

Predicting brain functional connectivity from structural connectivity using fully connected neural networks

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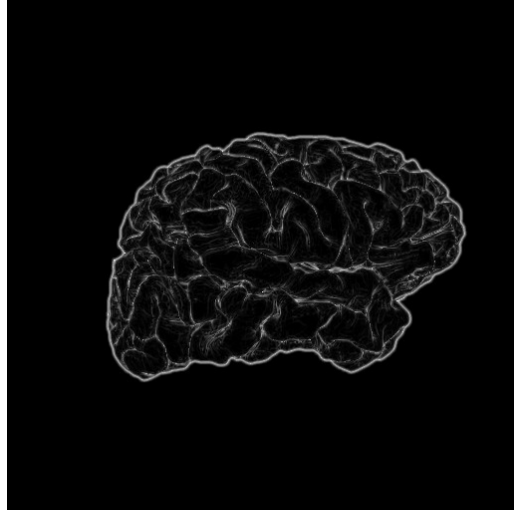
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The complexity of the brain



The complexity of the brain is immense:

~1200 cm³

~40-130 billion glial cells

~86 billion interconnected neurons

It is impossible to gain any insight into its global operation without simplifying assumptions.

Brain atlases

The brain can be divided into homogeneous areas



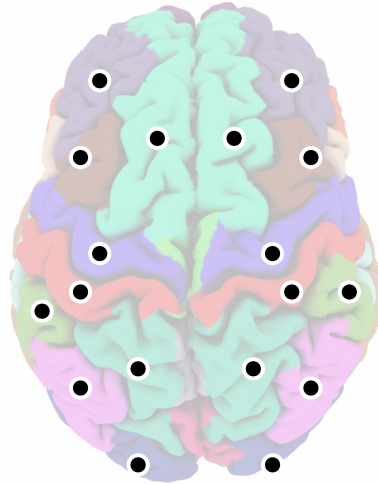
It has been subdivided based on its cytoarchitecture [1], gyri [2], functional organization [3], axonal connectivity [4], and combinations of these and other features [5].

Brain network

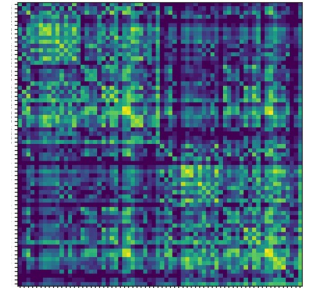
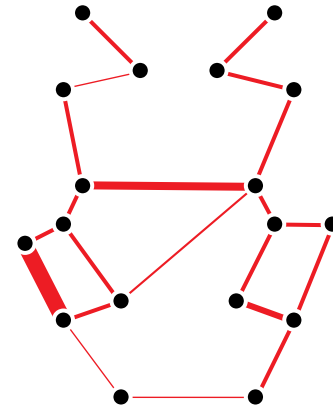
Cortical / Subcortical areas



Network nodes

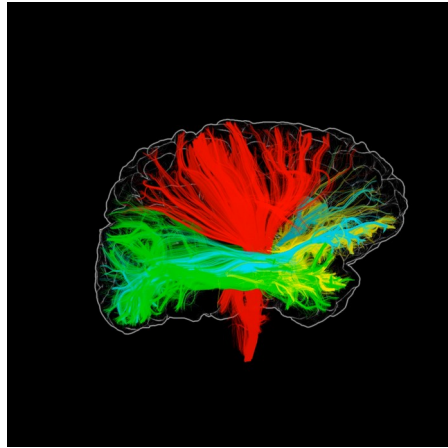


Network edge strengths



The focus is shifted from understanding how information is segregated in the brain, to how it is integrated.

Structural vs functional networks

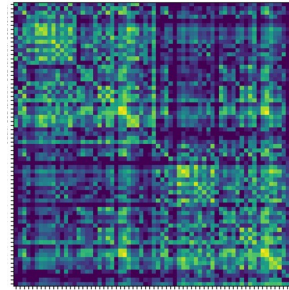


Diffusion MRI

Streamline count



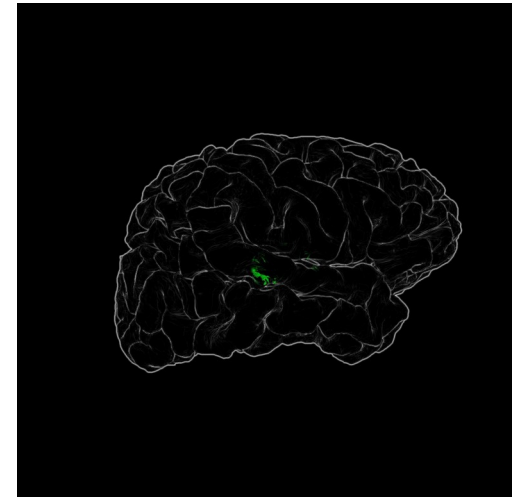
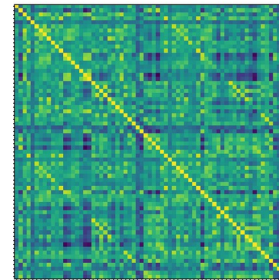
Structural connectivity



Correlation



Functional connectivity



Resting state functional MRI

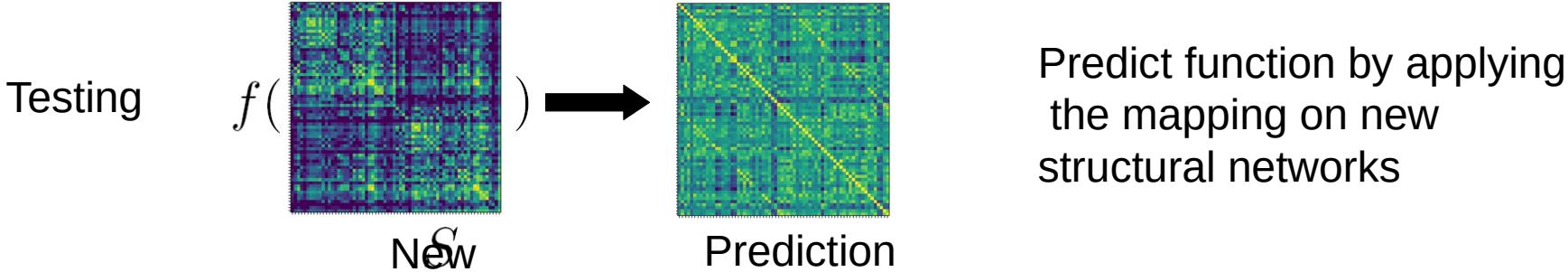
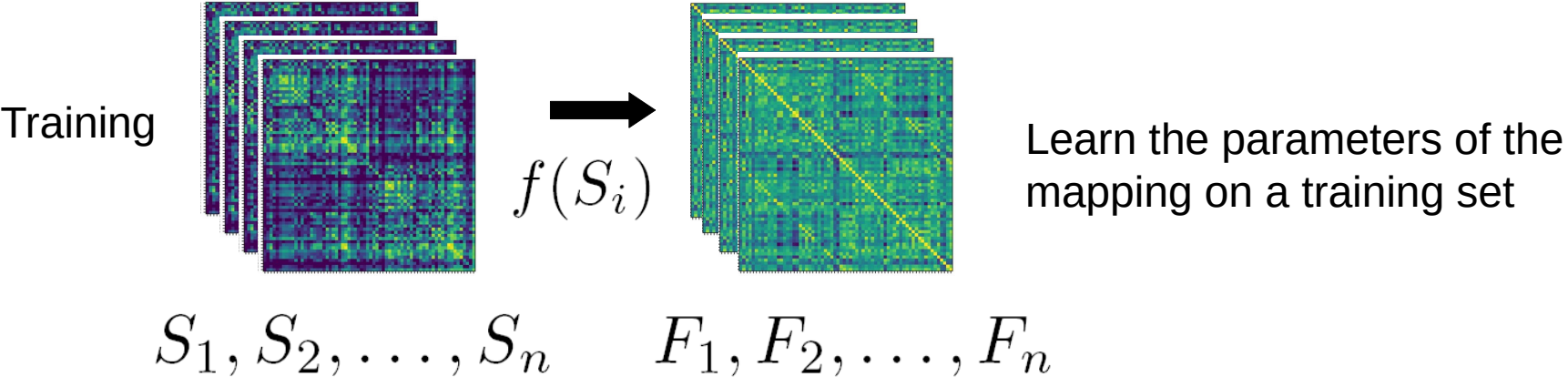
Brain structure-function mapping

It should be possible to predict, at least partially, functional connectivity given the structural network.

Why?

- To reduce acquisition times
- To predict functional changes caused by structural changes
- To gain a better understanding of the structure-function relationship

Brain structure-function mapping



Problem statement

Training

$$\underset{f}{\text{minimize}} \sum_{k=1}^K \|f(\mathbf{S}_k) - \mathbf{F}_k\|_{\mathcal{F}}^2$$

Testing

$$\text{corr}(\mathbf{A}, \mathbf{B}) = \frac{\sum_{i=1}^{N-1} \sum_{j=0}^{i-1} (\mathbf{A}_{ij} - \bar{A})(\mathbf{B}_{ij} - \bar{B})}{\|\mathbf{A}\|_{\text{Sym}_N} \|\mathbf{B}\|_{\text{Sym}_N}}$$

Different mapping strategies



Matrix decompositions (eigenmodes) [1]



Neural networks

Eigenmode models

Solving the diffusion equation on a graph [1, 2]:

$$f(\mathbf{L}) = ae^{-\alpha \mathbf{L}} + b\mathbf{I}$$

Unified eigenmode model:

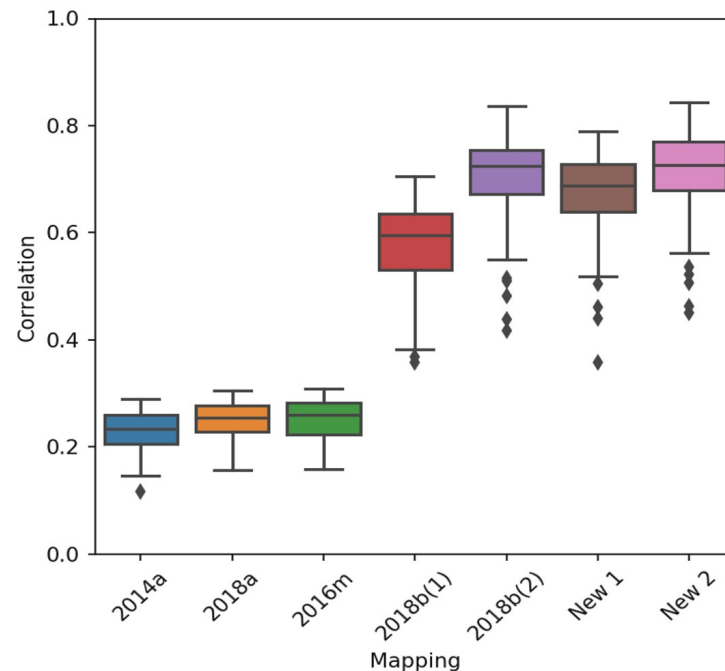
$$f(\mathbf{A}) = \sum_{n=0}^{N-1} g(\lambda_n)h(\mathbf{u}_n) + \mathbf{C}$$

Spectral mapping [3]

$$f(\mathbf{S}) = \sum_{m=0}^M a_m \mathbf{S}^m + \mathbf{C}$$

Results

	Reference	# of params
2014a	Abelnour et al. 2014	1
2018a	Abelnour et al. 2018	3
2016m	Meier et al. 2016	$M + 1$
2018b(1)	Becker et al. 2018	$M + 1 + (N^2 - N) / 2$
2018b(1)	Becker et al. 2018	$M + 1 + (N^2 - N) / 2$
New 1	Deslauriers-Gauthier et al. 2020	$M + 1 + N^2$
New 2	Deslauriers-Gauthier et al. 2020	$M + 1 + N^2$

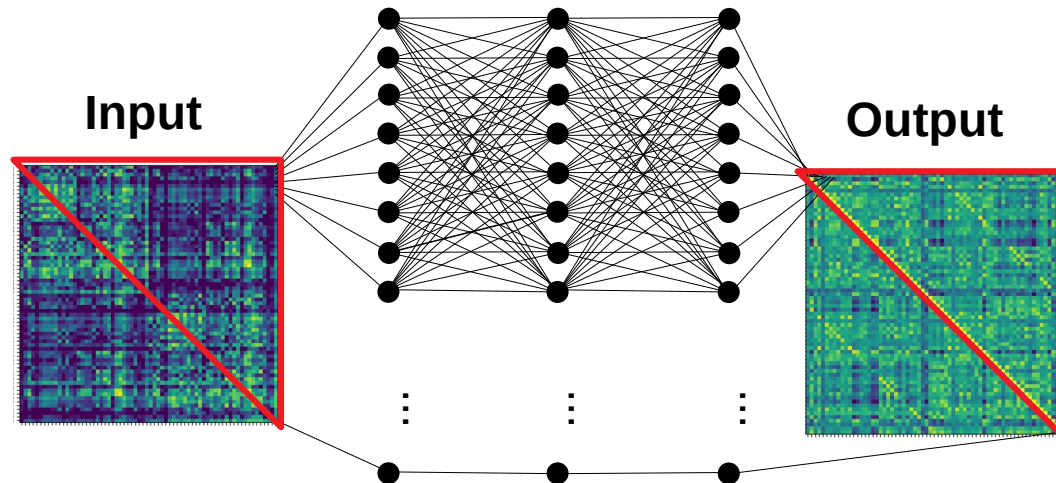


Function can be predicted from structure (~ 0.80)
using eigenmode models

ML brain structure-function mapping

Architecture:

- Fully connected neural networks
- 3, 4, and 5 layers
- 256, 128, 64, and 32 neurons
- ReLu



ML brain structure-function mapping

Dataset: 1050 subject of the Human Connectome Project

Training:

- 1049 subjects
- 70/30 training/validation split
- 128 batch size
- 2000 epochs
- Adam optimizer

Cost

$$\|f(\mathbf{S}_k) - \mathbf{F}_k\|_{\mathcal{F}}^2$$

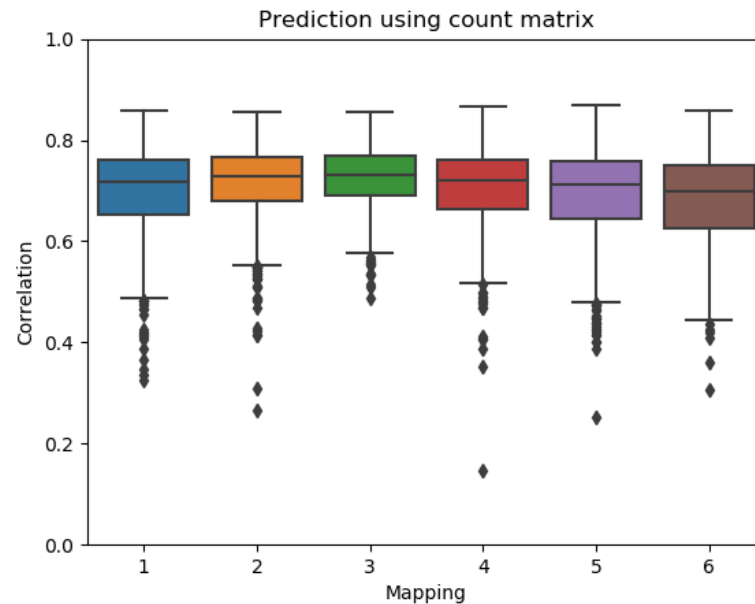
Testing: 1 subject (leave one out strategy)

Implementation:

- Tensorflow
- Python

Results

	Architecture
1	32-32-32
2	32-32-32-32
3	32-32-32-32-32
4	64-32-16
5	128-64-32
6	256-128-64



Fully connected neural networks have a performance similar to eigenmodes

Performance seems to be limited by the homogeneity of the input (healthy cohort)

Future work

- Test other ML architectures
- Apply to clinical healthy and non healthy data e.g. schizophrenia (in progress with collaborator Ashish Raj, UCSF)
- Explore other functional modalities (e.g. EEG, MEG)



Take Home Message

Brain structure can be used to predict brain function.

“Standard” ML approaches reach state of the art performance.

Performance may be limited by the homogeneity of the input.



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Acknowledgments

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