

# Statistical methods for functional brain connectivity mapping

Bertrand Thirion

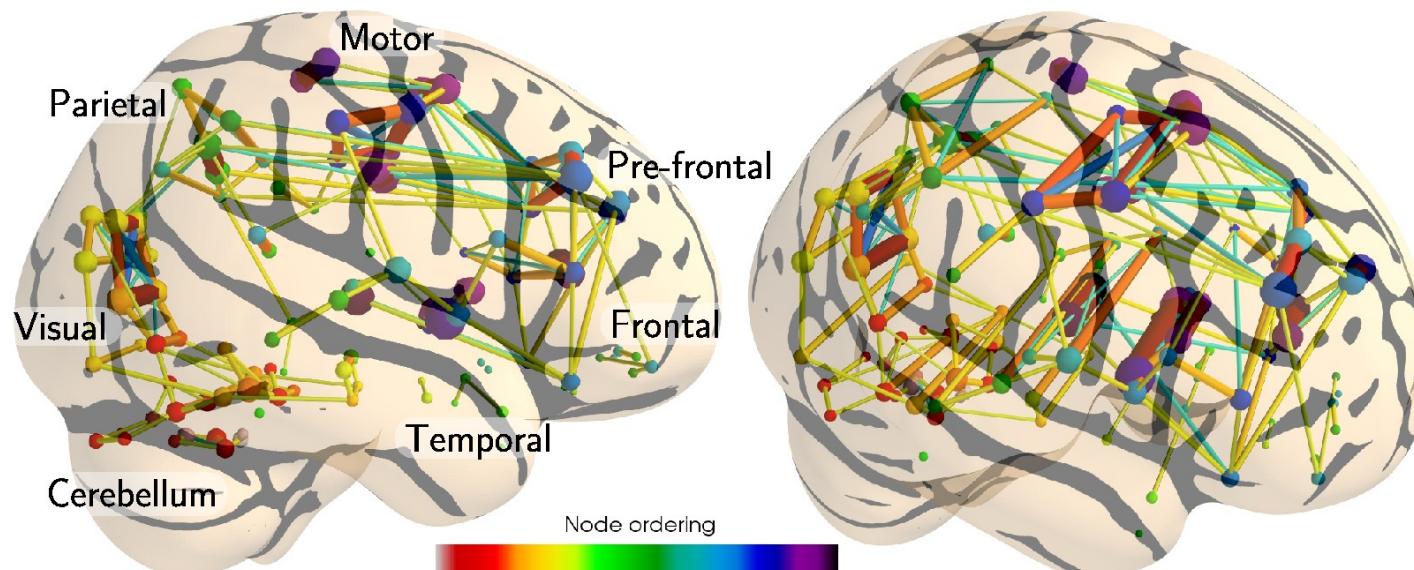
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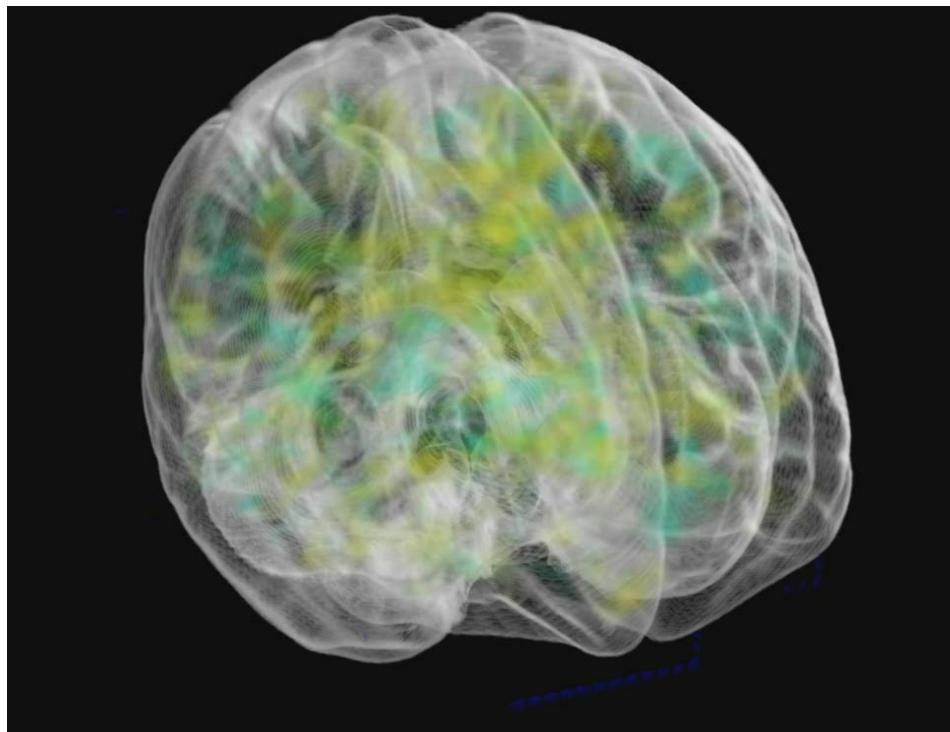
# Outline

- Introduction to functional connectivity analysis
- Defining regions from fMRI data
- Statistical inference on covariance models

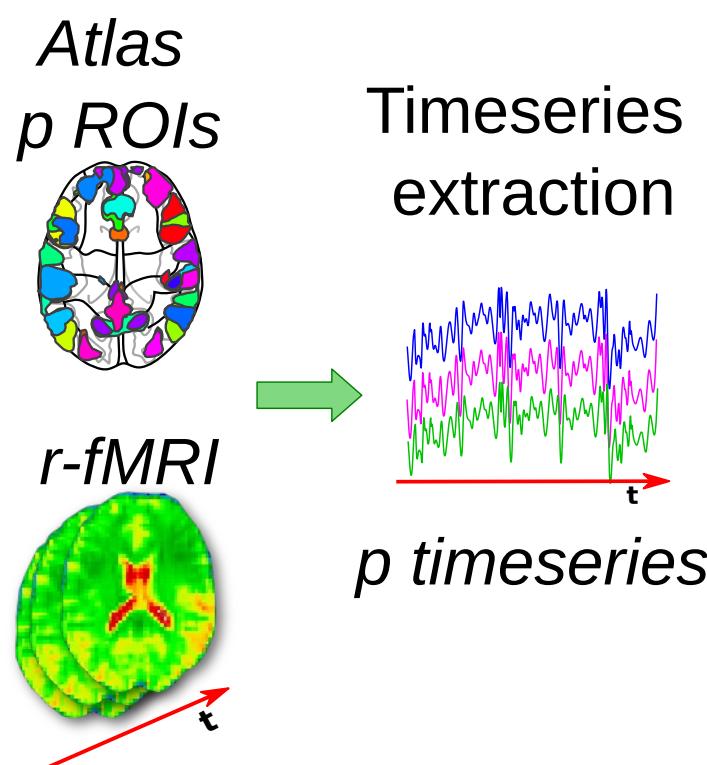


# Functional Connectivity

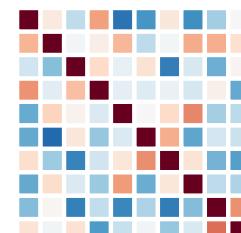
- **Resting-state experiments:** neural signals / absence of task
  - Informative on brain organization: **segregation & integration**
  - In task-fMRI, task covariates fit 2-5% of brain signals; remaining *intrinsic activity* not understood
  - Neural signals **mixed** with external signal: perceptual & motor activity, biological rhythms etc.



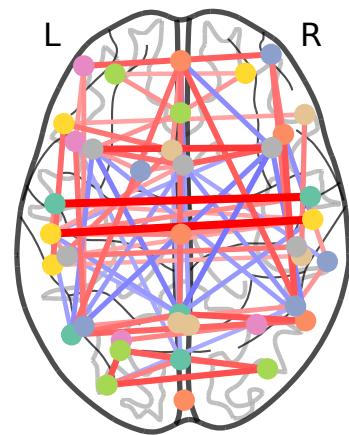
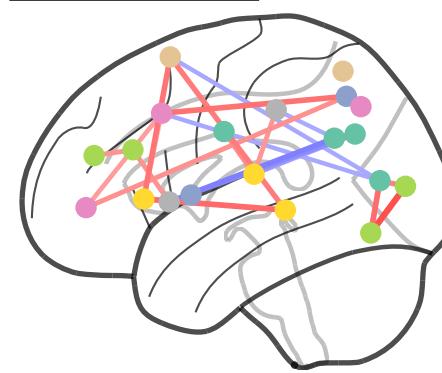
# The standard analysis pipeline



Empirical covariance

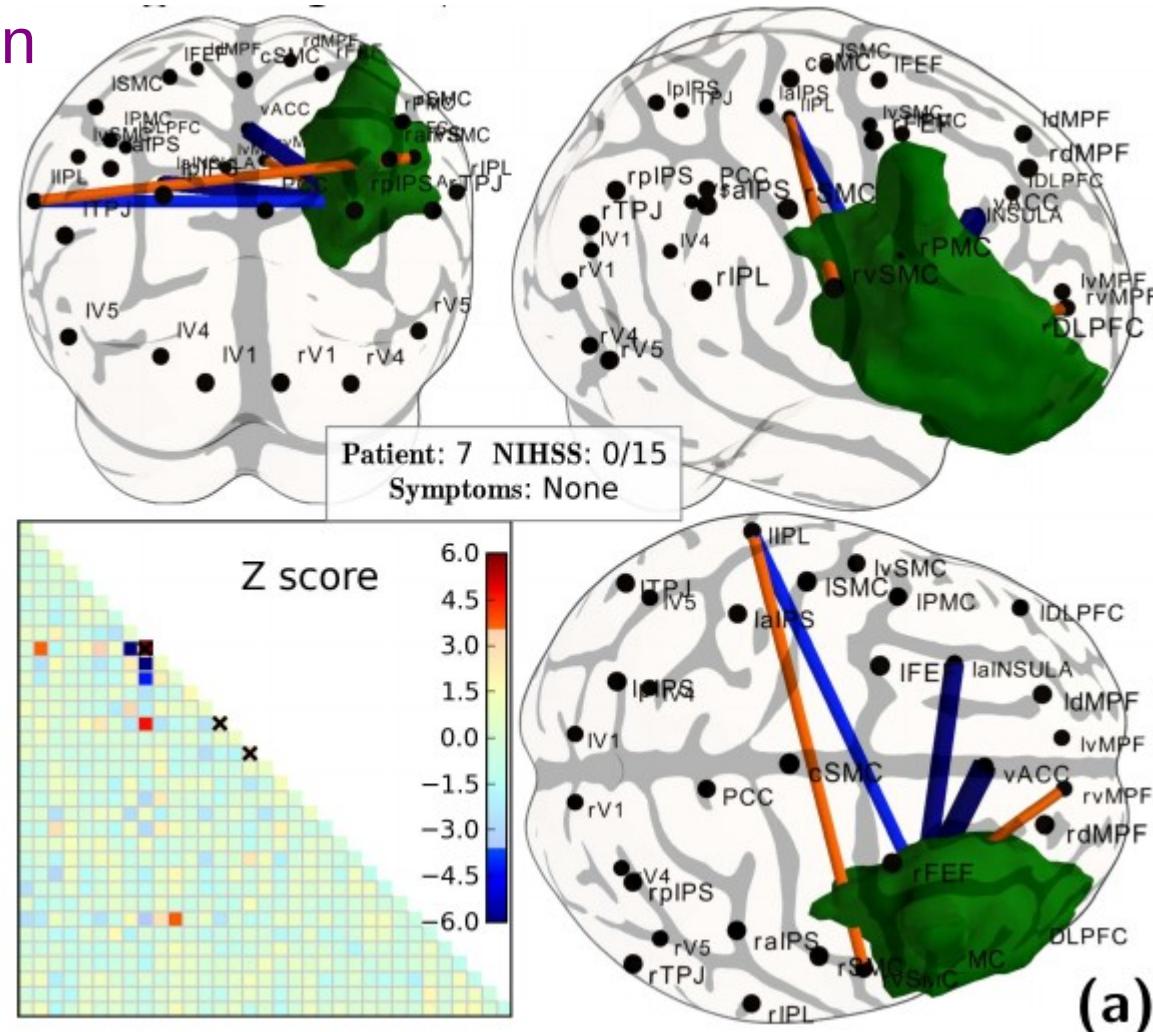


Covariance



# Functional connectivity: objectives

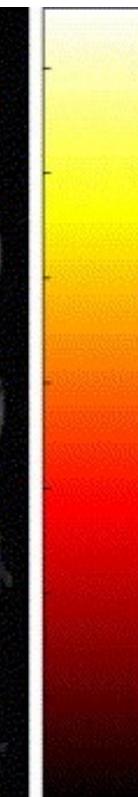
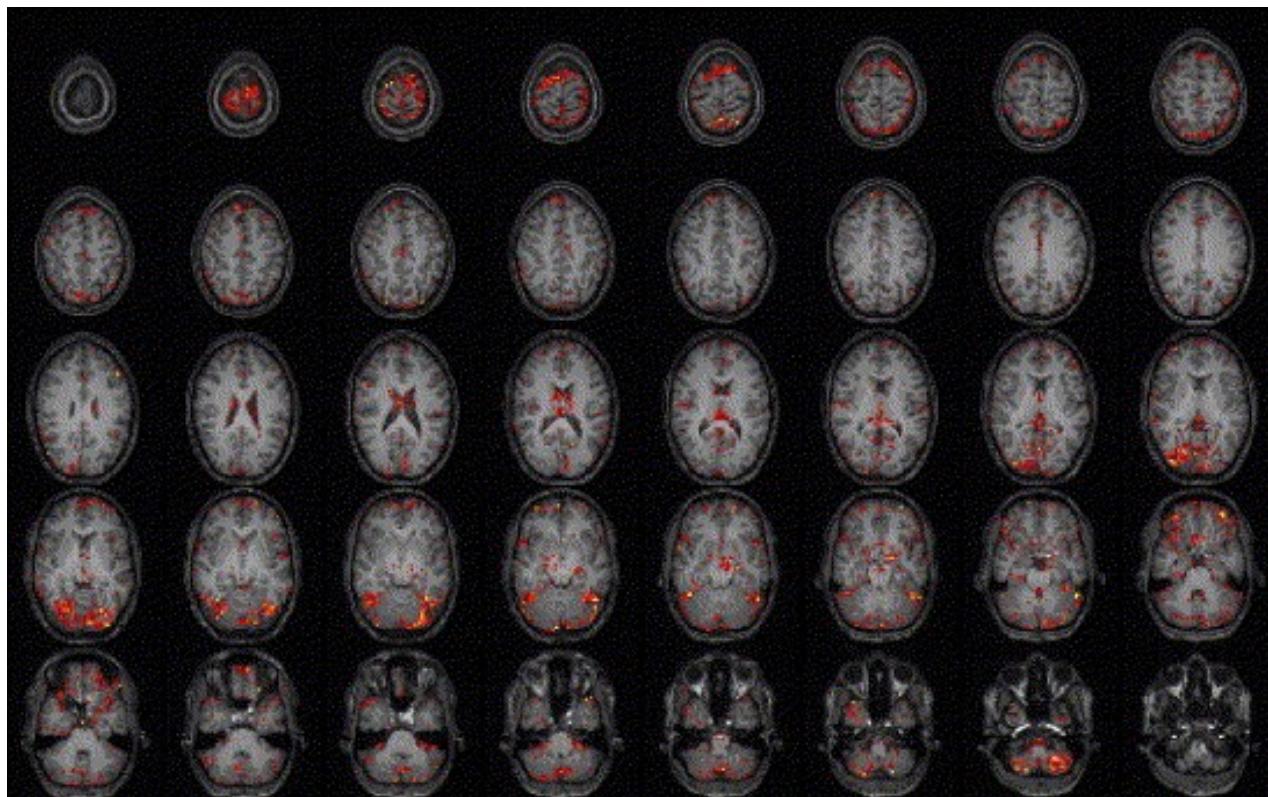
- Understand brain organization
  - Compare with anatomical connectivity
  - Compare with activation data
- marker for several brain diseases, and recovery processes
- Understand some brain diseases
- Interplay of ongoing with evoked activity



# Signal cleaning

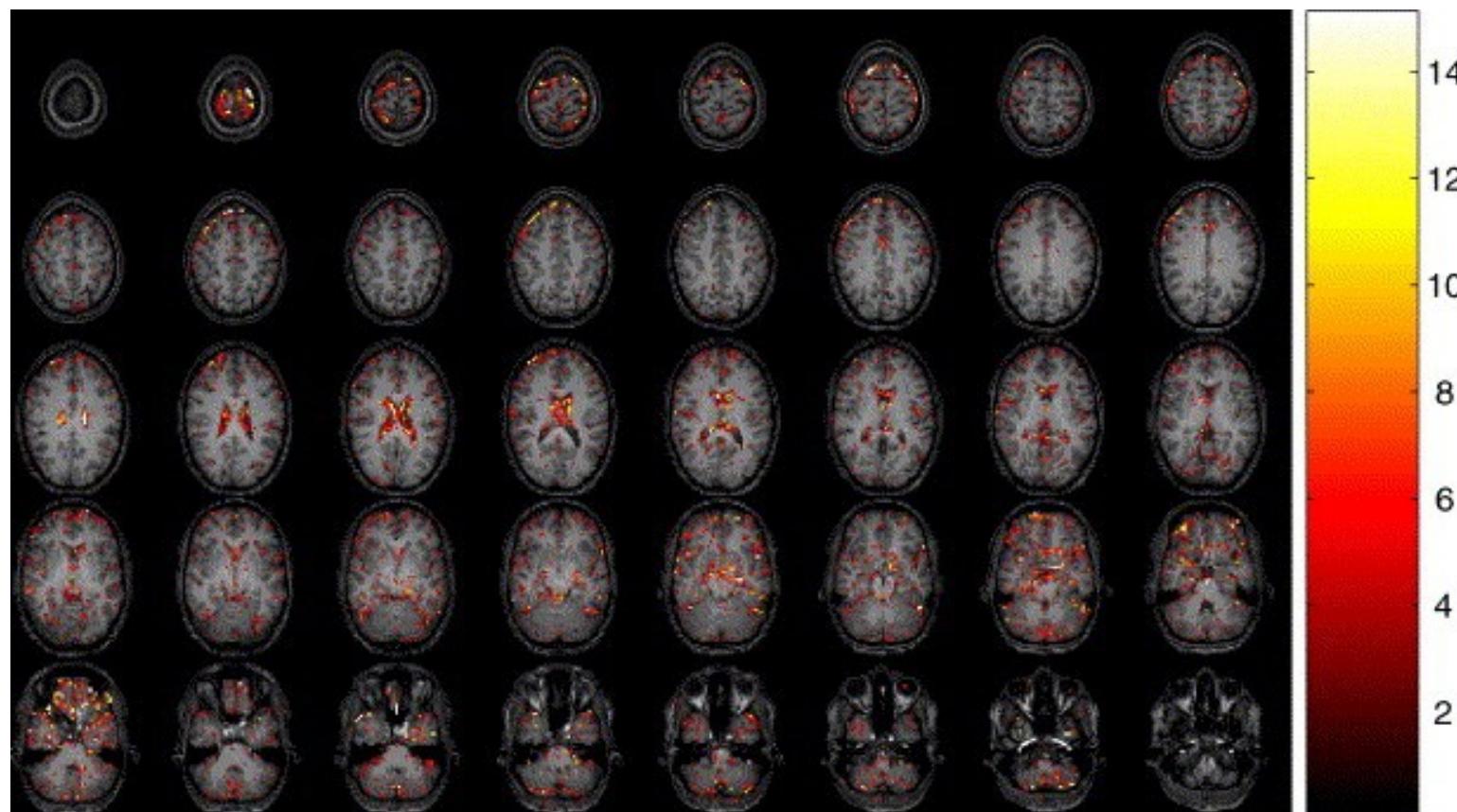
- Removing spurious physiology based signal

[Lund et al., NeuroImage 2006]



Residual movement effects.  
Significant ( $FDR < 0.05$ ) effect of residual movement effects.  
dominant near the **edges of the brain**.

# Respiratory...

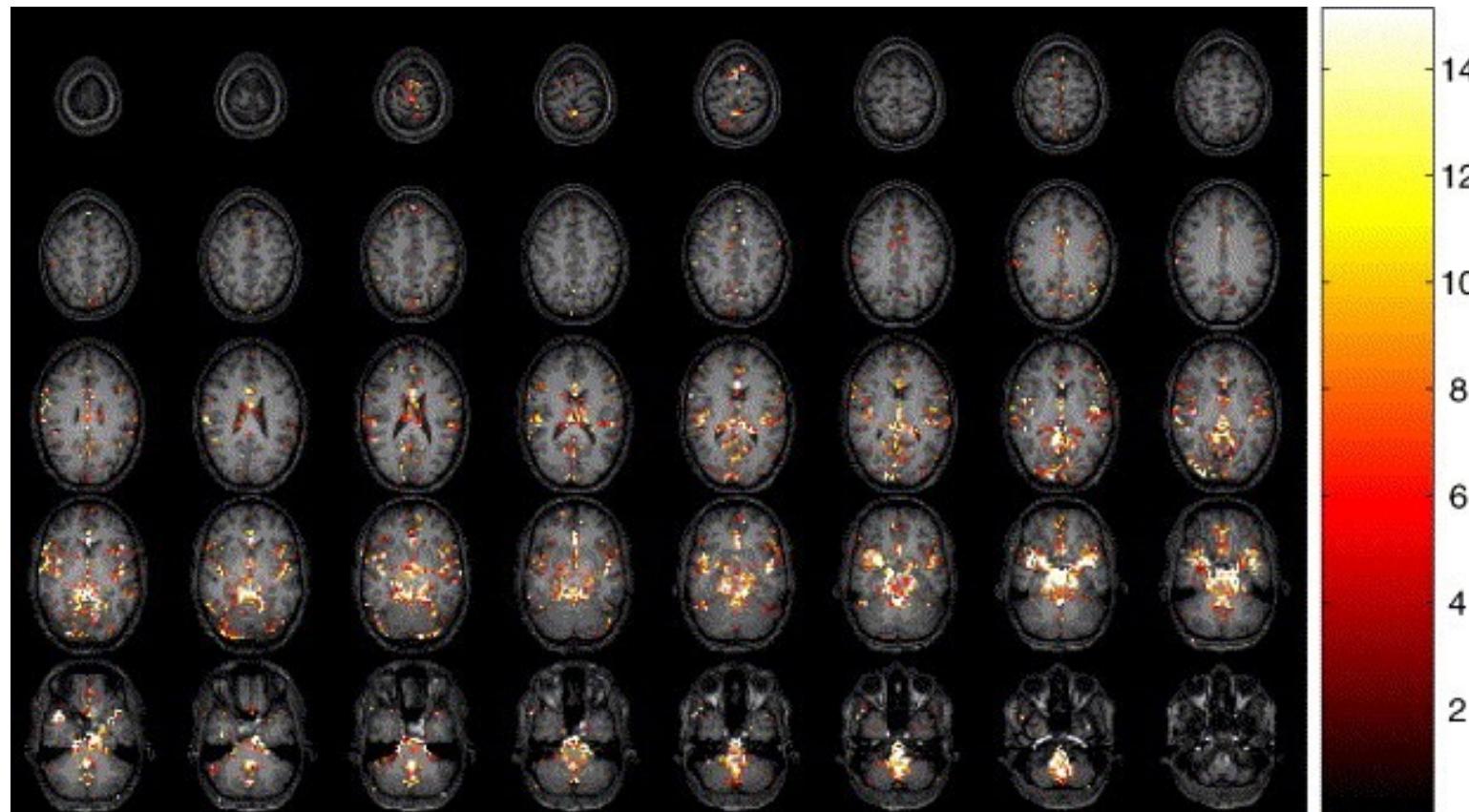


Respiratory-induced noise. significant ( $FDR < 0.05$ ) effect of respiratory oscillations.

Dominant near the **edges of the brain** as well as near in the **larger veins** and in the **ventricles**.

[Lund et al., NeuroImage 2006]

# Cardiac ...



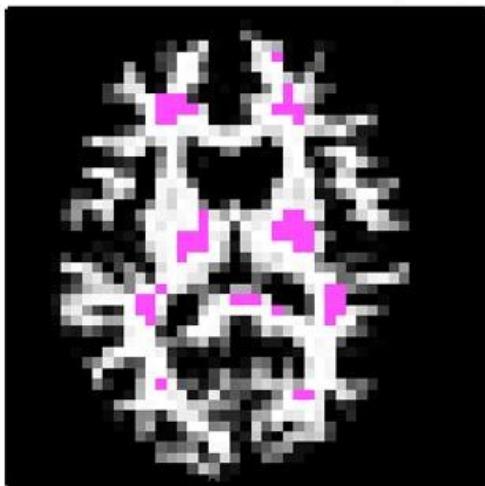
Significant  
( $f_{\text{WER}} < 0.05$ )  
effect of  
aliased cardiac  
oscillations.

Dominant near  
**larger vessels**  
(e.g. medial  
cerebral artery  
and Circle of  
Willis).

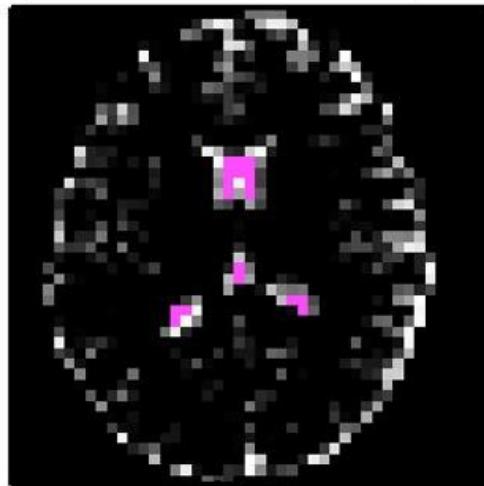
# Signal cleaning in practical settings

## 1. Band-pass filtering: [0.01, 0.1 Hz]

a) White Matter Partial Volume Mask, Subject 1



b) CSF Partial Volume Mask, Subject 1



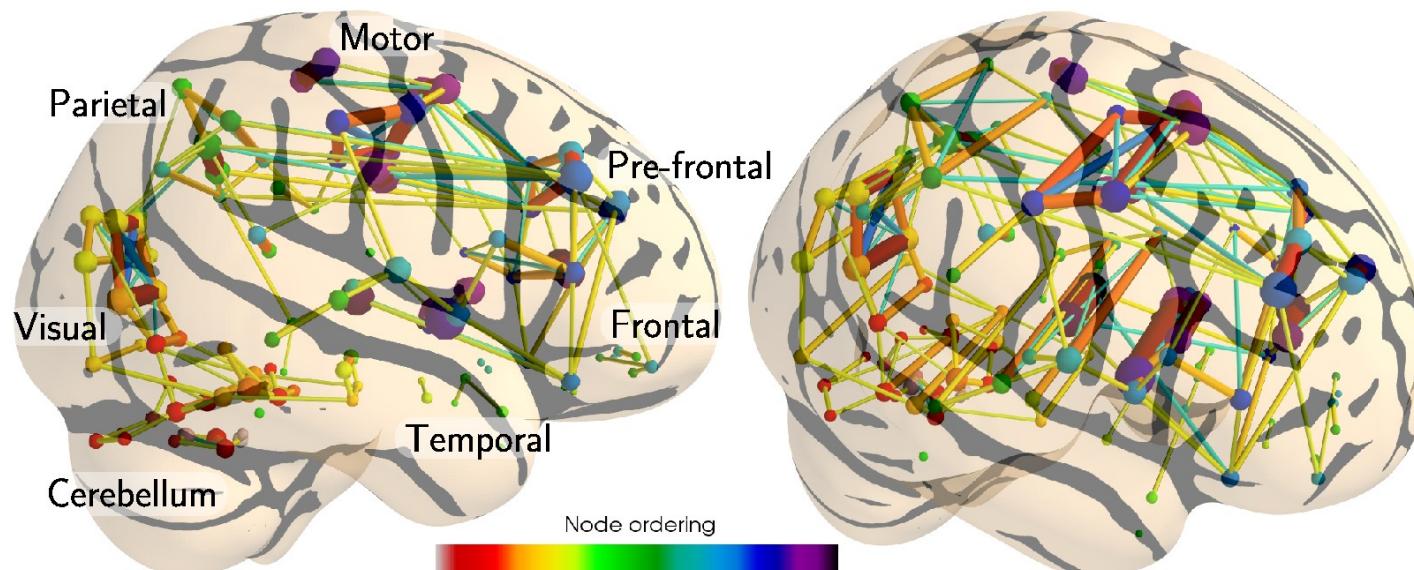
## 2. Confound removal

[Behzadi et al. Nimg 2007]

PCA of the signals in the voxels with highest variance  
or  
remove signal components from WM, ventricles

# Outline

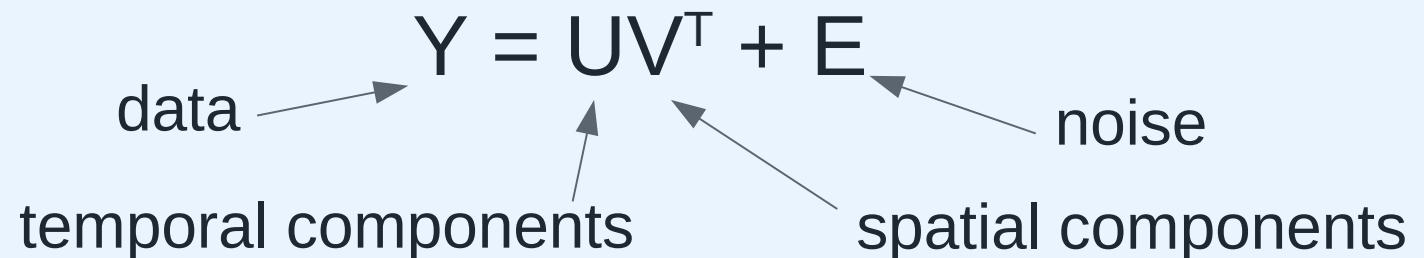
- Objectives & data preparation
- Multivariate decompositions of brain images
- Statistical inference on covariance models



# Learn brain atlases from fMRI data:

- Capture the structure of interest in **multivariate decompositions**

$Y : (n, p)$  matrix  
 $n = \#$  time samples  
 $p = \#$  voxels



PCA:  $\mathbf{U}_k \perp \mathbf{U}_l$  and  $\mathbf{V}_k \perp \mathbf{V}_l$  if  $k \neq l$

Clustering:  $\mathbf{V}_k \in \{0, 1\} \forall k$  and  $\mathbf{V} \cdot \mathbf{e}_K = \mathbf{e}_p$

ICA:  $\mathbf{V}_k$  independent of  $\mathbf{V}_l$  if  $k \neq l$

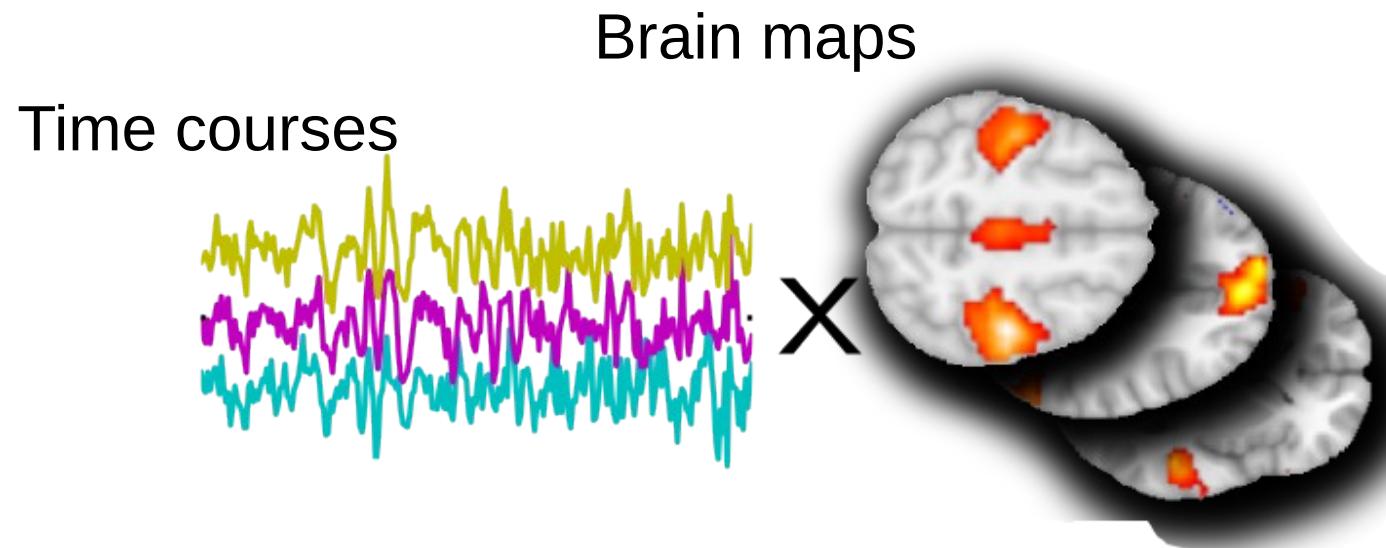
sparse PCA:  $\mathbf{V}_k \perp \mathbf{V}_l$  if  $k \neq l$ ,  $\|\mathbf{V}_k\|_1$  small  $\forall k$

Choice of  $K$ : model selection problem

# Learn brain atlases from fMRI data

Analogy with the GLM

$$\begin{aligned}\mathbf{Y} &= \mathbf{U}\mathbf{V}^T + \varepsilon \\ &= \mathbf{X}\boldsymbol{\beta} + \varepsilon\end{aligned}$$



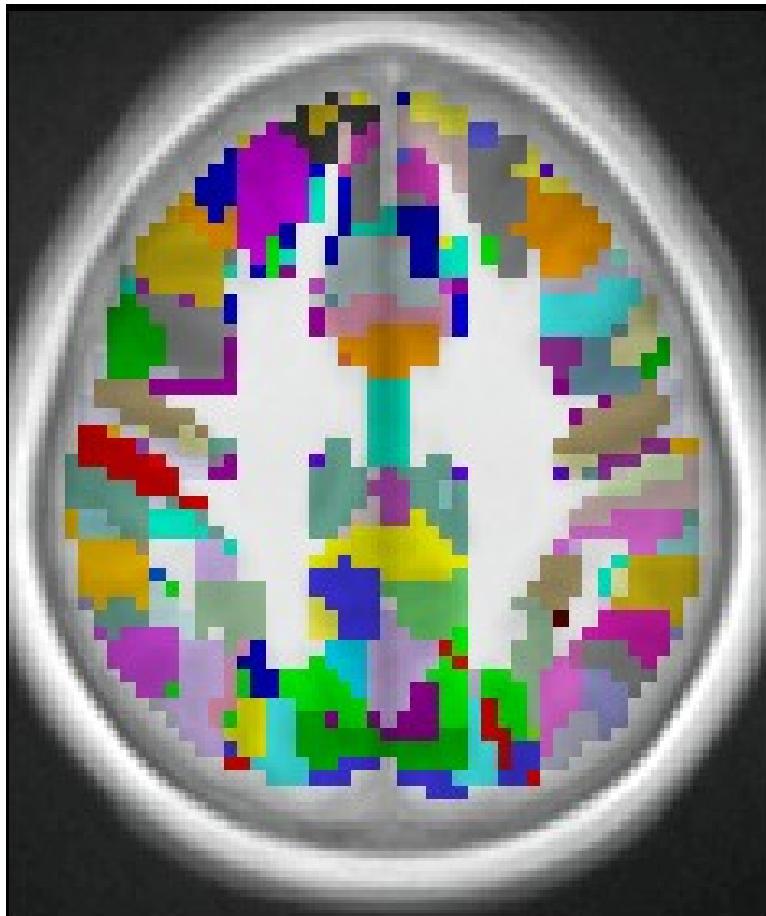
**Main difference:** “design matrix” unknown; to be estimated from data  
→ “mixing matrix”

# Learning brain atlases: Estimation techniques

- Clustering: k-means, Ward
- PCA: centering + singular value decomposition
- ICA: minimize marginal entropy of the reconstructed sources
- Sparse PCA: alternated optimization
  - Update of U: least squares
  - Update of V: K lasso problems  $\min_{\mathbf{V}, \mathbf{U}: \|\mathbf{U}_k\| \leq 1, \forall k} \|\mathbf{Y} - \mathbf{U}\mathbf{V}^T\|^2 + \lambda \|\mathbf{V}\|_1$

Online algorithms for  $L_1$  penalty in [Mairal et al. JMLR 2010]

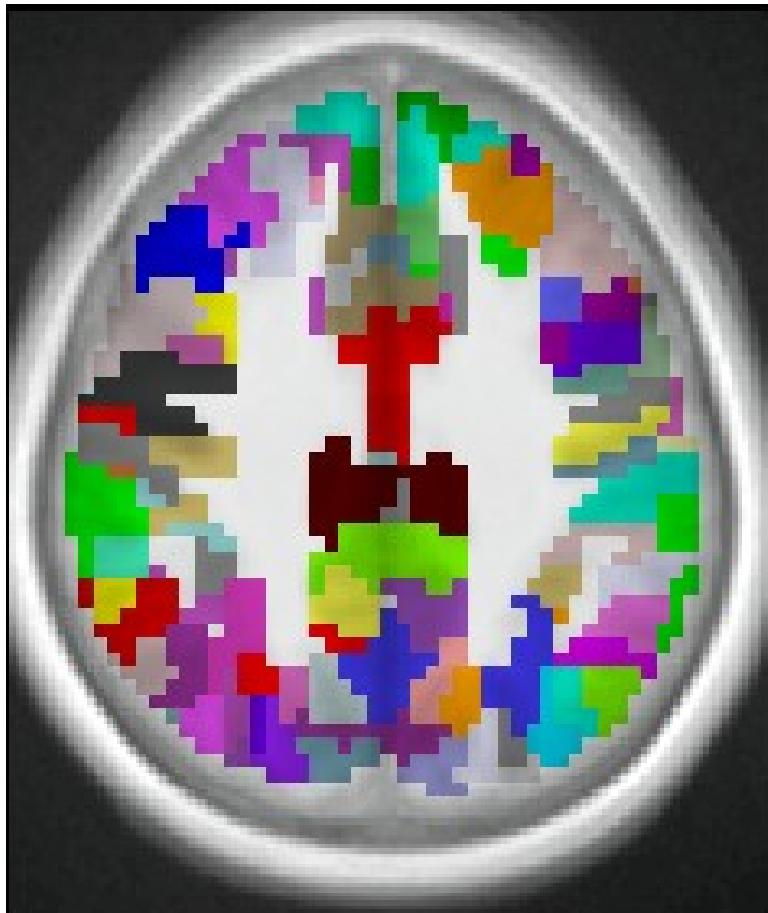
# Clustering: k-means



- Works well for small  $k$
- No priors
- Need prior data smoothing

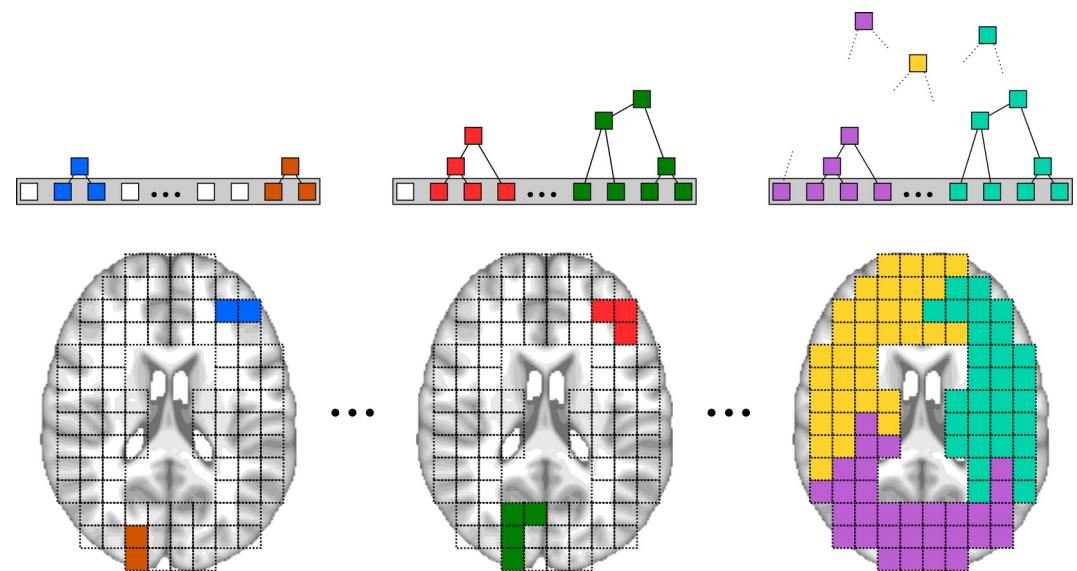
[Yeo et al. J Neurophysiol 2011]

# Clustering: Ward



[Michel et al. PR 2011]

- Works well for large  $k$
- Fast
- Includes spatial constraints



# Independent Components Analysis (ICA)

Generative model analysis

$$\mathbf{Y} = \mathbf{U}\mathbf{V}$$

(k,p) (k, k) (k,p)

$$\hat{\mathbf{V}} = \mathbf{W}\mathbf{Y}$$

Classical (noise-free)  
ICA setting

First step Dimension reduction / denoising

$$\mathbf{Y} = \mathbf{U}\mathbf{V} + \mathbf{E}$$

(n, p) (n, k) (k,p) (n, p)

SVD of  $\mathbf{Y}$  :  $\mathbf{Y} = \mathbf{A}\Lambda\mathbf{D}$

(n, p) (n, p) (p,p) (p, p)

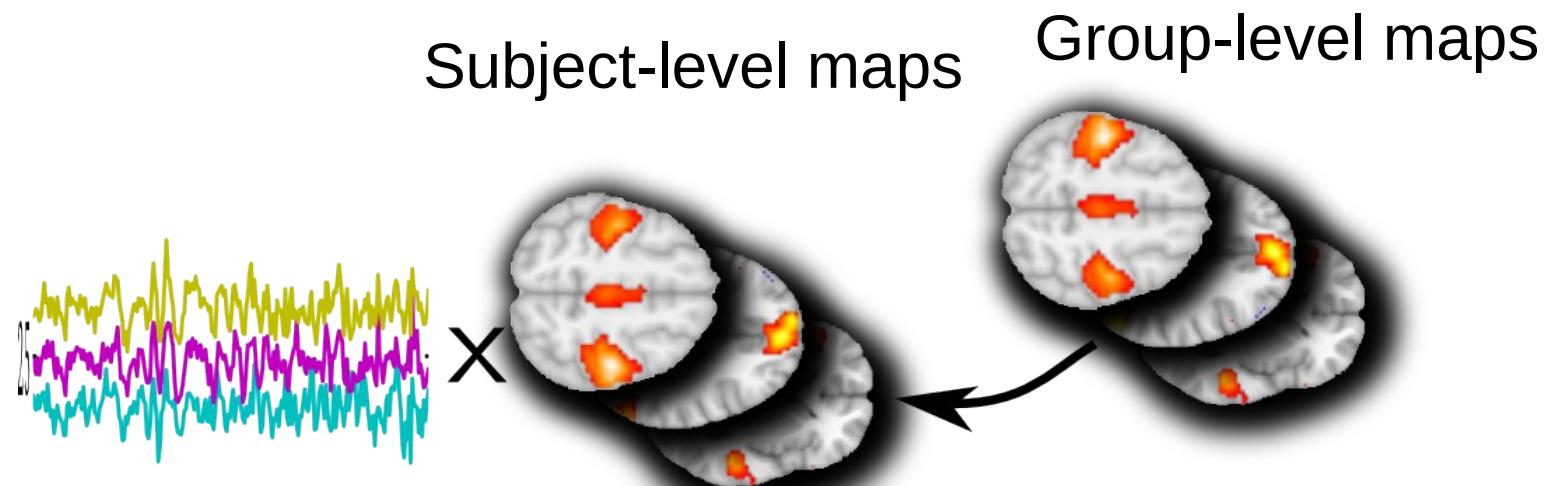
denoising  $\mathbf{Y} = \mathbf{A}\Lambda[:, :k]\mathbf{D}[:, k] + \mathbf{A}\Lambda[:, k :]\mathbf{D}[k :, :]$

whitening: set singular values to 1  $\tilde{\mathbf{Y}} \leftarrow \mathbf{A}\mathbf{D}[:, k]$

$k =$  rank of  
decomposition

# Brain atlases: multi-subject setting

Goal: consistent region segmentation across individuals



- Concatenated ICA [Beckmann et al. 2005]
- generalized Canonical correlation analysis [Varoquaux et al. Nimg2010]
- Multi-subject dictionary learning [Varoquaux et al. IPMI 2011]

# computational strategies

images  $[Y_1]$   
voxels

**Concatenation  
approach**

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} U_1 \\ U_2 \\ \vdots \\ U_n \end{bmatrix} [V]$$

# computational strategies

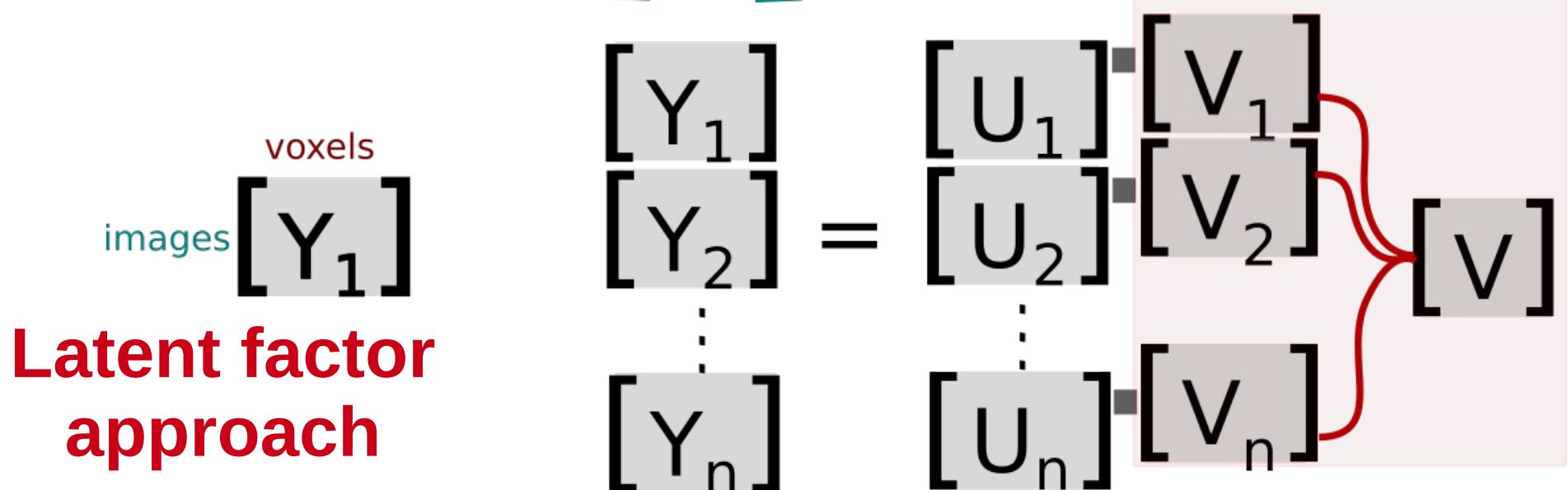
voxels  
images  $[Y_1]$

**Concatenation approach**

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} U_1 \\ U_2 \\ \vdots \\ U_n \end{bmatrix} [V]$$

voxels  
images  $[Y_1]$

**Latent factor approach**

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} U_1 \\ U_2 \\ \vdots \\ U_n \end{bmatrix} \begin{bmatrix} V_1 \\ V_2 \\ \vdots \\ V_n \end{bmatrix}$$


# Dictionary Learning in a data-rich context

voxels  
images  $[Y_1]$

$$\begin{bmatrix} Y_1 \\ Y_2 \\ \vdots \\ Y_n \end{bmatrix} = \begin{bmatrix} U_1 \\ U_2 \\ \vdots \\ U_n \end{bmatrix} [V]$$

$$\min_{\mathbf{V}, \mathbf{U}: \|U_k\| \leq 1, \forall k} \|\mathbf{Y} - \mathbf{U}\mathbf{V}^T\|^2 + \lambda \|\mathbf{V}\|_1$$

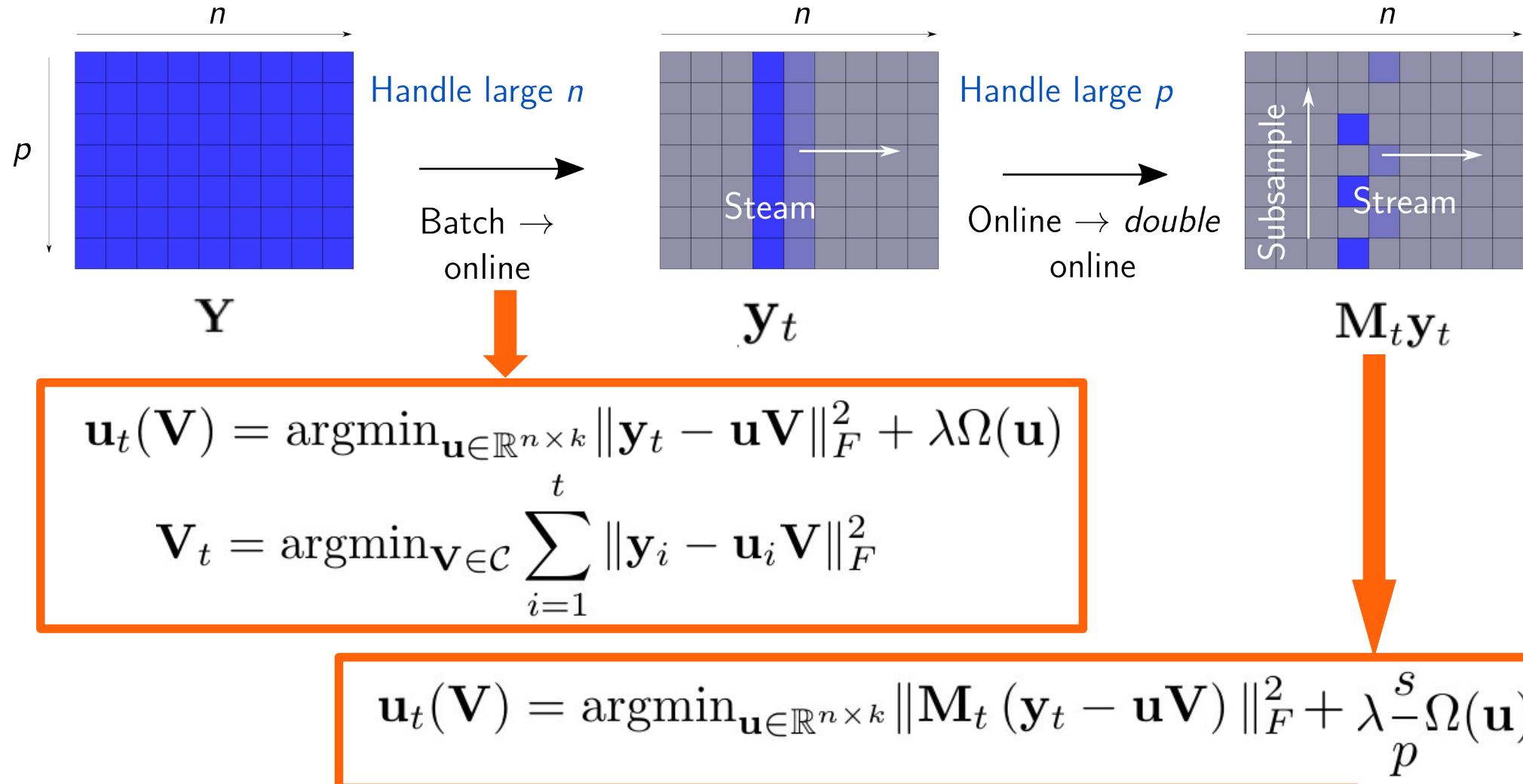
Concatenation mode for multi-subject → long “time courses”

# Upscaling the model

- Human Connectome project  $n=4.10^6$ ,  $p=2.10^5$ , 4**TB** of data
- Spatially-concatenated DL [varoquaux IPMI 2013] does not scale well:
  - Requires loading the data [Mensch et al. ISBI 2016]
- Solution
  - Work on batches of images **and** voxels
    - Online method in both samples and feature dimensions

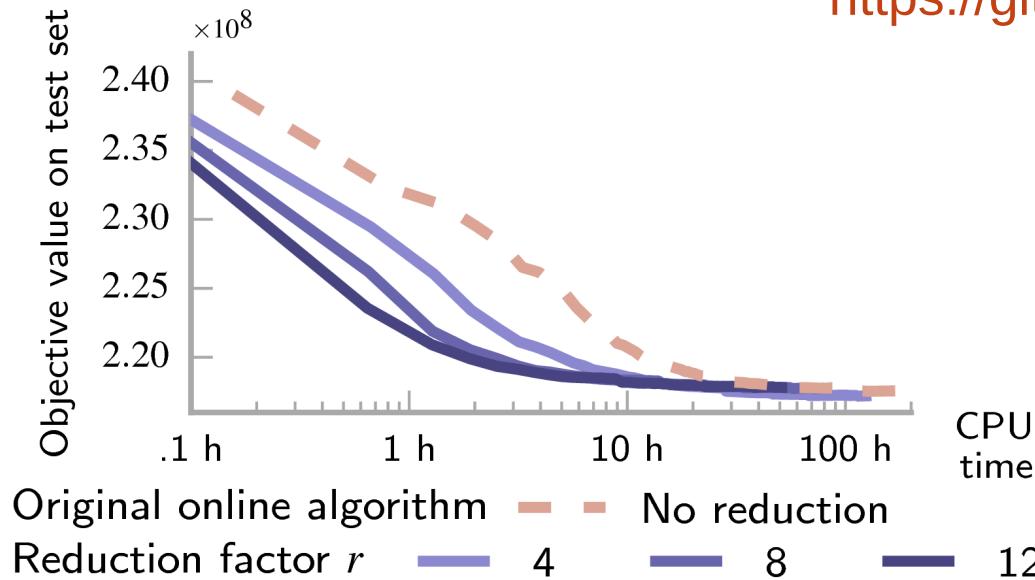
# Stochastic gradient approaches

<https://github.com/arthurmensch/modl>



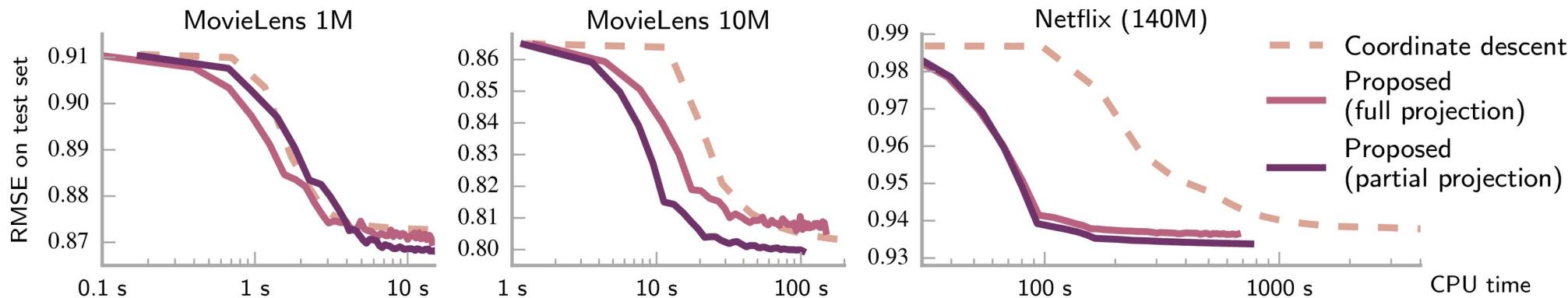
# Stochastic gradient approaches

<https://github.com/arthurmensch/modl>

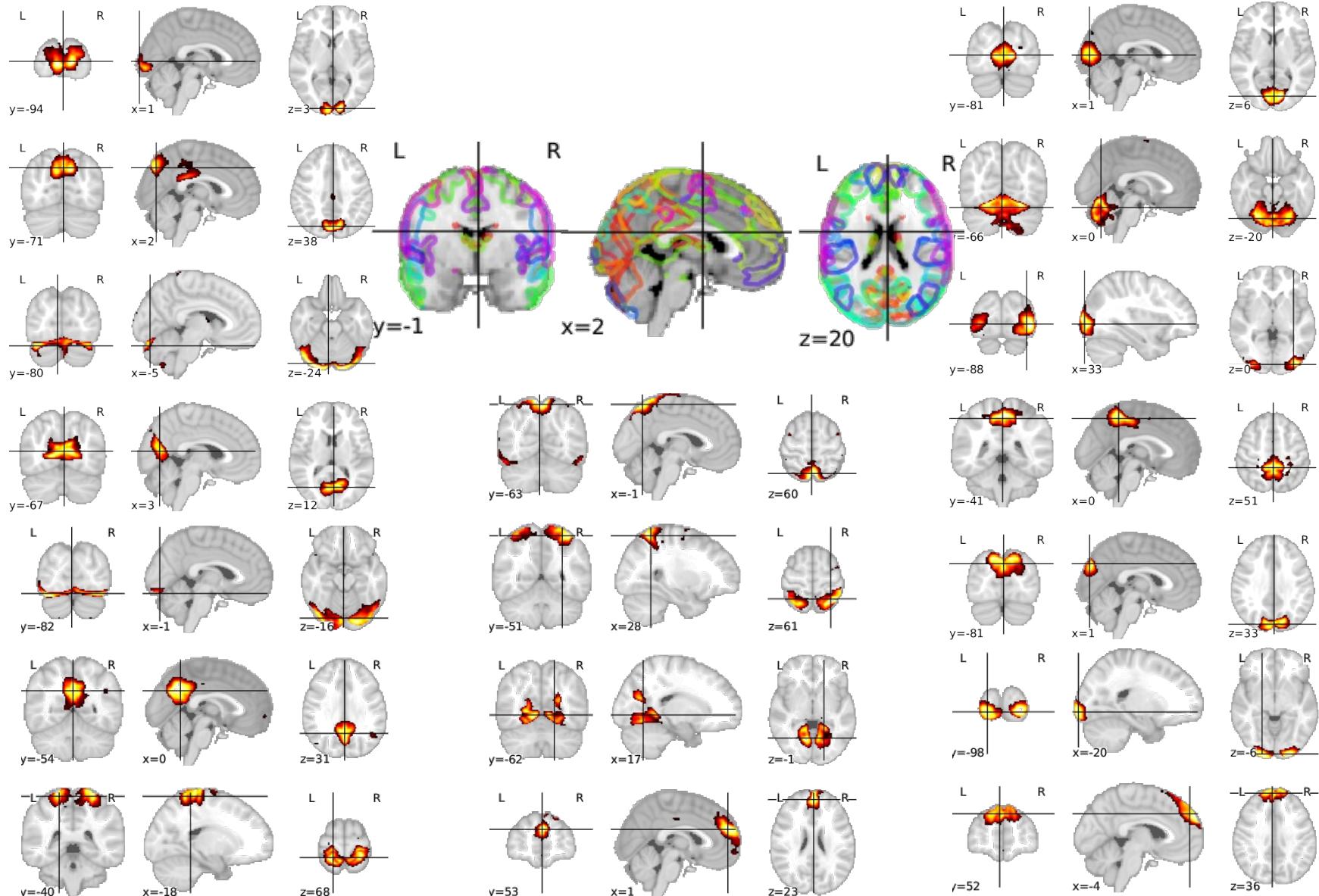


10-fold gain in CPU time  
without loss in accuracy

Can be used for recommender systems



# Brain atlases



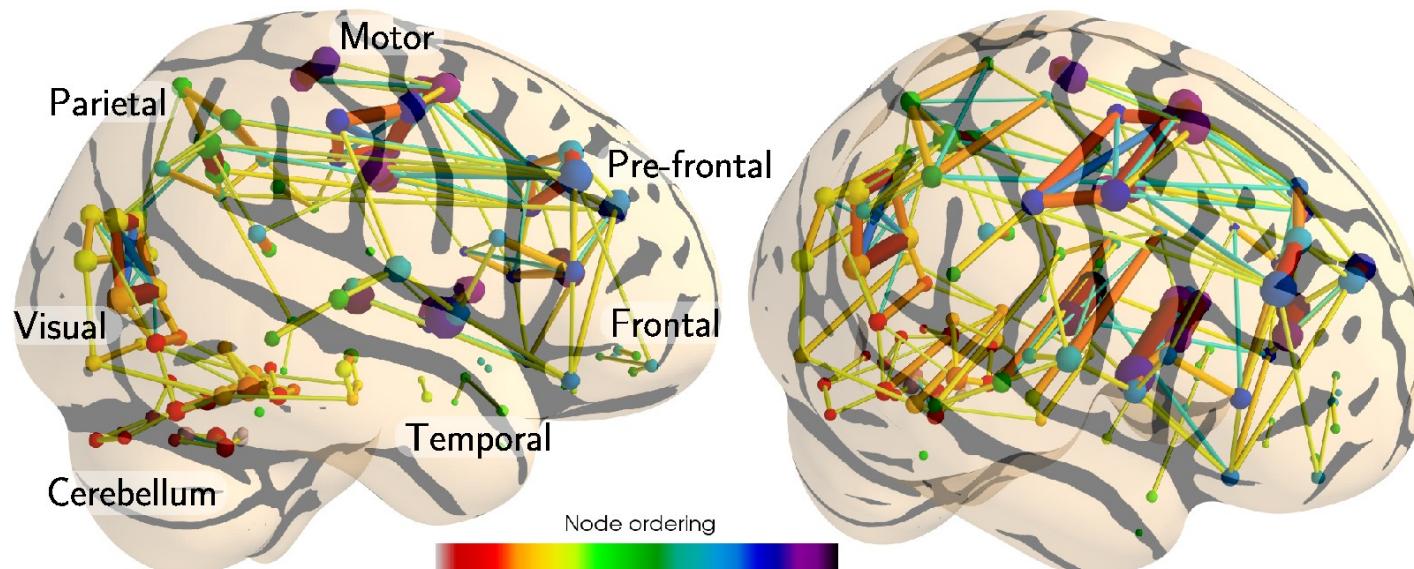
[Mensch et al. ICML 2016, IEEE TSP 2018]

# Brain atlases from fMRI data

- Relax clustering to spatio-temporal decompositions
- Model selection is hard
- Sparse-/smooth- PCA algorithms perform well
  - Fine-tuning to individual data is expensive
  - Sophisticated penalties (eg TV+L1) expensive
- Development of online methods to scale to large data [Mairal et al. JMLR 2010, Mensch et al. ICML 2016, Mensch et al IEEE TSP 2018]

# Outline

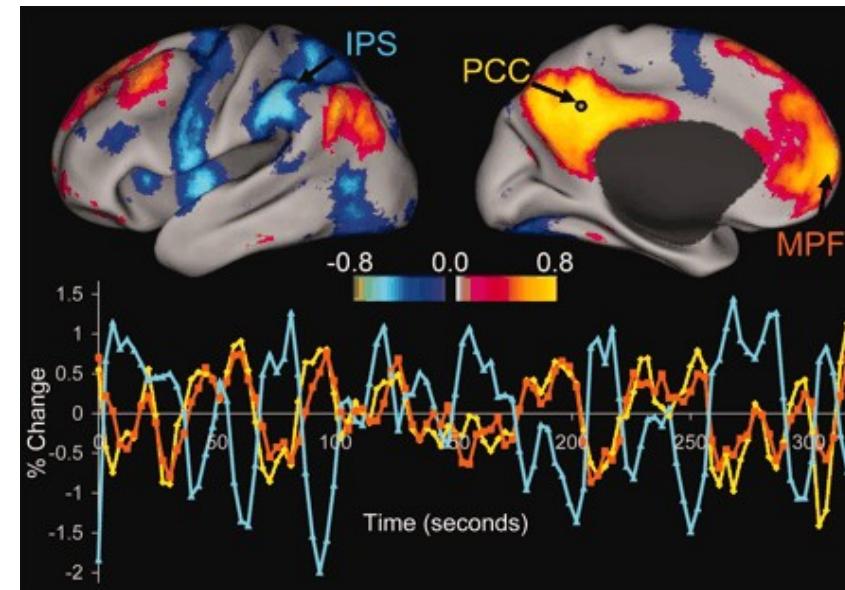
- Objectives & techniques
- Multivariate decompositions and ICA
- Statistical inference on covariance models
  - Covariance estimation
  - Statistical modeling and inference



# The covariance structure of fMRI signals: From descriptive statistics to models

## Problem setting:

- R regions
- Functional connectivity = statistical dependence of the signals cross regions
  - Integration of brain systems,
  - Population comparison,
  - Normal brain function/ diseases



[Fox et al PNAS 2005]

## Main issues

- Relatively short time series (<10<sup>3</sup> samples in R regions)
- noise (physiological signals)
- between-subject variability

# Covariance structure of fMRI signals

- Alternative: Generative model
  - fMRI time series  $Y_1, \dots, Y_R$  as  $n$  samples from centered  $R$ -dimensional Gaussian variable
  - Infer the covariance/precision of this variable

$$\hat{\mathbf{K}} = \operatorname{argmin}_{\mathbf{K} \succ 0} \operatorname{tr}(\hat{\Sigma} \mathbf{K}) - \log \det(\mathbf{K})$$

- Where  $\hat{\Sigma}$  is the empirical covariance (correlation) matrix

$(\hat{\Sigma}_{i,j}), (i, j) \in [1, p]^2$  sample (Pearson) correlations

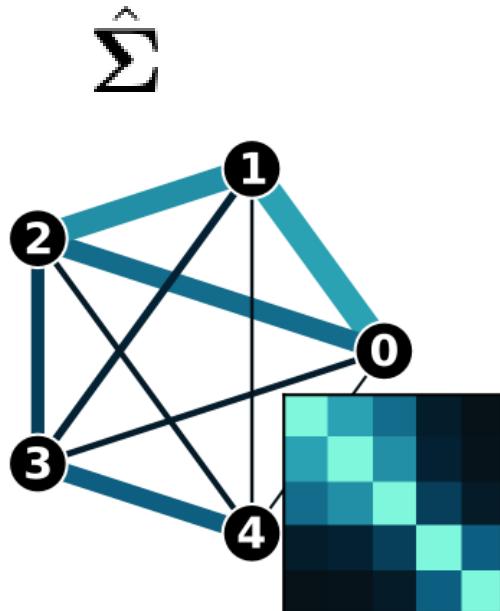
$\left( \frac{-\mathbf{K}_{i,j}}{\sqrt{\mathbf{K}_{i,i} \mathbf{K}_{j,j}}} \right), (i, j) \in [1, p]^2$  partial correlations

[Marrelec et al. 2006, Fransson et al. 2008]

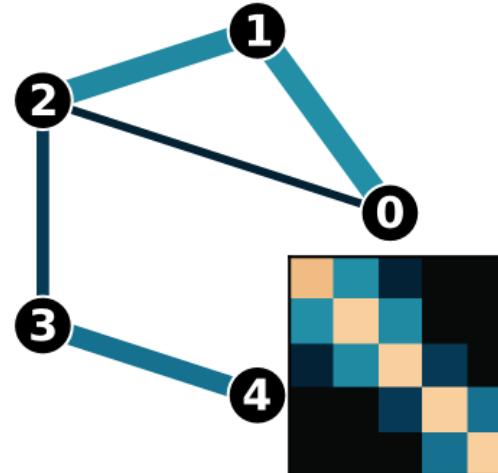
# The covariance structure of fMRI signals

$$\hat{\mathbf{K}} = \operatorname{argmin}_{\mathbf{K} > 0} \operatorname{tr}(\hat{\Sigma} \mathbf{K}) - \log \det(\mathbf{K})$$

Empirical correlations



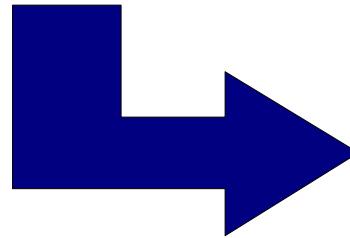
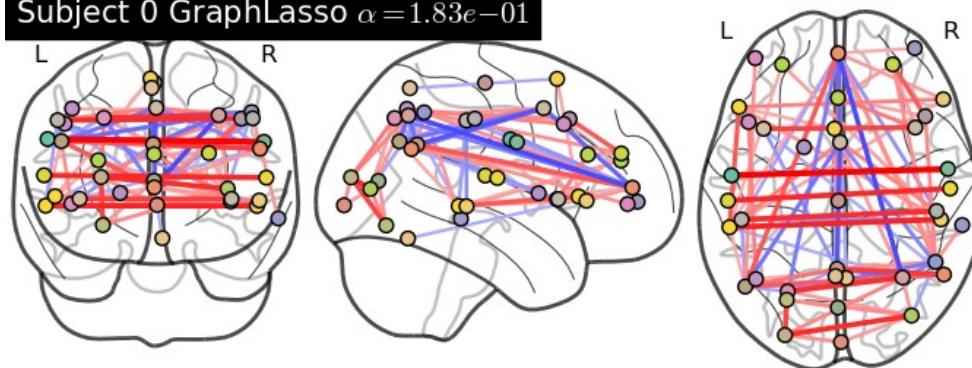
Underlying interactions  
(=partial correlations)  $\mathbf{K}$



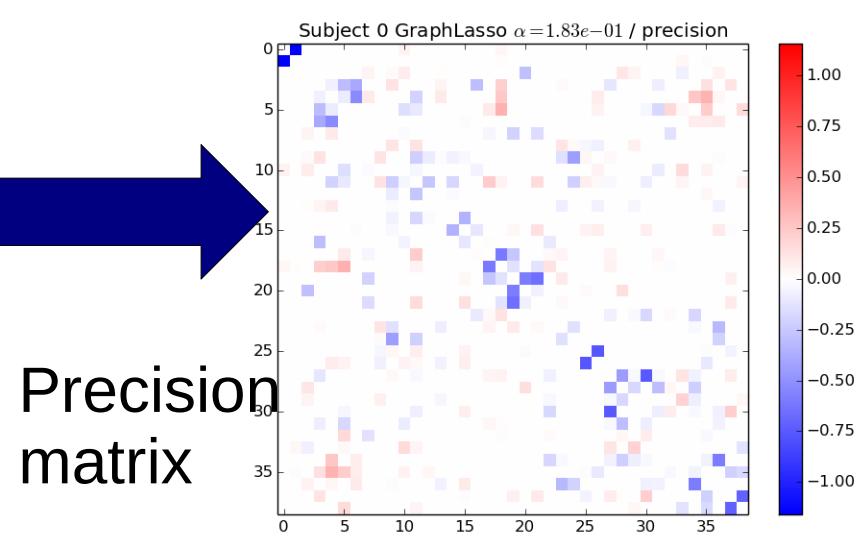
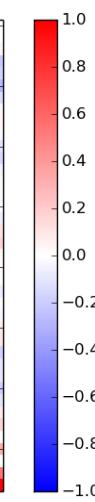
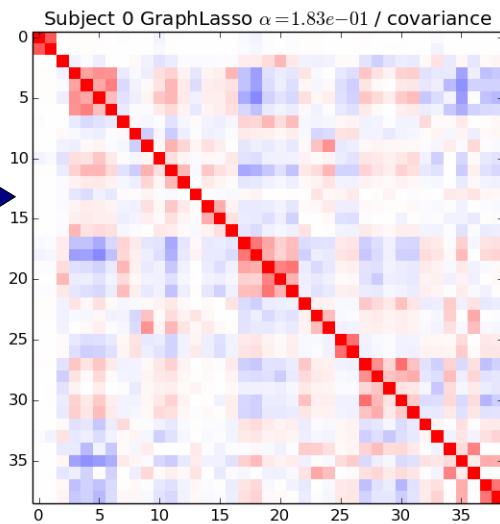
[Fransson et al. 2008]  
Partial correlations  
highlight the  
**backbone** of brain  
networks

# The covariance structure of fMRI signals

Subject 0 GraphLasso  $\alpha = 1.83e-01$



Covariance  
matrix



Precision  
matrix

# The Ledoit Wolf estimator

Shrink empirical covariance  $\min_{\rho_1, \rho_2} \mathbb{E} (\|\Sigma^* - \Sigma\|^2)$  s.t.  $\Sigma^* = \rho_1 \mathbb{I} + \rho_2 \hat{\Sigma}$

Solution [Ledoit & Wolf, 2004]

$$\rho_1 = \frac{b^2}{d^2} Tr(\hat{\Sigma}) \quad \rho_2 = 1 - \frac{b^2}{d^2}$$
$$d^2 = \|\hat{\Sigma} - Tr(\hat{\Sigma})\mathbb{I}\|^2 \quad b^2 = \frac{1}{n^2} \sum_{k=1}^n \|(\mathbf{X}_k \mathbf{X}_k)^T - \hat{\Sigma}\|^2$$

CF L<sub>2</sub>-shrinkage:

$$\hat{\mathbf{K}} = \operatorname{argmin}_{\mathbf{K} \succ 0} \operatorname{tr}(\hat{\Sigma} \mathbf{K}) - \log \det(\mathbf{K}) + \lambda \operatorname{tr}(\mathbf{K})$$

$$\hat{\mathbf{K}} = (\hat{\Sigma} + \lambda \mathbb{I})^{-1}$$

# The covariance of fMRI signals: Covariance selection

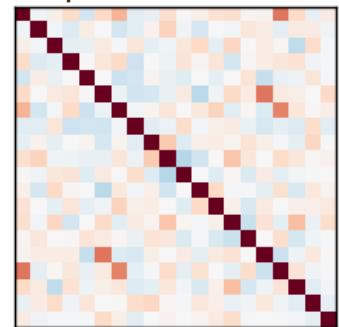
- **enforce sparsity** instead of shrinkage
  - Few brain regions anatomically connected
  - Benefits to covariance estimation: **covariance selection** [Dempster et al. 1972]
  - 0's of  $\mathbf{K}$   $\Leftrightarrow$  independence conditional to the other nodes [Lauritzen, 1996]
  - L1 shrinkage on off-diagonal precision coefficients  $\rightarrow$  convex estimation [Banejee et al. ICML 2006] [Friedmann et al. Biostat 2008]

$$\hat{\mathbf{K}}_{\ell_1} = \operatorname{argmin}_{\mathbf{K} > 0} \operatorname{tr}(\mathbf{K} \hat{\Sigma}_{\text{sample}}) - \log \det \mathbf{K} + \lambda \|\mathbf{K}\|_1$$

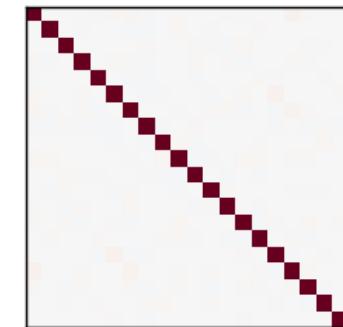
Main issue: set  $\lambda$

# Covariance estimators

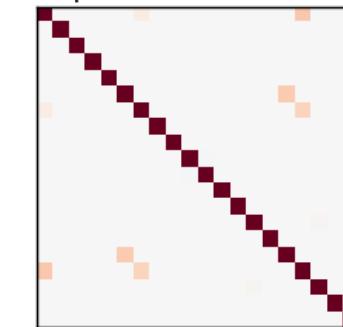
Empirical covariance



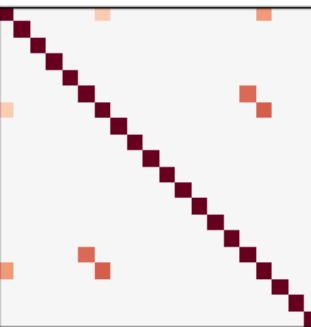
Ledoit-Wolf covariance



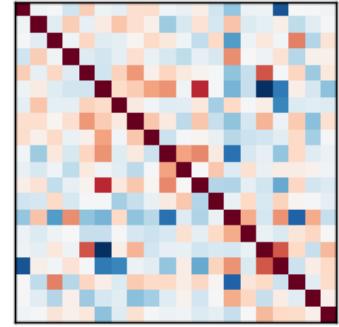
GraphLasso covariance



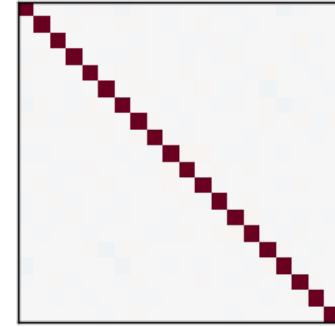
True covariance



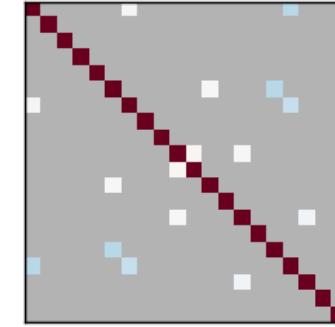
Empirical precision



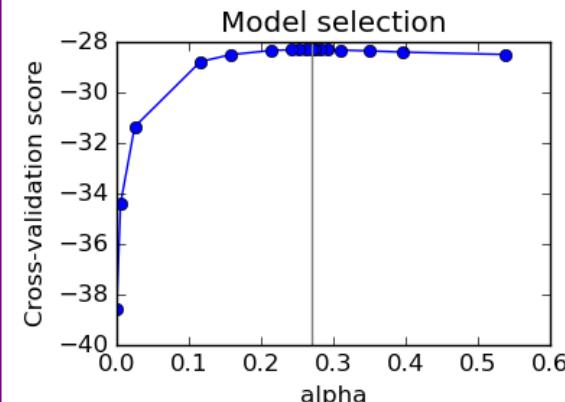
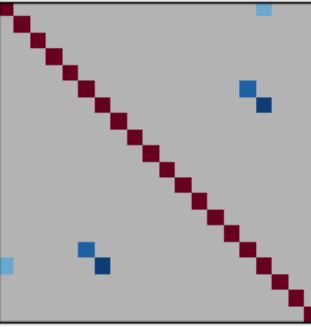
Ledoit-Wolf precision



GraphLasso precision



True precision

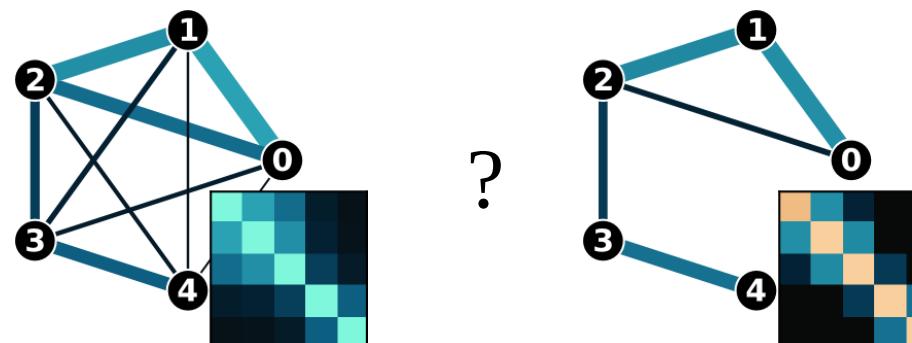


Ground truth

[http://scikit-learn.org/stable/auto\\_examples/covariance/plot\\_sparse\\_cov.html#example-covariance-plot-sparse-cov-py](http://scikit-learn.org/stable/auto_examples/covariance/plot_sparse_cov.html#example-covariance-plot-sparse-cov-py)

# Statistical testing on graphical models

- State of the art: t-test [Fair et al. PNAS 2007] or discriminative models [Richiardi et al. Neuroimage 2011] on pairwise correlations
- Known issues
  - a test on correlations is not the optimal test
    - correlations are **not** observed **independently**
  - **diluted effects**: a local perturbation has widespread effects
  - Non-independent tests → **cannot localize** the true effects



# Statistical testing on graphical models

- Use of affine invariant metric on SPD matrices

$$\text{dist}_g(\Sigma_1, \Sigma_2) = \left\| \text{Log} \left( \Sigma_1^{-\frac{1}{2}} \Sigma_2 \Sigma_1^{-\frac{1}{2}} \right) \right\|_2$$

- Geometric mean

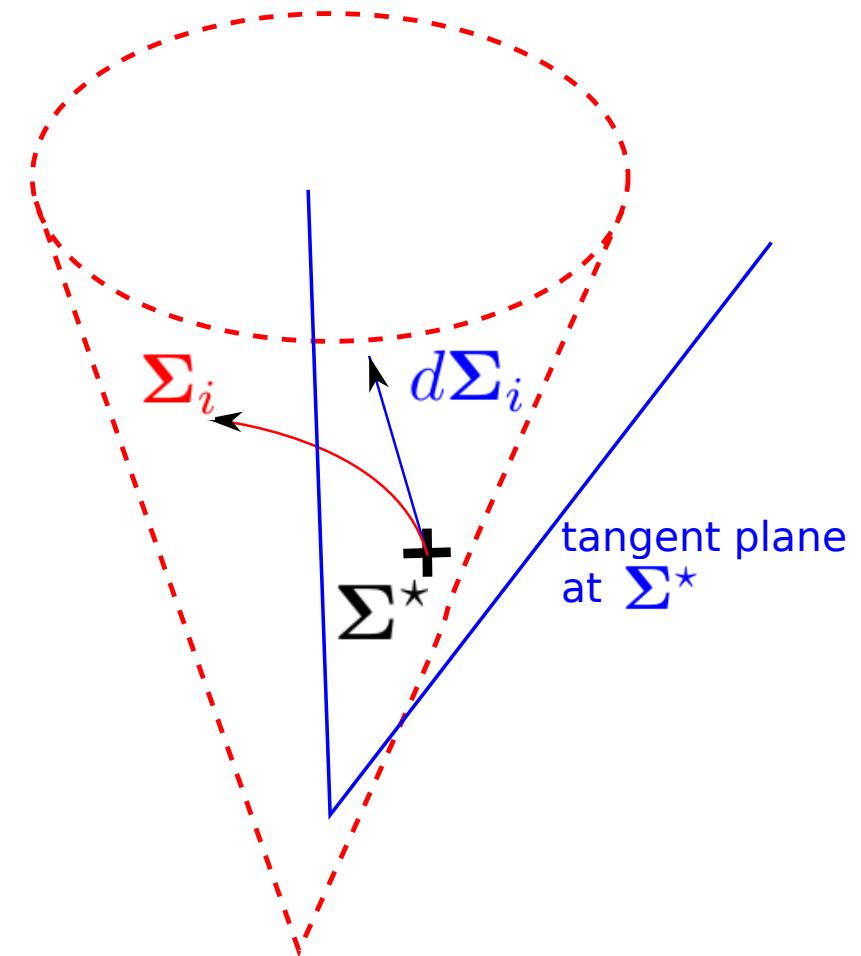
$$\Sigma_* = \operatorname{argmin}_{\Sigma} \sum_{i=1}^n \text{dist}_g(\Sigma, \Sigma_i)^2$$

- Geometric deviations

$$\text{Let } \Phi_{\Sigma} : \mathbf{S} \rightarrow \text{Log} \left( \Sigma^{-\frac{1}{2}} \mathbf{S} \Sigma^{-\frac{1}{2}} \right)$$

$$d\Sigma_i = \Phi_{\Sigma_*}(\Sigma_i)$$

“tangent” representation



[Varoquaux et al. MICCAI 2010]

# Statistical testing on graphical models

Geometric distance  
on SPD matrices

$$\text{dist}_g(\Sigma_1, \Sigma_2) = \left\| \text{Log} \left( \Sigma_1^{-\frac{1}{2}} \Sigma_2 \Sigma_1^{-\frac{1}{2}} \right) \right\|_2$$

Geometric matrix  
average

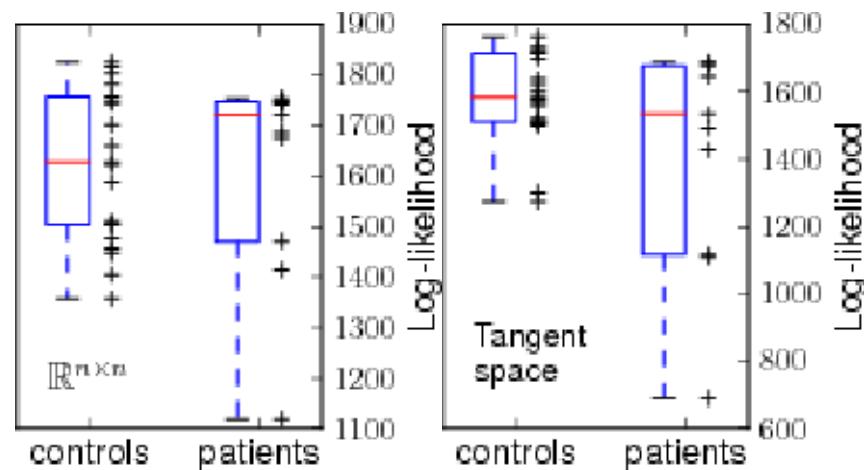
$$\Sigma_{\star} = \operatorname{argmin}_{\Sigma} \sum_{i=1}^n \text{dist}_g(\Sigma, \Sigma_i)^2$$

Geometric deviation

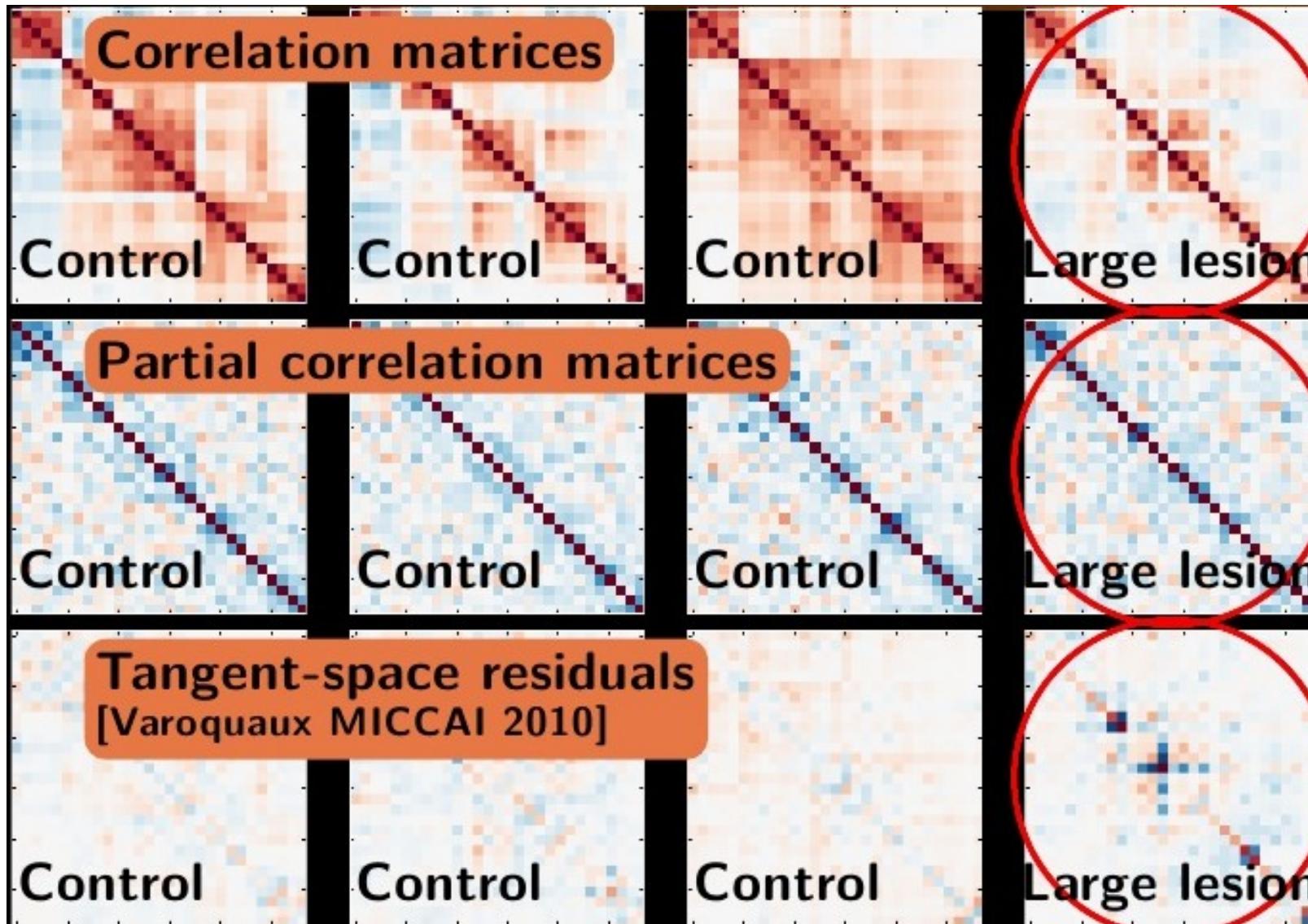
Let  $\Phi_{\Sigma} : \mathbf{S} \rightarrow \text{Log} \left( \Sigma^{-\frac{1}{2}} \mathbf{S} \Sigma^{-\frac{1}{2}} \right)$   
 $\Phi_{\Sigma_{\star}}(\Sigma_i)$

[Varoquaux et al. MICCAI 2010]

Ensuing test discriminates  
patients from controls

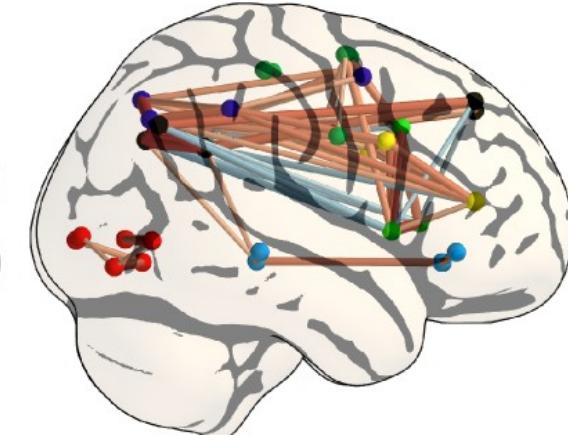
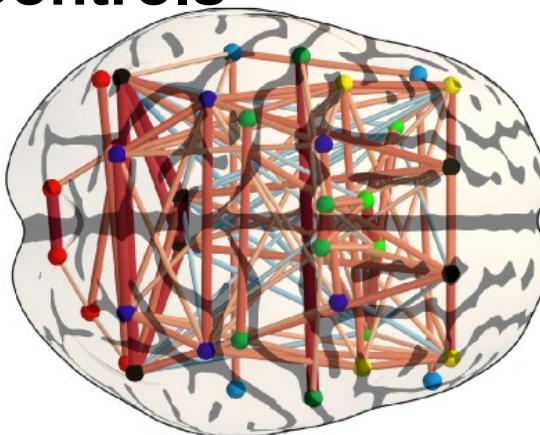
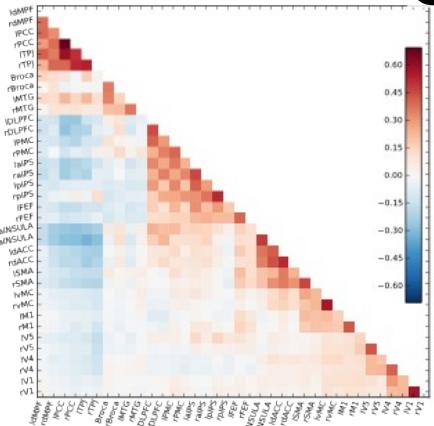


# Statistical testing on graphical models

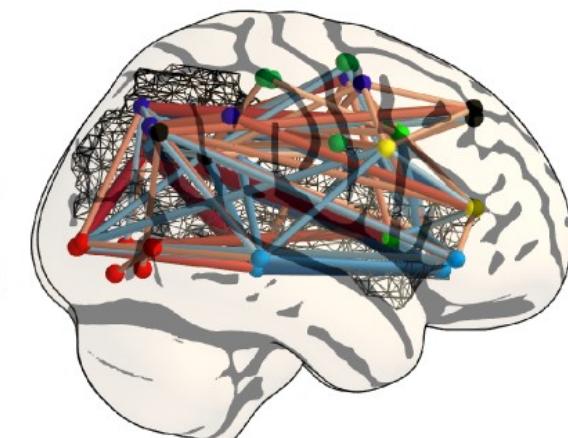
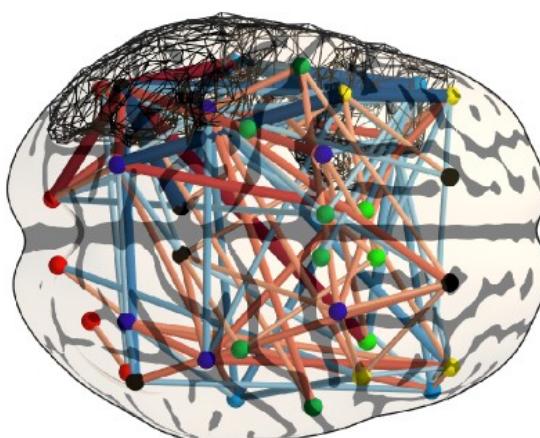
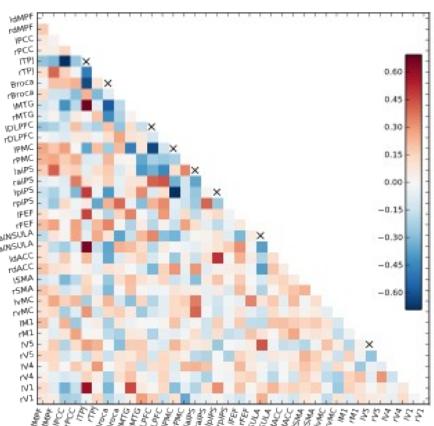


# Statistical testing on graphical models

Controls



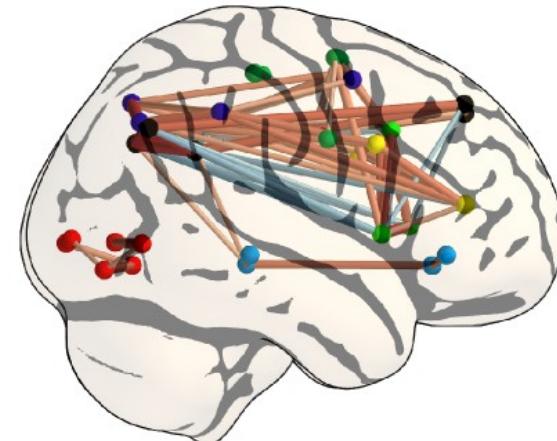
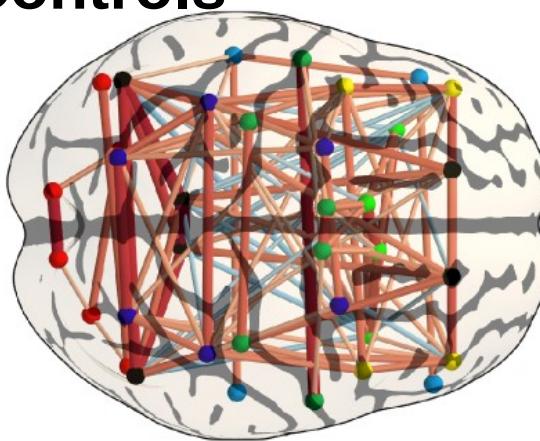
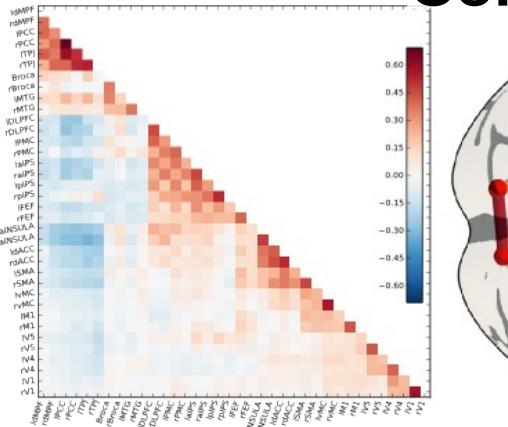
Perturbated Correlations after a stroke



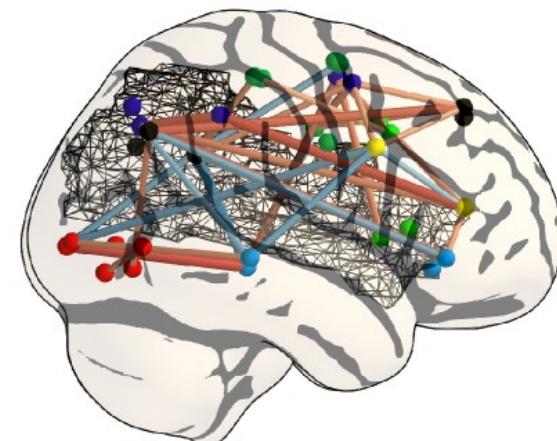
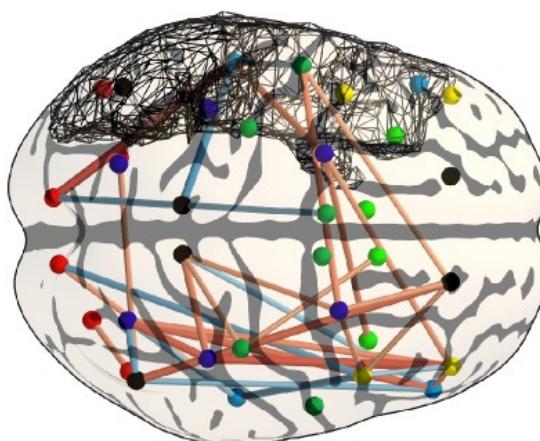
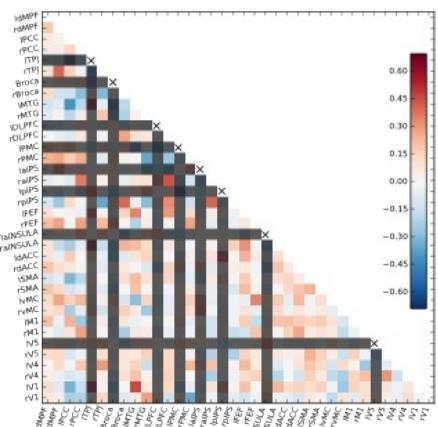
Data by F. Baronnet and A. Kleinschmidt. See [Varoquaux et al MICCAI 2010]

# Statistical testing on graphical models

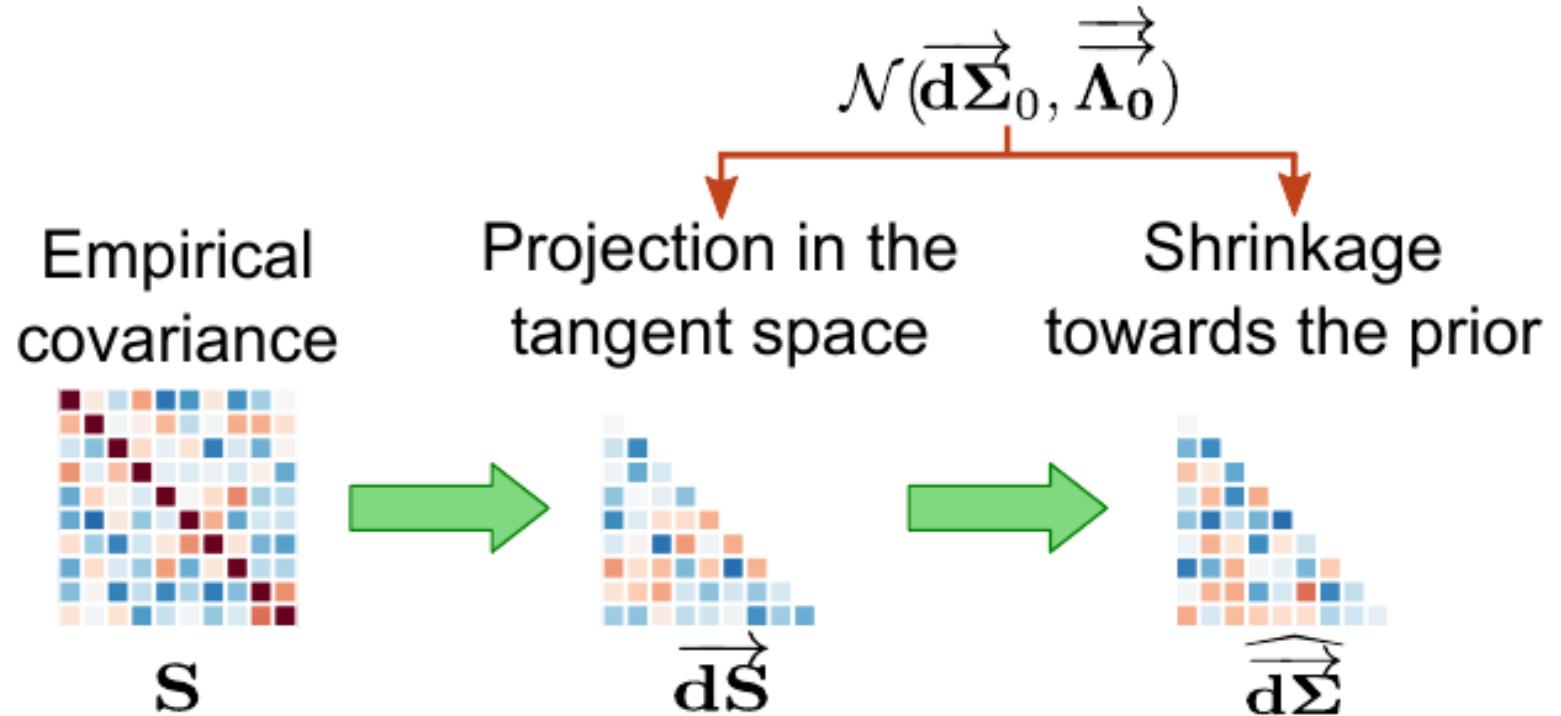
Controls



Perturbated Correlations after a stroke



# Population model covariance



- Idea: regularize estimation in tangent representation
  - shrinkage toward population distribution
- Low-variance, biased estimator

# Population model covariance

Tangent model  $\mathbf{d}\Sigma = \text{logm}(\Sigma_0^{-\frac{1}{2}} \Sigma \Sigma_0^{-\frac{1}{2}})$

Vector model  $\vec{d\Sigma} = \text{vec}(\mathbf{d}\Sigma) = \{\sqrt{2} \mathbf{d}\Sigma_{i,j}, j < i, \mathbf{d}\Sigma_{i,i}, i = 1 \dots p\}$

prior  $\vec{d\Sigma} \sim \mathcal{N}(\vec{d\Sigma}_0, \vec{\Lambda}_0)$

$\vec{d\Sigma}_0 = \vec{0}$

$$\vec{\Lambda}_0 = \frac{1}{N_{\text{train}} - 1} \sum_{i=1}^{N_{\text{train}}} \vec{dS}_i \otimes \vec{dS}_i$$

likelihood  $p(\vec{dS} | \vec{d\Sigma}) = \mathcal{N}(\vec{dS}, \vec{\Lambda})$

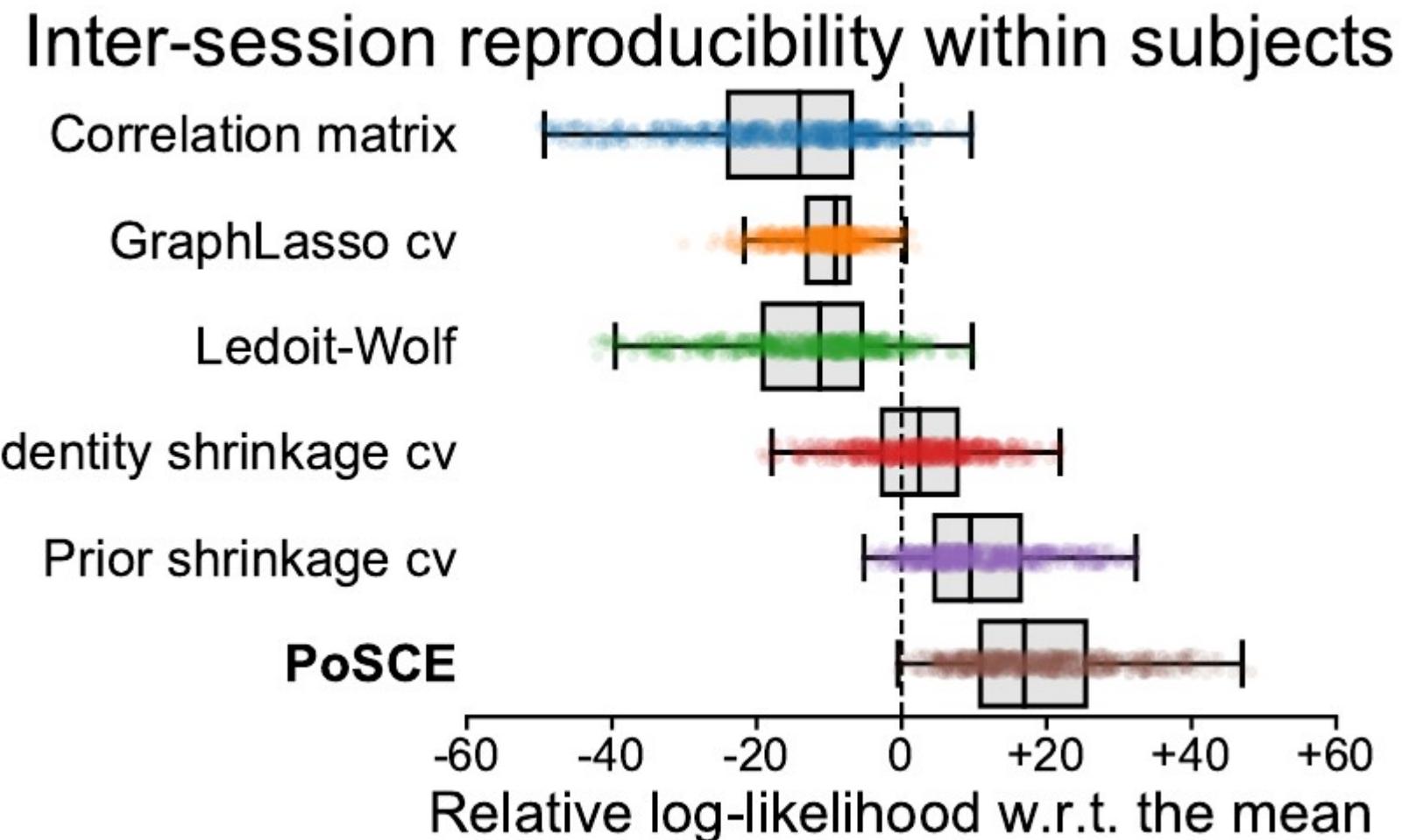
Posterior inference  $p(\vec{d\Sigma} | \vec{dS}) = \mathcal{N}(\widehat{\vec{d\Sigma}}, \vec{\bar{C}})$

$$\vec{\bar{C}}^{-1} = \vec{\Lambda}^{-1} + \vec{\Lambda}_0^{-1}$$
$$\widehat{\vec{d\Sigma}} = (\vec{\Lambda}^{-1} + \vec{\Lambda}_0^{-1})^{-1} \vec{\Lambda}^{-1} \vec{dS}$$

Back to covariance matrices  $\hat{\Sigma}_{\text{PoSCE}} = \Sigma_0^{\frac{1}{2}} \text{expm}(\widehat{\vec{d\Sigma}}) \Sigma_0^{\frac{1}{2}}$

# Applications of POSCE

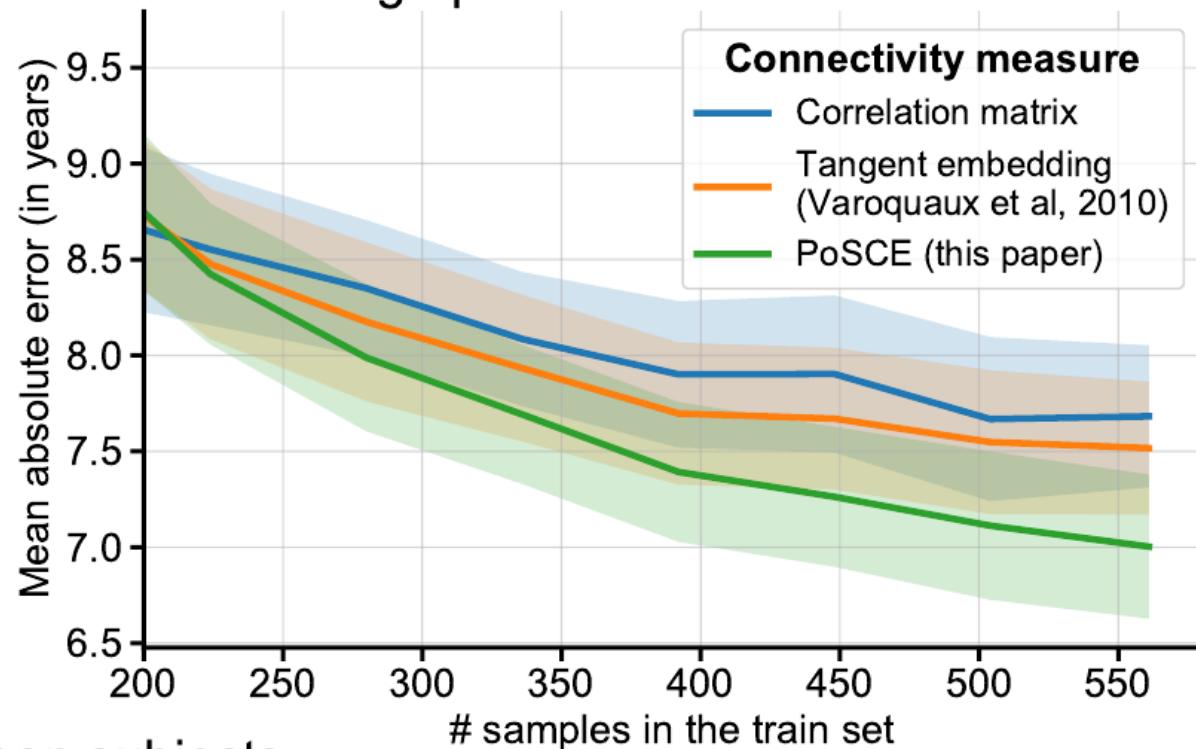
Repeated measures experiment:  
POSCE better generalizes to data from same subject



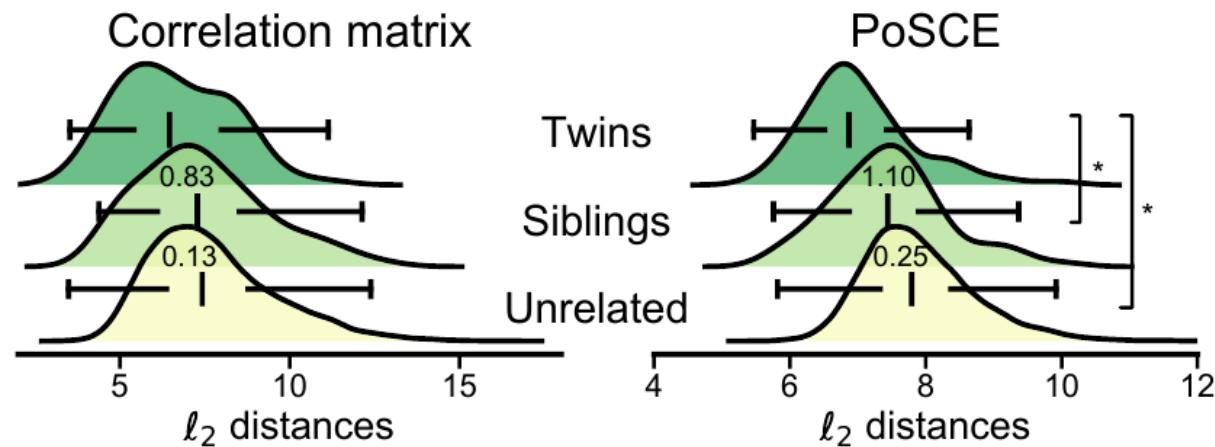
# Applications of POSCE

Age prediction experiment:  
regularization improves estimation

Age prediction on CAMCAN



Connectivity-based similarities between subjects

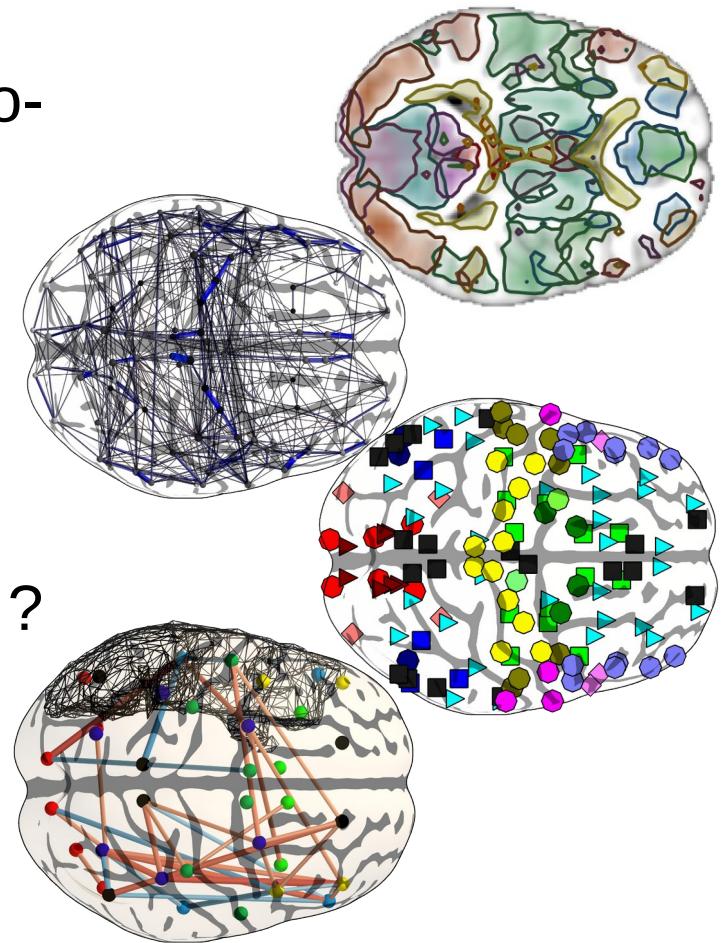


Genetic similarity better represented by POSCE estimator

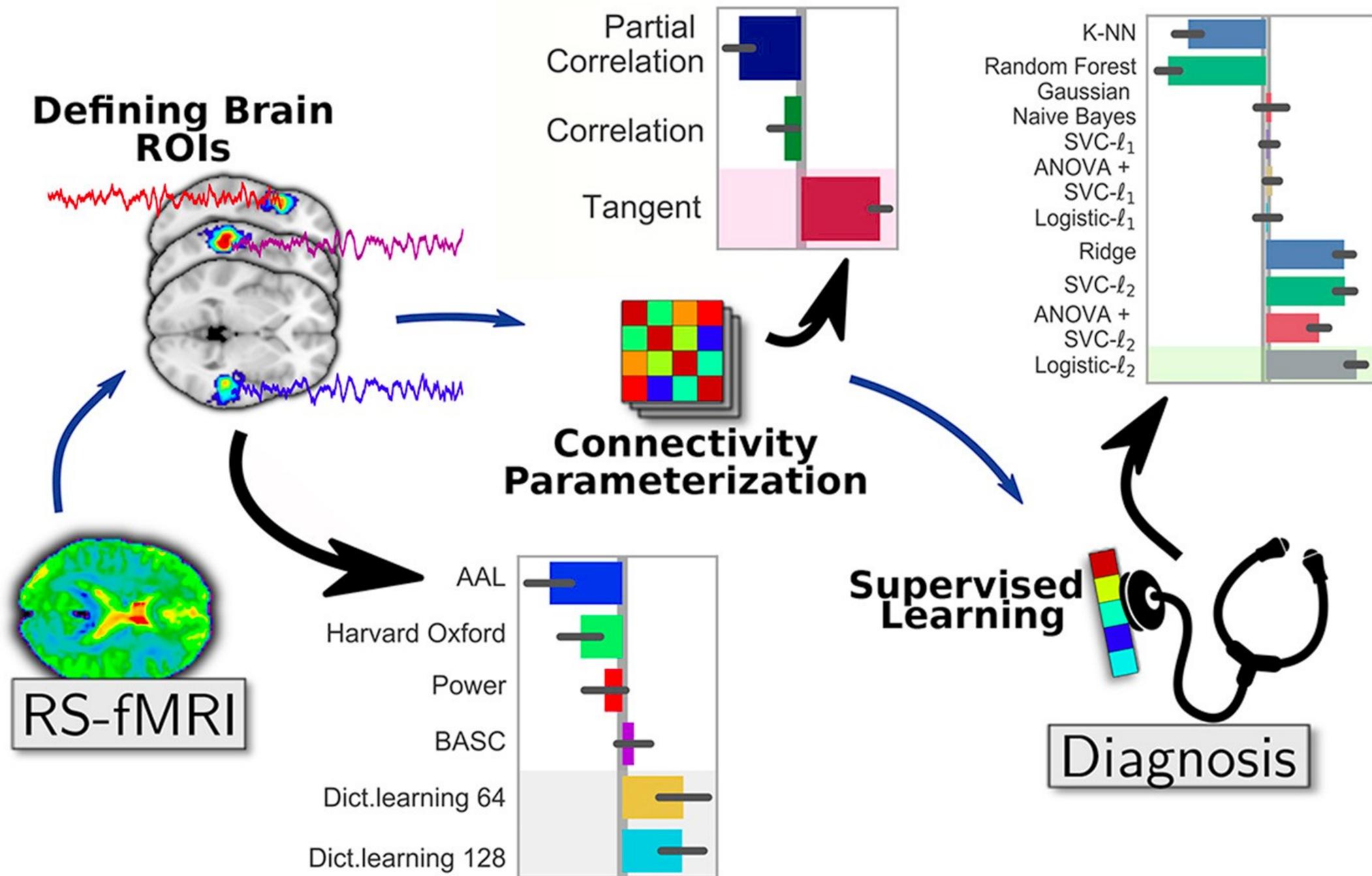
# The covariance structure of fMRI signals

- Deriving brain atlases from functional co-activations
- Graph of functional interactions
- Intrinsic structures in brain connectivity
- Individualized diagnostic markers
- Towards a functional-anatomical model ?

Weak SNR, weak specificity  
of resting-state signals



# What matters most for diagnosis accuracy?



# The best brain atlas

AAL  
(116 regions)

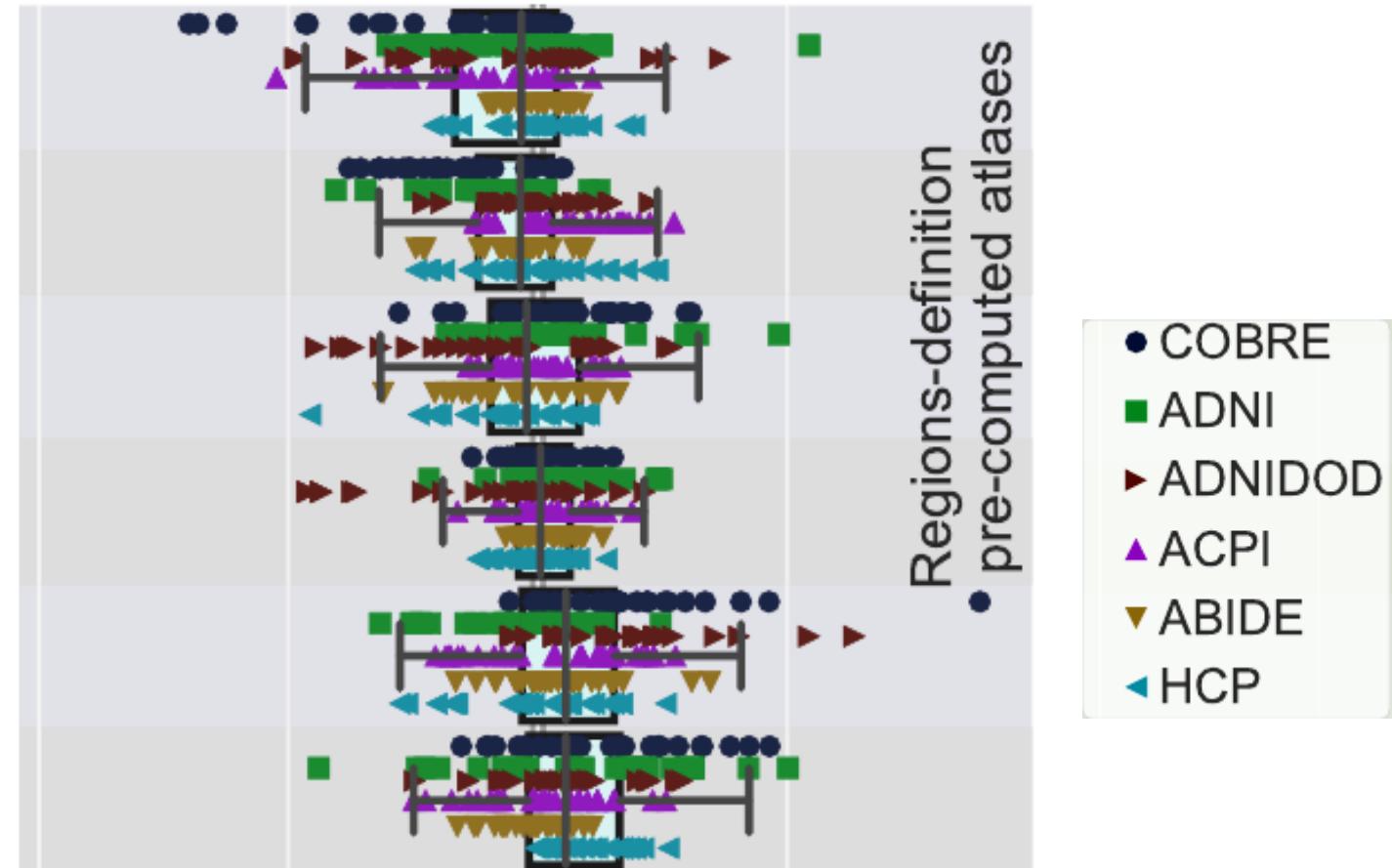
Harvard Oxford  
(118 regions)

Power  
(264 regions)

BASC  
(122 networks)

MODL dict. learning  
(64 networks)

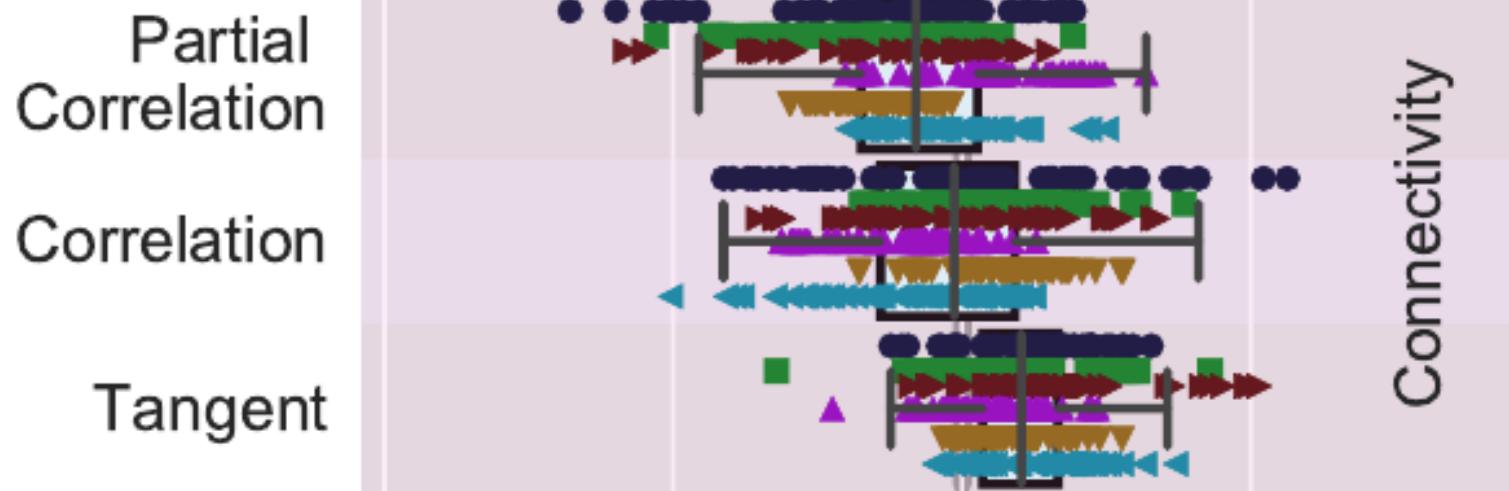
MODL dict. learning  
(128 networks)



Across 6 datasets & cross-validation folds

[Dadi et al. Nimg 2019]

# The best connectivity model



Across 6 datasets & cross-validation folds

Tangent outperforms alternatives

[Dadi et al. Nimg 2019]

# The best classifier

K-NN  
Random Forest

Gaussian  
Naive Bayes

SVC- $\ell_1$

ANOVA +  
SVC- $\ell_1$

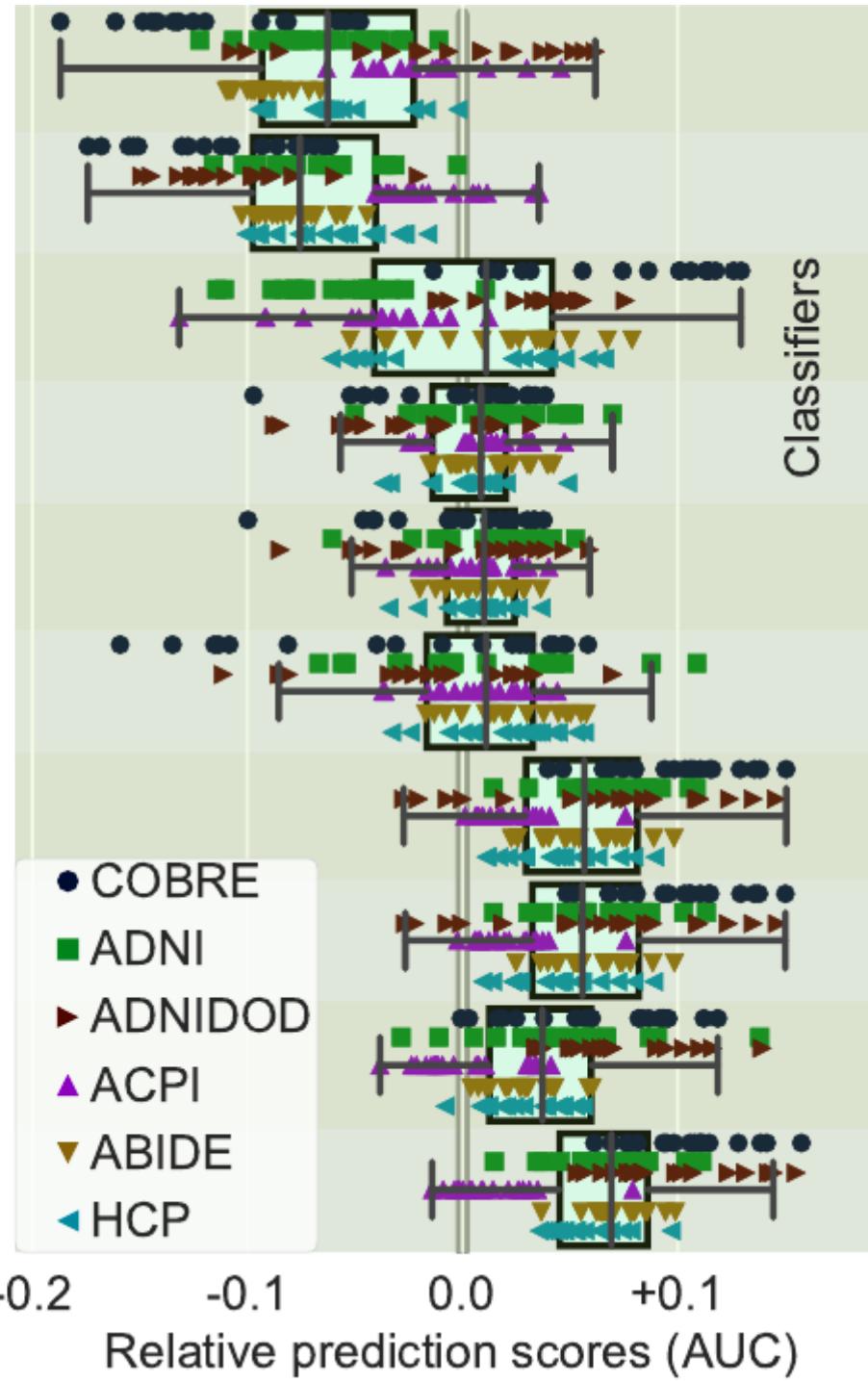
Logistic- $\ell_1$

Ridge

SVC- $\ell_2$

ANOVA +  
SVC- $\ell_2$

Logistic- $\ell_2$



# IMPAC



IMPAC

IMaging-PsychiAtry Challenge: predicting autism  
A data challenge on Autism Spectrum Disorder detection

## Incentives and goals:

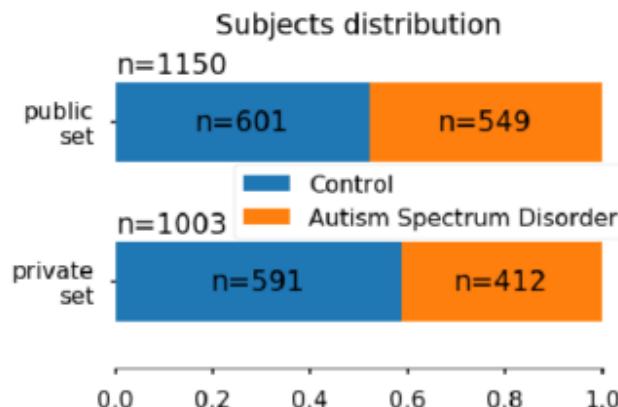
- 3000€ for the best prediction of autism status

## Web-based:

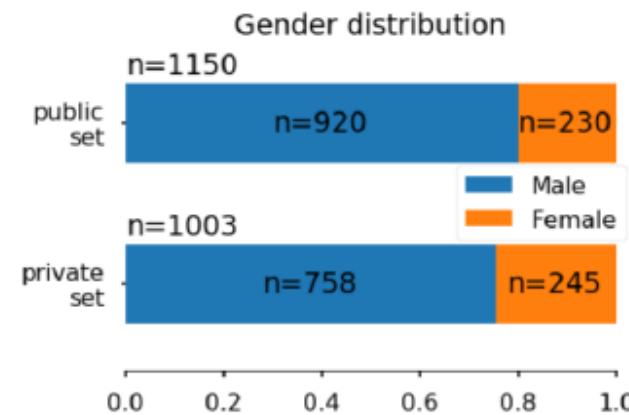
- Participants submit code
- Competition open during 3 months

# Blind assessment of biomarkers

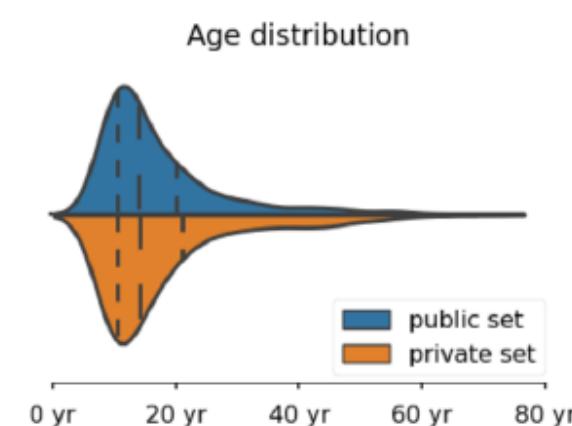
Patient vs Control distribution



Gender distribution



Age distribution



## Hidden test set:

Participants never see the private set

Private-set prediction scores are published at the end

# Learning curve

