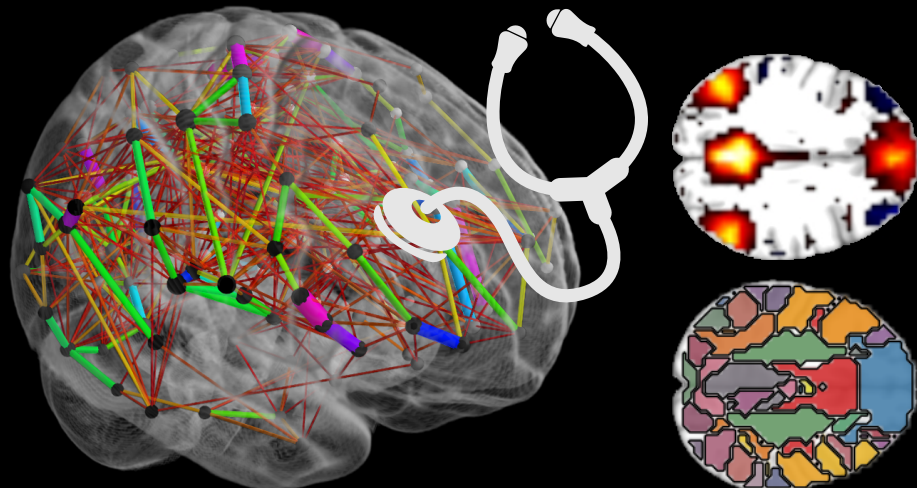


Statistical markers of pathologies from the brain at rest

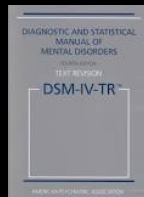
Gaël Varoquaux



Probing variations of the mind

Psychiatry is defined by symptoms

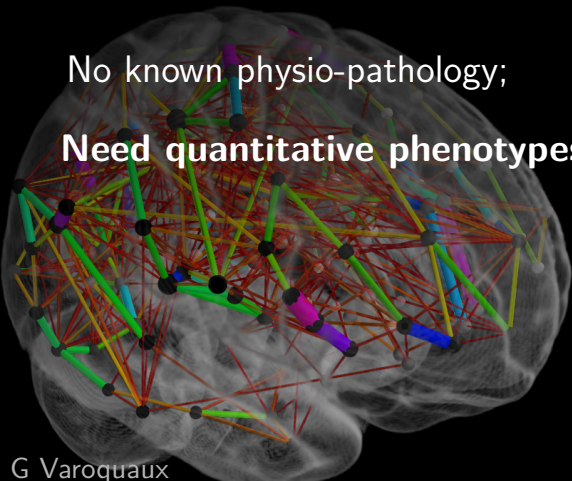
Diagnostic and Statistical
Manual of Mental Disorders



No known physio-pathology;

Autism \neq Asperger

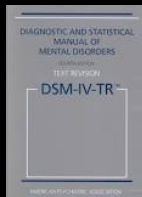
Need quantitative phenotypes of brain function



Probing variations of the mind

Psychiatry is defined by symptoms

Diagnostic and Statistical
Manual of Mental Disorders



No known physio-pathology; Autism \neq Asperger

Need quantitative phenotypes of brain function

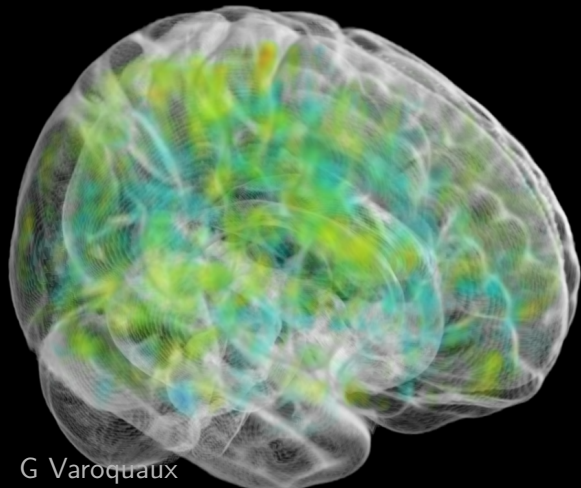
Population imaging with rest fMRI

UK Biobank [Miller... 2016]

- Easy to set up reproducibly
- Suitable for diminished patients
- Connectivity captures traits

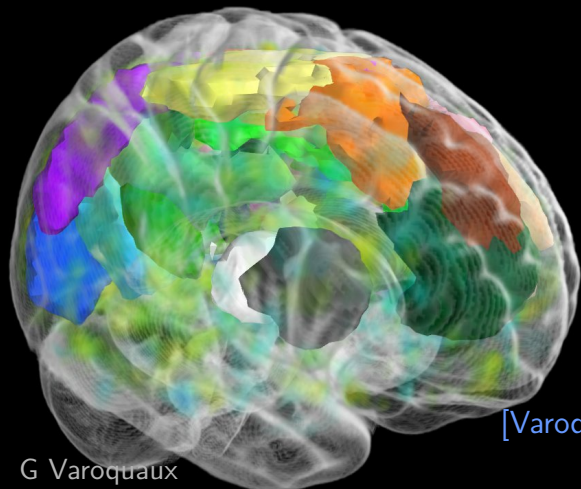
Functional connectomes: brain graphs

No salient features in rest fMRI



Functional connectomes: brain graphs

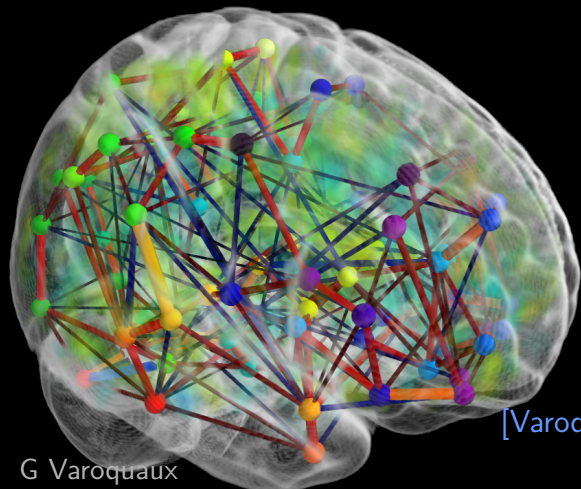
- Define functional regions



[Varoquaux and Craddock 2013]

Functional connectomes: brain graphs

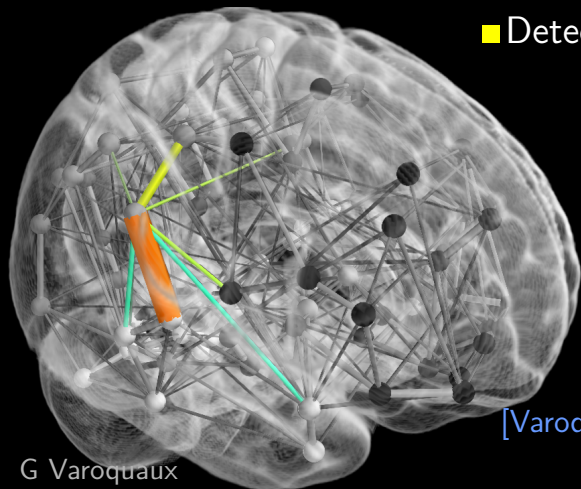
- Define functional regions
- Learn interactions



[Varoquaux and Craddock 2013]

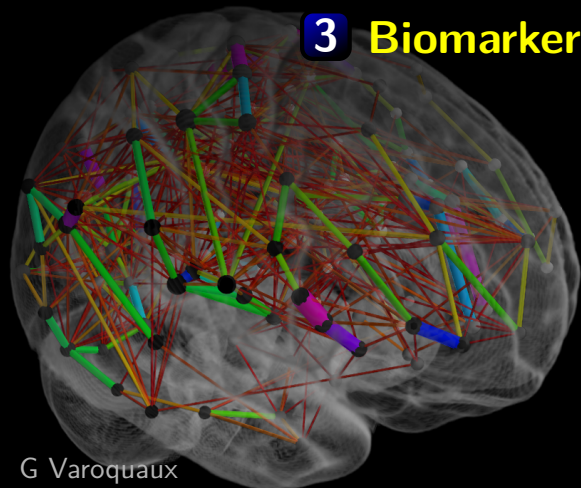
Functional connectomes: brain graphs

- Define functional regions
- Learn interactions
- Detect differences



[Varoquaux and Craddock 2013]

- 1 Functional regions**
- 2 The connectome matrix**
- 3 Biomarkers of autism**



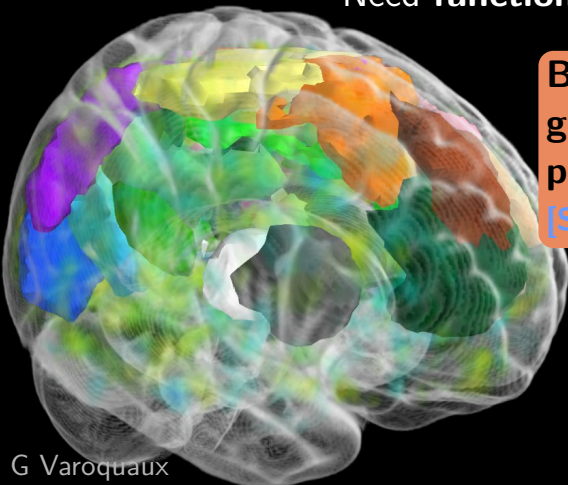
1 Functional regions

Need **functional** regions for nodes

Bad choice of regions
gives wrong graph
properties

[Smith... 2011]

⇒ Spatial analysis



1 Functional regions

Available “on the market”

anatomical atlases, functional atlases, region-extraction methods



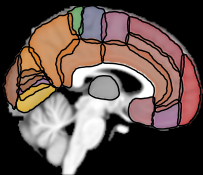
1 Functional regions

- Atlases based on anatomy
- Clustering tools
- Models based on linear decompositions

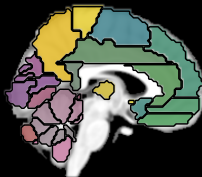
1 Anatomical atlases

- Anatomical atlases do not resolve functional structures

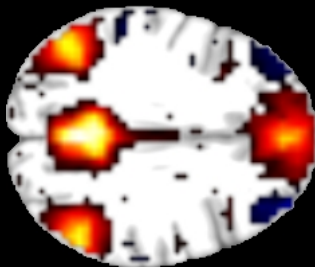
Harvard Oxford



AAL

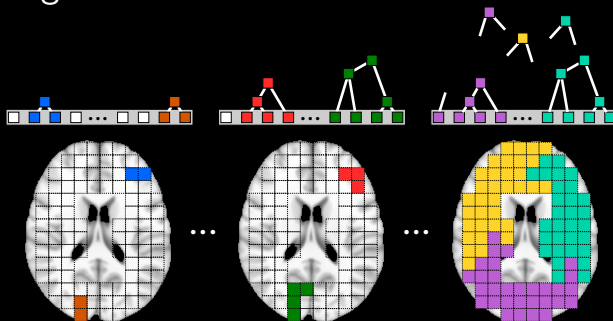


Default mode network:
most stable network at
rest



1 Clustering approaches

- Group together voxels with similar time courses



1 Clustering approaches

K-Means

- Fast
- No spatial constraint
(smooth the data)

Related to [Yeo... 2011]

KMeans



Normalized cuts

- Slow [Craddock... 2012]
- Spatial constraints
- Very geometrical

Ncuts [Craddock 2011]



Ward clustering

- Very fast
(even with many clusters)
- Spatial constraints

Ward



1 Clustering approaches

[Thirion... 2014]

K-Means

- Fast
- No spatial constraint
(smooth the data)

KMeans



Model selection: empirical results

Based on cluster stability and fit to data

- Large number of clusters: Ward
- Small number of clusters: Kmeans

[Thirion... 2014]

Ward clustering

- Very fast
(even with many clusters)
- Spatial constraints

Ward

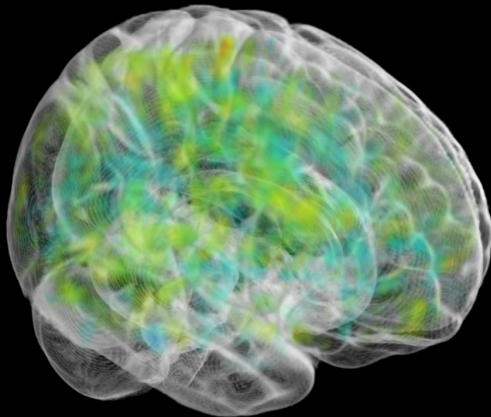


1 Mixture models: linear decompositions

Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



1 Mixture models: linear decompositions

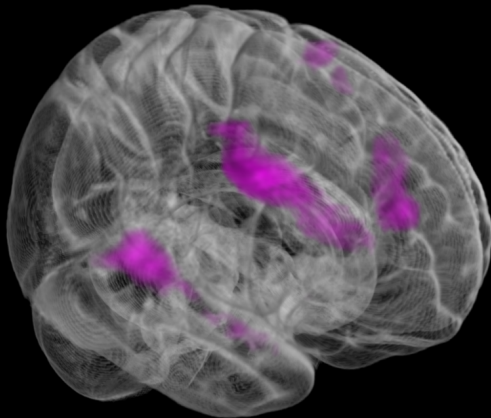
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Language

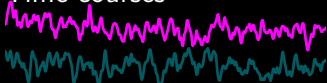


1 Mixture models: linear decompositions

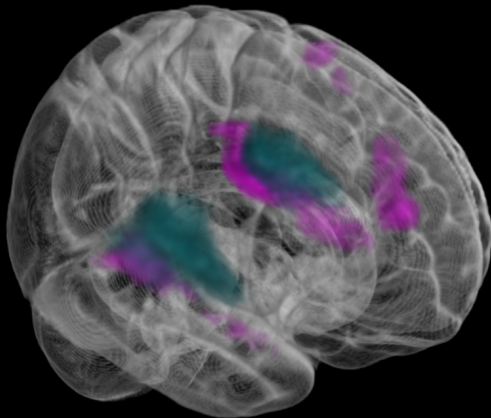
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Audio

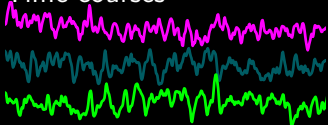


1 Mixture models: linear decompositions

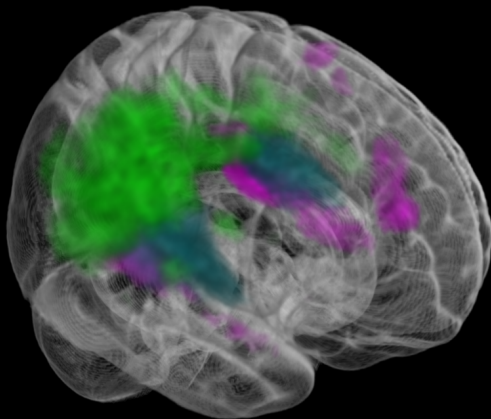
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Visual

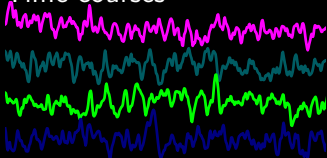


1 Mixture models: linear decompositions

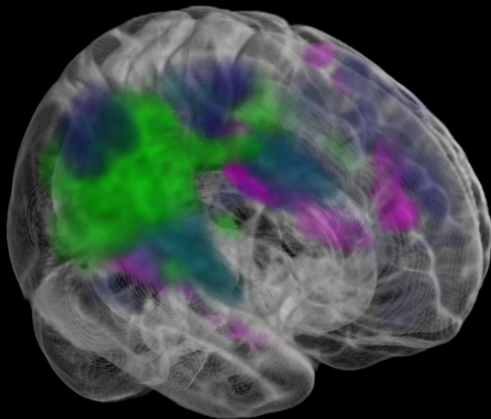
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Dorsal Att.

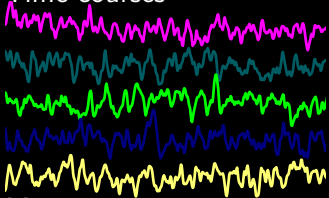


1 Mixture models: linear decompositions

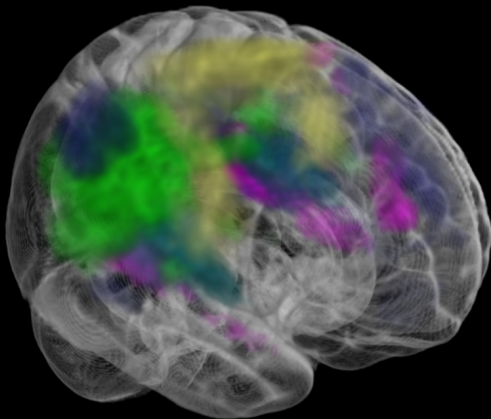
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Motor

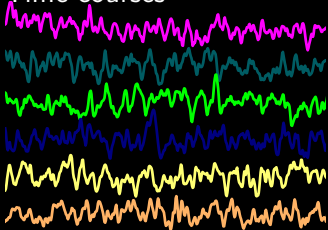


1 Mixture models: linear decompositions

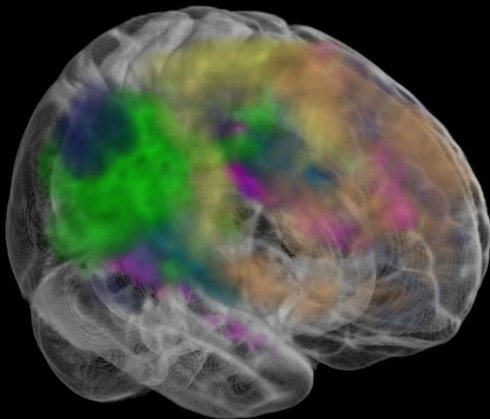
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Saliency

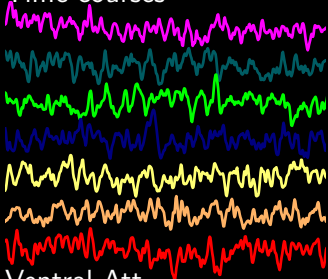


1 Mixture models: linear decompositions

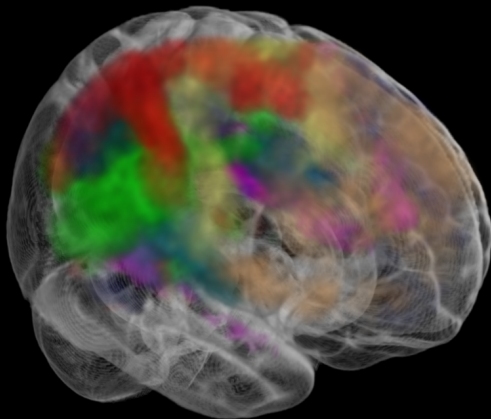
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Ventral Att.

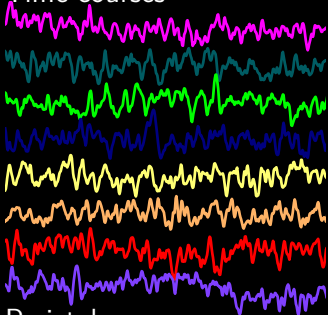


1 Mixture models: linear decompositions

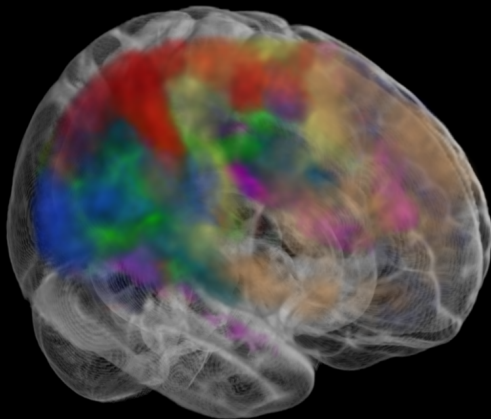
Working hypothesis / model:

Observing linear mixtures of networks at rest

Time courses



Parietal

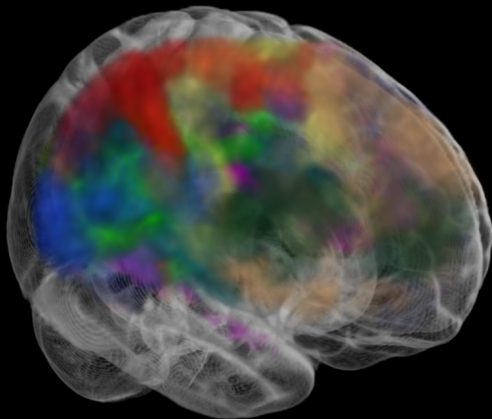
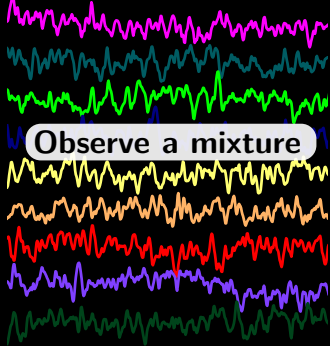


1 Mixture models: linear decompositions

Working hypothesis / model:

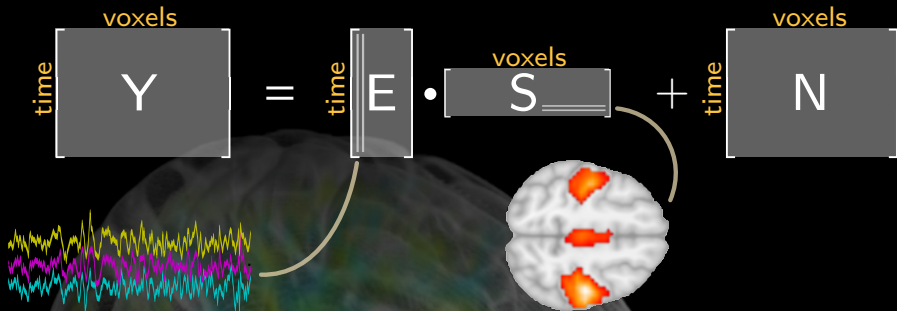
Observing linear mixtures of networks at rest

Time courses



How to unmix networks?

1 Spatial modes: ICA decomposition

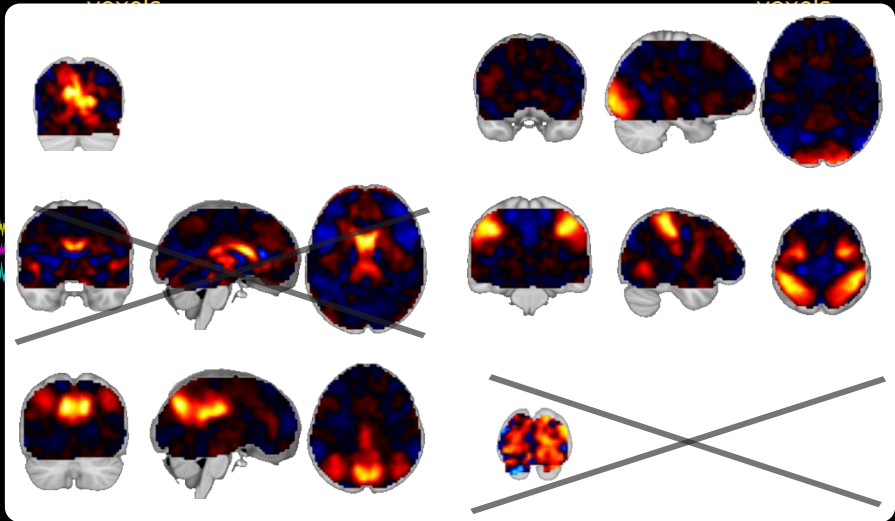


Decomposing time series into:

- covarying spatial maps, S
- uncorrelated residuals, N

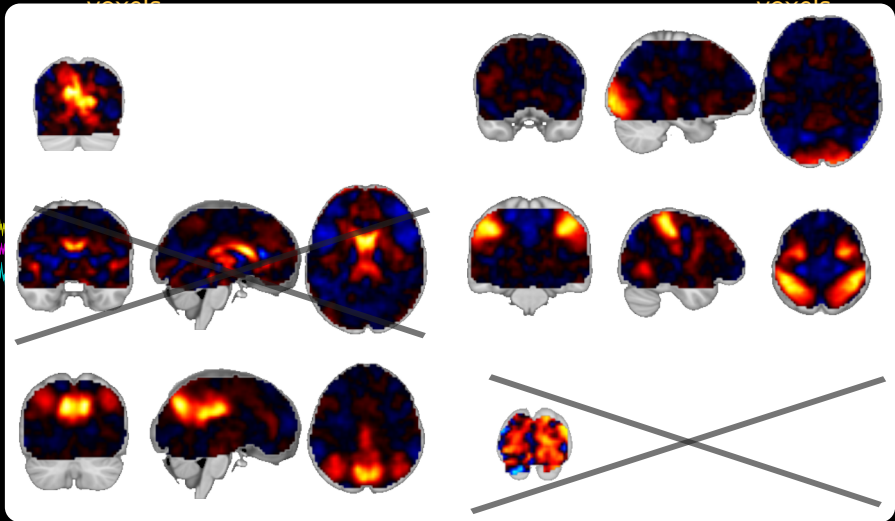
ICA: minimize mutual information across S

1 Spatial modes: ICA decomposition



ICA: minimize mutual information across S

1 Spatial modes: ICA decomposition



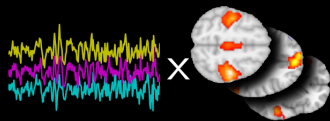
Sparse decompositions: sparse penalty on maps

1 ICA versus sparse decompositions

ICA

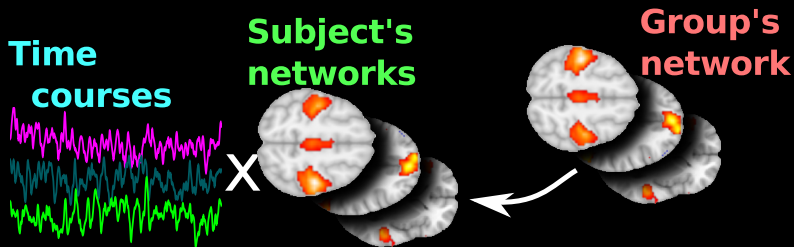
1. Select signal of interest
2. Select “maximally independent” ICs

Sparse decomposition



$$\hat{\mathbf{E}}, \hat{\mathbf{S}} = \underset{\mathbf{S}, \mathbf{E}}{\operatorname{argmin}} \underbrace{\|\mathbf{Y} - \mathbf{E}\mathbf{S}\|_2^2}_{\text{Data fit}} + \lambda \underbrace{\|\mathbf{S}\|_1}_{\text{Penalization: sparse maps}}$$

Joint estimation of signal space + components



Multi-Subject Dictionary Learning

$$\operatorname{argmin}_{\mathbf{E}^s, \mathbf{S}^s, \mathbf{S}} \sum_{\text{subjects}} \left(\underbrace{\|\mathbf{Y}^s - \mathbf{E}^s \mathbf{S}^{sT}\|_{\text{Fro}}^2}_{\text{Data fit}} + \underbrace{\mu \|\mathbf{S}^s - \mathbf{S}\|_{\text{Fro}}^2}_{\text{Subject variability}} \right) + \underbrace{\lambda \Omega(\mathbf{S})}_{\text{Penalization: inject structure}}$$

[Varoquaux... 2011, Abraham... 2013]

Create a region-forming penalty:

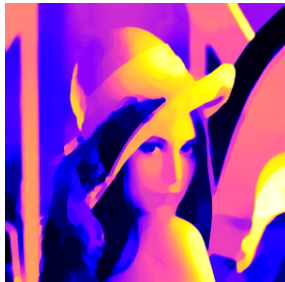
Original



Clustering



Total-variation



$$\operatorname{argmin}_{\mathbf{E}^s, \mathbf{S}^s, \mathbf{S}} \sum_{\text{subjects}} \left(\underbrace{\|\mathbf{Y}^s - \mathbf{E}^s \mathbf{S}^s T\|_{\text{Fro}}^2}_{\text{Data fit}} + \underbrace{\mu \|\mathbf{S}^s - \mathbf{S}\|_{\text{Fro}}^2}_{\text{Subject variability}} \right) + \underbrace{\lambda \Omega(\mathbf{S})}_{\text{Penalization: inject structure}}$$

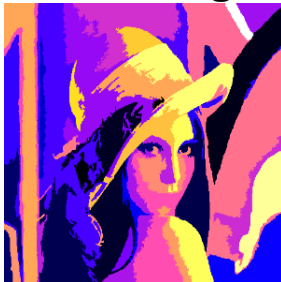
[Varoquaux... 2011, Abraham... 2013]

Create a region-forming penalty:

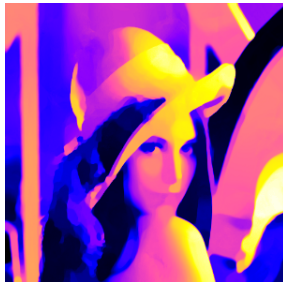
Original



Clustering



Total-variation



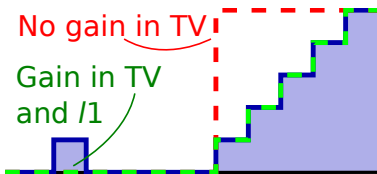
TV- ℓ_1 penalty: $\|\mathbf{w}\|_1 + TV(\mathbf{w})$

- sparse and smooth regions
- TV \neq "piecewise constant"

[Gramfort... 2013]

No gain in TV

Gain in TV
and ℓ_1

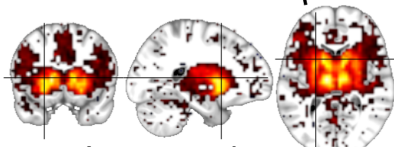
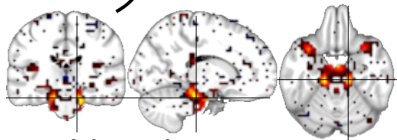
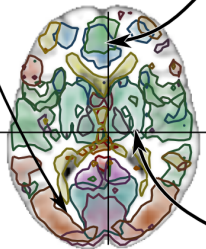
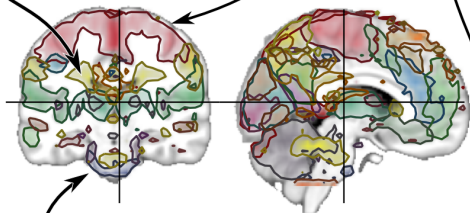
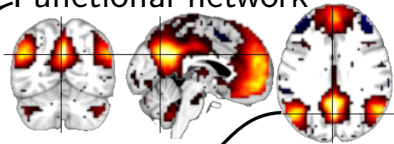
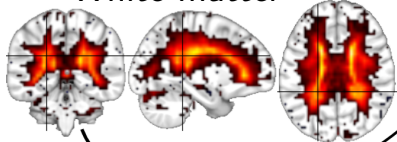


[Varoquaux... 2011, Abraham... 2013]

Visual and motor system

Functional network

White matter

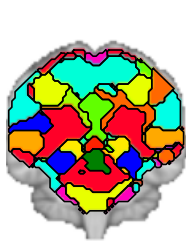


Vascular system

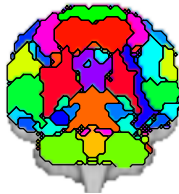
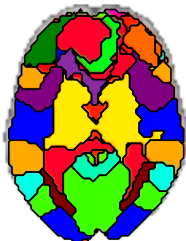
Inner nuclei

Downloadable from Parietal webpage <http://team.inria.fr/parietal>

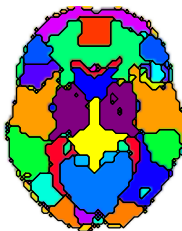
Brain parcellations



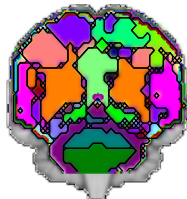
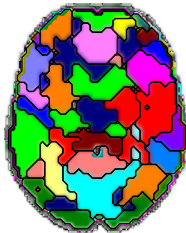
MSDL



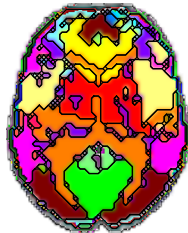
Group ICA



Ward



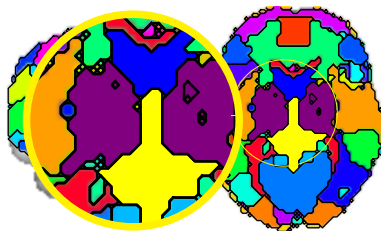
K-Means



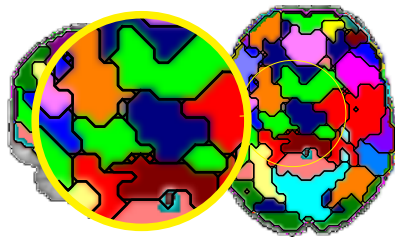
Brain parcellations



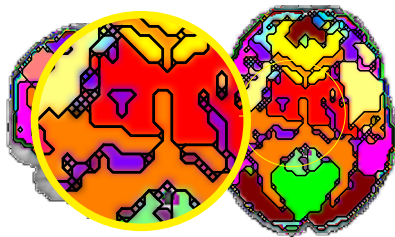
MSDL



Group ICA

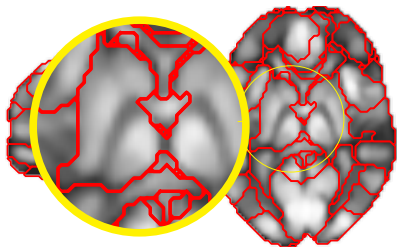


Ward

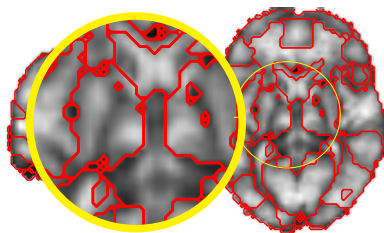


K-Means

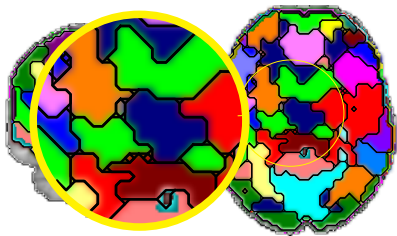
Brain parcellations



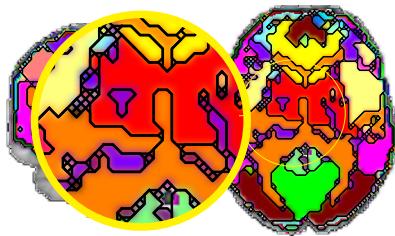
MSDL



Group ICA

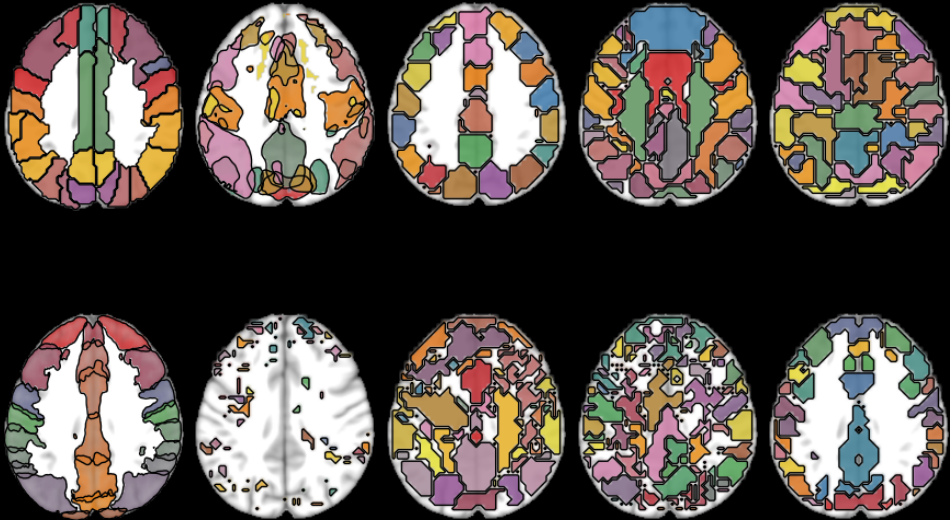


Ward



K-Means

Functional regions



Functional regions



AAL



Smith 2009
ICAs



Craddock
2011 Ncuts



Abraham 2013
TV-MSDL



Ward



Harvard-
Oxford



High model
order ICA



K-Means



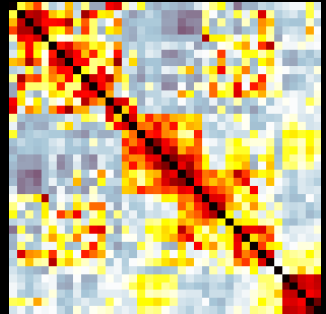
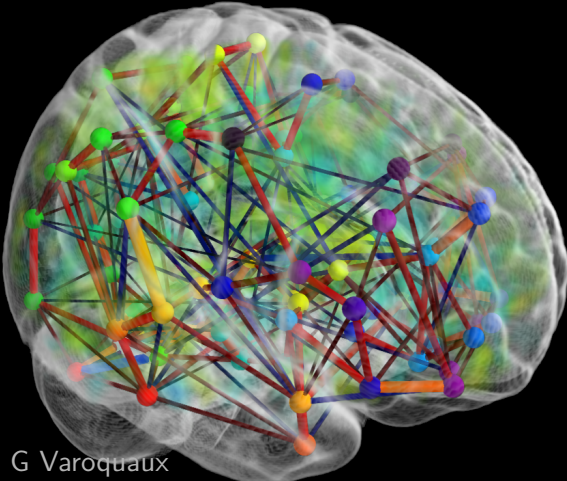
Varoquaux
2011 Smooth-
MSDL



Yeo 2011

2 The connectome matrix

How to capture and represent interactions?



2 Data processing induces structure

Small-world:

"The friends of my friends are my friends"

Correlation:

If **A** and **B** are very correlated,
and **C** is correlated with **A**,
C is also correlated with **B**

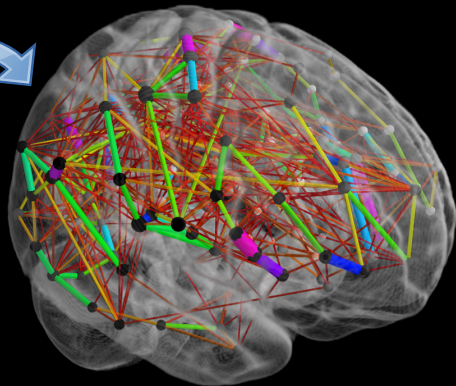
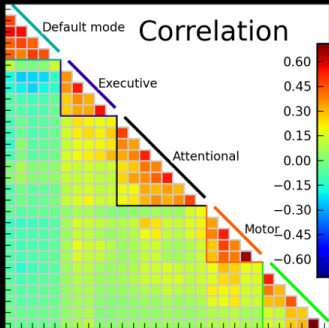
⇒ Thresholded correlations are small-world

[Zalesky... 2012]

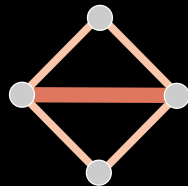
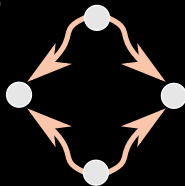


Need careful statistics

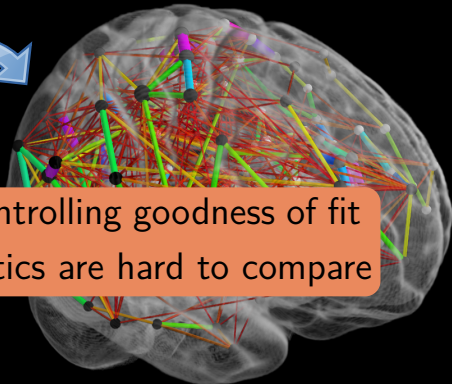
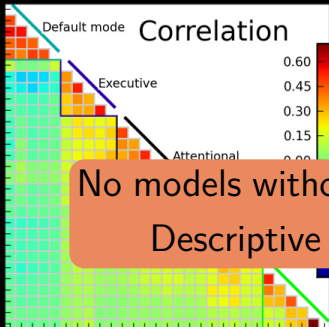
2 From correlations to connectomes



Threshold?



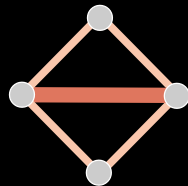
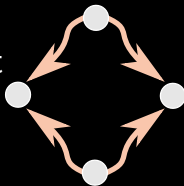
2 From correlations to connectomes



No models without controlling goodness of fit
Descriptive statistics are hard to compare

Threshold?

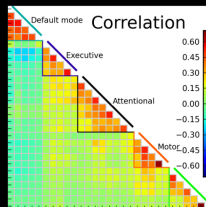
How to check that we are not
throwing out the baby
with the bath water



2 Probabilistic model for interactions

- Simplest **data generating process**
= multivariate normal:

$$\mathcal{P}(\mathbf{X}) \propto \sqrt{|\boldsymbol{\Sigma}^{-1}|} e^{-\frac{1}{2} \mathbf{x}^T \boldsymbol{\Sigma}^{-1} \mathbf{x}}$$



- Model parametrized by inverse covariance matrix,
 $\mathbf{K} = \boldsymbol{\Sigma}^{-1}$: **conditional** covariances

- Goodness of fit:

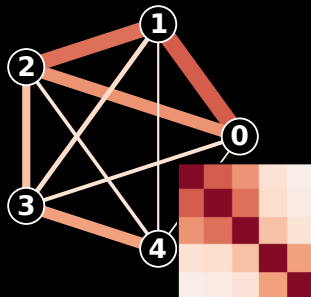
likelihood of observed covariance $\hat{\boldsymbol{\Sigma}}$ in model $\boldsymbol{\Sigma}$

$$\mathcal{L}(\hat{\boldsymbol{\Sigma}} | \mathbf{K}) = \log |\mathbf{K}| - \text{trace}(\hat{\boldsymbol{\Sigma}} \mathbf{K})$$

2 Correlations: observations and indirect effects

Observations

Correlation

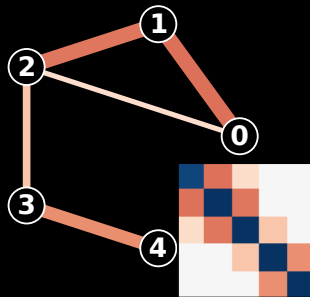


Covariance:
scaled by variance



Direct connections

Partial correlation



Inverse covariance:
scaled by partial variance

2 Correlations: observations and indirect effects

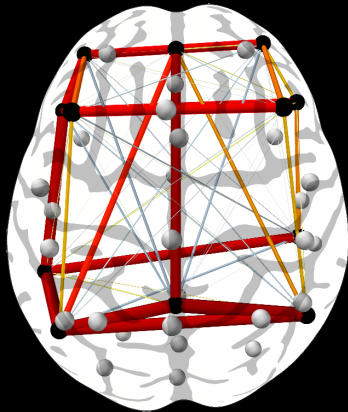
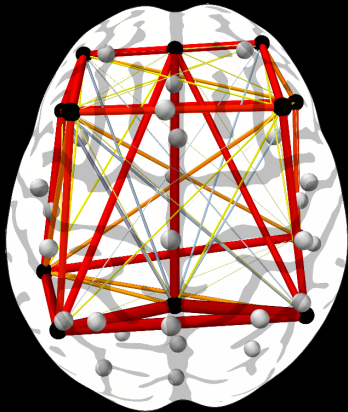
Observations

Correlation



Direct connections

Partial correlation

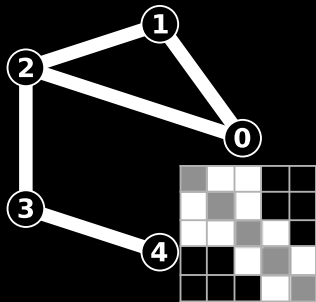


2 Estimating a graphical model

Gaussian graphical models

Zeros in inverse covariance give **conditional independence**

$$\Sigma_{i,j}^{-1} = 0 \iff \mathbf{x}_i, \mathbf{x}_j \text{ independent conditionally on } \{\mathbf{x}_k, k \neq i, j\}$$



Sparse inverse covariance

Estimator imposes zeros

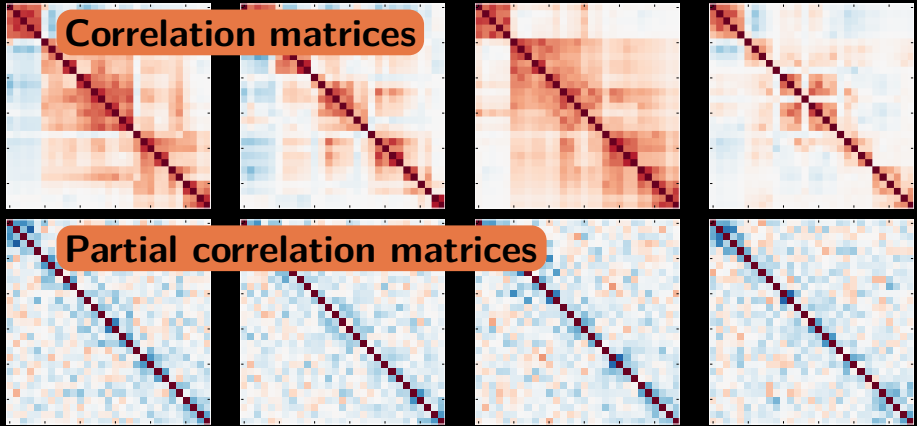
[Smith... 2011, Varoquaux... 2010b]

Shrunk estimator

Estimates closer to 0

[Varoquaux and Craddock 2013]

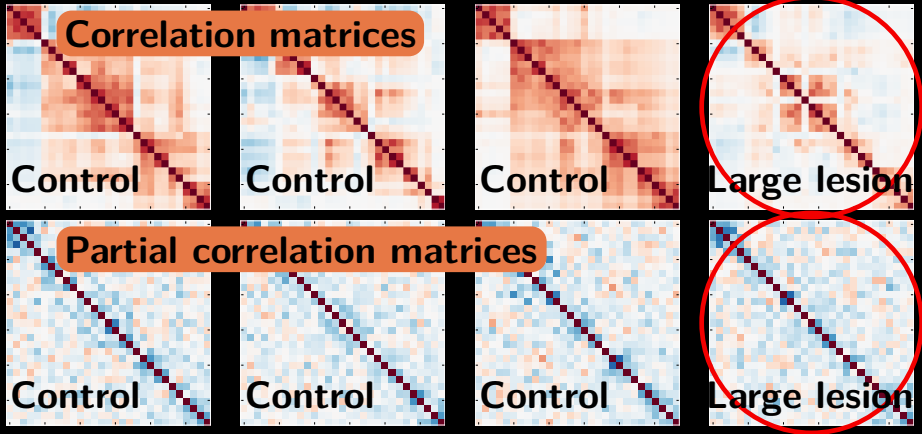
2 Differences in correlations across subjects



3 controls, 1 severe stroke patient

Which is which?

2 Differences in correlations across subjects



- Spread-out variability in correlation matrices
- Noise in partial-correlations

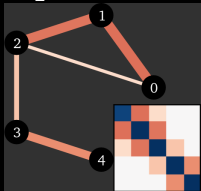
Strong dependence between coefficients

[Varoquaux... 2010a]

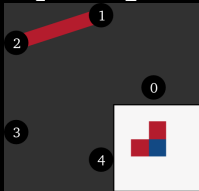
2 A toy model of differences in connectivity

- Two processes with different partial correlations

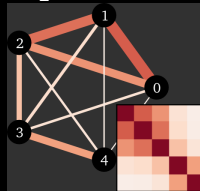
\mathbf{K}_1 :



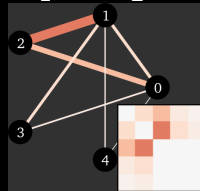
$\mathbf{K}_1 - \mathbf{K}_2$:



Σ_1 :

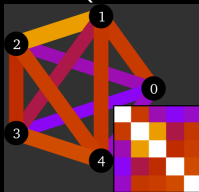


$\Sigma_1 - \Sigma_2$:

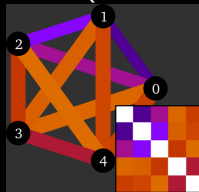


- + jitter in observed covariance

$\text{MSE}(\mathbf{K}_1 - \mathbf{K}_2)$:



$\text{MSE}(\Sigma_1 - \Sigma_2)$:



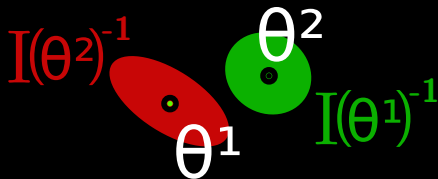
Non-local effects and non homogeneous noise

2 Error geometry

Estimation error of covariances

- Asymptotics given by Fisher matrix
Cramer-Rao bounds

[Rao 1945]

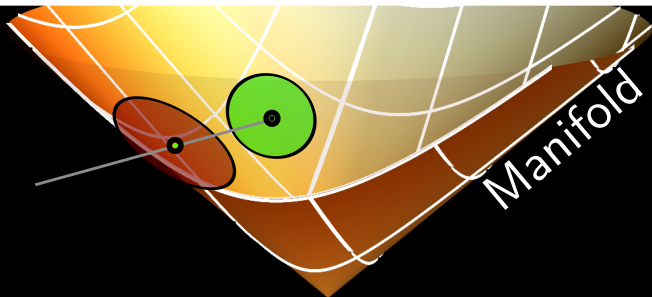


2 Error geometry

Estimation error of covariances

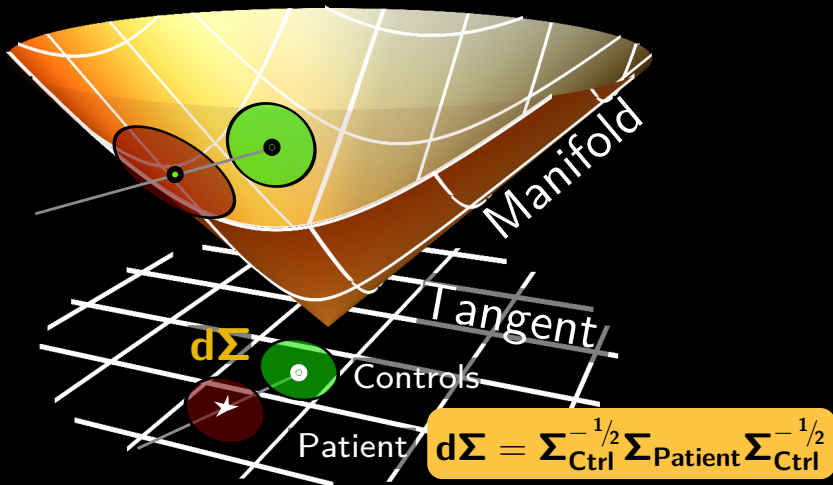
- Asymptotics given by Fisher matrix
- Defines a metric on a manifold of models
- With covariances: Lie-algebra structure

[Rao 1945]



2 Reparametrization for uniform error geometry

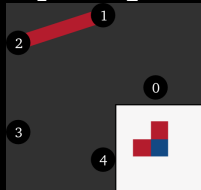
- Disentangle parameters (edge-level connectivities)
- Connectivity matrices form a manifold
⇒ project to tangent space



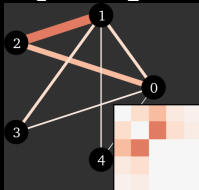
2 Reparametrization for uniform error geometry

The simulations

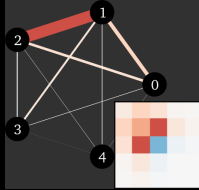
$\mathbf{K}_1 - \mathbf{K}_2$:



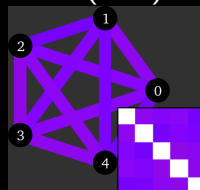
$\Sigma_1 - \Sigma_2$:



$d\Sigma$:



$\text{MSE}(d\Sigma)$:



Semi-local effects and homogeneous noise

2 Which parametrization capture differences

Correlation matrices

Control

Control

Control

Large lesion

Partial correlation matrices

Control

Control

Control

Large lesion

Tangent-space embedding
[varoquaux 2010]

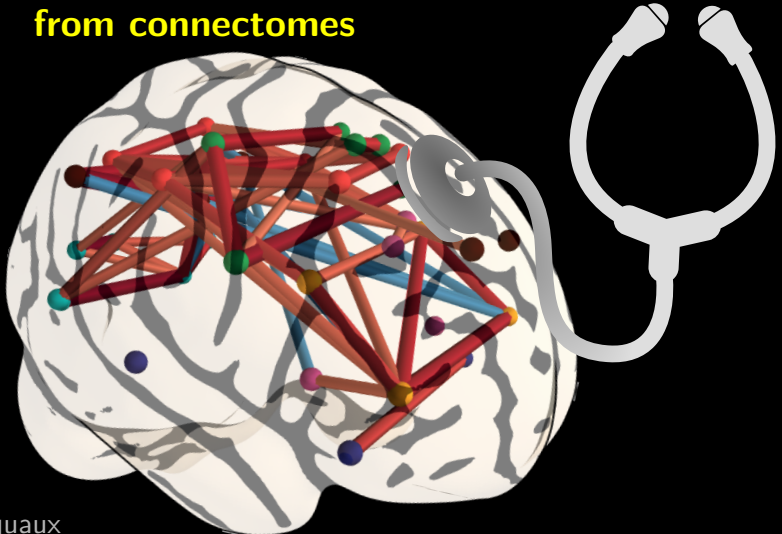
Control

Control

Control

Large lesion

3 Biomarkers of autism from connectomes



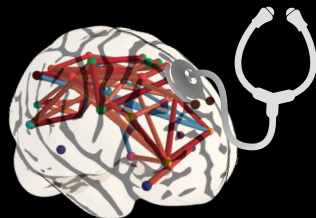
3 Intersite autism neurophenotypes

Predicting diagnostic status a good success metric

Multi-site large autism dataset: ABIDE

[Di Martino... 2014]

- Autism Spectrum Disorder
⇒ Patient/Control classification
- 16 sites
- ~ 1000 subjects



Biomarkers robust to inter-site variations

- Cross-validation predicting to new sites

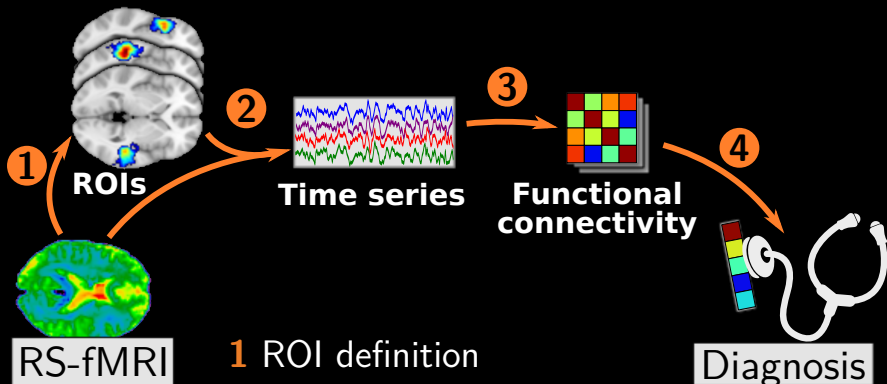


Training set



Testing set

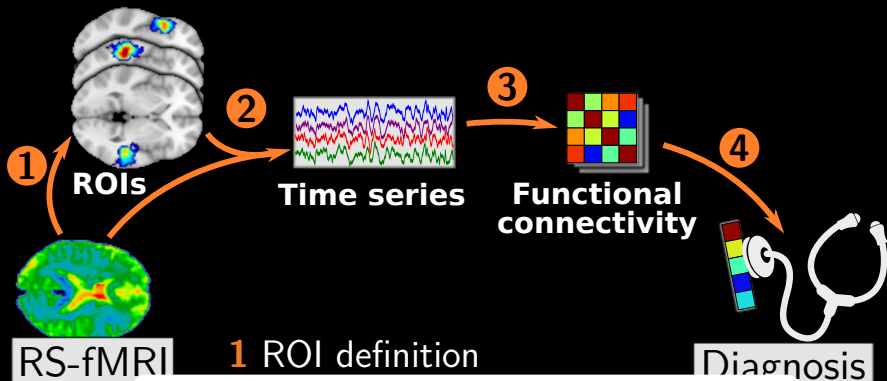
A connectome classification pipeline



- 1 ROI definition
- 2 Time-series extraction
- 3 Connectivity matrices
- 4 Supervised learning

[Abraham... 2016]

A connectome classification pipeline

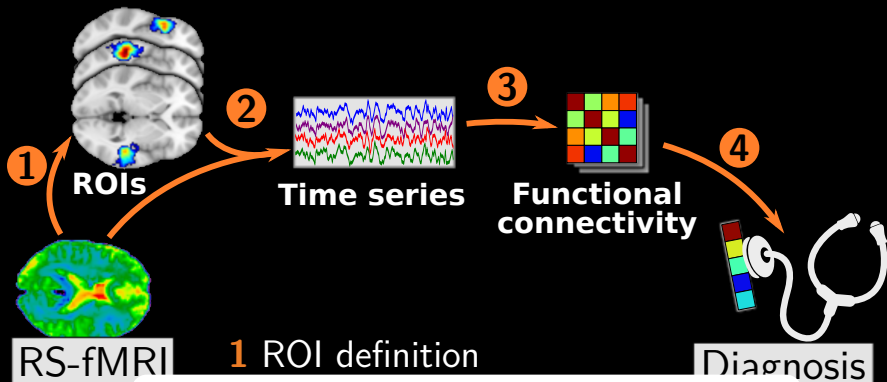


Prediction accuracy (%)

Seen sites	67 ± 3
Unseen sites	67 ± 5

016]

A connectome classification pipeline



Prediction accuracy (%)

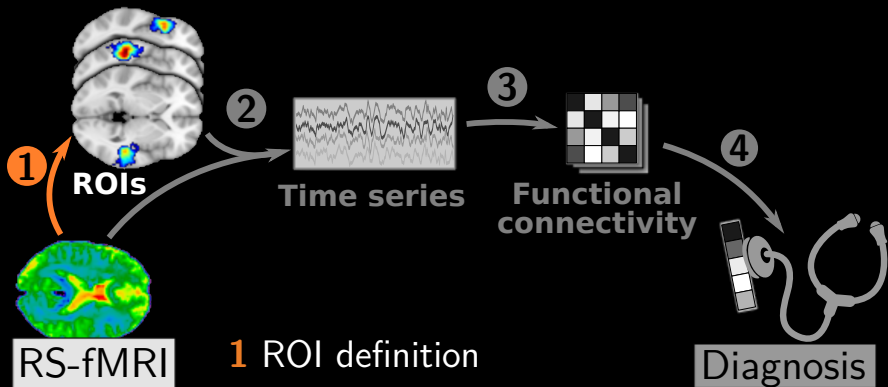
Seen sites 67 ± 3

Unseen sites 67 ± 5

What is important to predict?

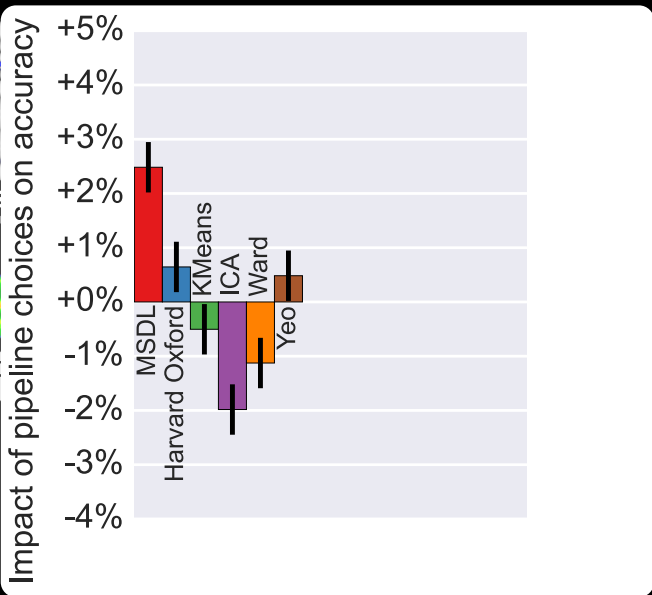
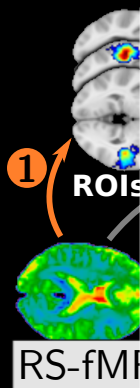
[016]

3 ROI definition: impact of choice

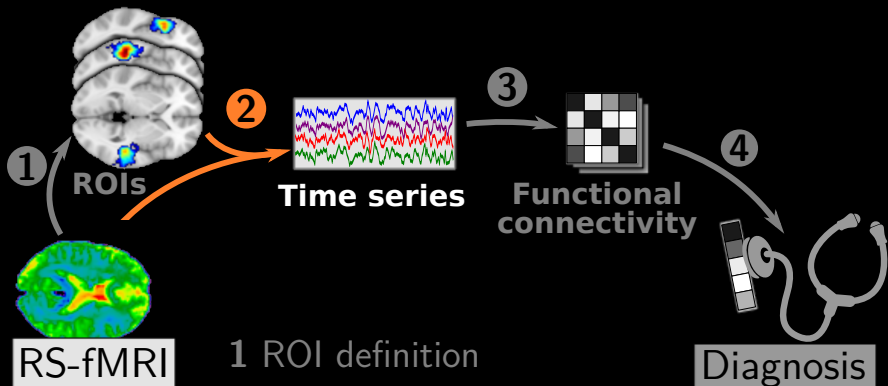


- 1 ROI definition
- 2 Time-series extraction
- 3 Connectivity matrices
- 4 Supervised learning

3 ROI definition: impact of choice

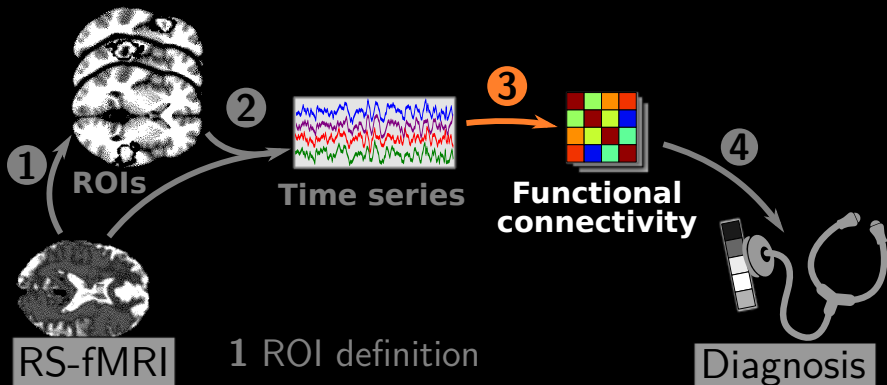


3 Time-series extraction



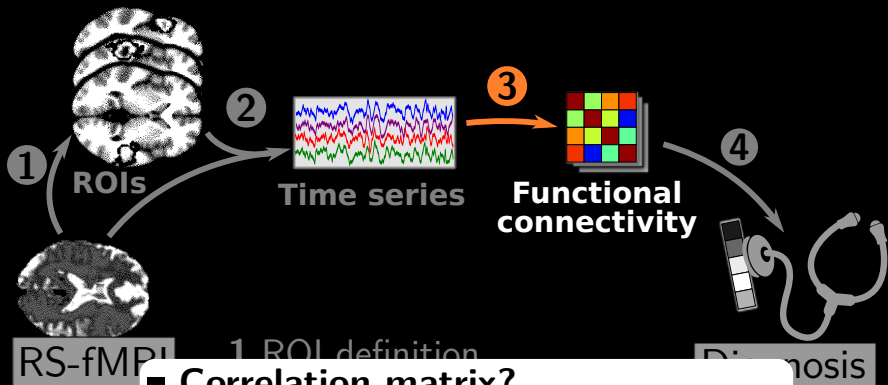
- 1 ROI definition
- 2 Time-series extraction
- 3 Connectivity matrices
- 4 Supervised learning

3 Functional-connectivity matrix



- 1 ROI definition
- 2 Time-series extraction
- 3 Connectivity matrices
- 4 Supervised learning

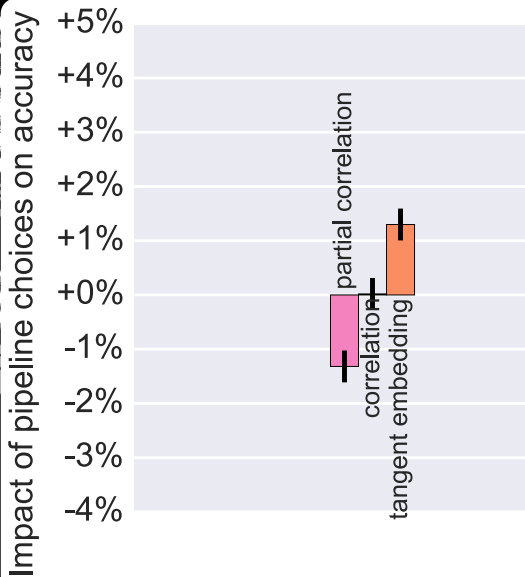
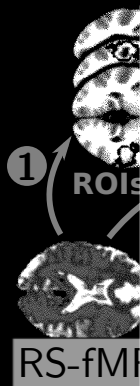
3 Functional-connectivity matrix



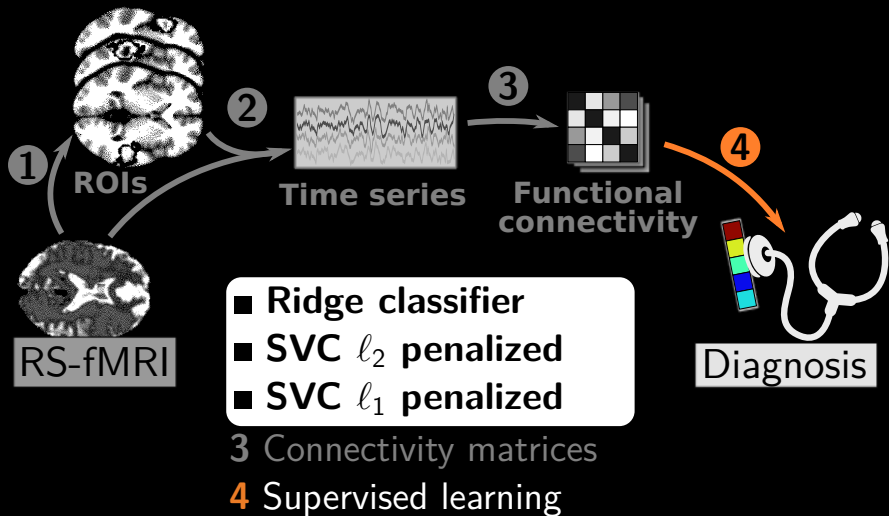
- Correlation matrix?
- Partial correlation matrix?
- Tangent-space embedding?

[Varoquaux... 2010a]

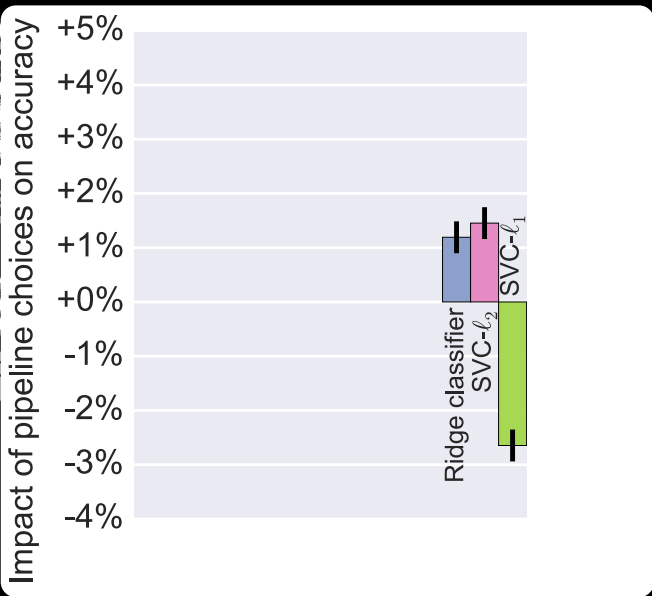
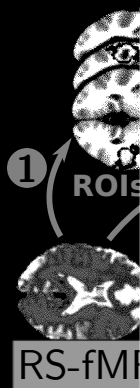
3 Functional-connectivity matrix



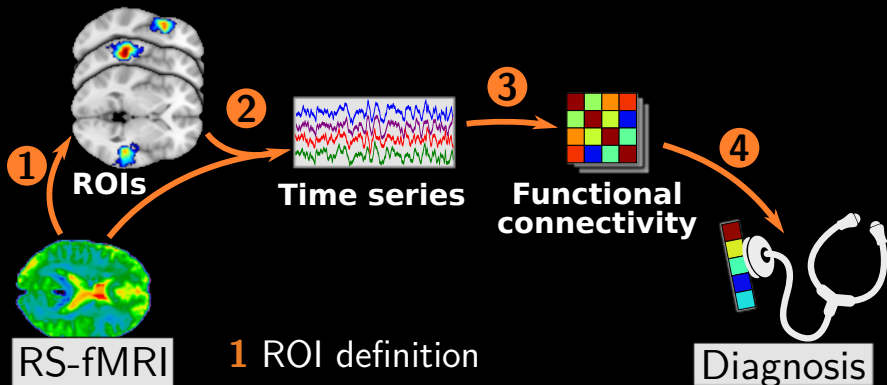
3 Supervised learning method



3 Supervised learning method: impact of choice

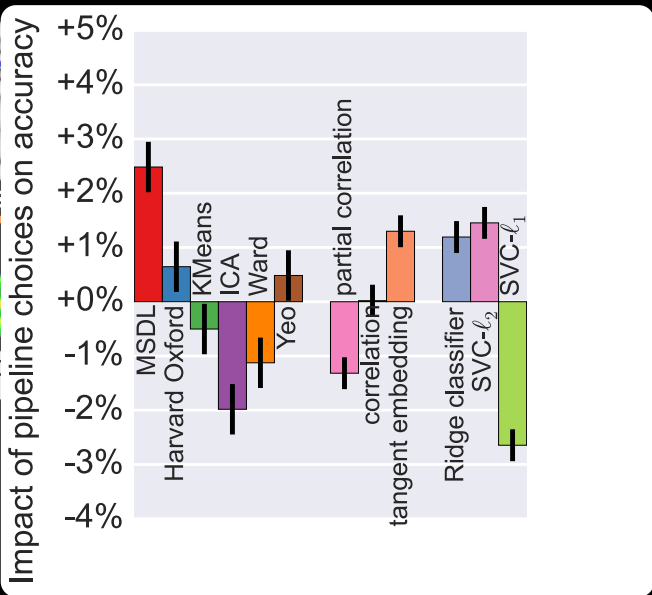
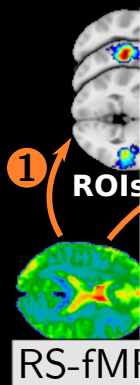


Importance of pipeline steps

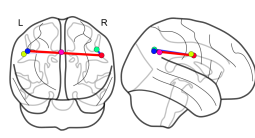
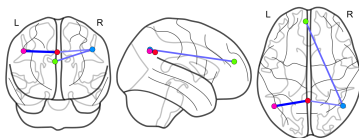
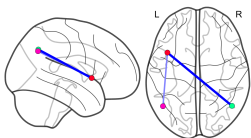
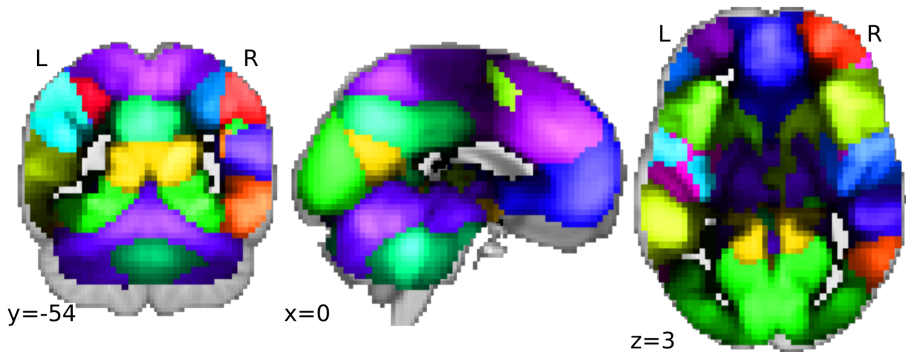


- 1 ROI definition
- 2 Time-series extraction
- 3 Connectivity matrices
- 4 Supervised learning

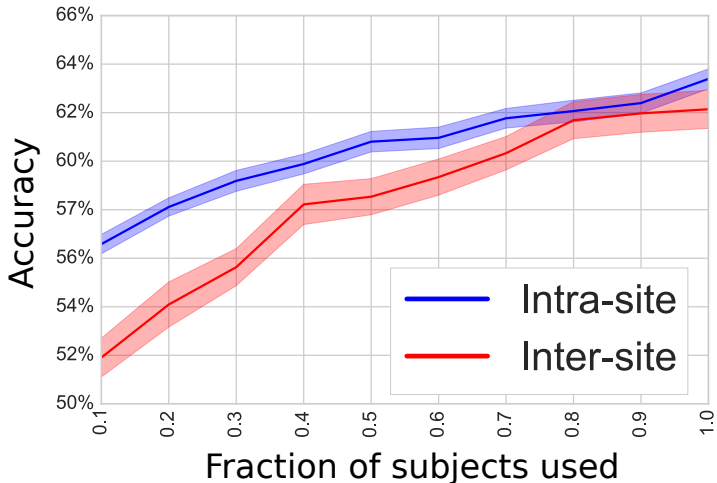
Importance of pipeline steps



MSDL atlas



More data is better



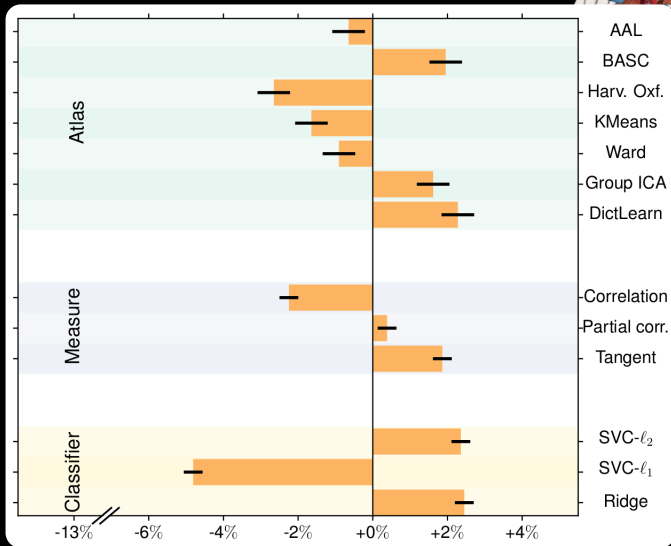
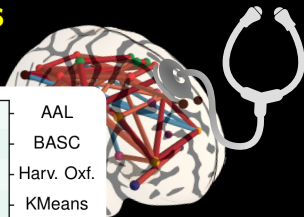
Multivariate processing of a 1Tb of heterogeneous data
is worth the trouble

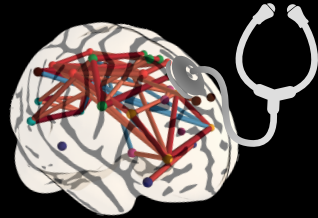
3 Results carry over (1)

[Dadi... 2016]

3 more cohorts and brain disorders

■ Schizophrenia, Alzheimer's, addiction





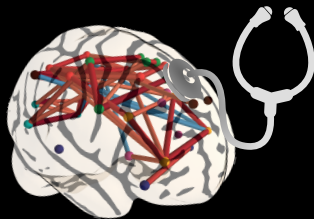
Brain aging

- Combines brain connectivity and morphology
- Predicts age with a mean absolute error of 4.3 years
- Prediction error correlates with cognitive impairment

3 Psychiatric neurophenotypes from rest-fMRI

Viable from data accumulation

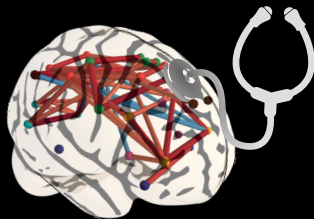
- ABIDE is a post-hoc aggregate
- Prediction across sites



3 Psychiatric neurophenotypes from rest-fMRI

Viable from data accumulation

- ABIDE is a post-hoc aggregate
- Prediction across sites



-
- Not (yet) for clinical diagnostic
 - Capture neural signatures of disorders

⇒ **Towards a redefinition of disorders**

Requires huge data accumulation

nilearn: machine learning for neuroimaging

Make it easy for

- Neuroscientists to use machine learning
- Machine learning research to do neuroimaging

Design goal: runs out of the box

Strong points

- Fast and versatile
- High-quality brain plotting
- Simple syntax



Meaningful neuroimaging analysis in examples.

Try it – <http://nilearn.github.io>

[Abraham... 2014]

Statistical markers of pathologies

Markers from brain graphs

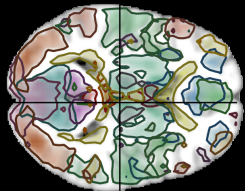
- Choice of regions critical (learn them)
- Valued graphs and estimation error
- Tangent-space embedding
- Standard SVM



Statistical markers of pathologies

Markers from brain graphs

- Choice of regions critical (learn them)
- Valued graphs and estimation error
- Tangent-space embedding
- Standard SVM



Dictionary learning

MSDL

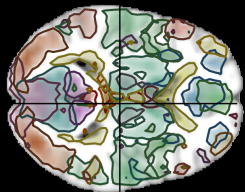
Good definitions of regions

Validation is very hard

Statistical markers of pathologies

Markers from brain graphs

- Choice of regions critical (learn them)
- Valued graphs and estimation error
- Tangent-space embedding
- Standard SVM



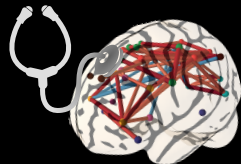
Dictionary learning

Good definitions of regions
Validation is very hard

MSDL

Prediction of autism across sites

[Abraham... 2016]



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