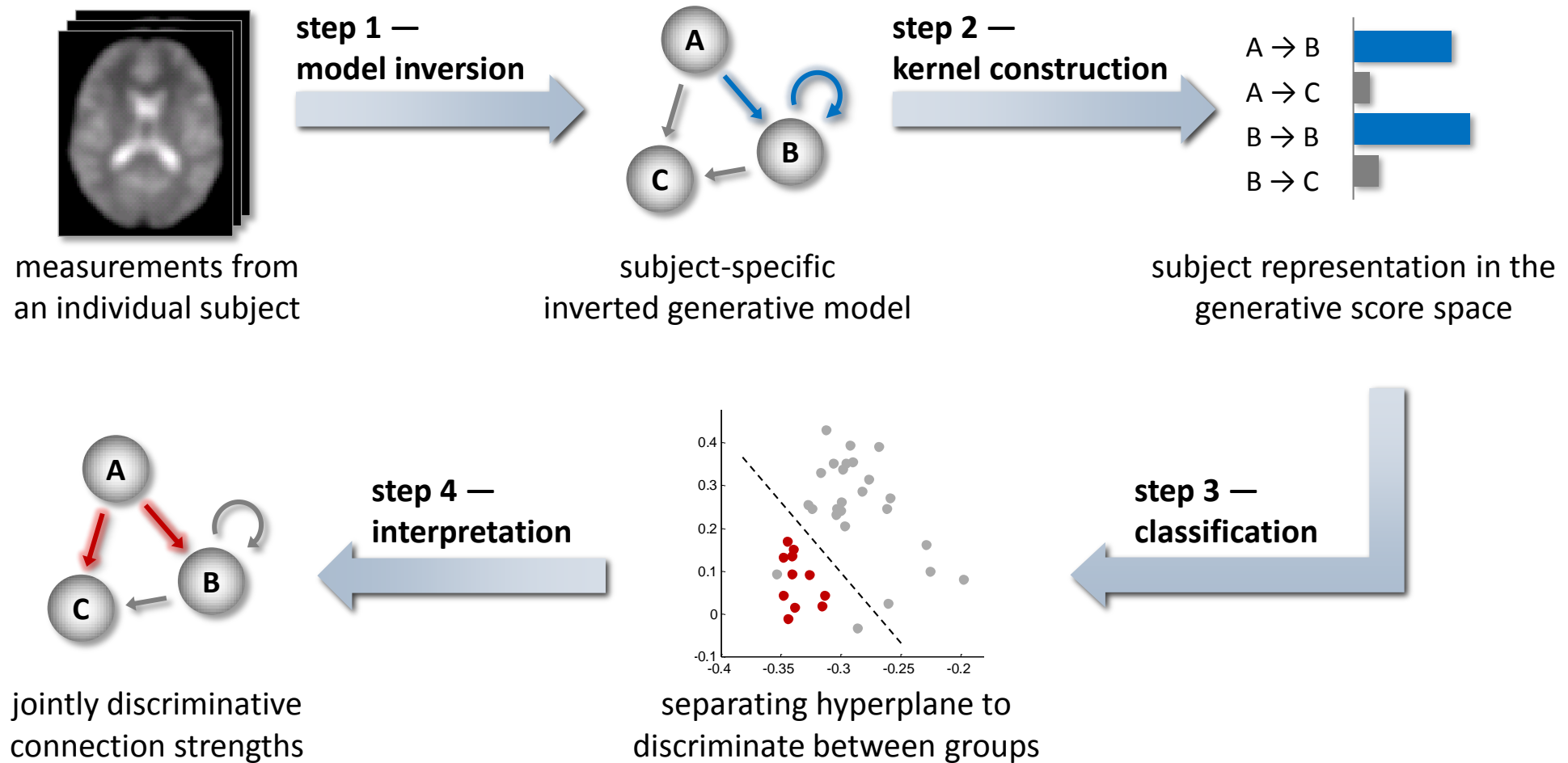


**Klaas Enno Stephan**  
University of Zurich · University College London



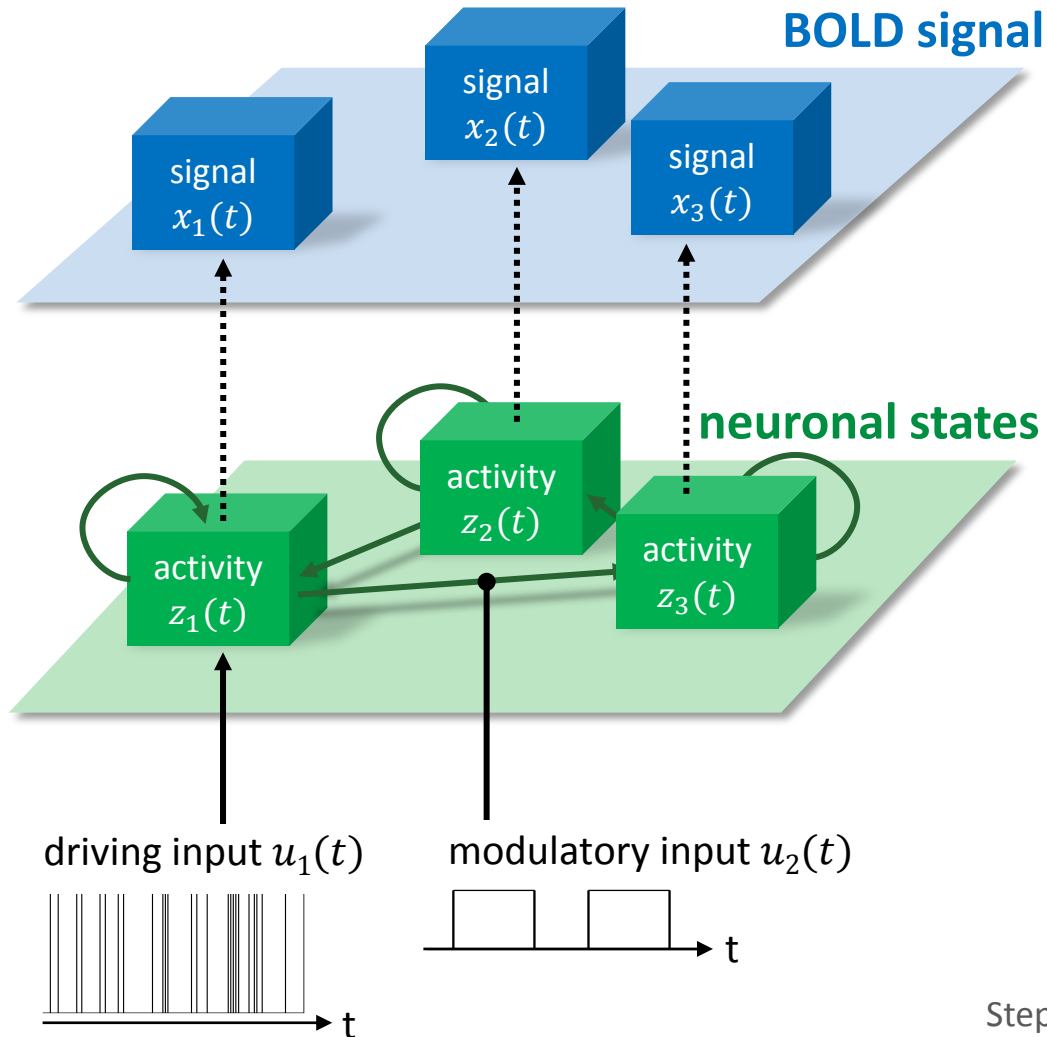
**Christoph Mathys**  
University of Zurich · ETH Zurich

# Model-based classification through generative embedding



Brodersen et al. (2011) *NeuroImage*; Brodersen et al. (2011) *PLoS Comput Biol*

# Choosing a generative model: DCM for fMRI



**haemodynamic forward model**

$$x = g(z, \theta_h)$$

**neural state equation**

$$\dot{z} = (A + \sum u_j B^{(j)})z + Cu$$

↑  
intrinsic  
connectivity

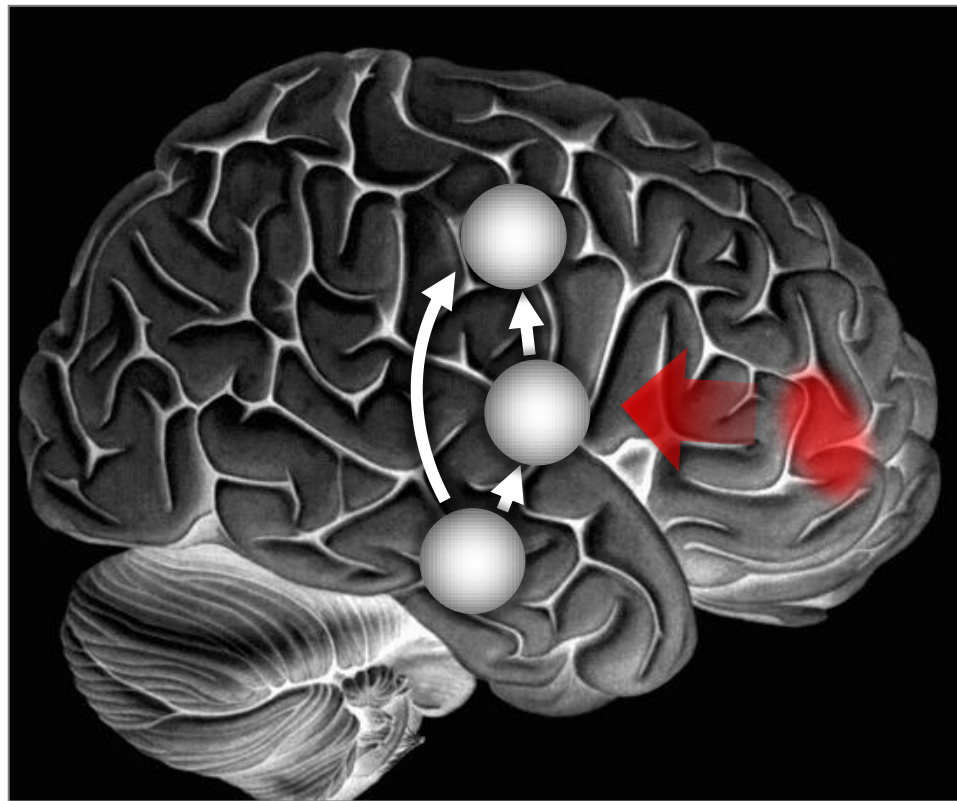
↑  
modulation of  
connectivity

↑  
direct inputs

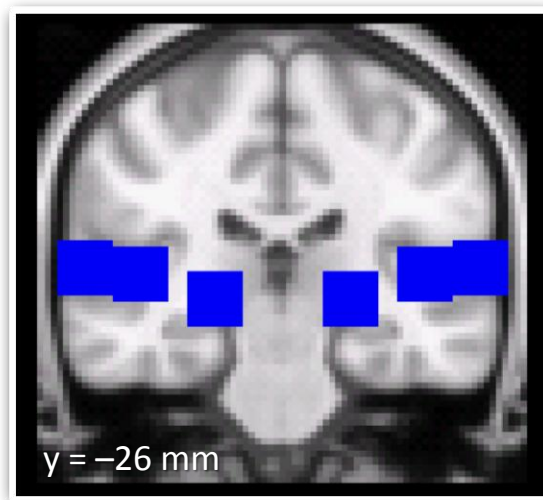
Friston, Harrison & Penny (2003) *NeuroImage*  
Stephan & Friston (2007) *Handbook of Brain Connectivity*


## Example: diagnosing stroke patients

To illustrate our approach, we aimed to distinguish between stroke patients and healthy controls, based on non-lesioned regions involved in speech processing.

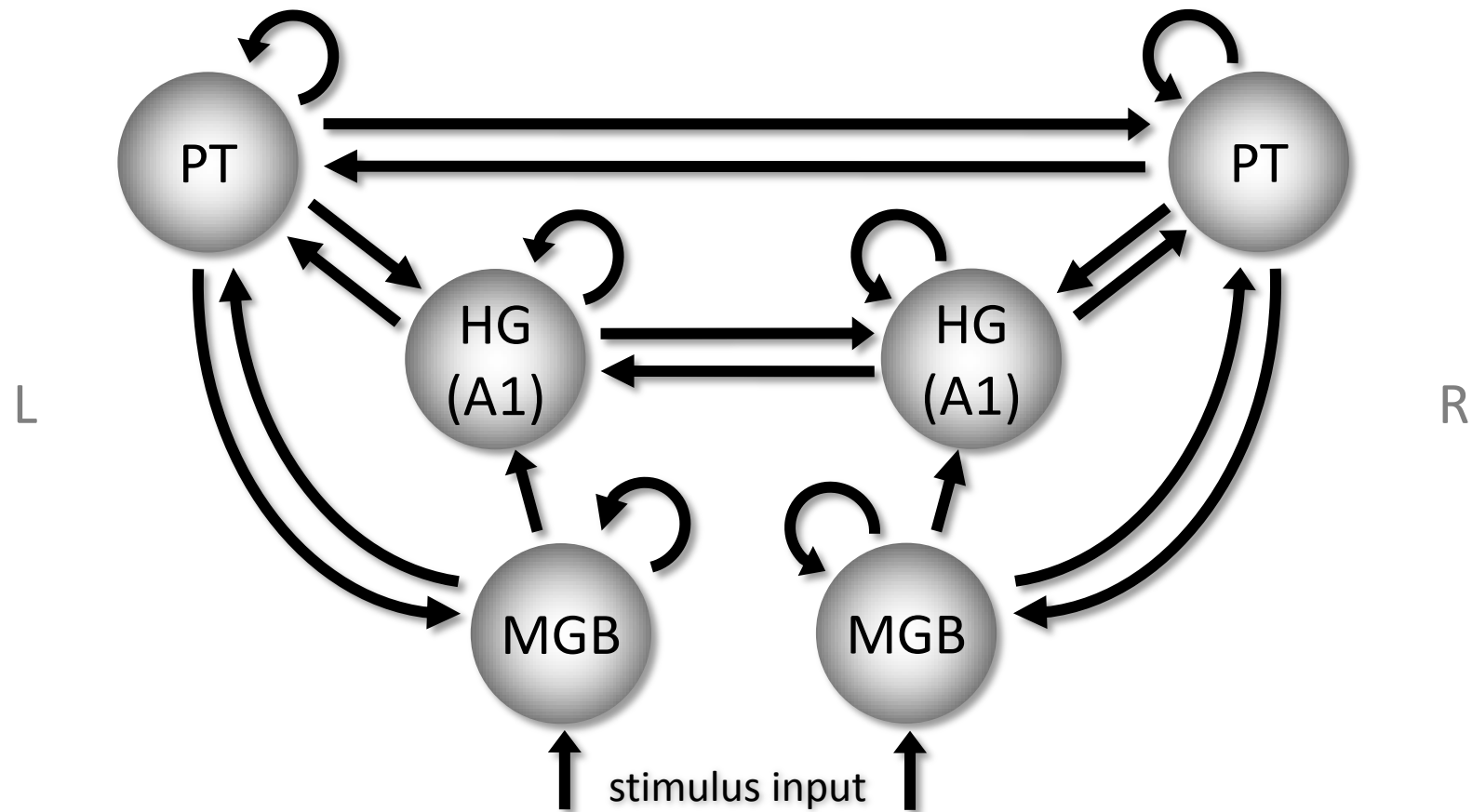


# Example: diagnosing stroke patients



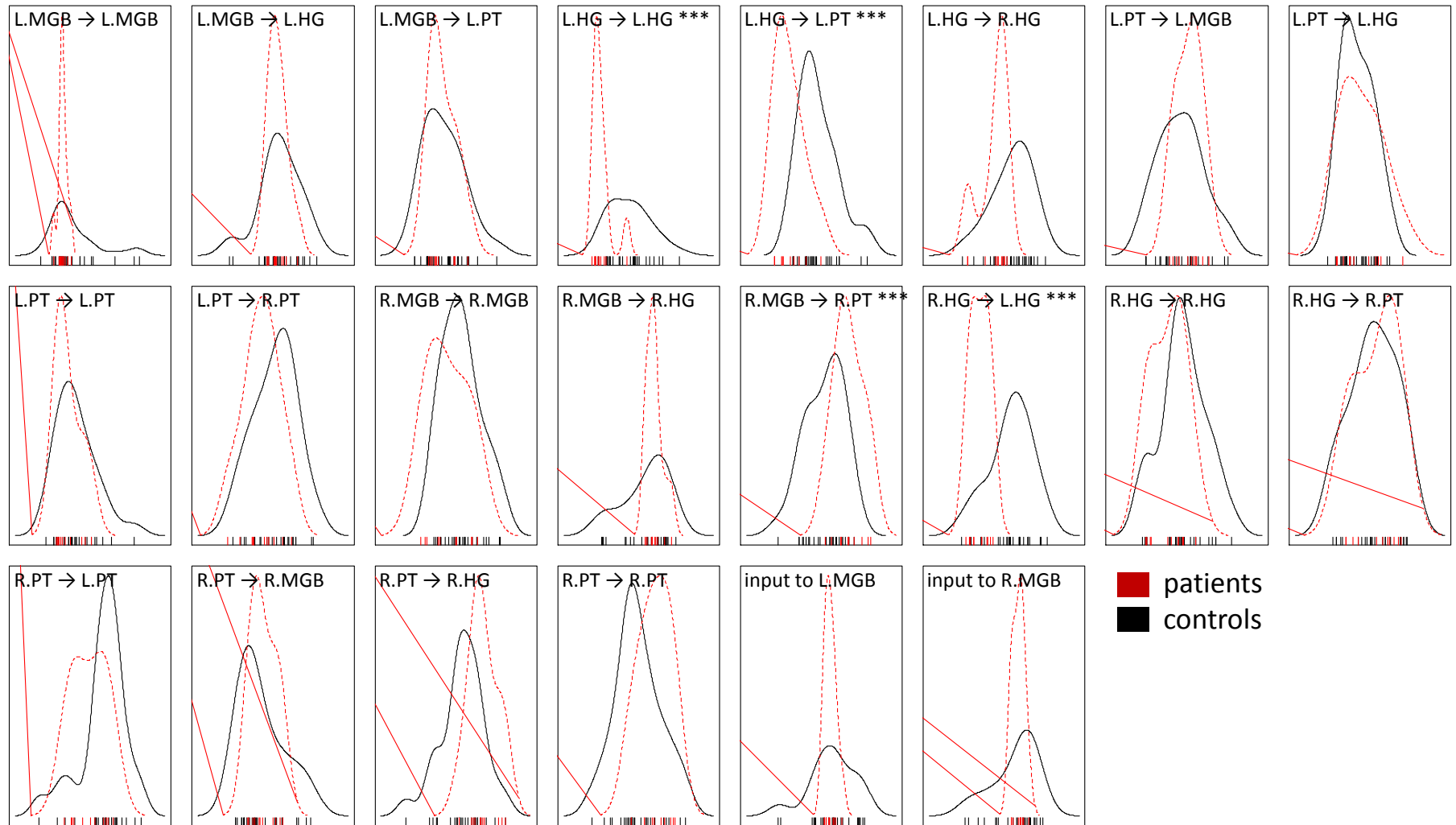
 anatomical regions of interest

## Example: diagnosing stroke patients

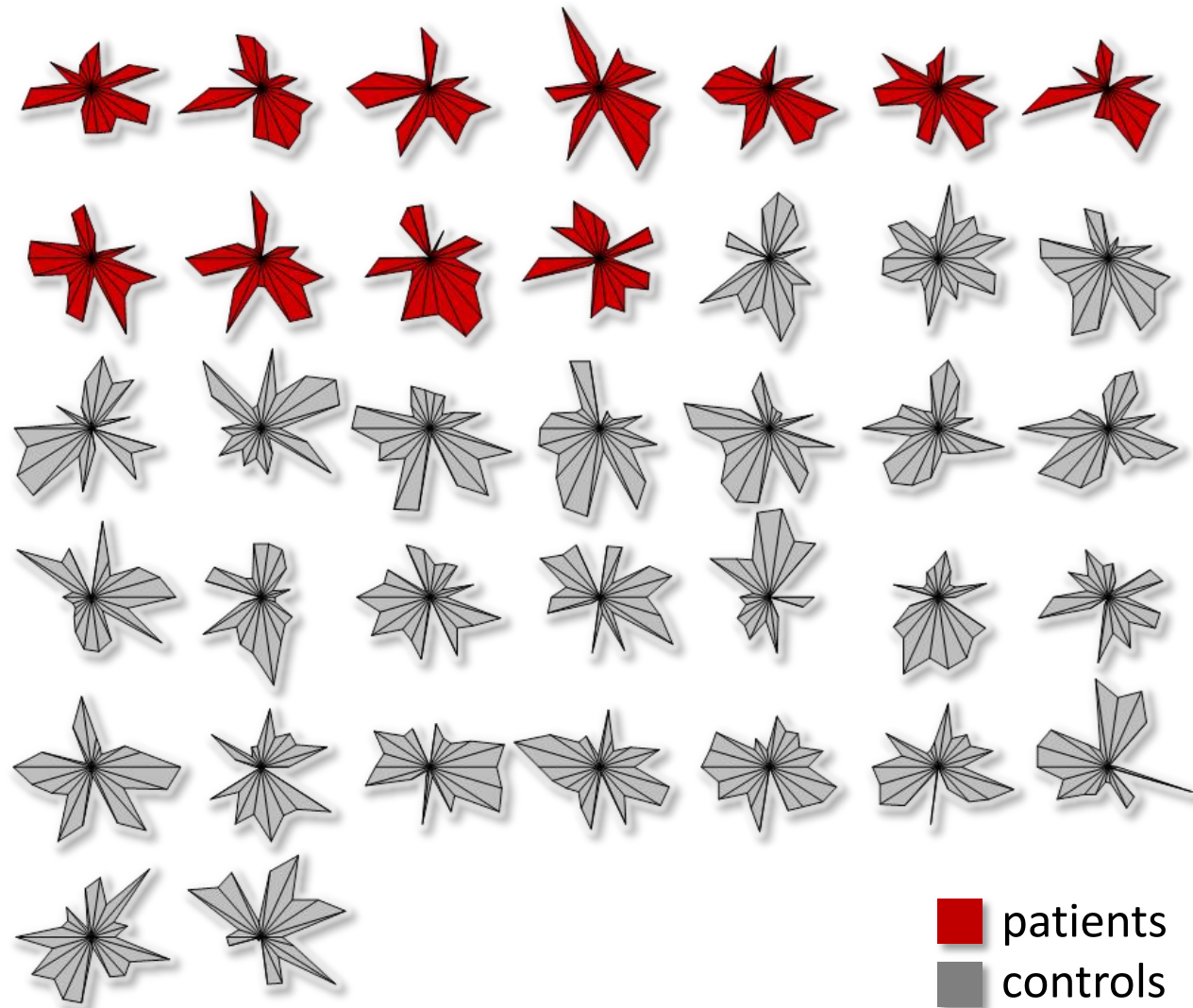




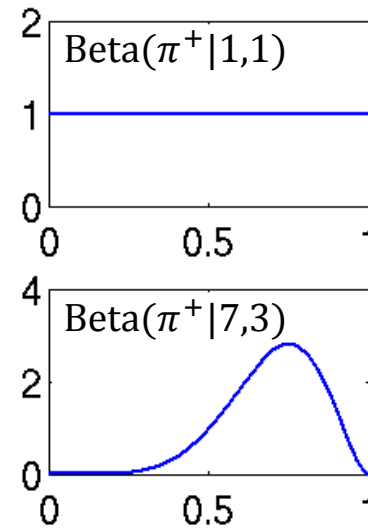
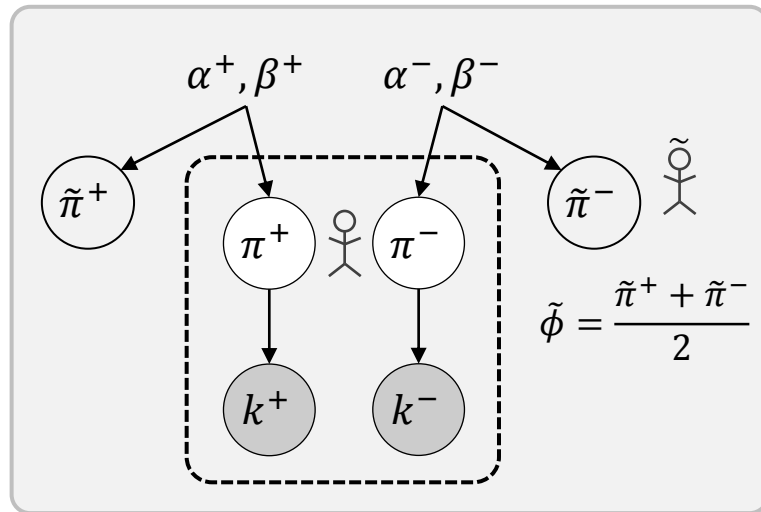
# Univariate analysis: parameter densities



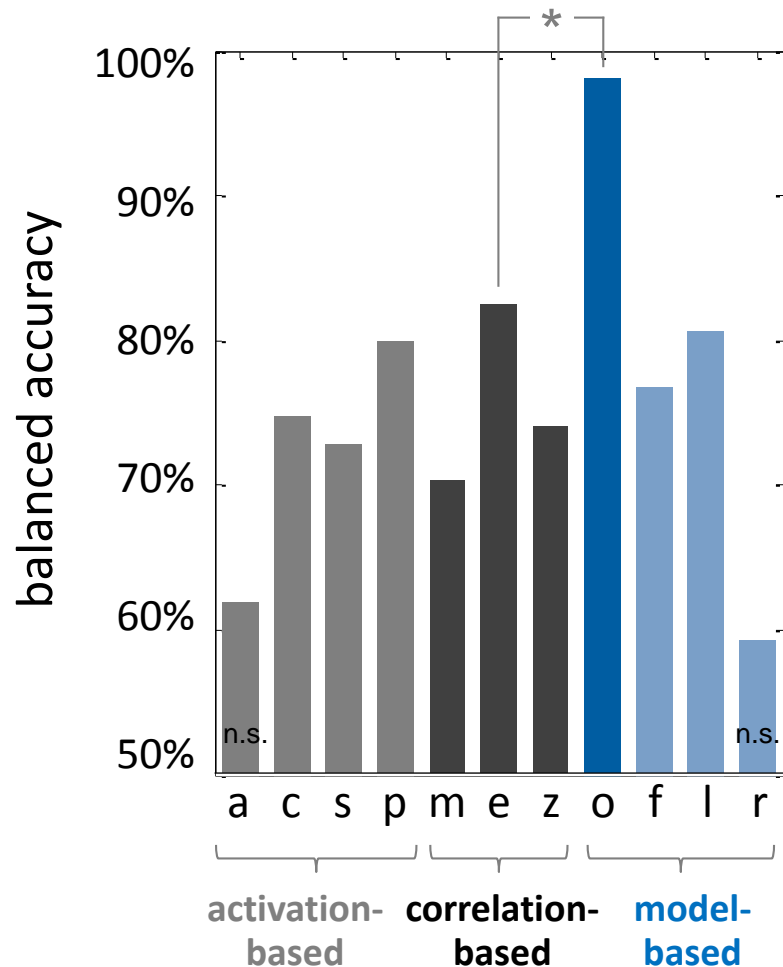
# Multivariate analysis: connectional fingerprints



# Full Bayesian approach to performance evaluation



# Classification performance



## Activation-based analyses

- a anatomical feature selection
- c mass-univariate contrast feature selection
- s locally univariate searchlight feature selection
- p PCA-based dimensionality reduction

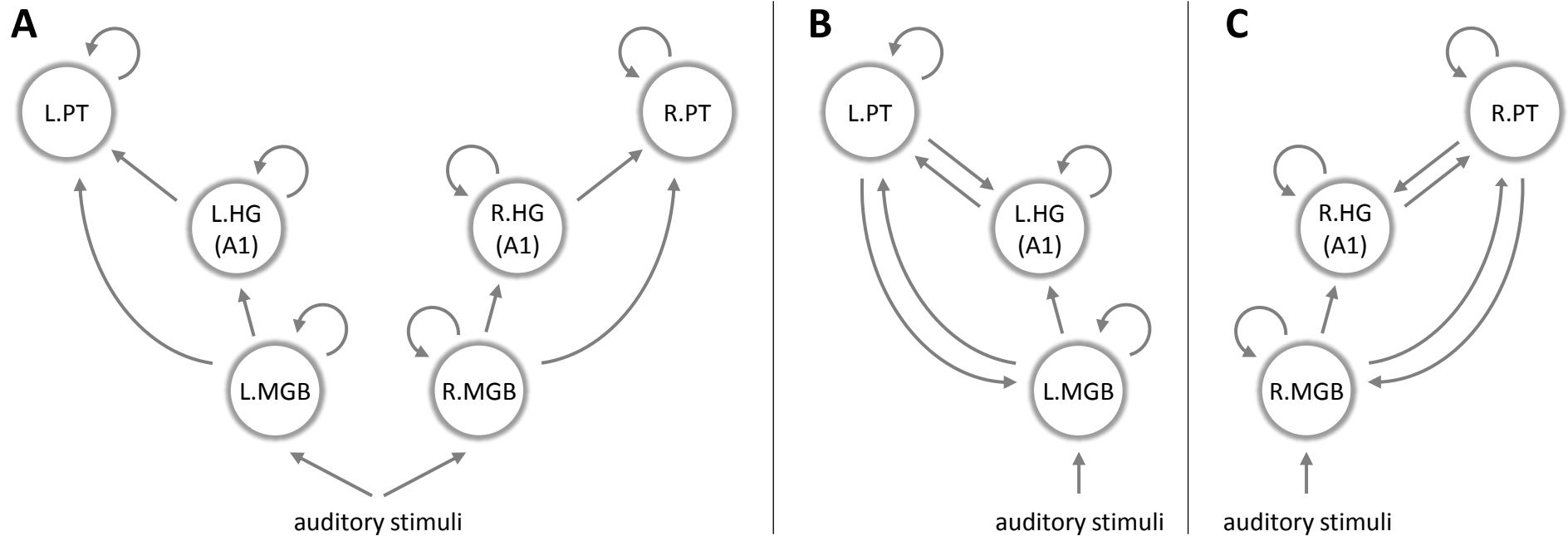
## Correlation-based analyses

- m correlations of regional means
- e correlations of regional eigenvariates
- z Fisher-transformed eigenvariates correlations

## Model-based analyses

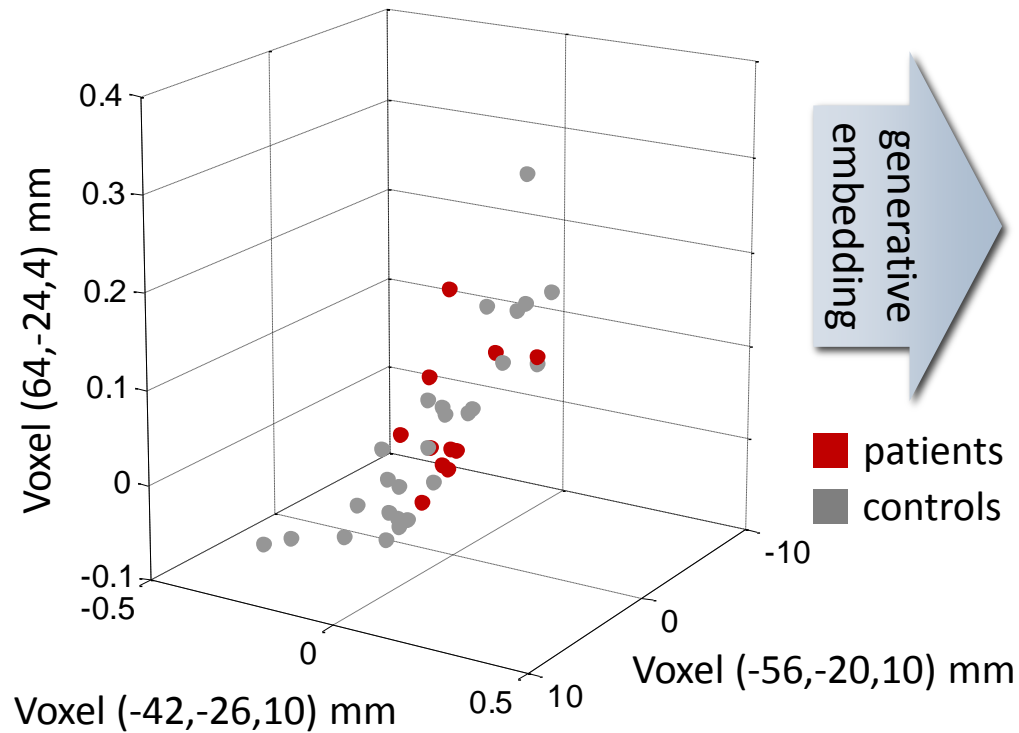
- o gen.embed., original full model
- f gen.embed., less plausible feedforward model
- l gen.embed., left hemisphere only
- r gen.embed., right hemisphere only

# Biologically less plausible models perform poorly

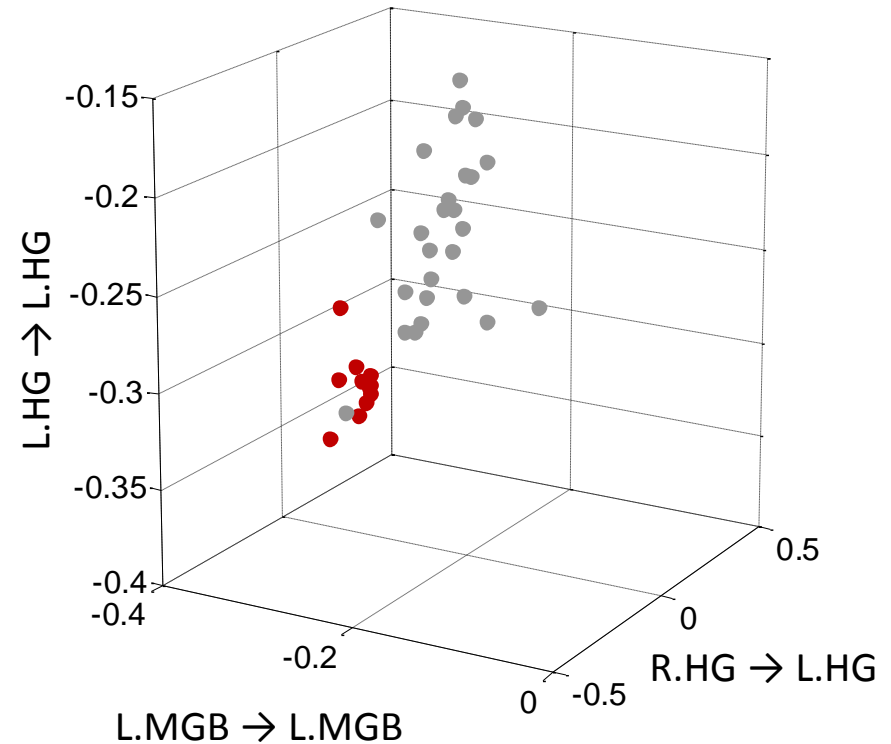


# The generative projection

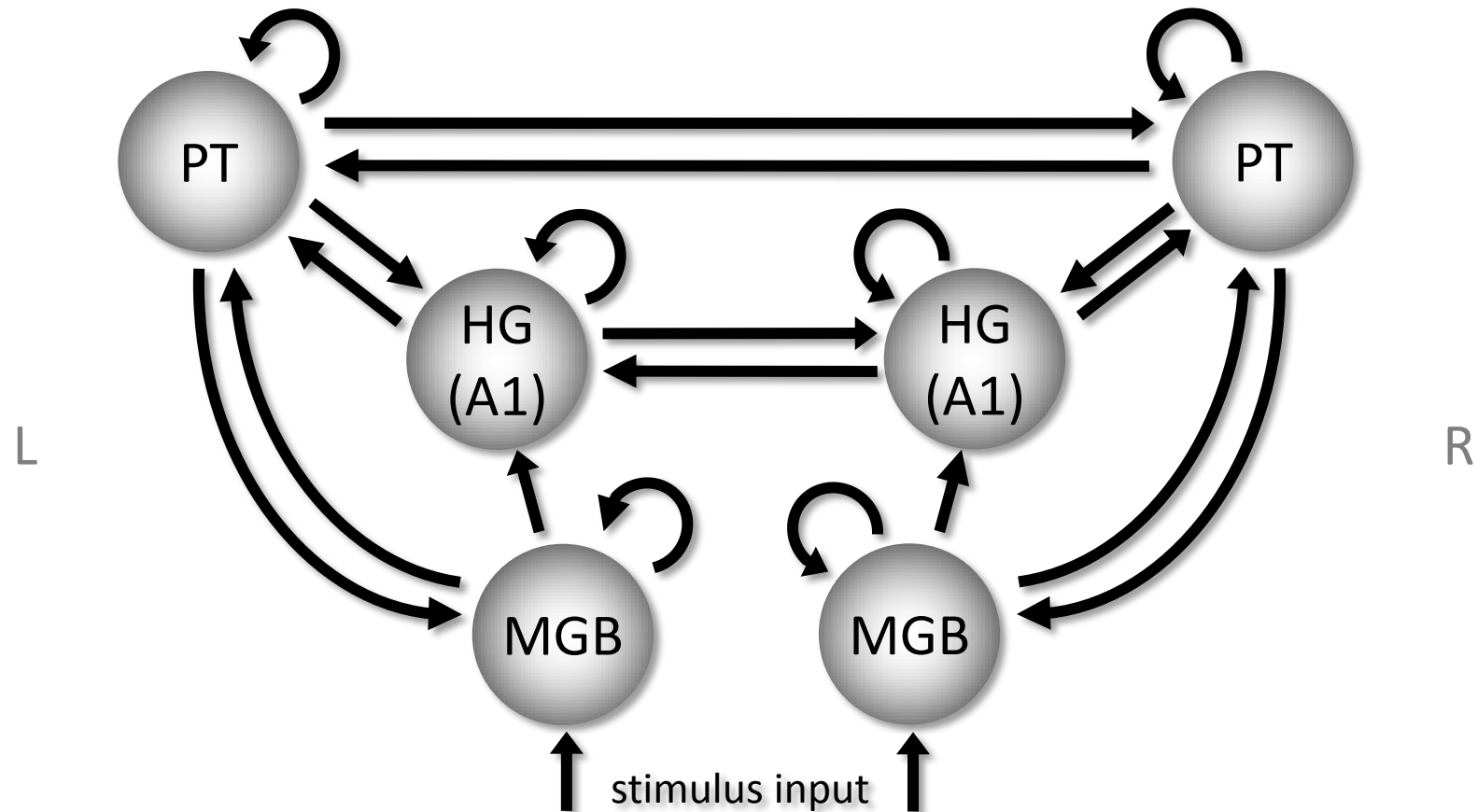
## Voxel-based activity space



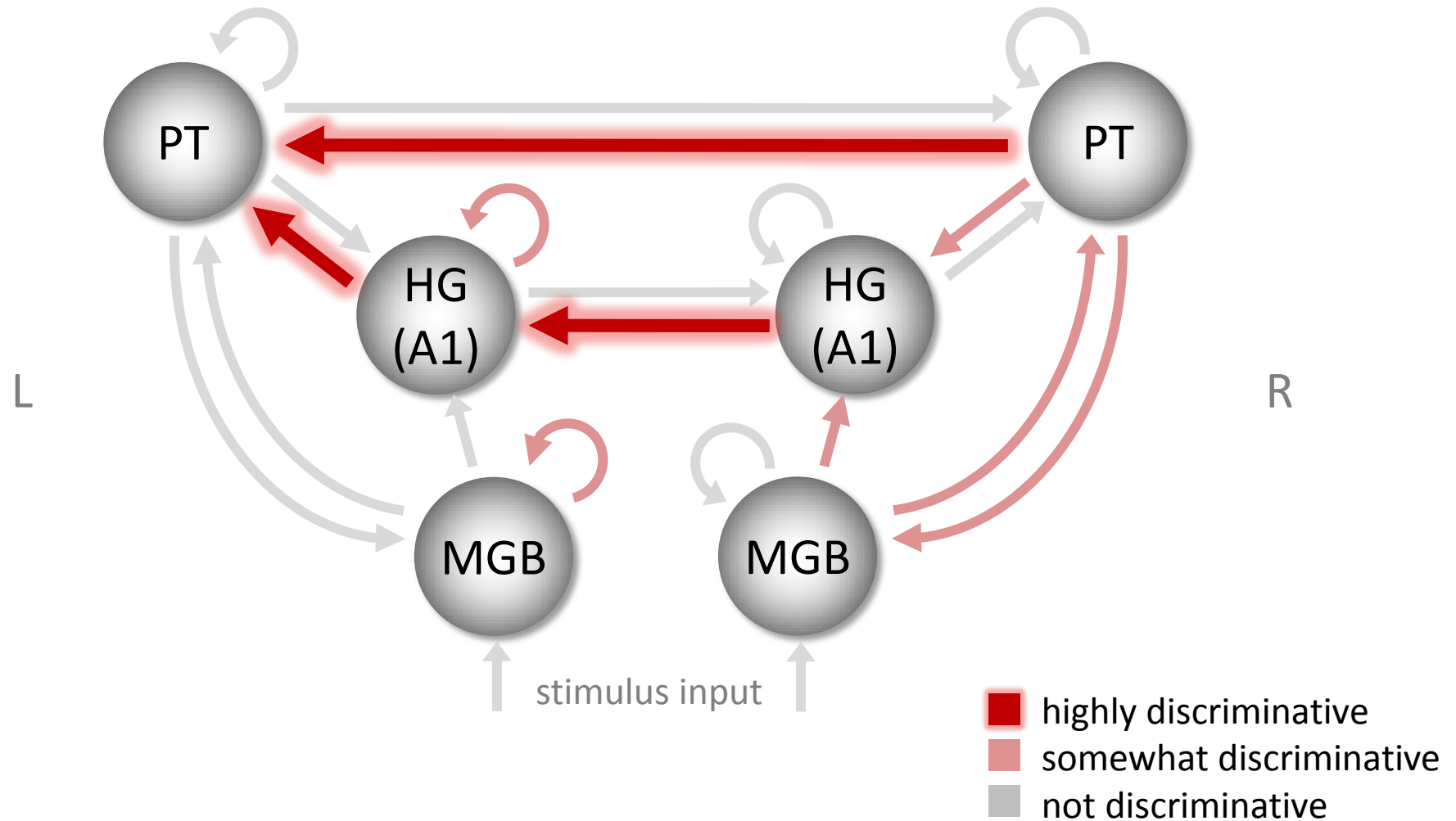
## Model-based parameter space



# Discriminative features in model space

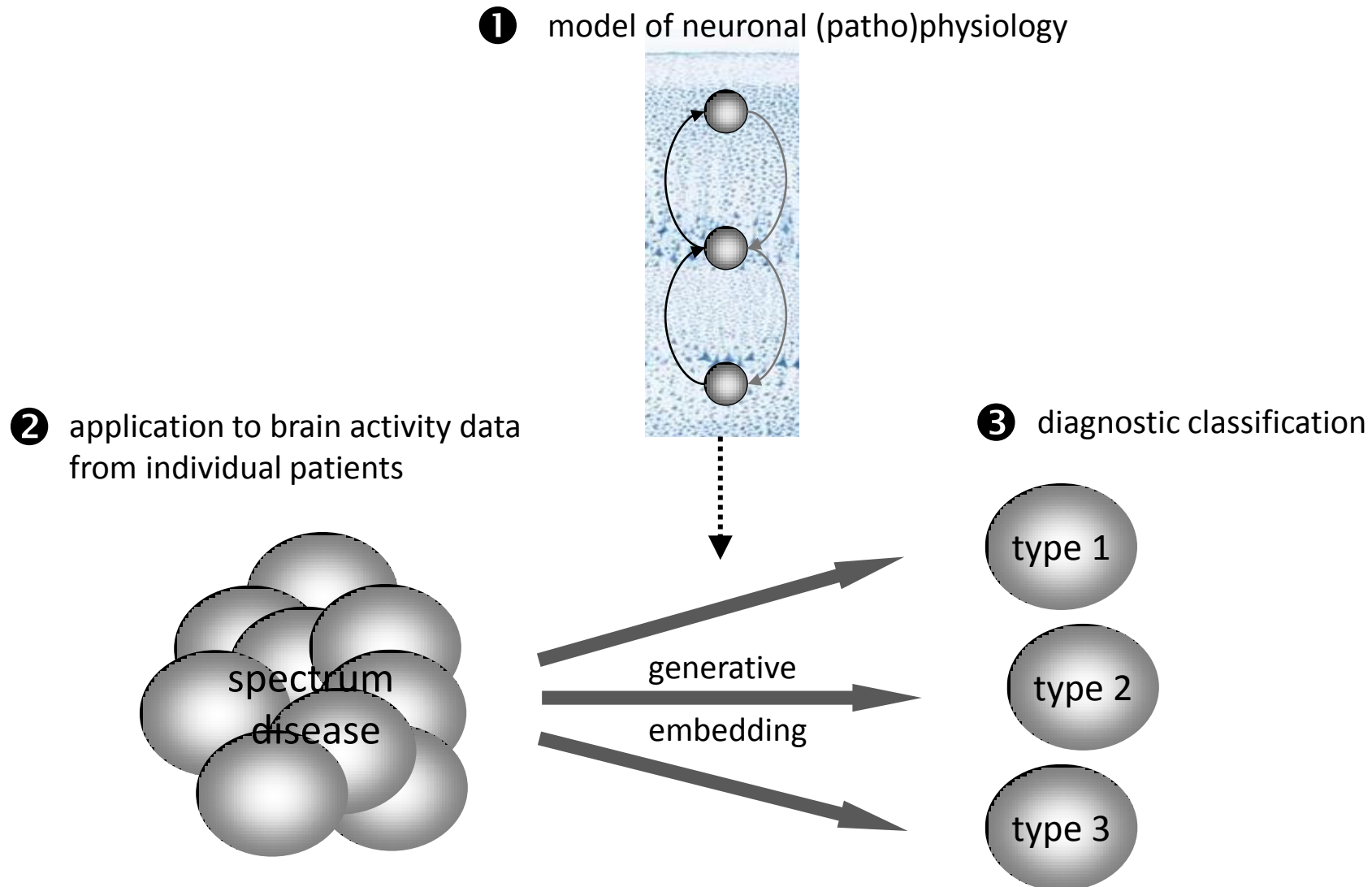


# Discriminative features in model space





# Model-based inference on individual pathophysiology



# Summary: generative embedding for fMRI

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- ① **Strong classification performance.** Generative embedding exploits the rich discriminative information encoded in 'hidden' quantities, such as coupling parameters.
- ② **Creation of an interpretable feature space.** High-dimensional fMRI data are replaced by low-dimensional subject-specific fingerprints with biologically interpretable axes.
- ③ **Future applications.** Generative embedding could help dissect spectrum disorders into physiologically defined subgroups (*in preparation*).