

Whole brain effective connectivity from fMRI data

Some subtitle

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THE ITALIAN ACADEMY
FOR ADVANCED STUDIES IN AMERICA



Whole brain connectivity

Whole brain connectivity

- ▶ Whole brain is divided in ROIs (parcellation)

Whole brain connectivity

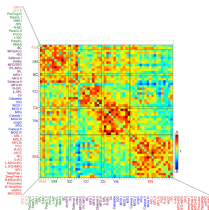
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Whole brain connectivity

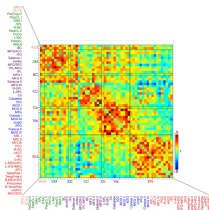
- ▶ Whole brain is divided in ROIs (parcellation)
- ▶ Average activity in each ROI
- ▶ Connectivity between ROIs



Functional Connectivity (FC)



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- Pearson correlation between ROIs

Effective Connectivity (EC)

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- ▶ Asymmetric: no directionality of interactions

Outline

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- ▶ EC based subject and condition identification

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- ▶ Estimation of model parameters

Network model

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Characterization of whole brain networks underlying “mental” states

Characterization of whole brain networks underlying watching a movie

Characterization of whole brain networks underlying remembering

Characterization of whole brain networks underlying calculating

Characterization of whole brain networks underlying pathological states (dementia, autism, depression, etc.)

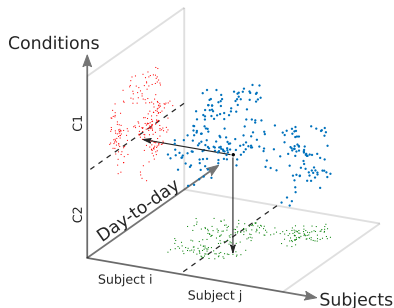
Characterization of whole brain networks underlying “mental” states

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- ▶ Separate different sources of variability

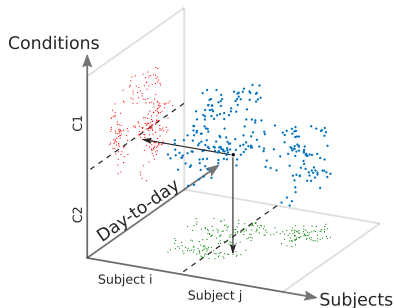
Characterization of whole brain networks underlying “mental” states

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Characterization of whole brain networks underlying “mental” states

- ▶ Separate different sources of variability
 - ▶ classify subjects
 - ▶ classify conditions
 - ▶ extract networks underlying each classification



Datasets

Dataset name	Acquisition	Number of subjects	Sessions per subject	Session duration
Dataset A1	Day2day project	6	40-50	5 minutes
Dataset B	CoRR	30	10	10 minutes
Dataset C	Gilson et al. 2017, Mantini et al. 2012	19	3 resting; 2 movie	10 minutes

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 - ▶ impact of training set size

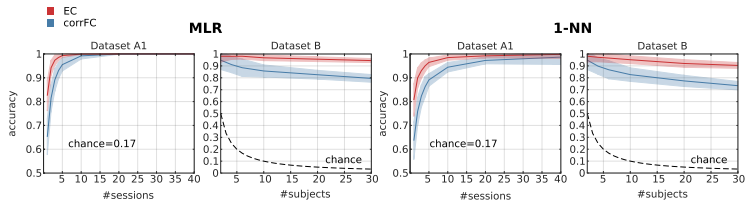
Multinomial Logistic Regression (MLR)

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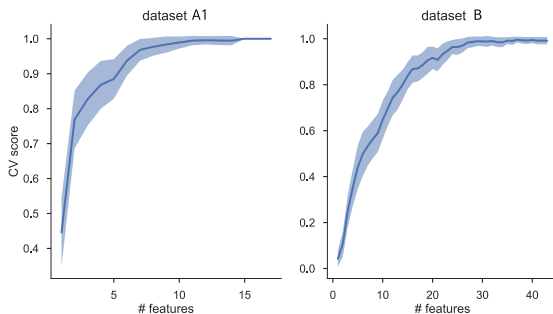
- ▶ $C_k = \sigma(\sum_j^N \beta_{jk} x_j)$
- ▶ allows to estimate the most relevant features for the classification
- ▶ Recursive feature elimination:
 - ▶ recursively remove feature $i = \arg \min_j \sum_k \beta_{jk}$
 - ▶ survival time reflects relevance of each link

Subjects classification

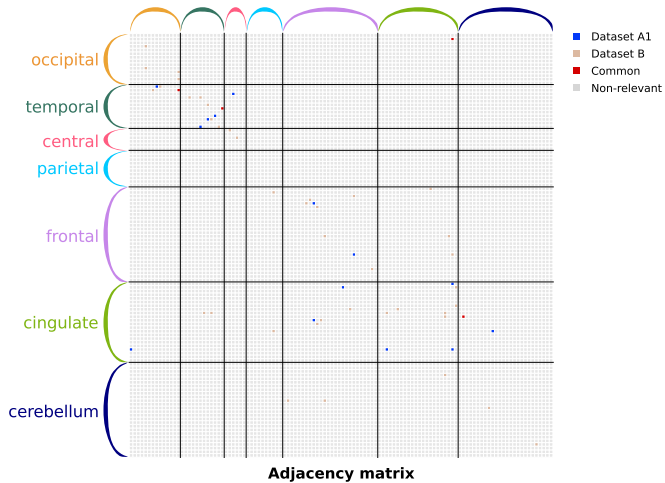


Subjects classification

Classification accuracy using subsets of links according to RFE ranking

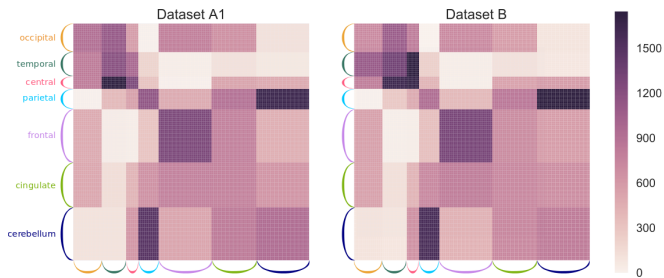


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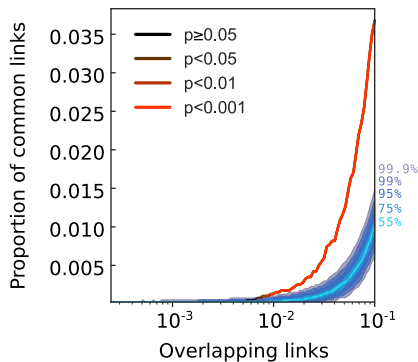
Subjects classification

Average ranking by subsystem



Subjects classification

Number of overlapping links is much higher than expected by chance



Condition classification

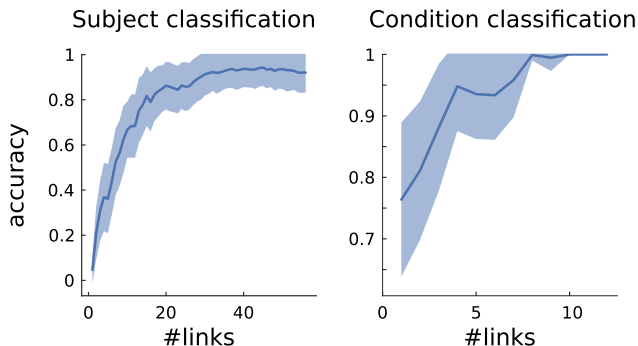
resting VS movie viewing

Condition classification

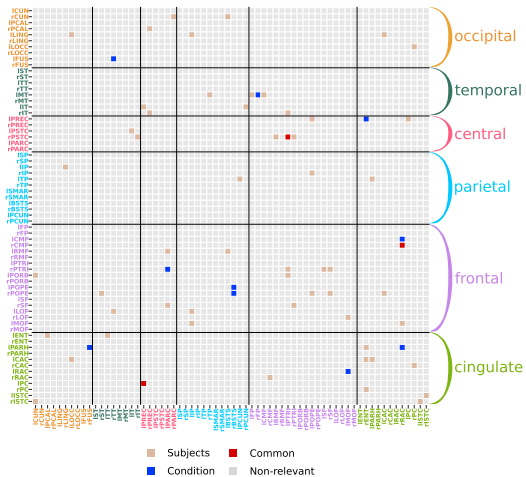
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Classification accuracy using subsets of links according to RFE ranking

B

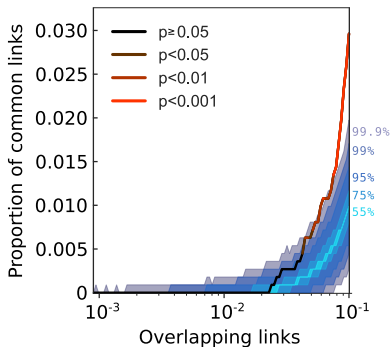


Condition classification



Condition classification

Number of overlapping links is similar to that expected by chance

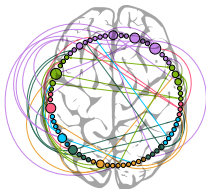
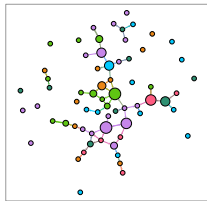


Condition classification

Subjects and conditions networks

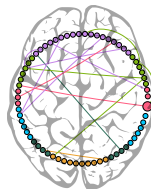
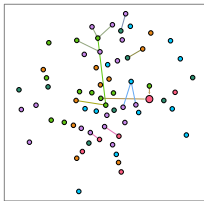
A

Support network of **subject** classification



B

Support network of **condition** classification



- frontal
- cingulate
- central
- parietal
- temporal
- occipital

Summary (ad interim)



Estimation of parameters in the MOU model

Estimation of parameters

- ▶ Lyapunov optimization (Gilson et al. PLoS Comp Biol 2015)
- ▶ minimize $V = \sum_{m,n} (\mathbf{Q}_{mn}^0 - \hat{\mathbf{Q}}_{mn}^0)^2 + \sum_{m,n} (\mathbf{Q}_{mn}^\tau - \hat{\mathbf{Q}}_{mn}^\tau)^2$

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- ▶ Regularization \rightarrow better estimation with few timepoints
- ▶ Model comparison

Bayesian estimation of parameters

- ▶ Bayesian MAP estimate with uniform prior (\equiv MLE): Tizio et al. 2017
- ▶ $C^* = \text{logm}[(\mathbf{Q}^0)^{-1}\mathbf{Q}^1]$

MAP estimate for large scale networks

MAP estimate for small time samples

Influence of weight values

True and predicted weights

Summary



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Matthieu Gilson

Ana Sanjuan

Simone Kuhn

Dante Mantini

Gustavo Deco

John Cunningham



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