

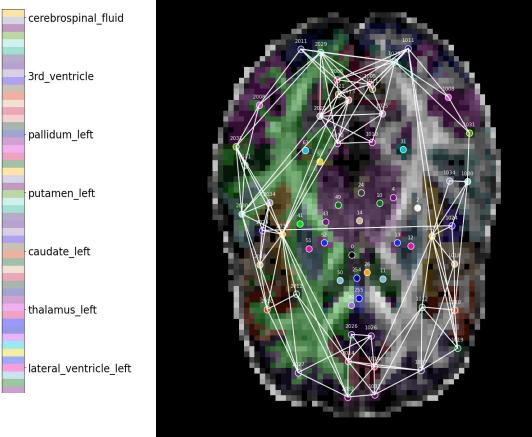
MODELLING THE RELATIONSHIP BETWEEN STRUCTURAL AND FUNCTIONAL CONNECTOMES



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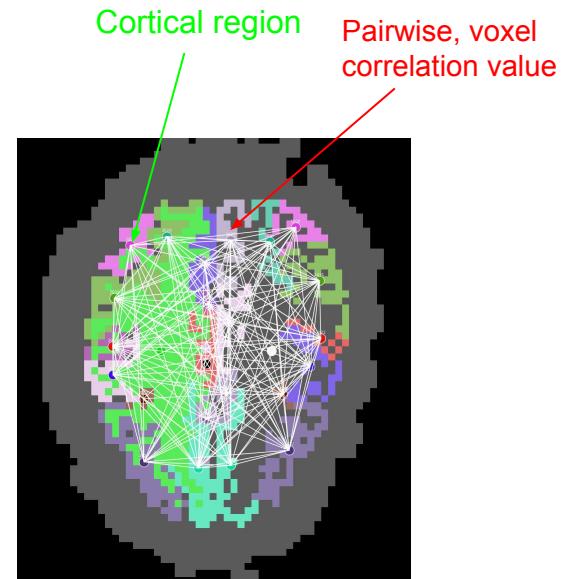
Outline

- Part 1:
 - What do graphs, structural and functional, elucidate?
- Part 2:
 - Can we predict the functional from the structural?



Structural connections

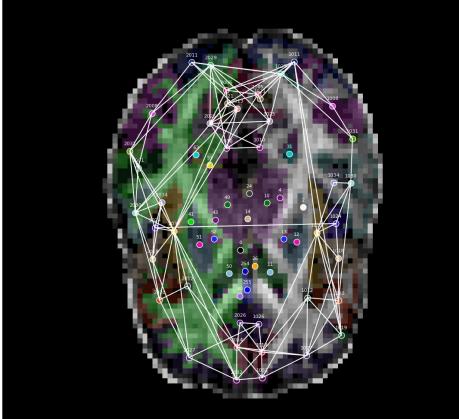
+ Indirect
connections



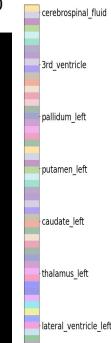
Functional connections

Structural connectome

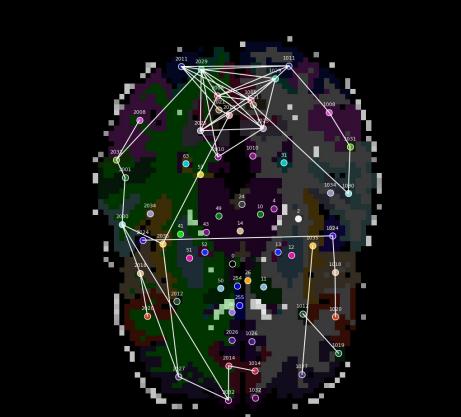
Color-coded FA Parcellation Connectome of slice 30
overlaid with FA graph at threshold 0.1



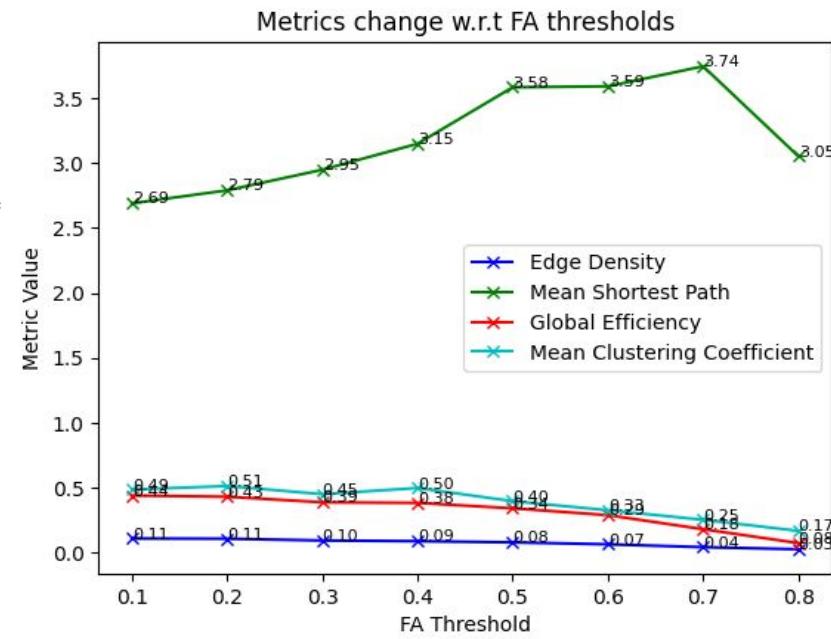
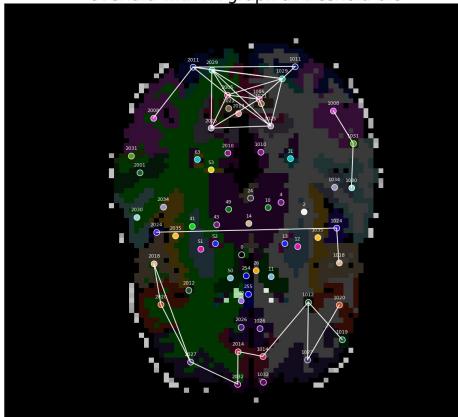
Color-coded FA Parcellation Connectome of slice 30
overlaid with FA graph at threshold 0.4



Color-coded FA Parcellation Connectome of slice 30
overlaid with FA graph at threshold 0.8

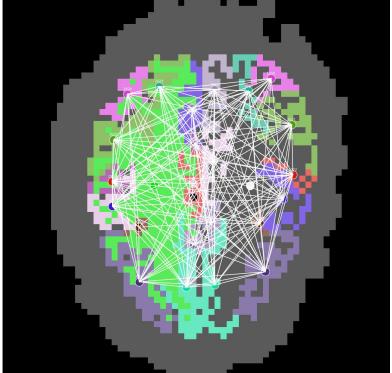


Color-coded FA Parcellation Connectome of slice 30
overlaid with FA graph at threshold 0.8

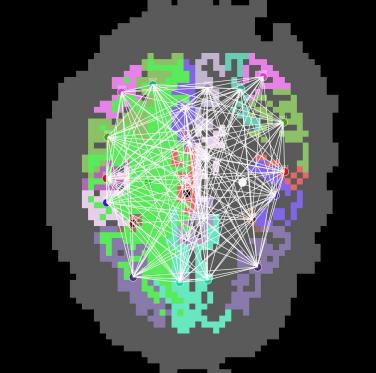


Functional connectome

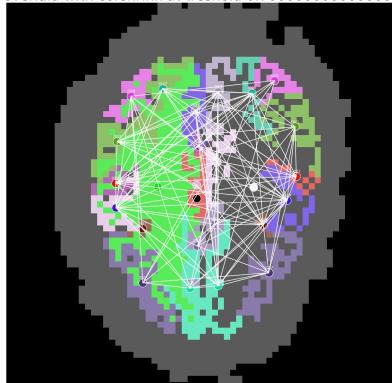
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.1



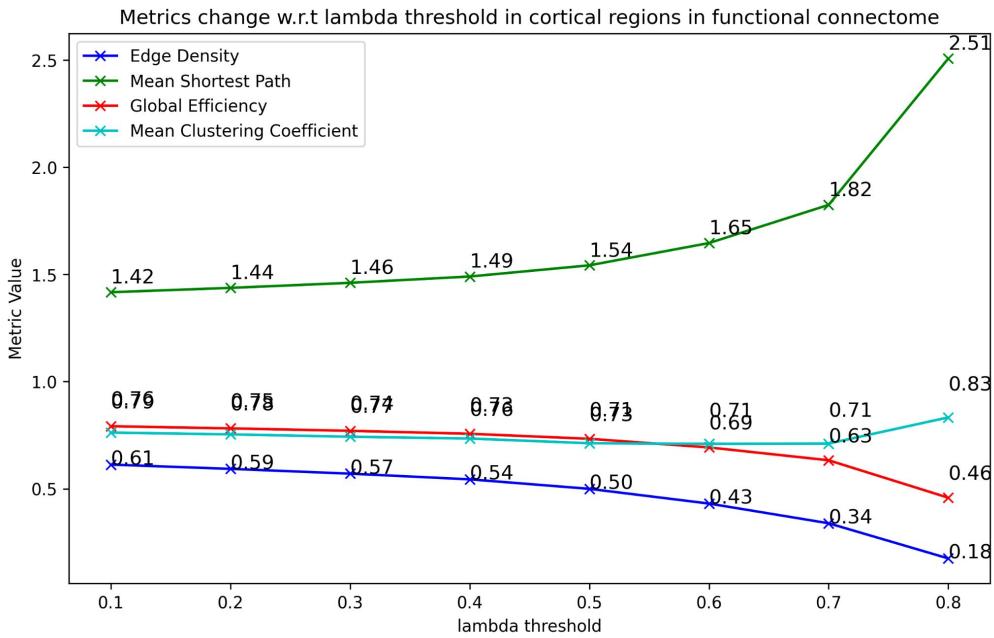
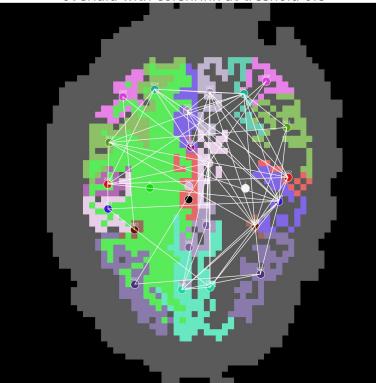
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.2



Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.7000000000000001

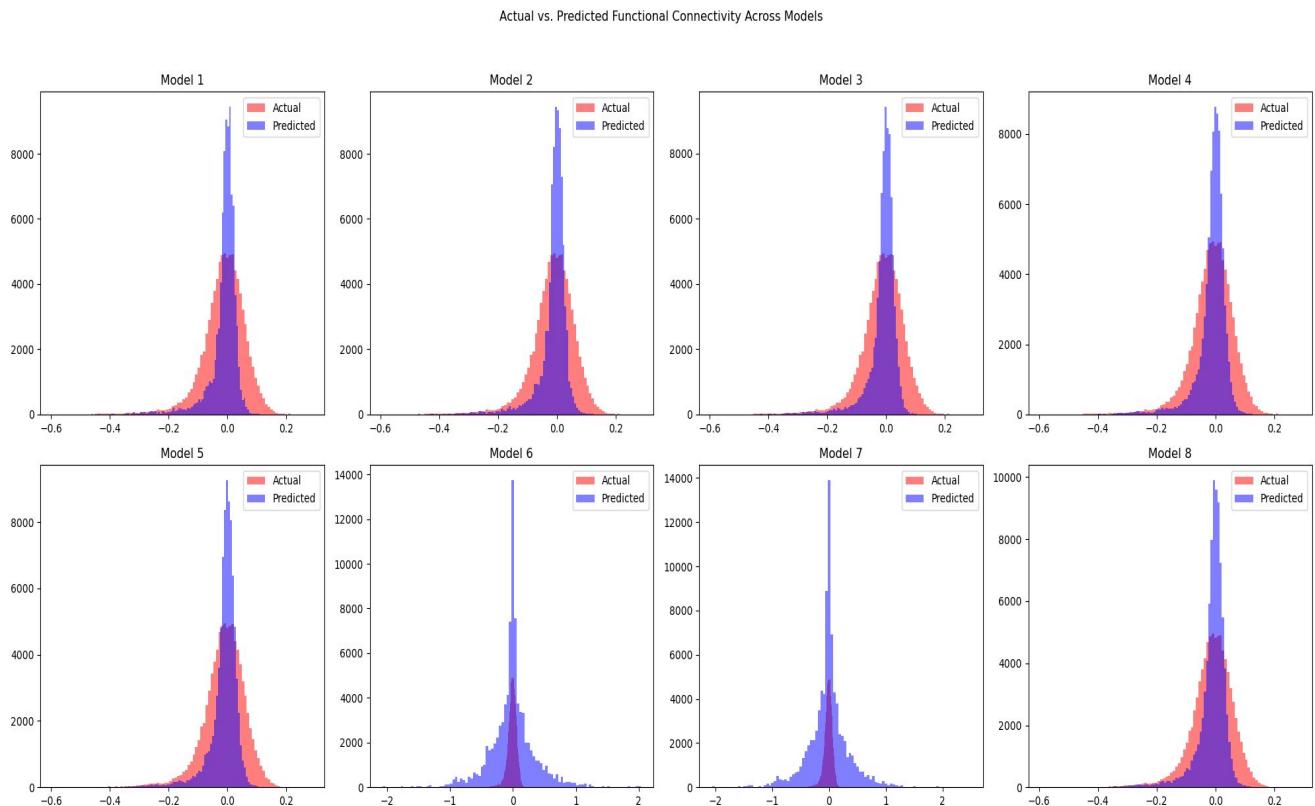


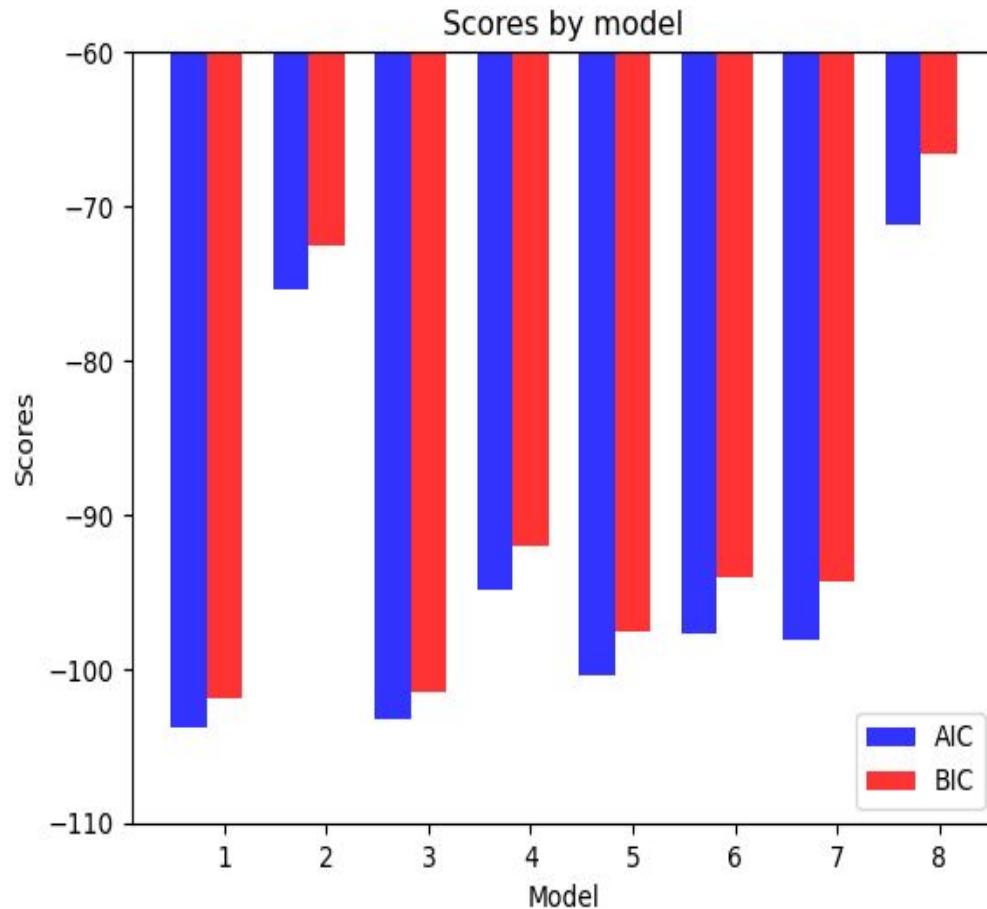
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.8



Part 2: Modelling the relationships between connectomes

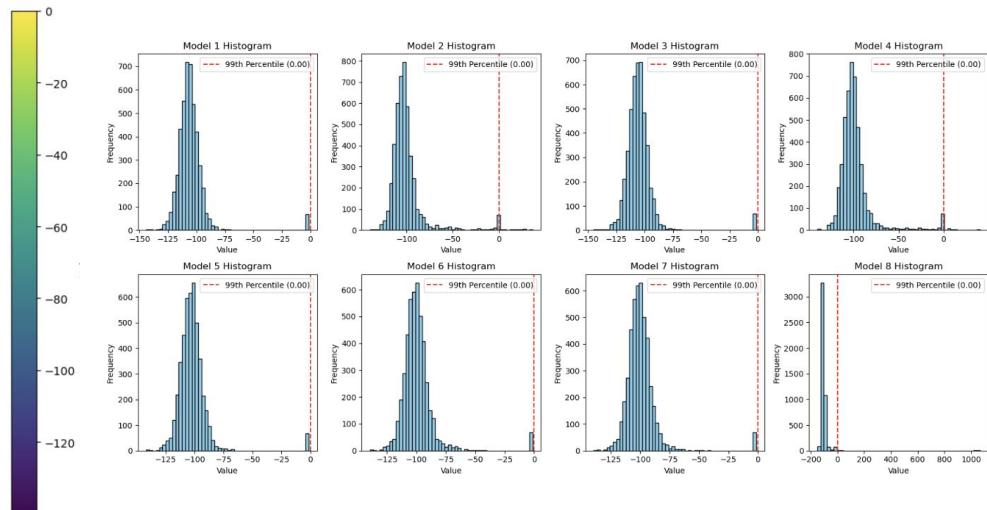
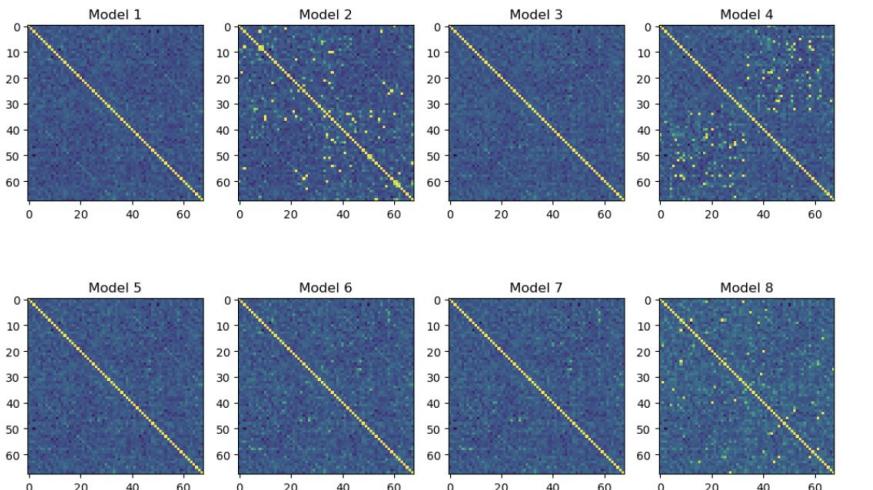
- functional structural
- $$1. f_{ij} = \alpha_{ij} + \beta_{ij}s_{ij}$$
- $$2. f_{ij} = \alpha_{ij} + \beta_{ij}s_{ij} + \gamma_{ij}s_{ij}^2$$
- indirect
- $$3. f_{ij} = \alpha_{ij} + \beta_{ij}t_{ij}$$
- $$4. f_{ij} = \alpha_{ij} + \beta_{ij}t_{ij} + \gamma_{ij}t_{ij}^2$$
- $$5. f_{ij} = \alpha_{ij} + \beta_{ij}s_{ij} + \gamma_{ij}t_{ij}$$
- $$6. f_{ij} = \alpha_{ij} + \beta_{ij}\sqrt{s_{ij}}$$
- $$7. f_{ij} = \alpha_{ij} + \beta_{ij}s_{ij}^2 + \gamma_{ij}\sqrt{t_{ij}}$$
- $$8. f_{ij} = \alpha_{ij} + \beta_{ij}s_{ij} + \gamma_{ij}t_{ij} + \delta_{ij}(s_{ij} \cdot t_{ij})$$



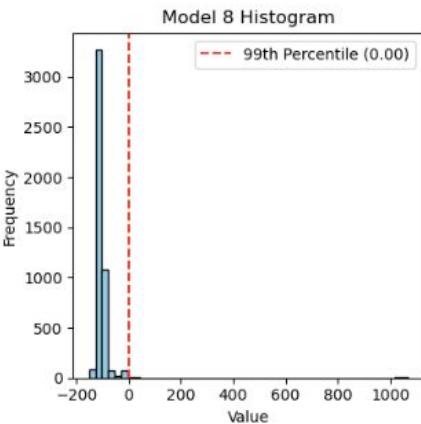
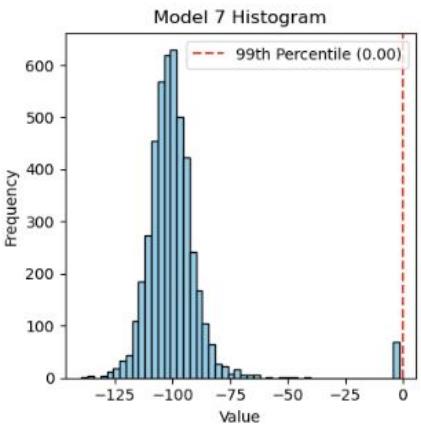
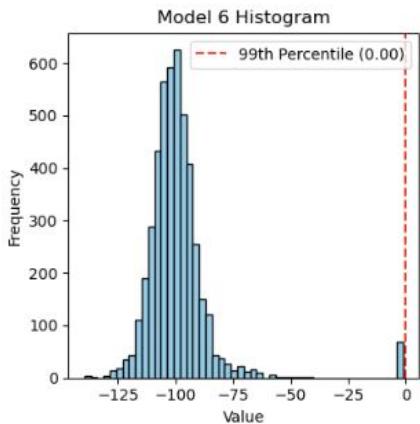
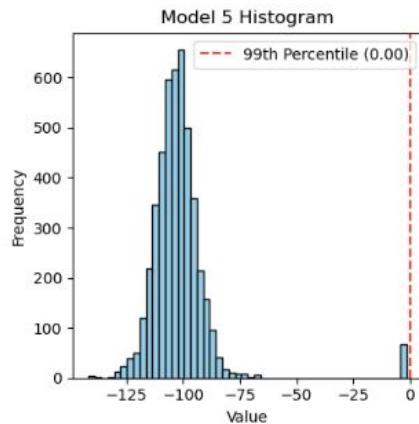
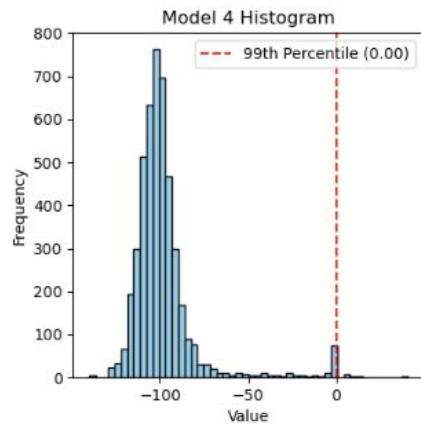
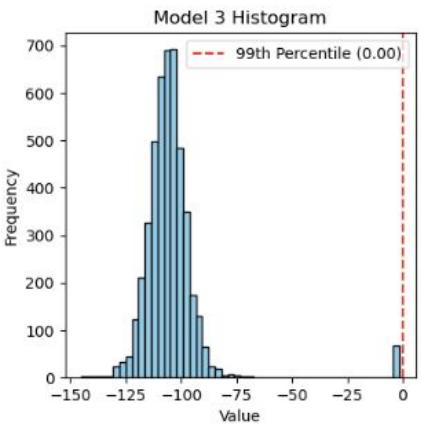
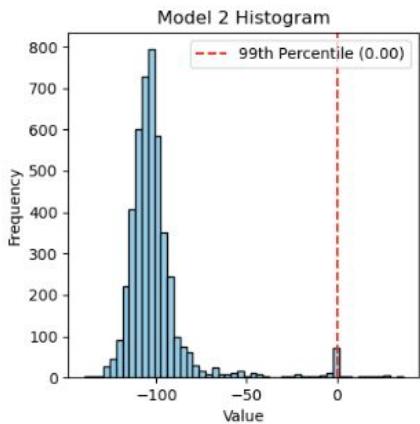
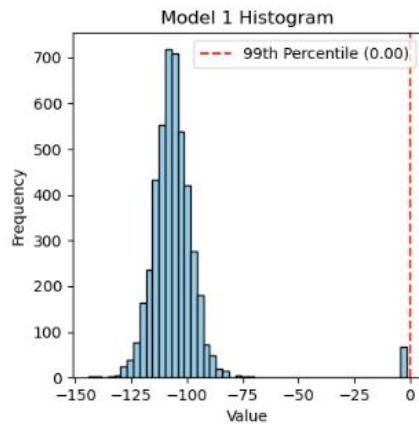


Other Experiments:

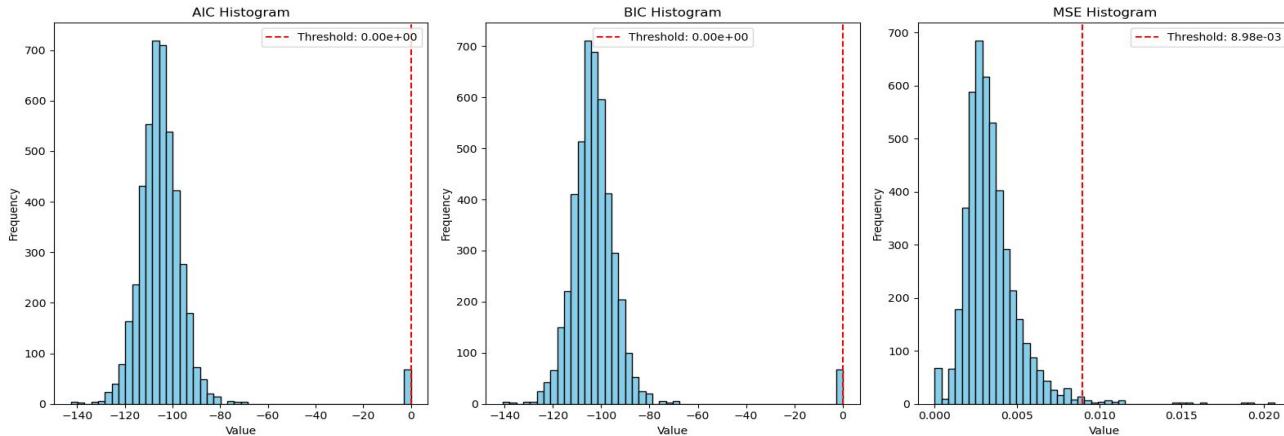
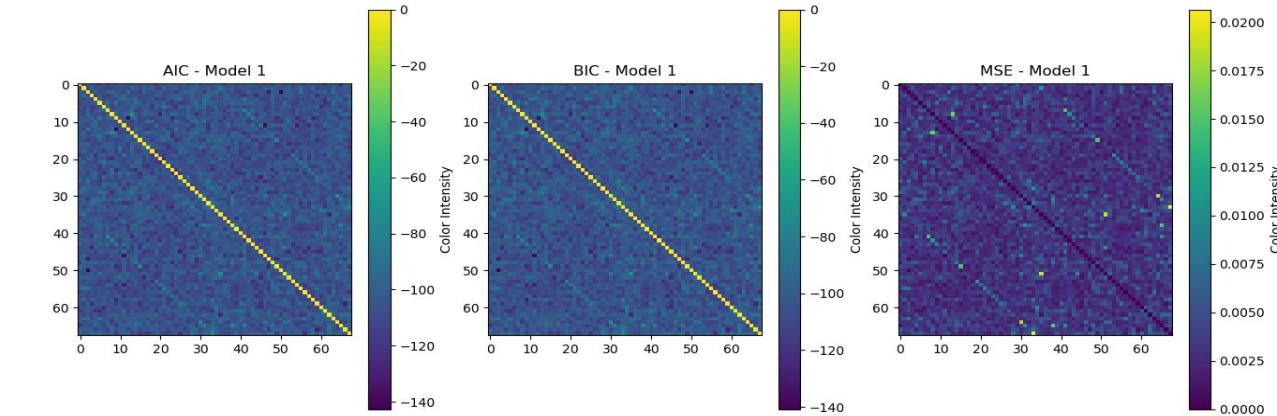
- Simplifying the problem - have worse results, ignore the regions and get one AIC of the Different Models



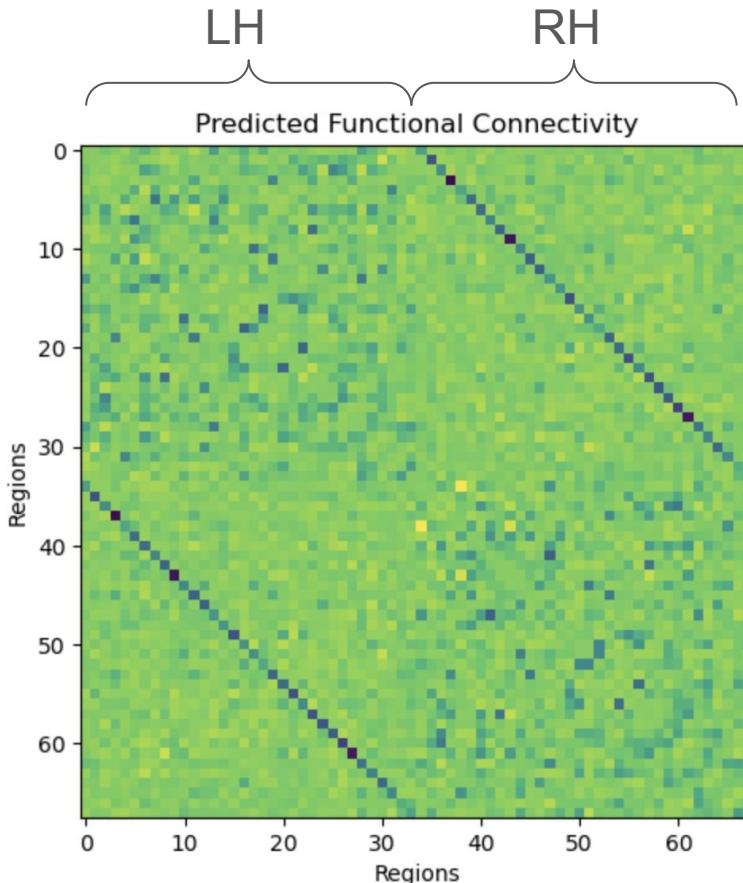
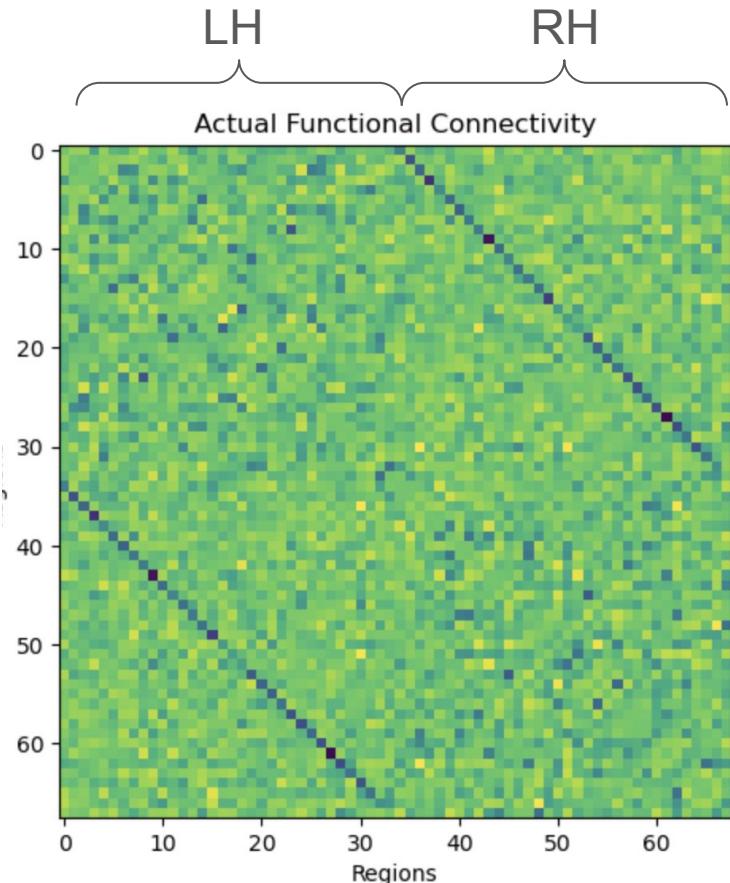
AIC of the Different Models



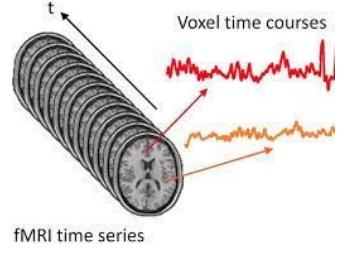
Best Model Fit: $f_{ij} = \alpha_{ij} + \beta_{ij}s_{ij}$



Model Functional Connectivity vs Prediction:



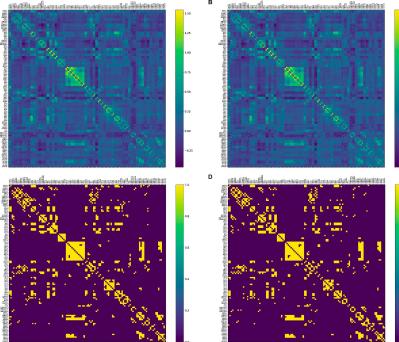
fMRI time series



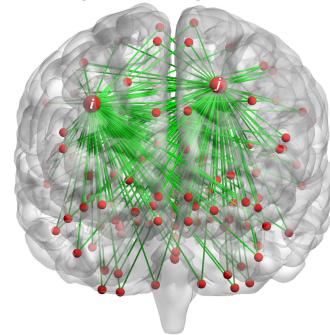
Parcellation maps



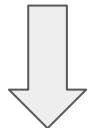
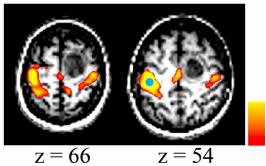
Correlation matrix and binarised connectivity



Functional brain network and graph theory analysis



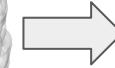
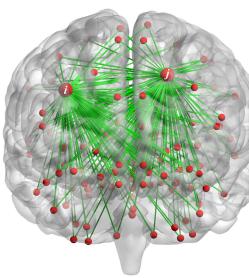
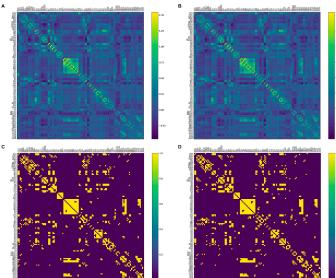
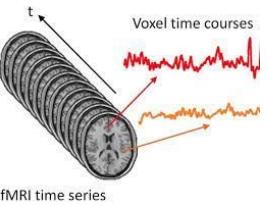
Resting State



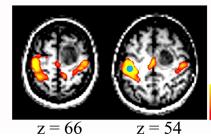
Relationship between structural and functional connectivity

Conclusions and limitations

1. Attempted to identify the Default Mode Network
2. Reconstruction of Graph Networks is insightful but challenging:
 - a) graph metrics can show abnormality
 - b) no defined pipeline, threshold dependent
3. Functional connectivity found between regions that are structurally connected and disconnected



Resting State



Conclusions and limitations: “*All models are wrong, some are useful*”

1. *Without exception, connector hubs are located within the anterior-posterior medial axis of the cortex*
2. Reconstructing graph network of connectivity is challenging even for a single patient with limited conclusions that can be drawn
3. Choice of thresholds significantly impacts the reconstruction of the graph nodes
4. Confirmation that consistent functional connectivity can be observed between regions which are **not directly connected anatomically**

Appendix Q&A

Structural connectome

Nodes: cortical brain regions

Edges: (binarized) correlation values between pair of regions in FA map

(96, 96, 60) # 60 slices

(68,68) # 68 cortical brain regions / corr.
matrix

Functional connectome

Nodes: cortical brain regions

Edges: (binarized) correlation values between pair of regions in RS-MRI

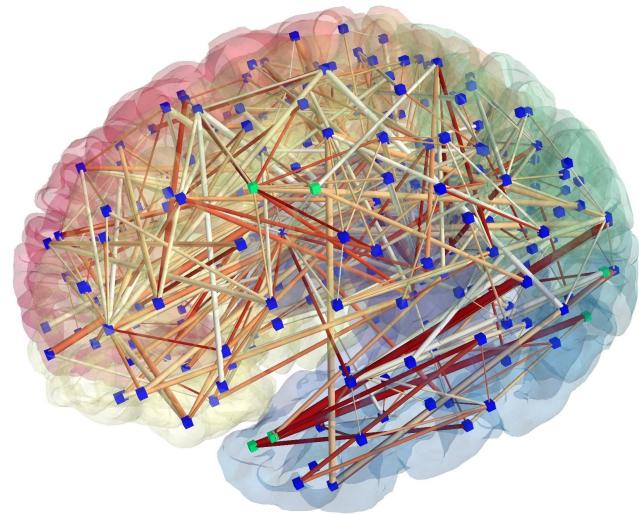
(64, 64, 30, 15) # 30 brain slices, 15 timesteps

(68, 15) # 68 cortical brain regions
(68,68) # correlation matrix

No unifying pipeline for extracting graph

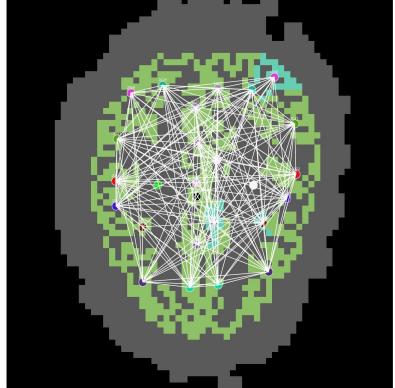
- Graph is just an (inaccurate) abstraction,
but useful nonetheless

“All models are wrong, some are useful”

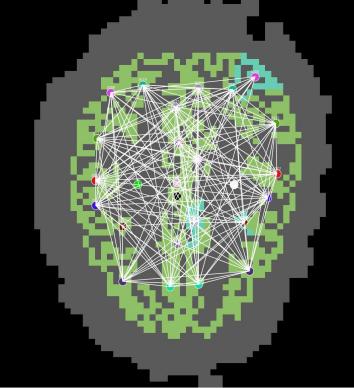


Functional connectome

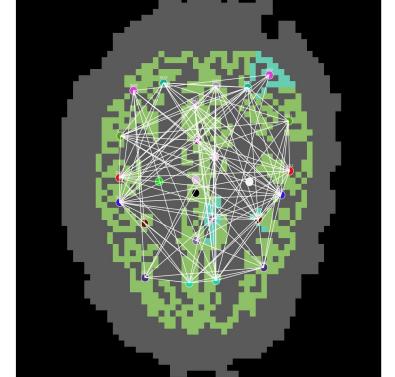
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.0.1



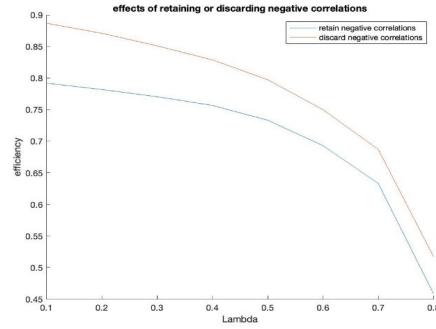
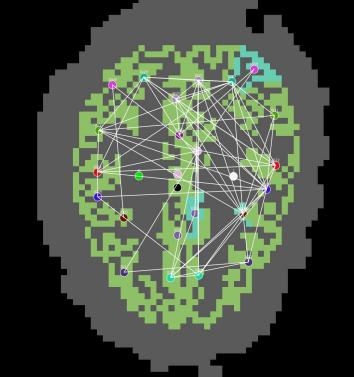
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.0.4



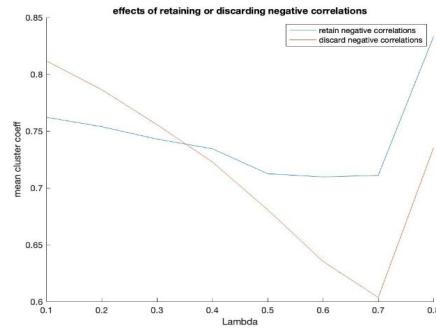
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.0.7000000000000001



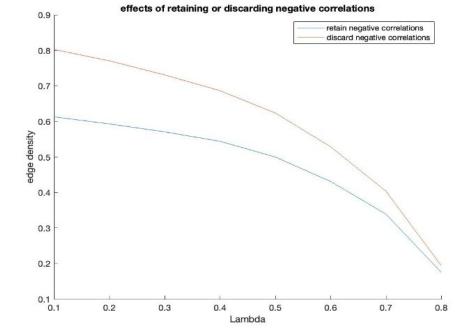
Color-coded RS-MRI Parcellation Connectome of slice 17
overlaid with corshrink at threshold 0.0.8



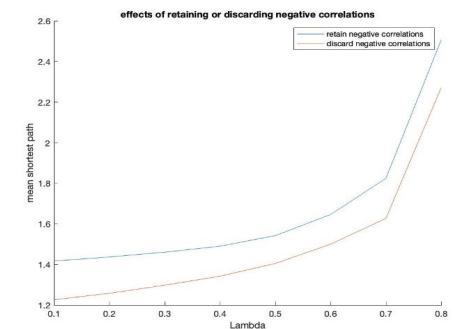
(a) Efficiency change with lambda.



(c) Mean clustering coefficient change with lambda.

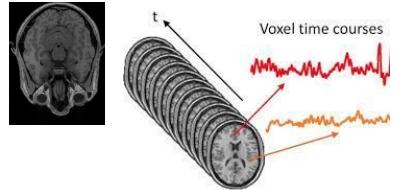


(b) Edge density change with lambda.



(d) Mean shortest path change with lambda.

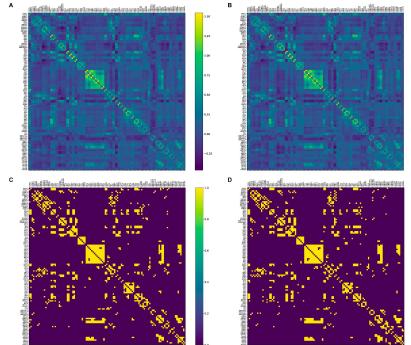
[a] dMRI and rs-fMRI
(time series)



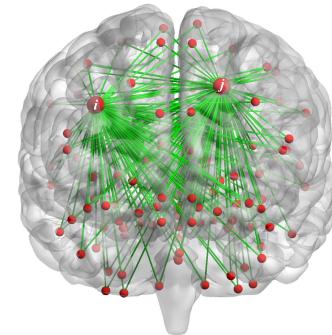
[b] Parcellation maps



[c] Correlation matrix and
binarised connectivity



[d] Functional brain network
and graph theory analysis



Relationship between
structural and functional
connectivity

