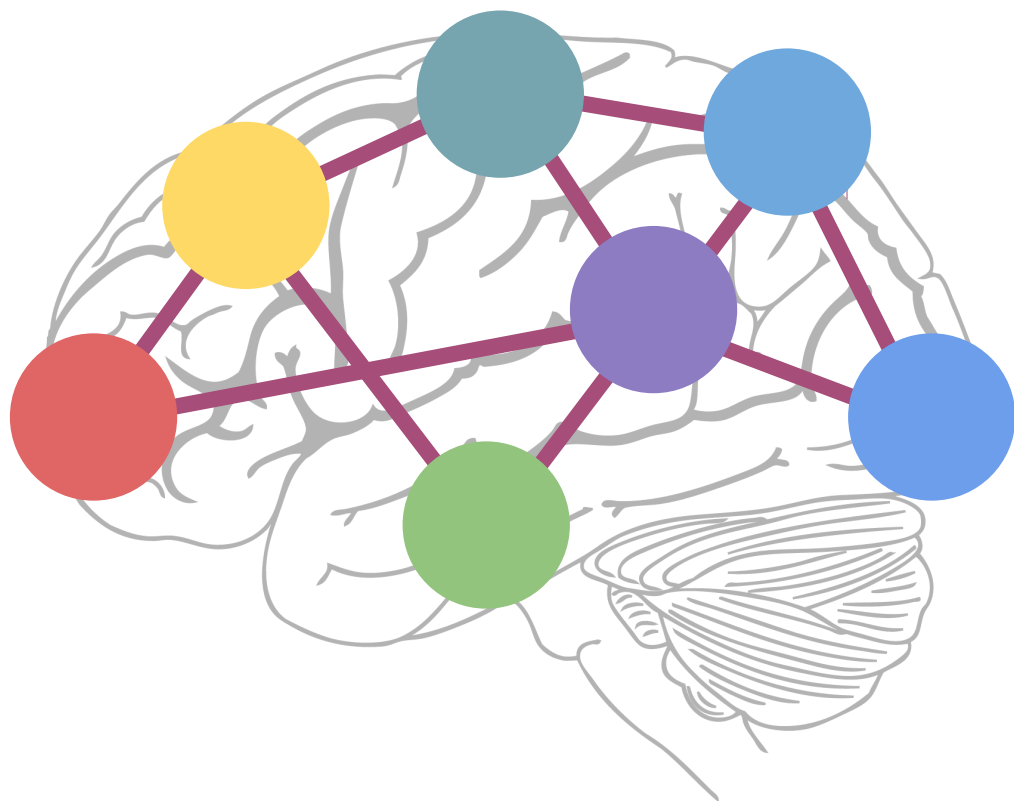
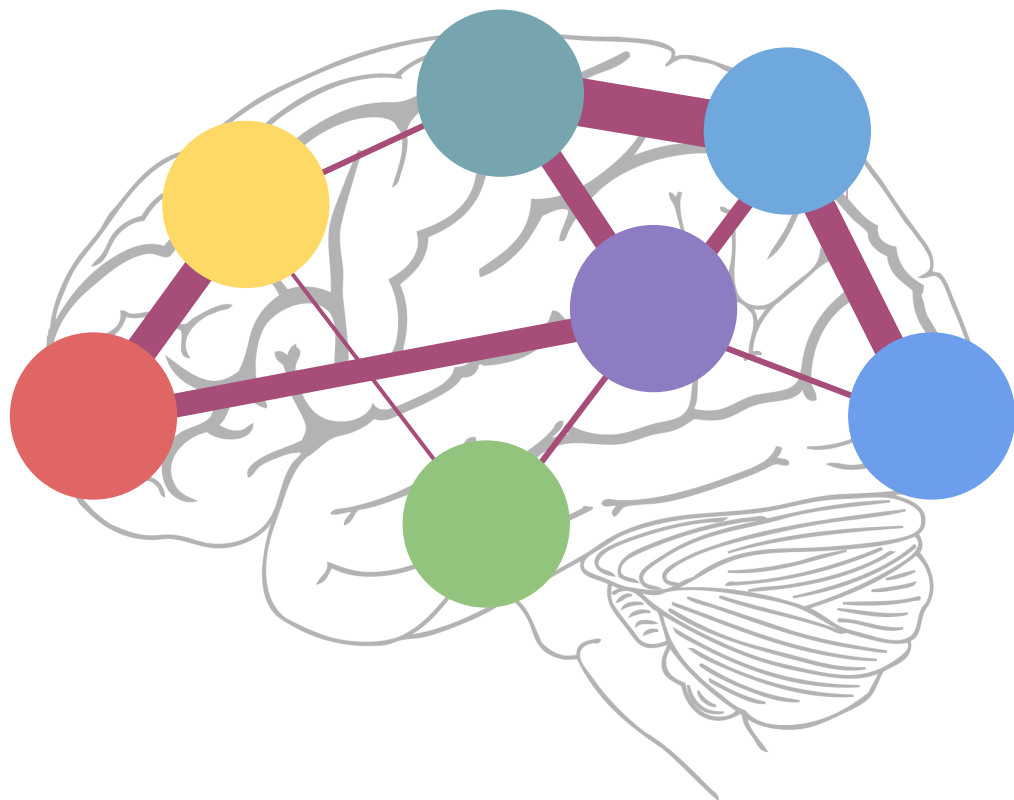
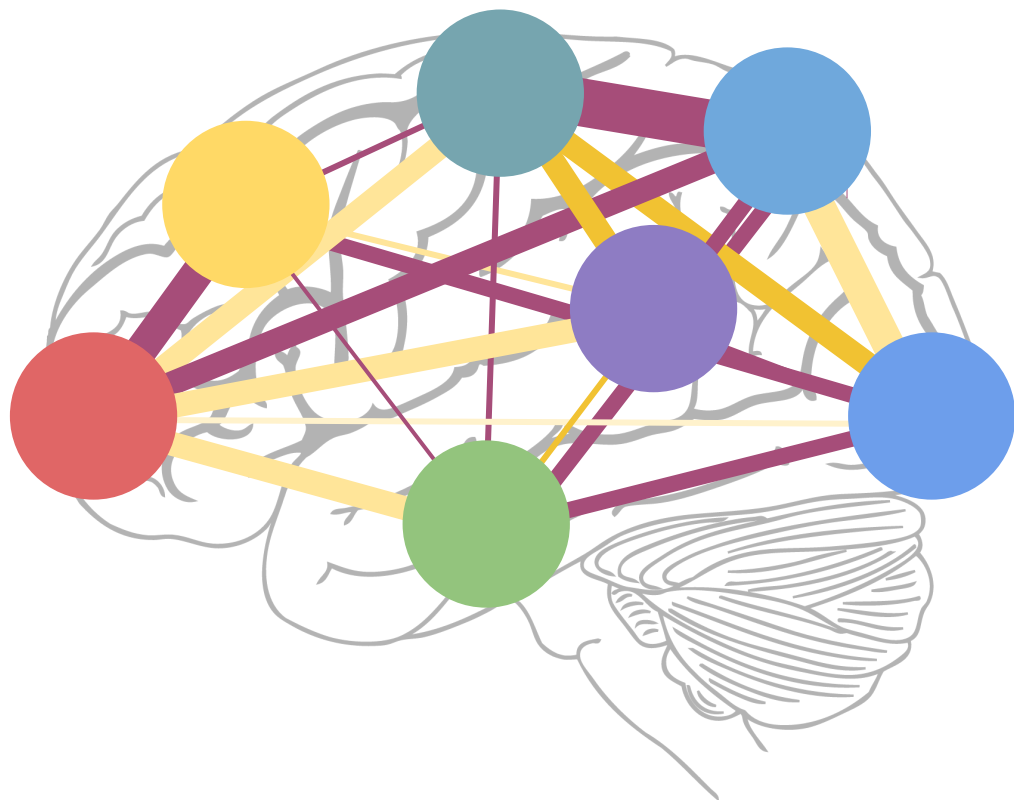


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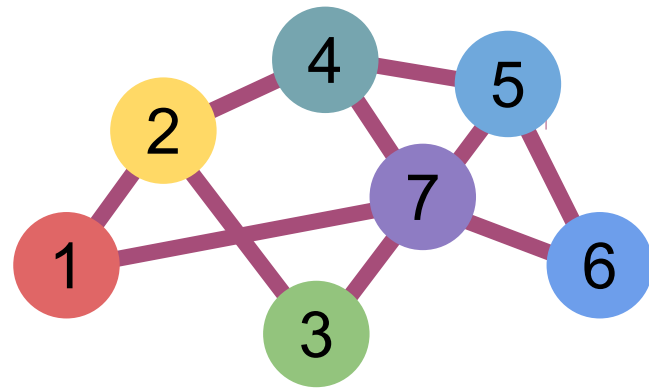
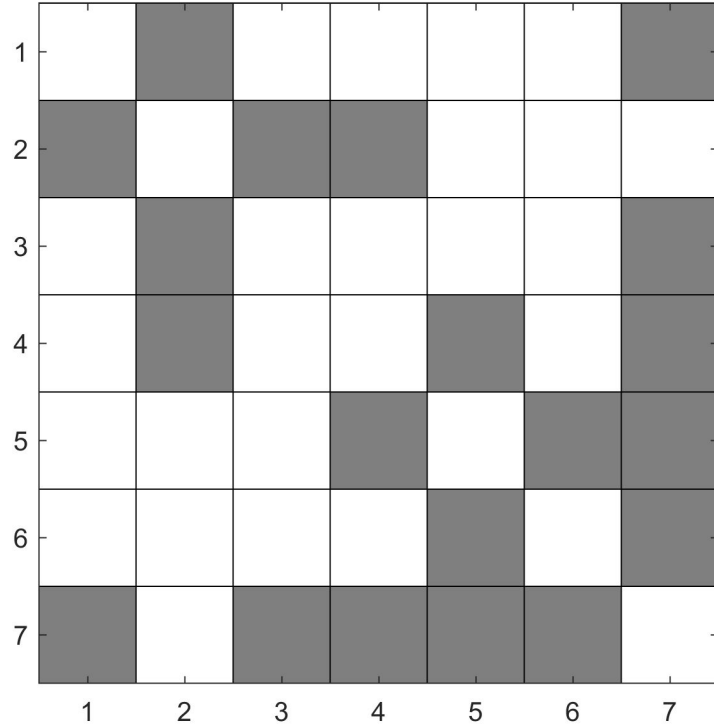




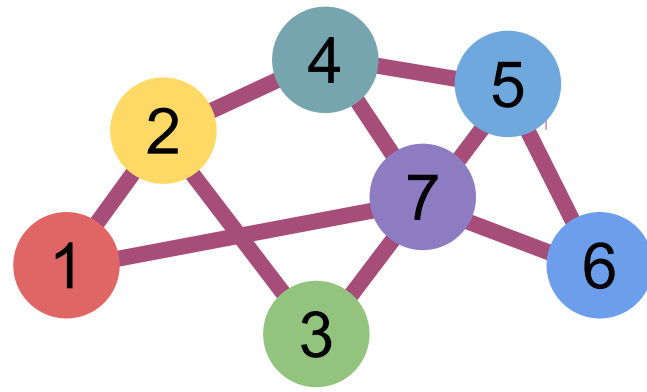
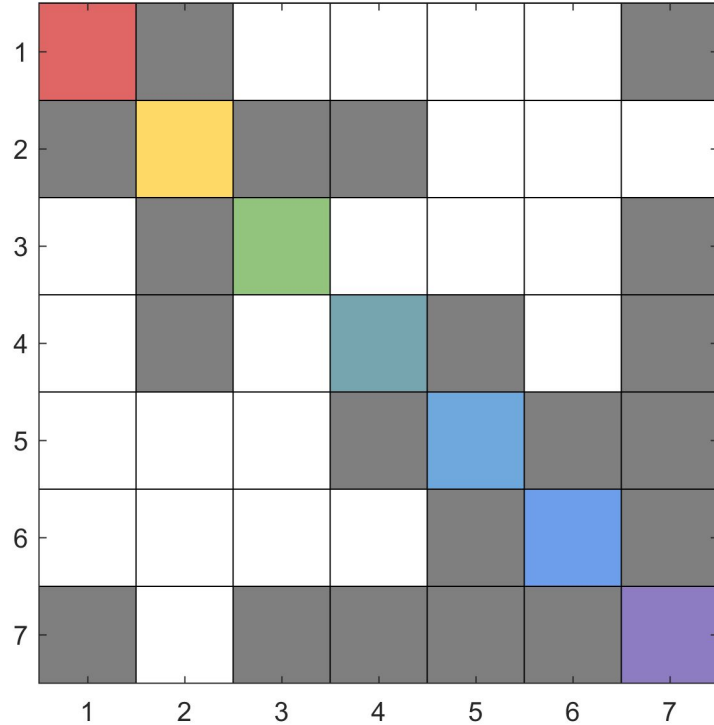




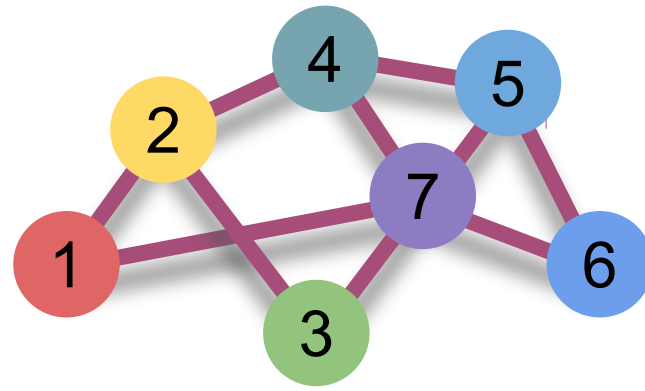
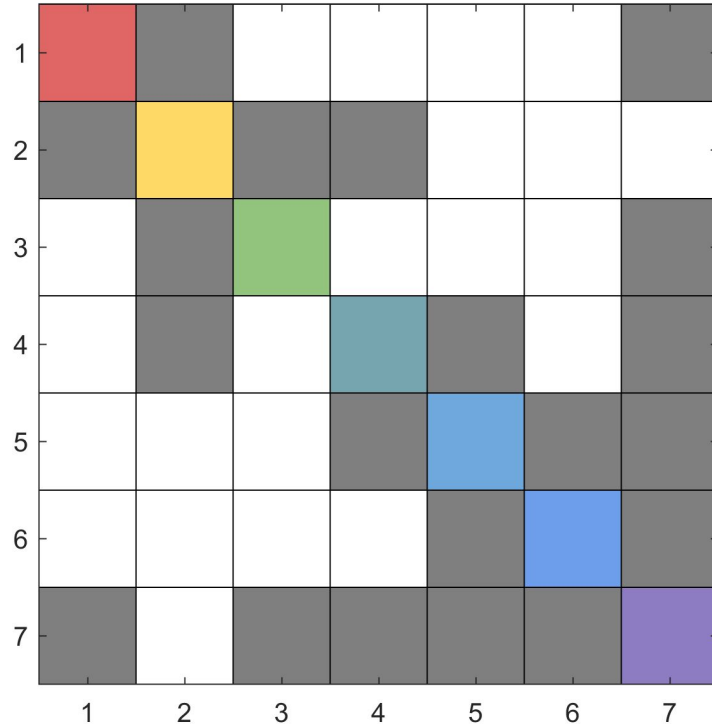
Adjacency matrix



Adjacency matrix

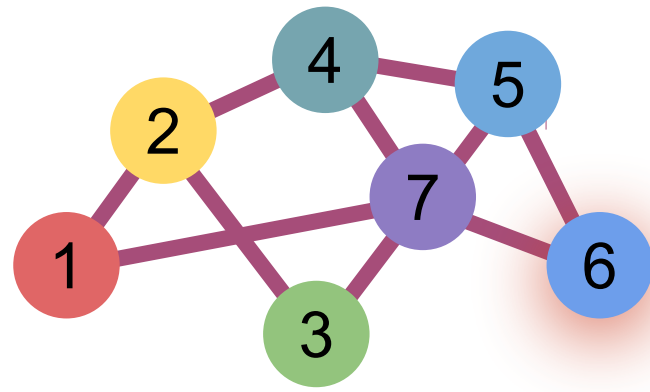
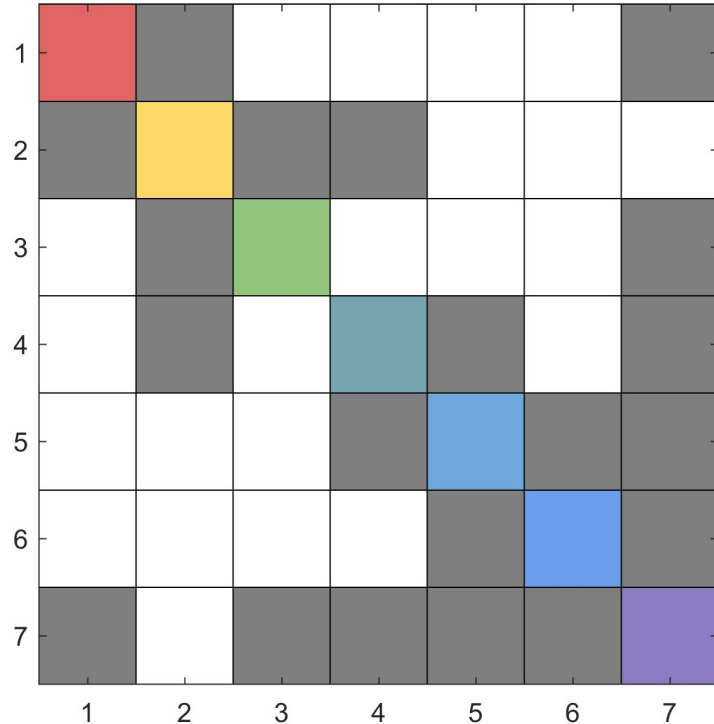


Adjacency matrix



Topology - Overall pattern of interrelationships, which might be described by generating principles

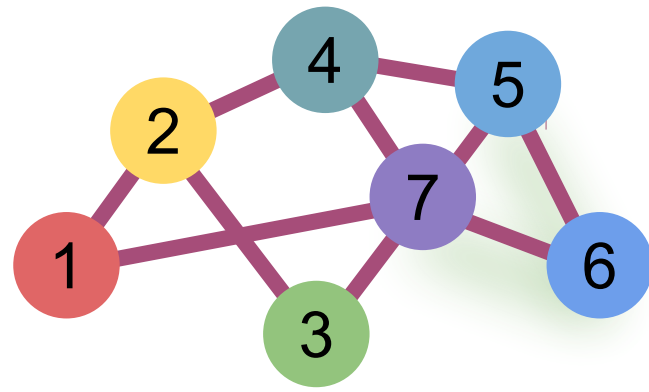
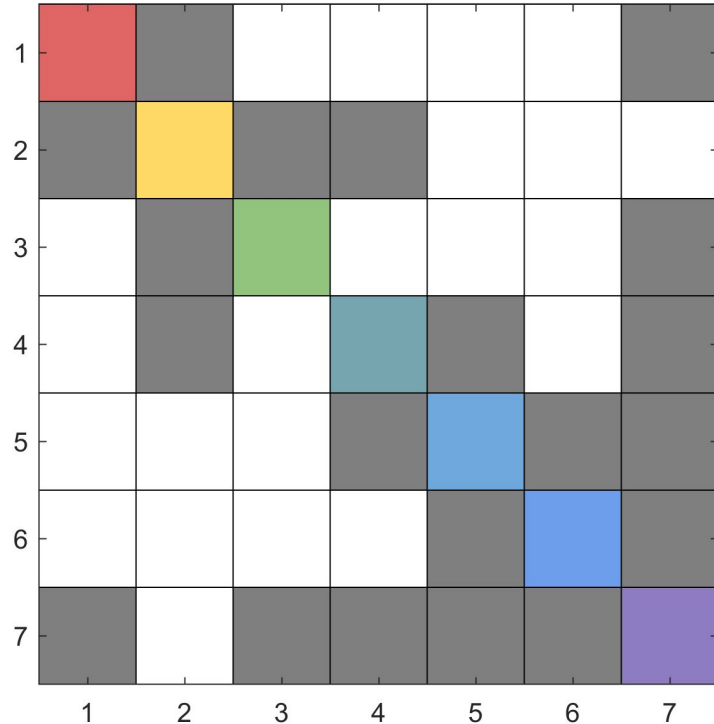
Adjacency matrix



Topology - Overall pattern of interrelationships, which might be described by generating principles

Node - Distinct components of the system

Adjacency matrix

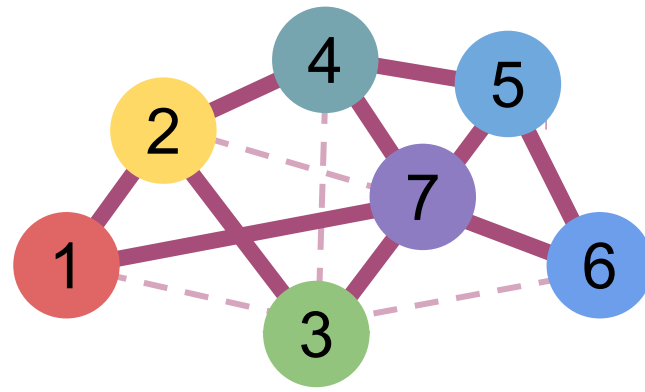
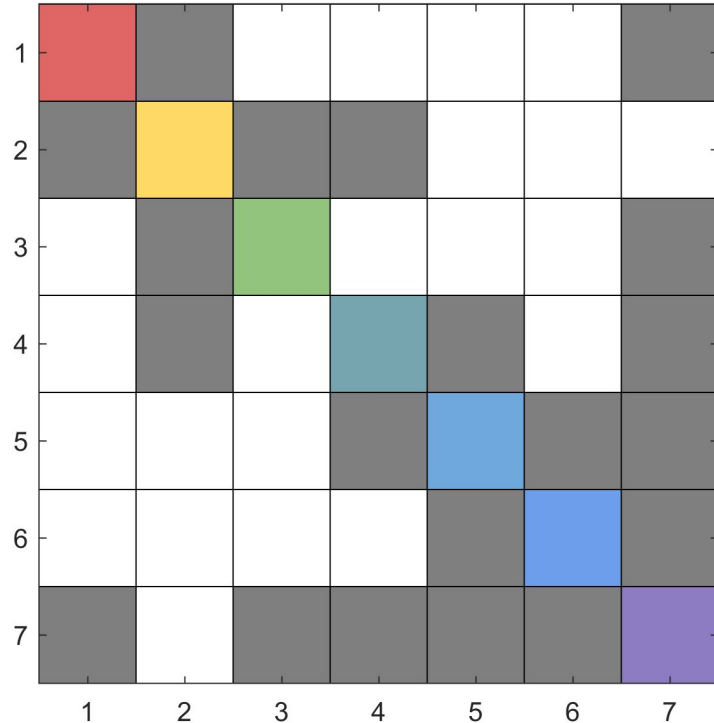


Topology - Overall pattern of interrelationships, which might be described by generating principles

Node - Distinct components of the system

Edge - Relationships quantified between system components

Adjacency matrix



Topology - Overall pattern of interrelationships, which might be described by generating principles

Node - Distinct components of the system

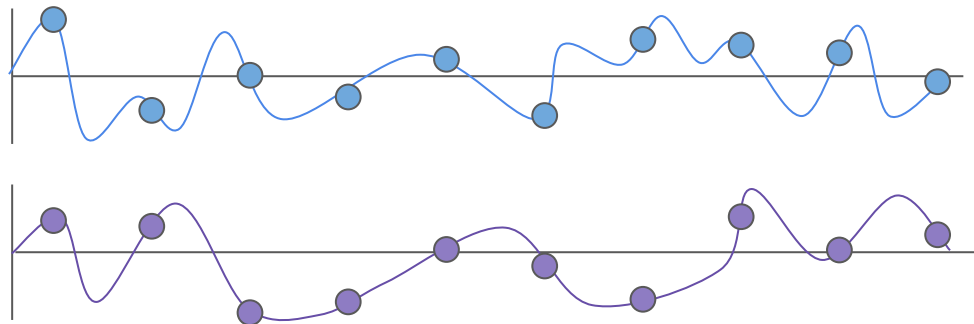
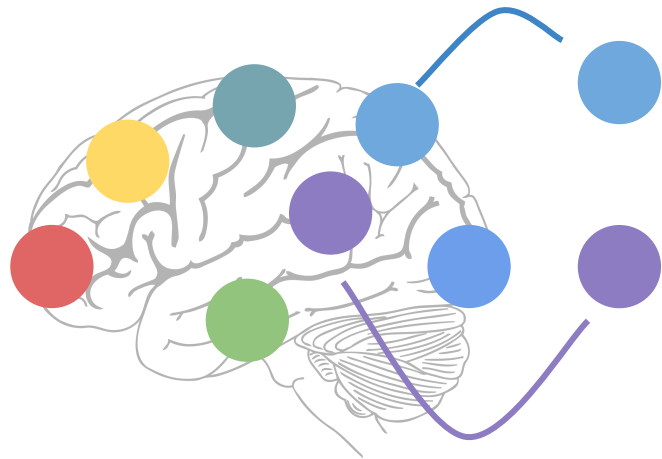
Edge - Relationships quantified between system components

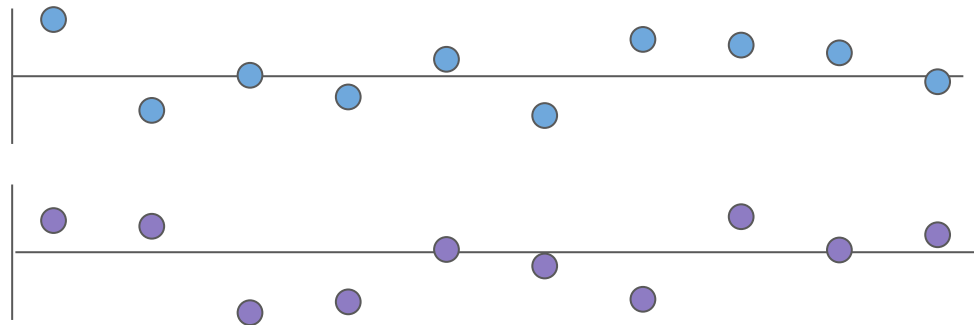
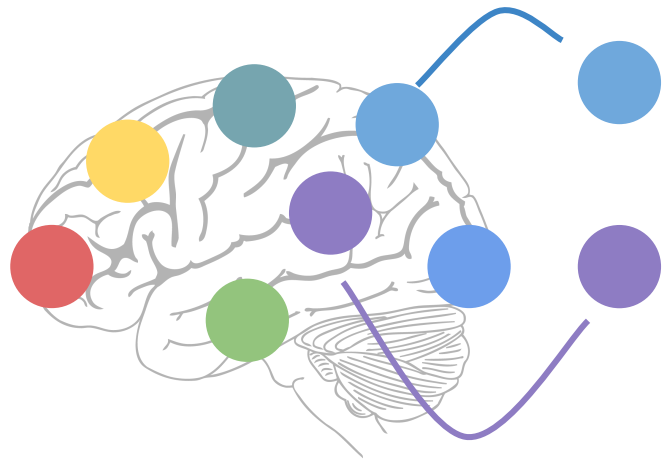
Density - Number of edges present relative to all possible pairs of nodes

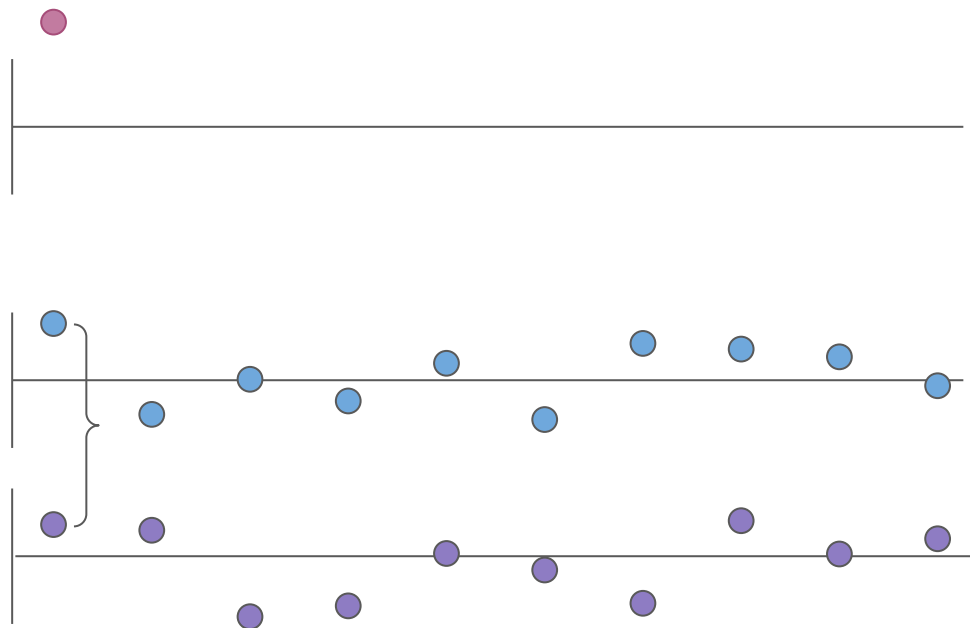
Edges in space

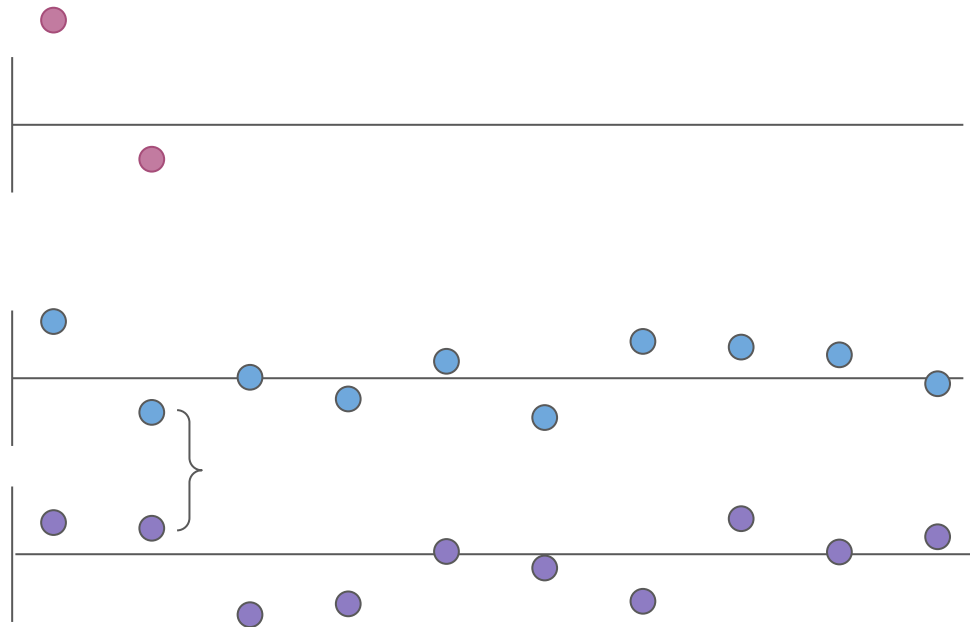
Josh Faskowitz

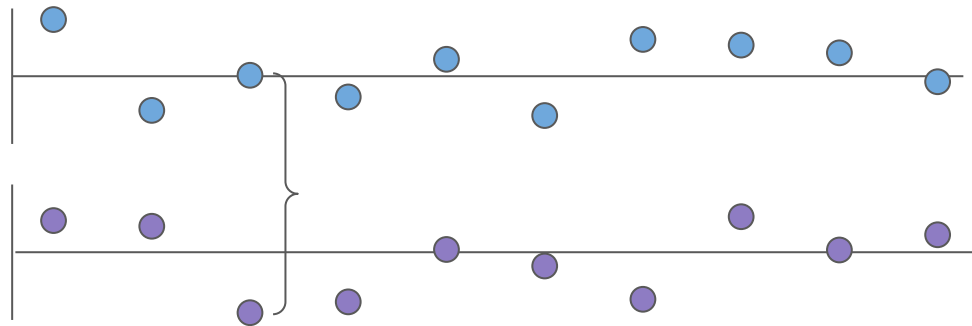
Calculating correlation

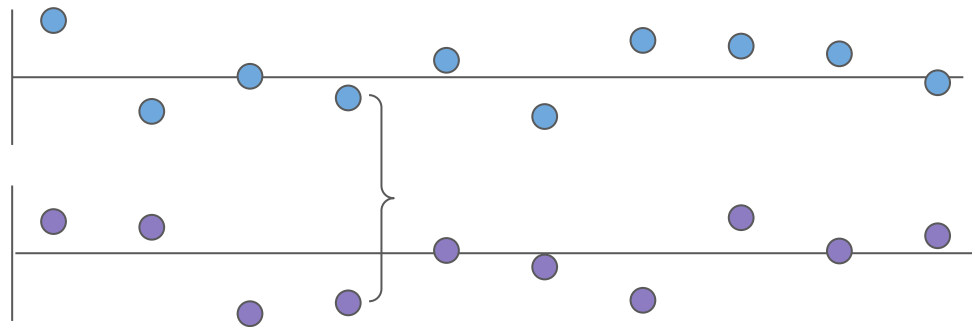


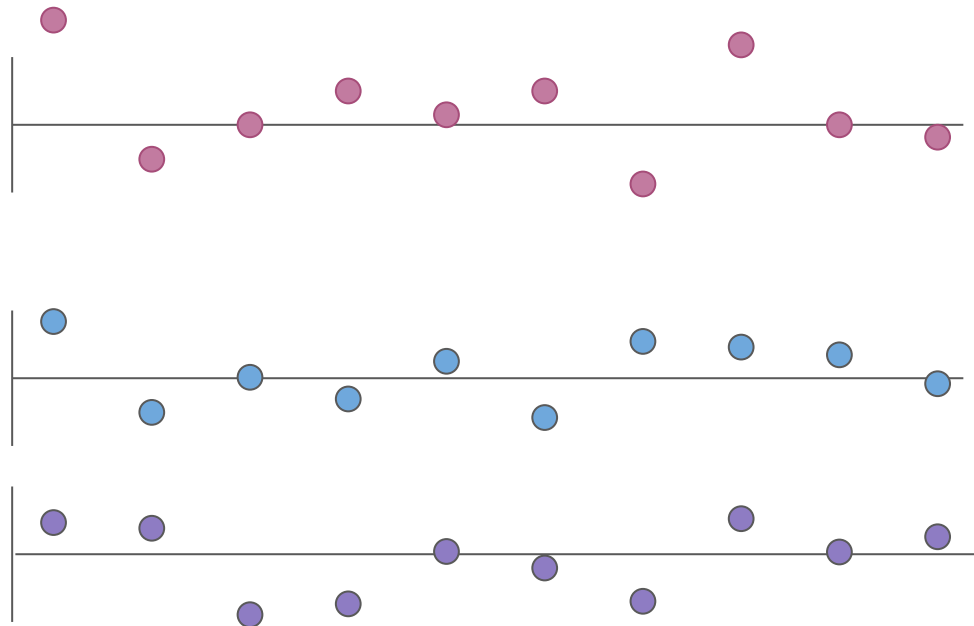












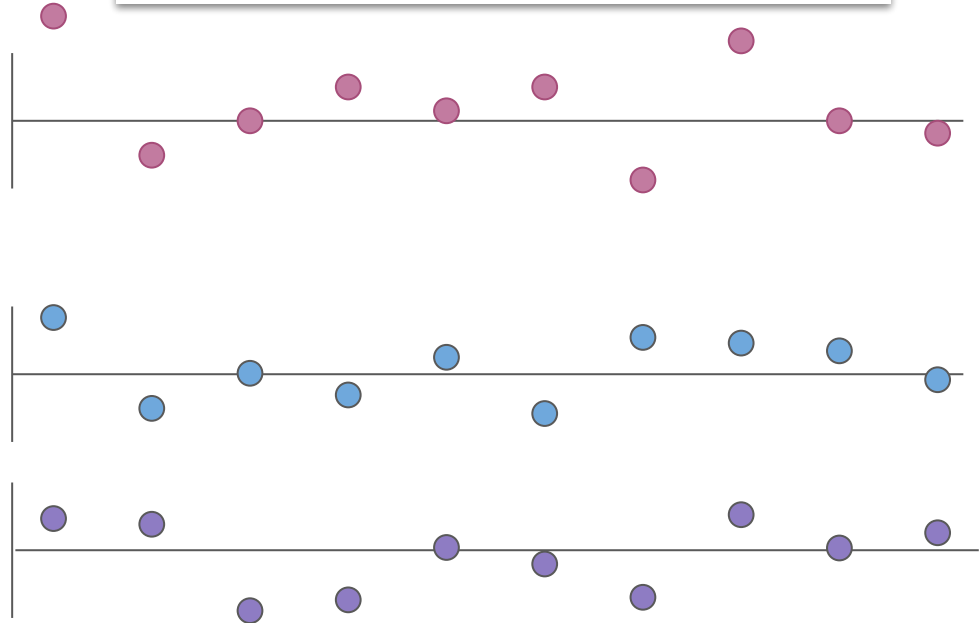
An equivalent expression gives the formula for r_{xy} as the mean of the products of the **standard scores** as follows:

$$r_{xy} = \frac{1}{n-1} \sum_{i=1}^n \left(\frac{x_i - \bar{x}}{s_x} \right) \left(\frac{y_i - \bar{y}}{s_y} \right)$$

where

$n, x_i, y_i, \bar{x}, \bar{y}$ are defined as above, and s_x, s_y are defined below

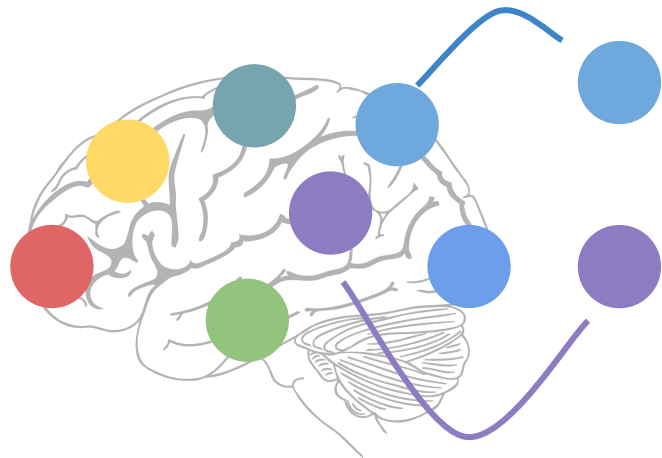
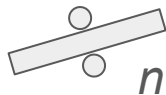
$\left(\frac{x_i - \bar{x}}{s_x} \right)$ is the **standard score** (and analogously for the standard score of y)



0.25



Σ



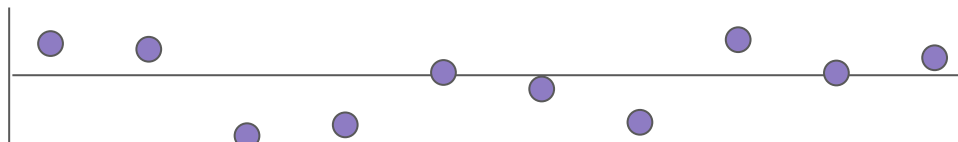
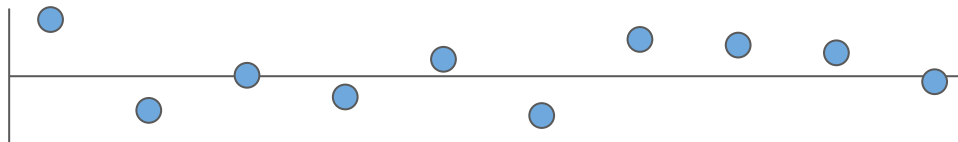
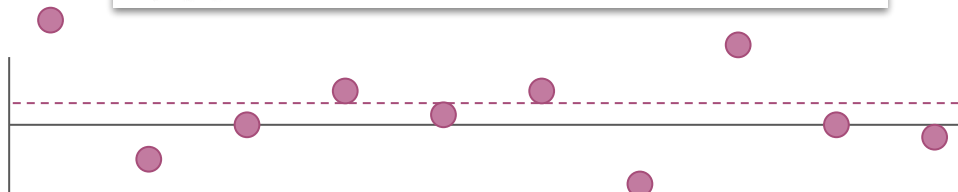
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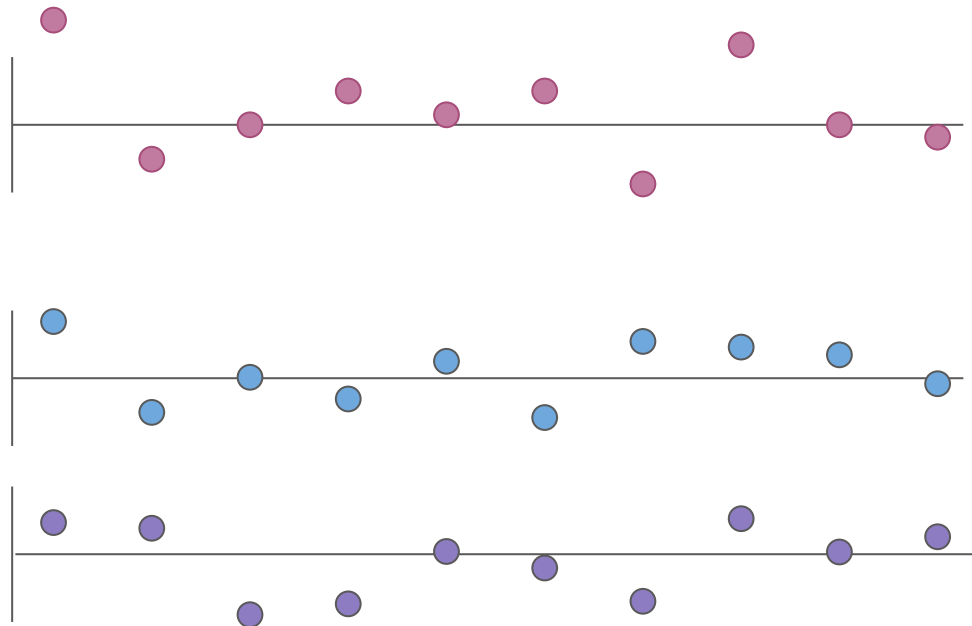
where

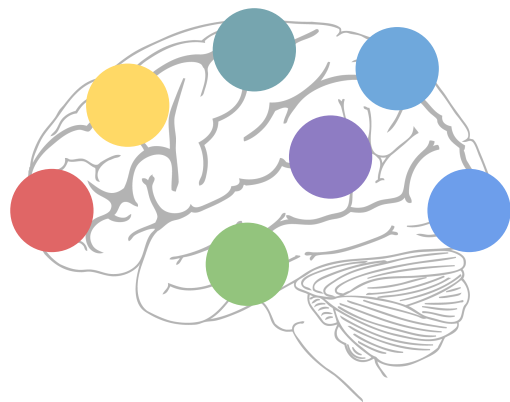
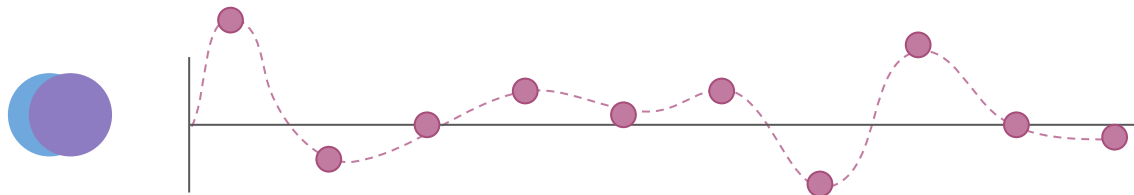
$n, x_i, y_i, \bar{x}, \bar{y}$ are defined as above, and s_x, s_y are defined below

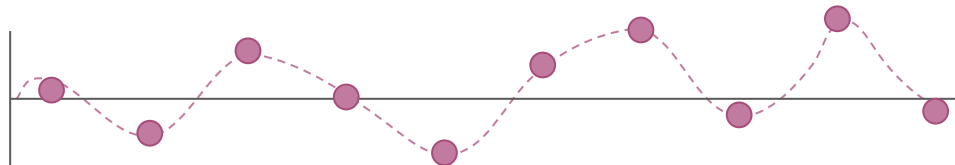
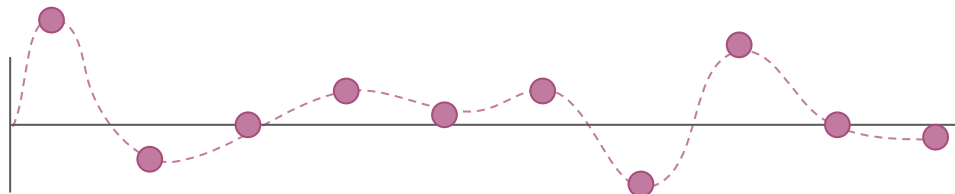
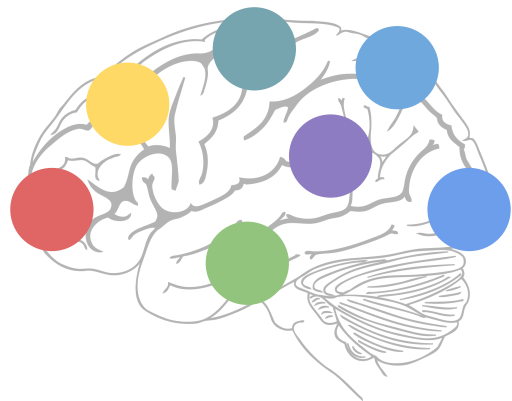
$\left(\frac{x_i - \bar{x}}{s_x} \right)$ is the **standard score** (and analogously for the standard score of y)



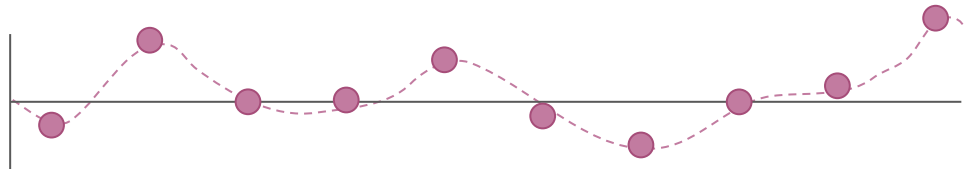
Time to get edgy

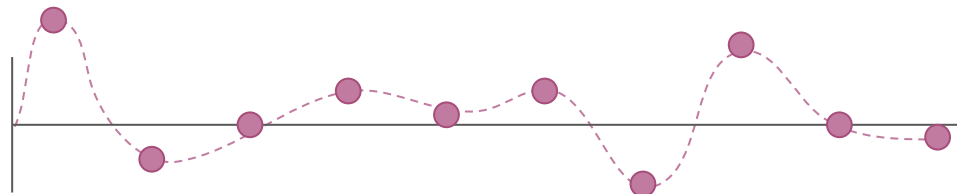
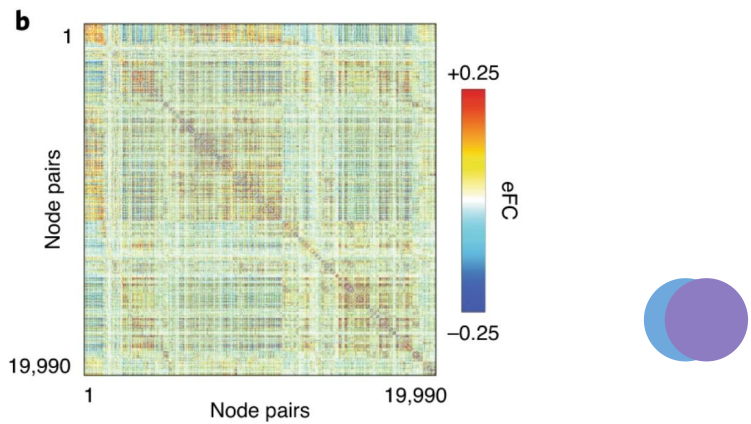




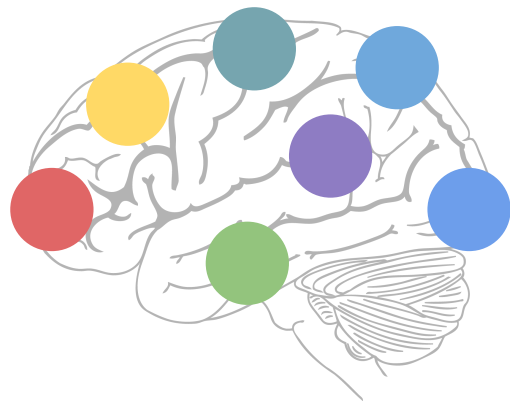


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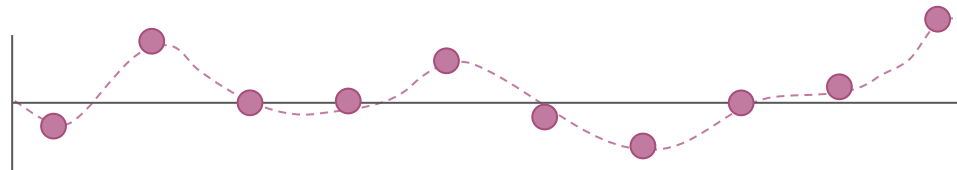
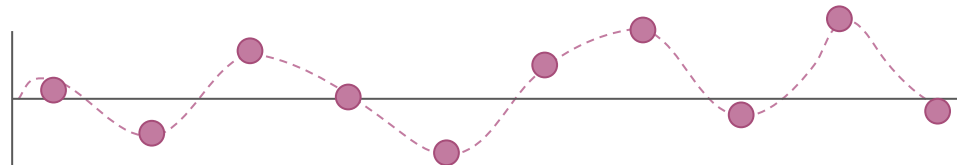




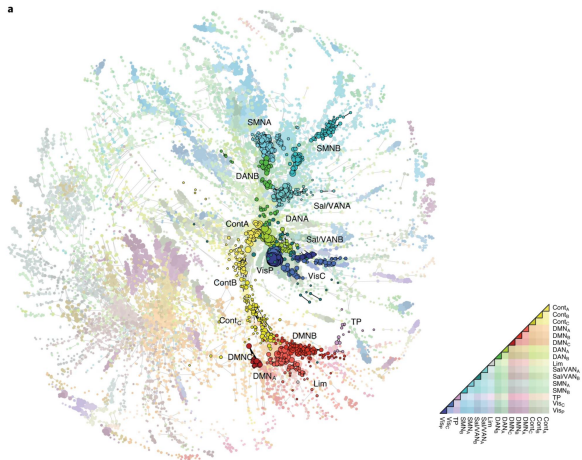
Faskowitz et al (2020) *Nat. Neuro*



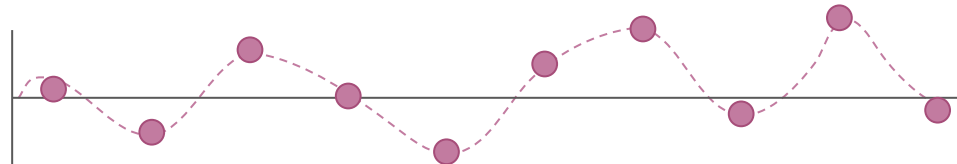
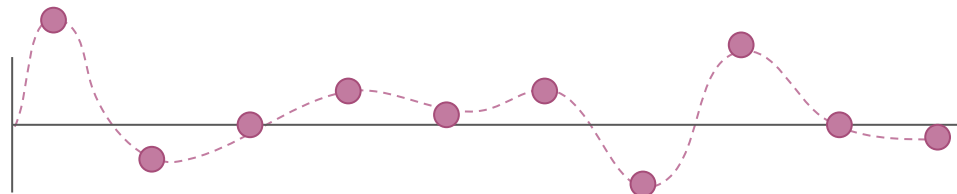
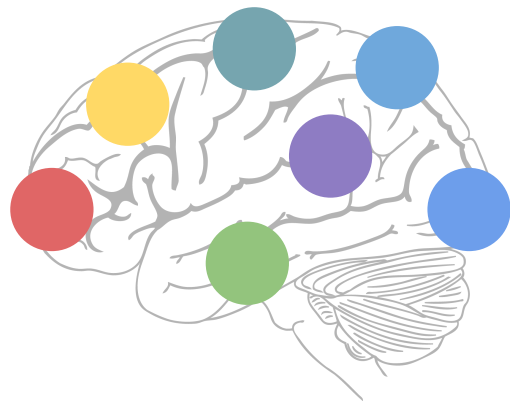
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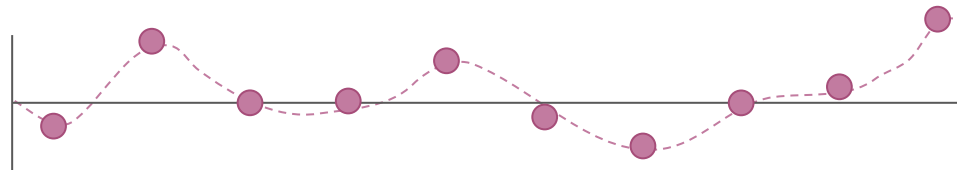
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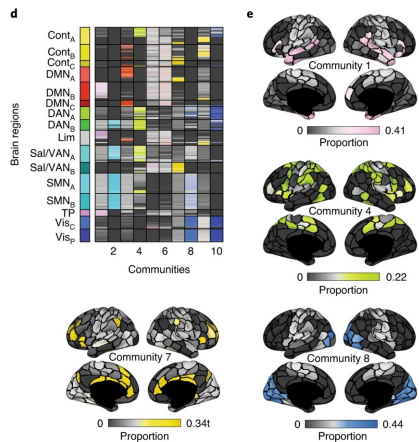


Faskowitz et al (2020) *Nat. Neuro*

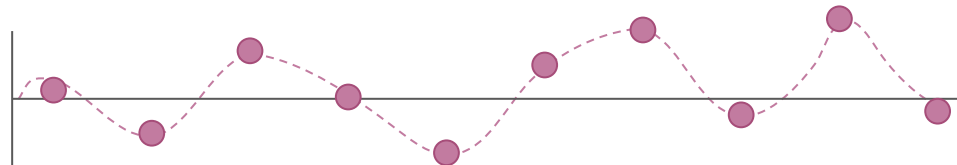
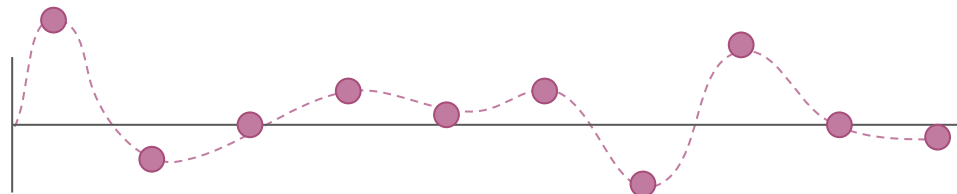
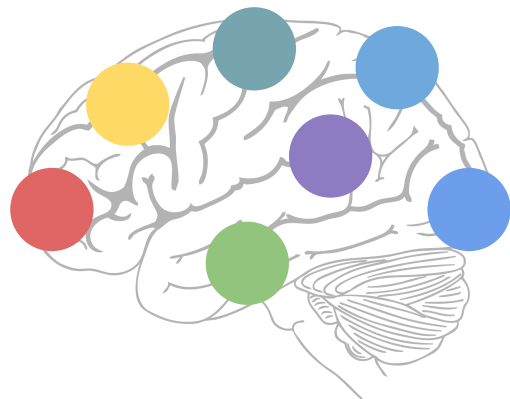


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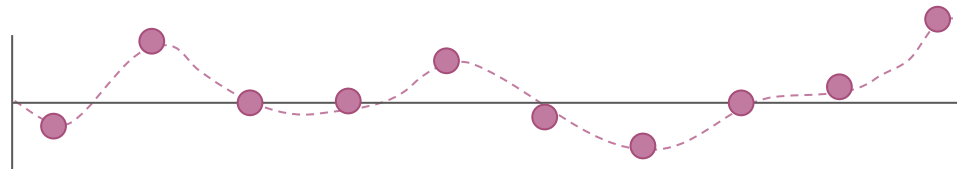


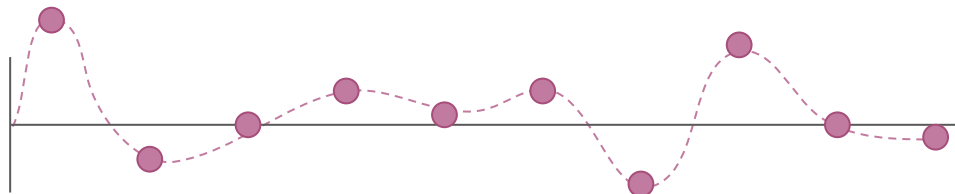
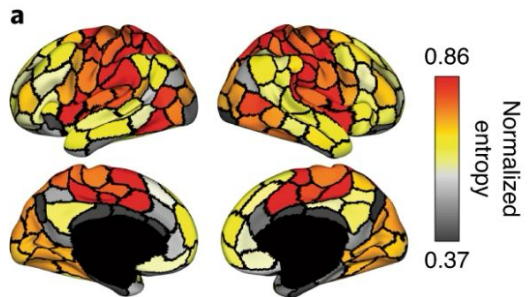


Faskowitz et al (2020) *Nat. Neuro*

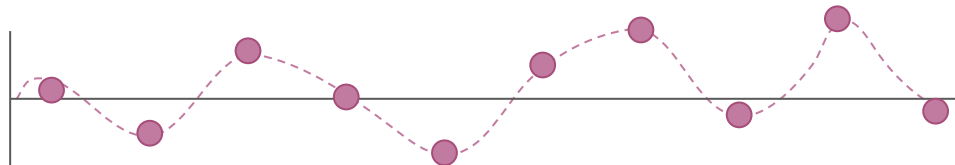
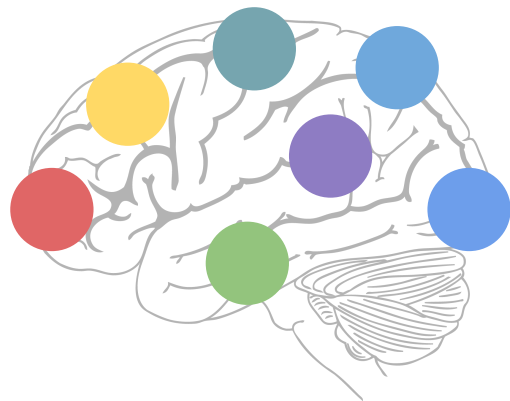


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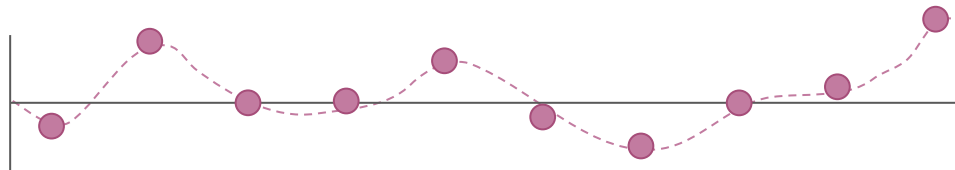




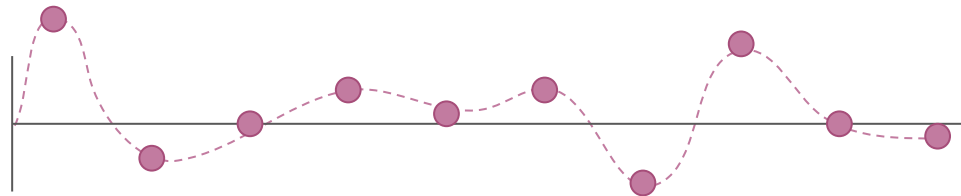
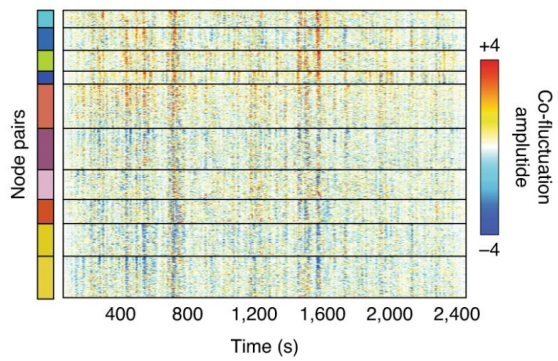
Faskowitz et al (2020) *Nat. Neuro*



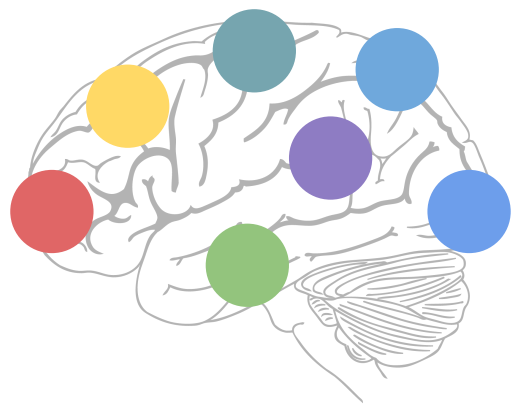
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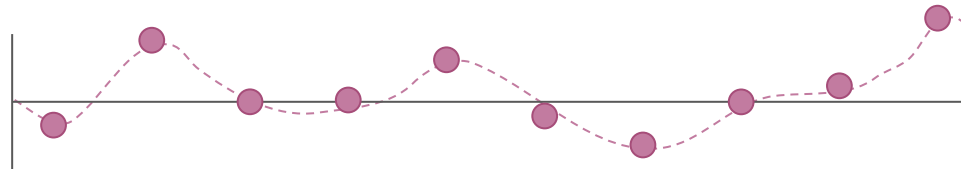
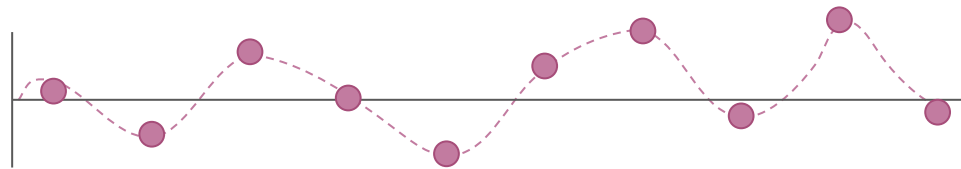
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Faskowitz et al (2020) *Nat. Neuro*



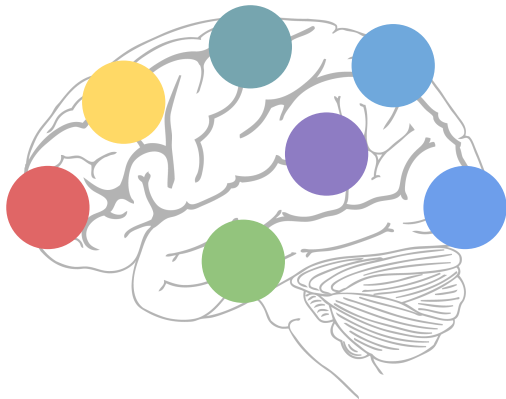
...



- No sliding step or window parameter
- Time-average is exactly correlation
- Same resolution as data input
 - Single frame information
 - Potential to measure “faster” phenomena

Faskowitz et al (2020) *Nat. Neuro*
 Zamani Esfahlani (2020) *PNAS*

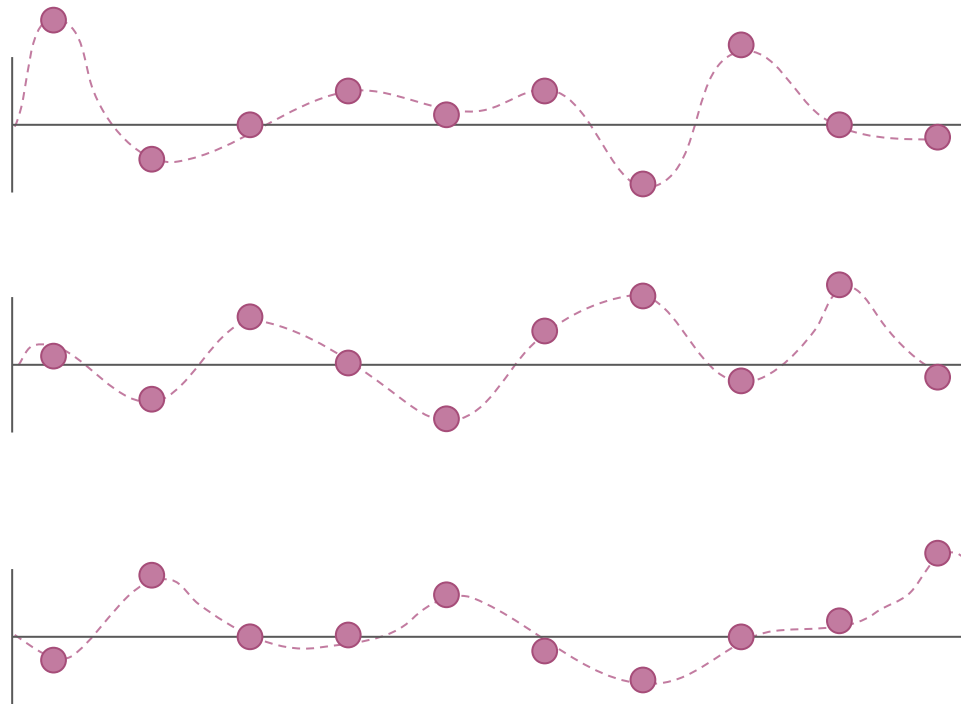
See also! Liu & Duyn (2013) *PNAS*,
 Lahnakoski et al (2017) *HBM*, van Oort et
 al (2018) *NeuroImage*...



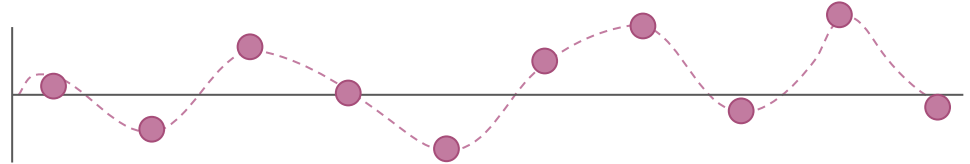
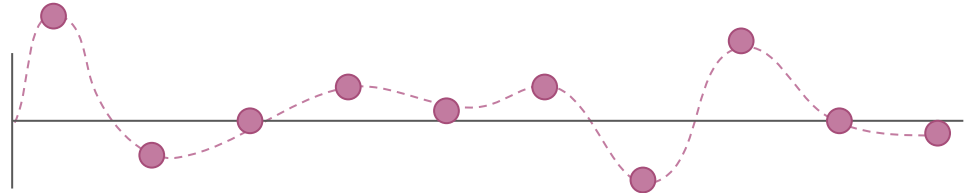
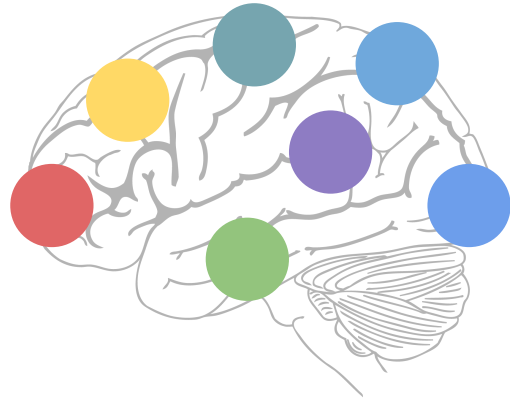
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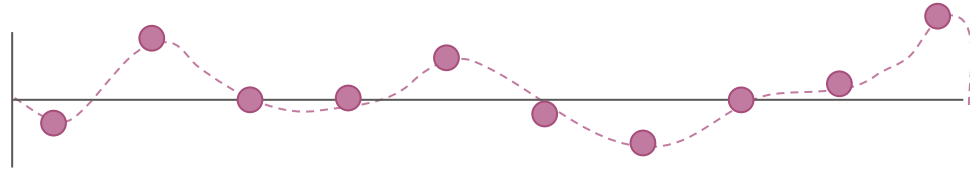
Instantaneous similarity after “unwrapping” the traditional correlation



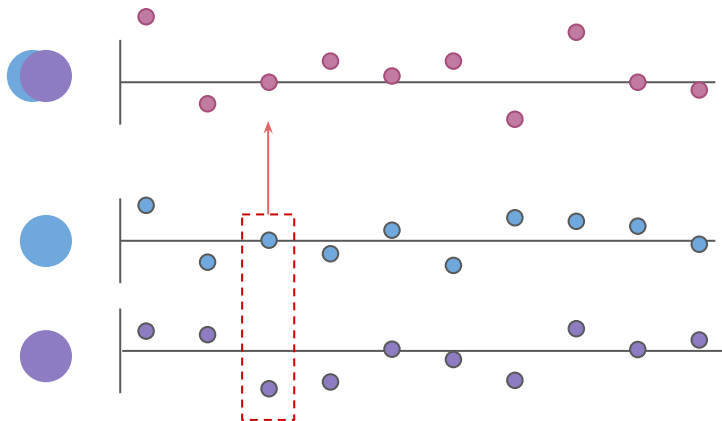
What does the
correlation
“unwrapped” get
you?



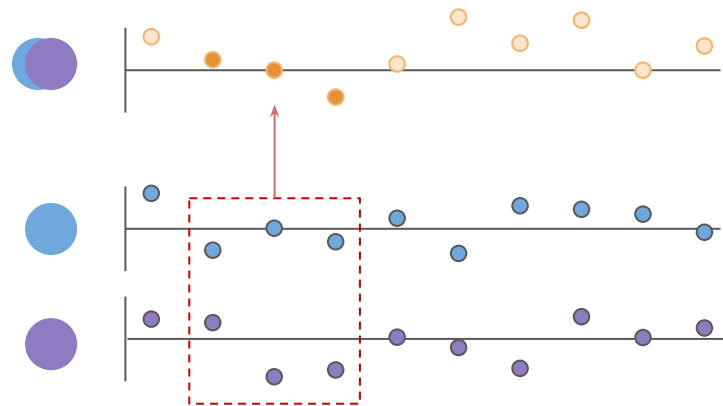
...



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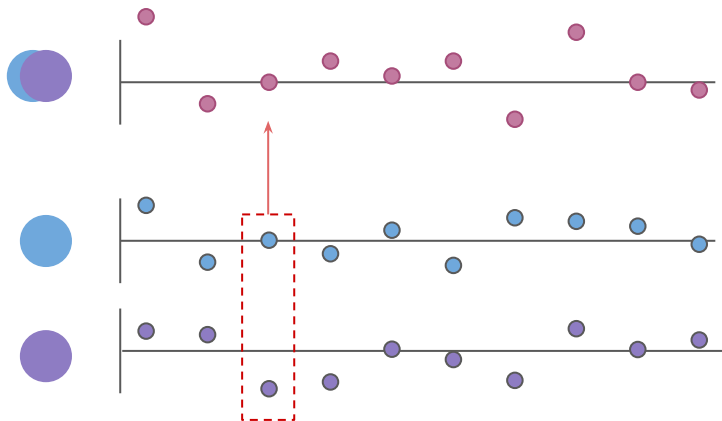
Edge time series



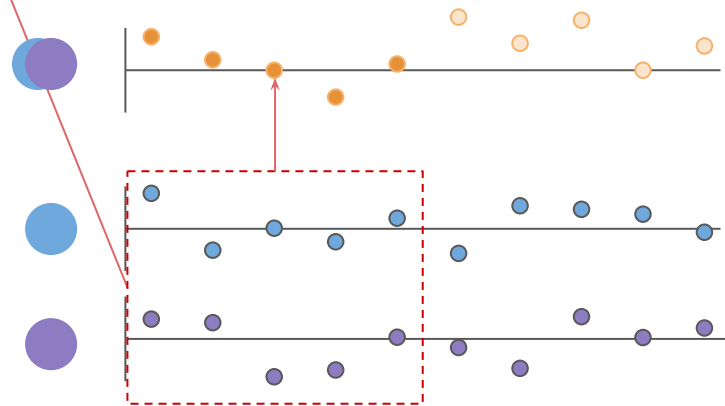
tv-FC

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Pick window size

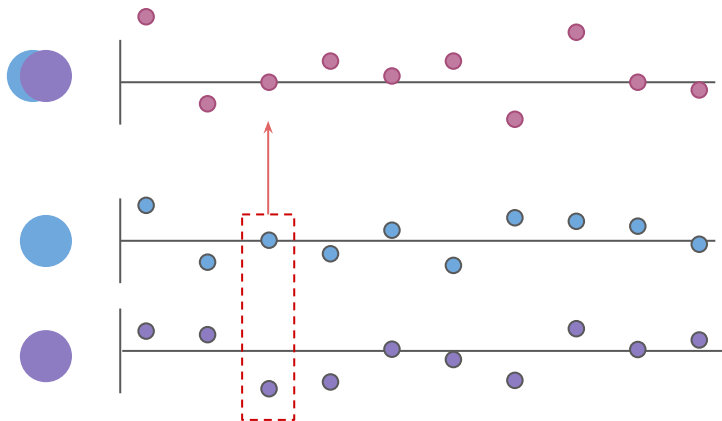


Edge time series

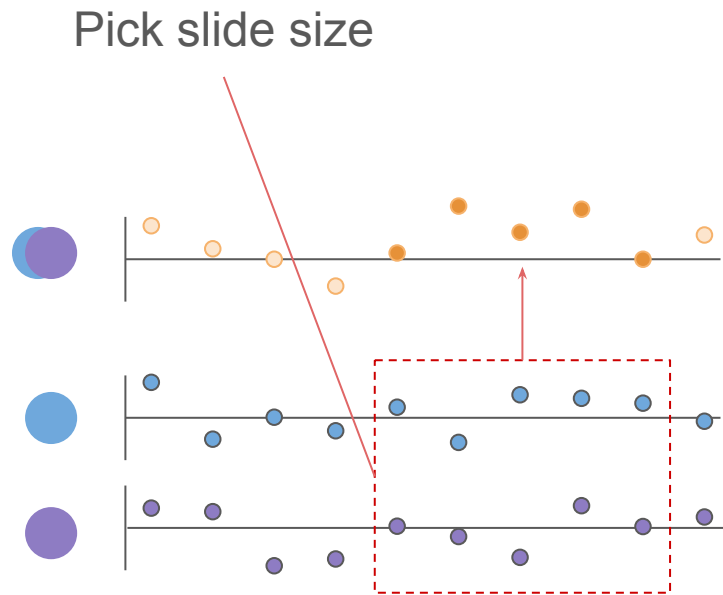


tv-FC

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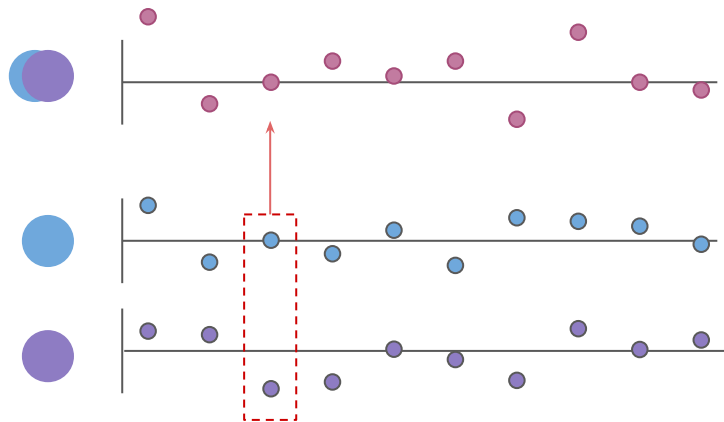


Edge time series



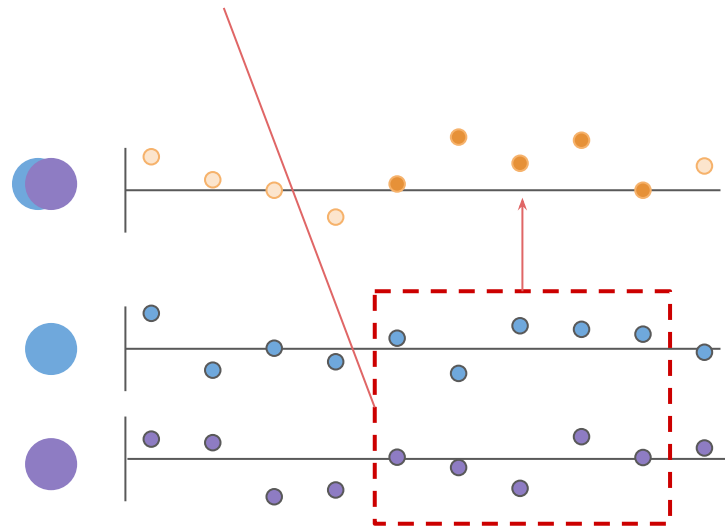
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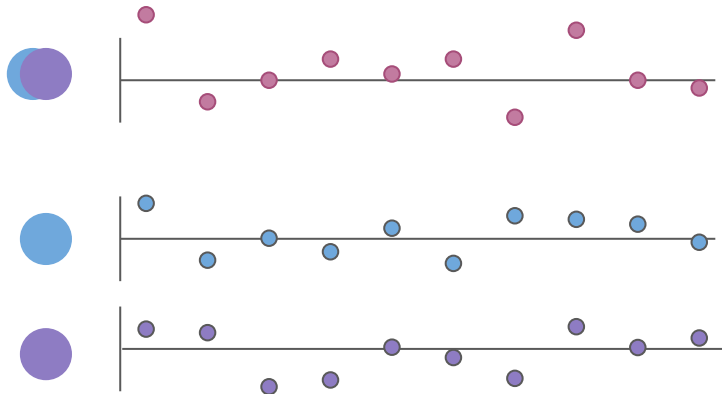
Edge time series

Normalize data within window

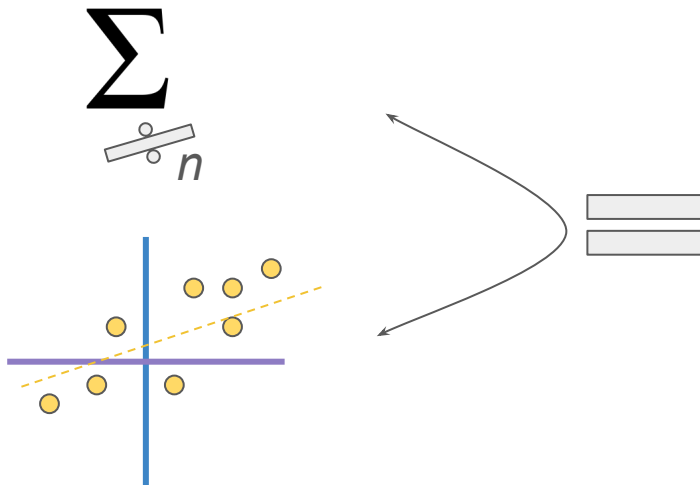


tv-FC

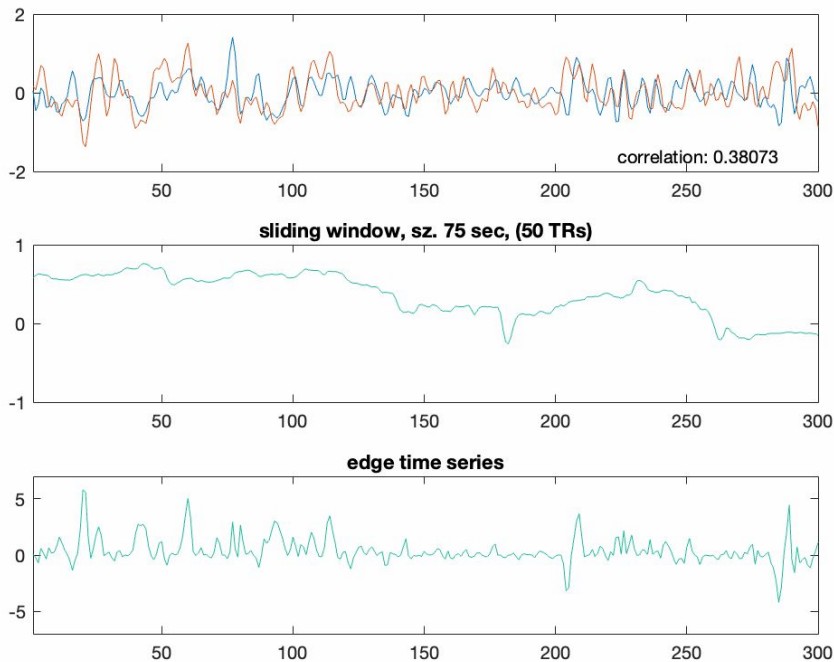
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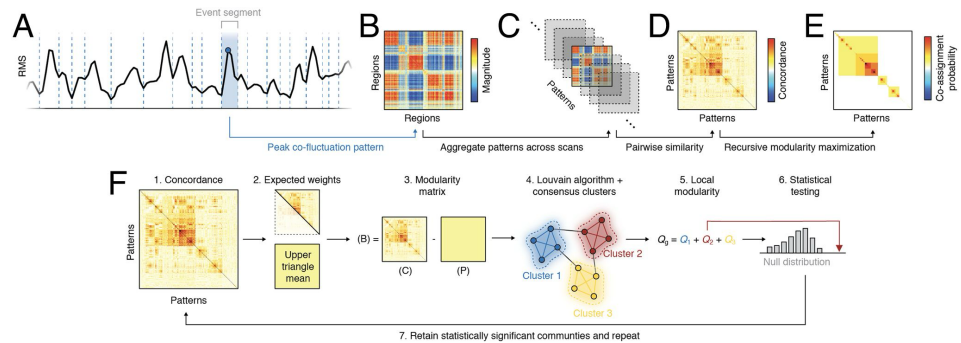
Edge time series



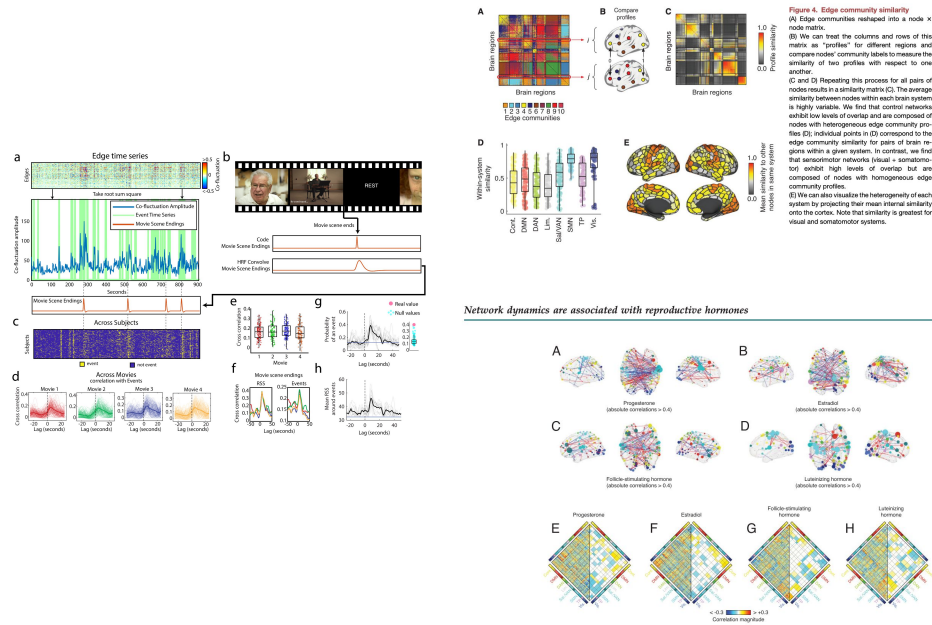
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 - **Potential to measure “faster” phenomena**



Difference in
synchronization
timing, variability,
shape (but *not*
claiming edges are
correct vs sliding
window)



Imaging Neuroscience, Volume 4, 2026





Edges in Space: An edgy sequel

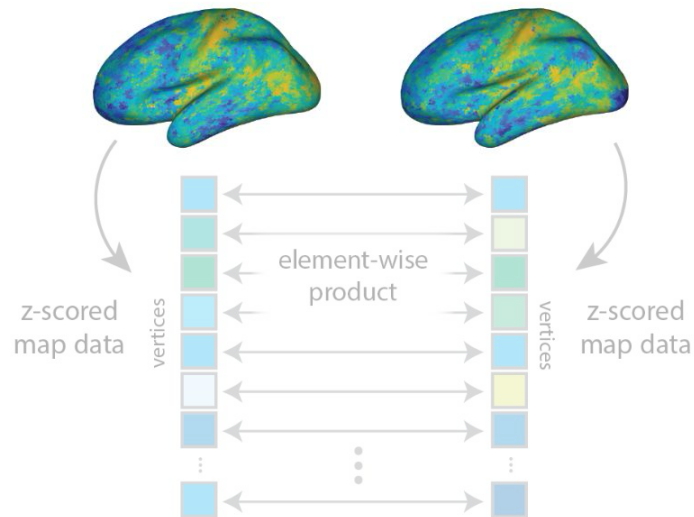
The method in a nutshell



- Obtain your spatially mapped data of interest
 - Two sets of data, as we are making a bivariate comparison!
- Z-score each set of mapped data
- Element-wise multiply the sets
- Look at that element-wise multiplication
 - That's the similarity rendered at each point in space

Map 1

Map 2

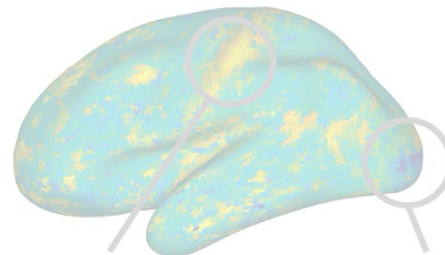


Map of point-wise
contribution to the
overall spatial
similarity btwn. input
data sources

$$\frac{\sum}{\text{num. points}} = \text{spatial correlation}$$

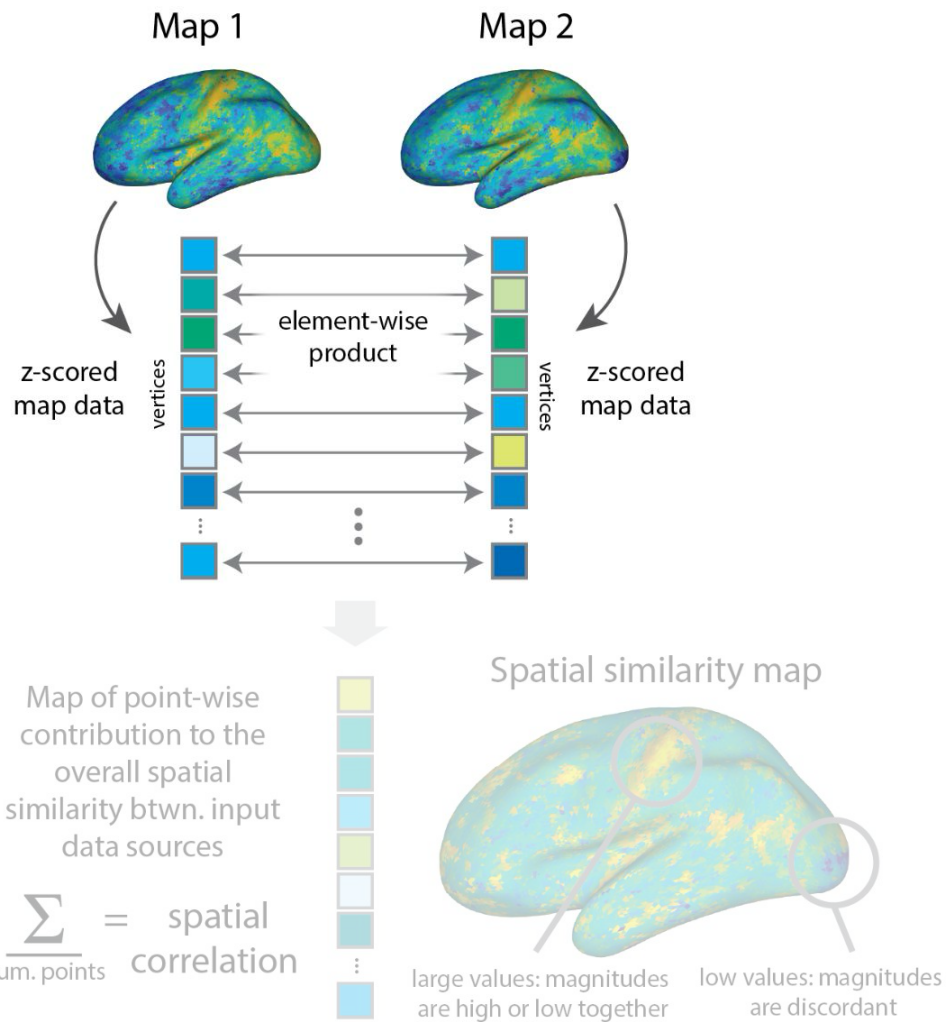


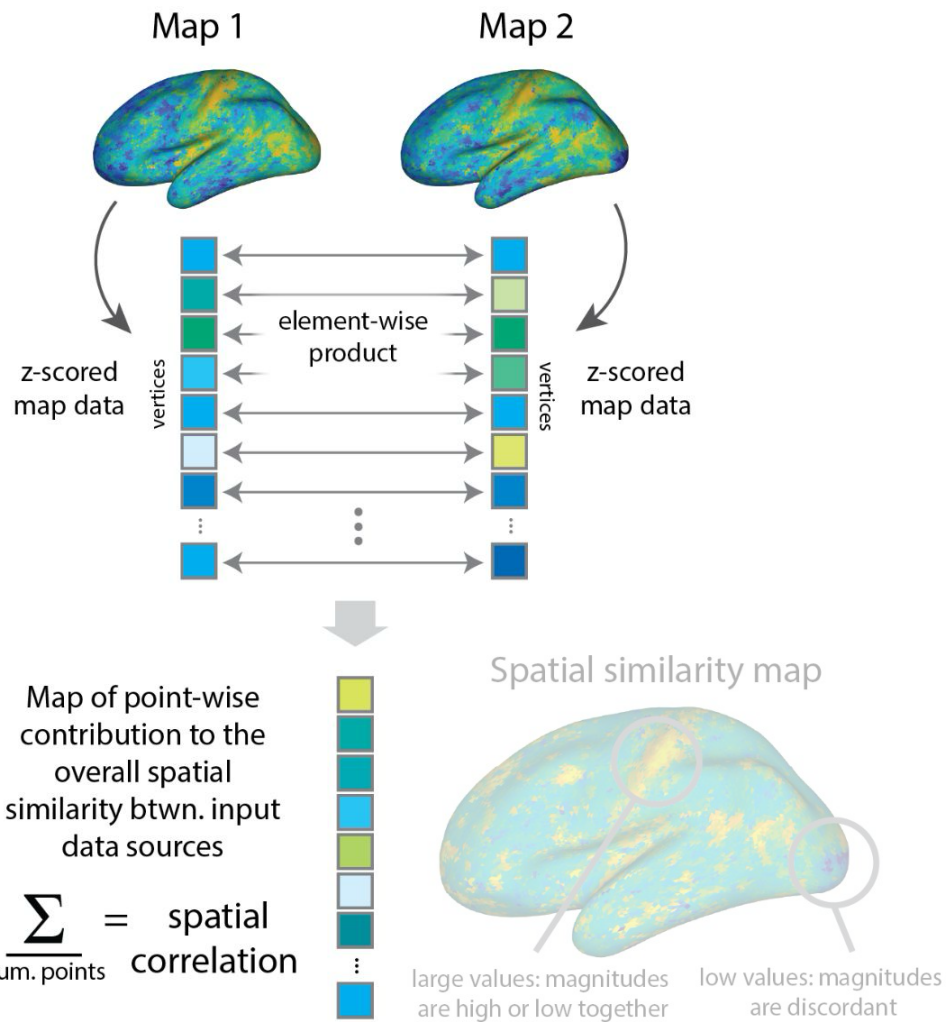
Spatial similarity map

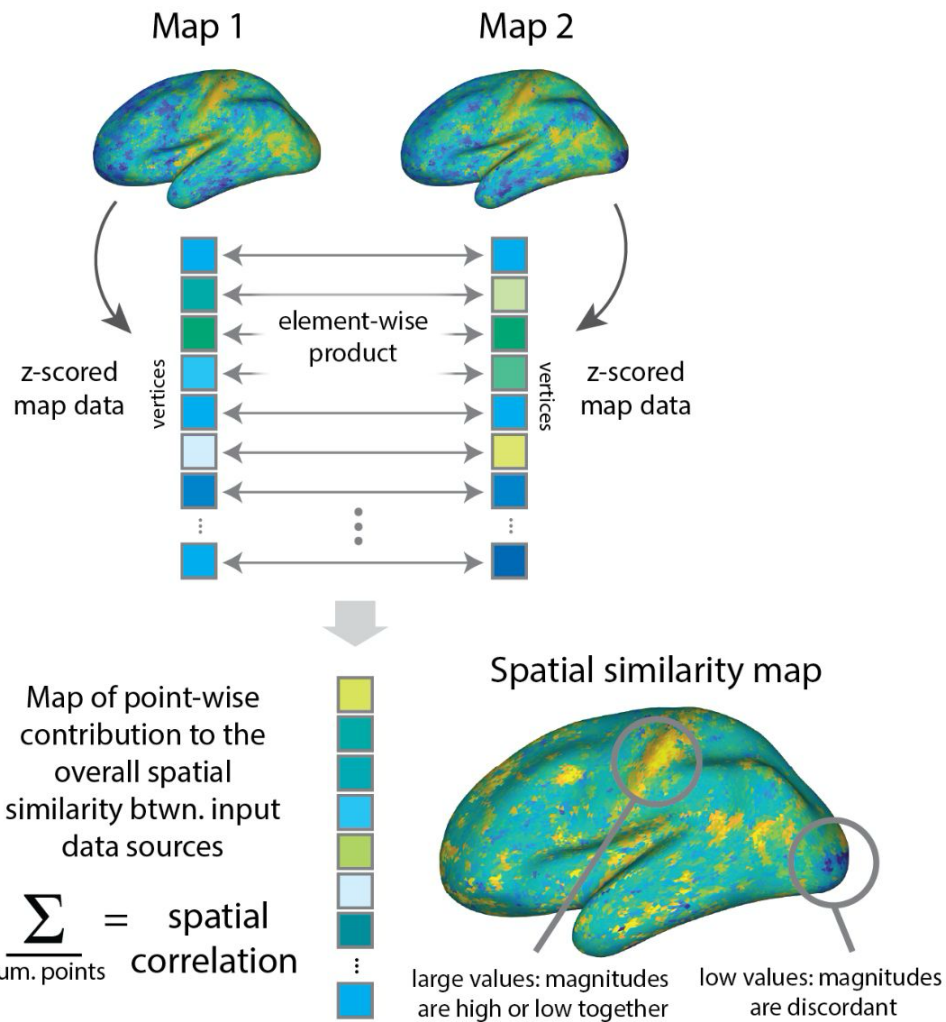


large values: magnitudes
are high or low together

low values: magnitudes
are discordant



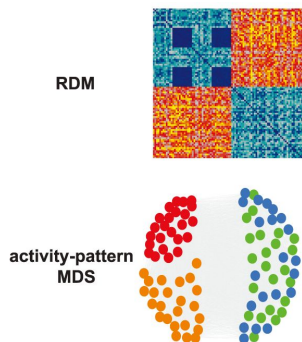




Why even do this? What is the point of doing the spatial version of the edge 'unrolling'?

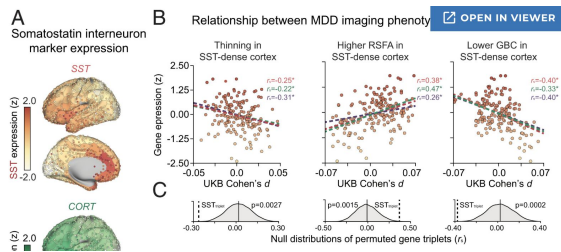
Spatial comparison is all around us (in neuroimaging)

Comparing mapped data within each subject can or be a finding itself



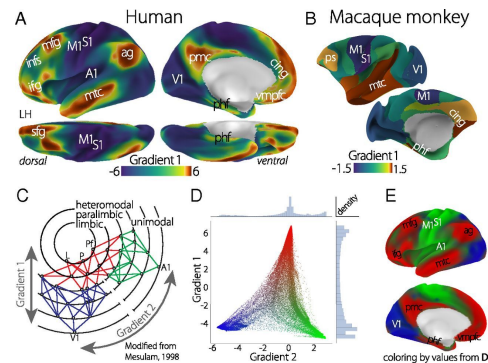
Nili et al (2014). *PLoS CB*

Andersen et al (2020). *PNAS*



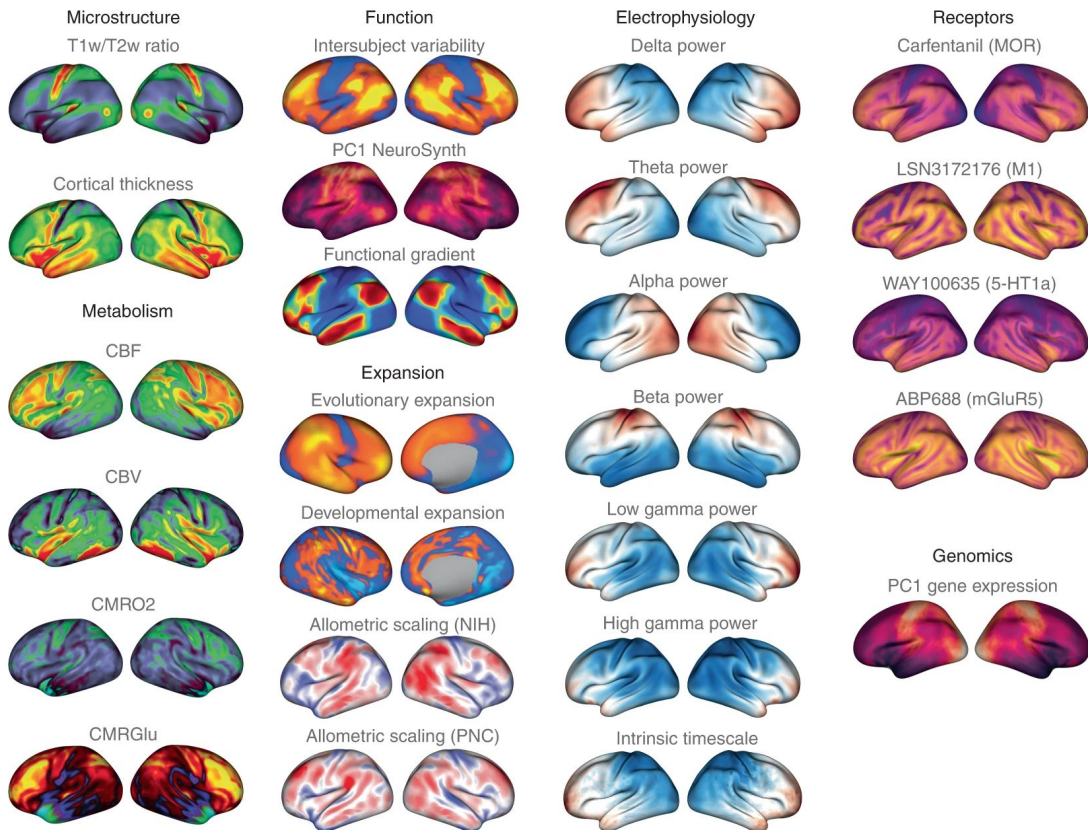
Comparing mapped data to a reference data serves to generate hypothesis / embellish theory

Comparing mapped data can identify shared spatial patterning



Margulies et al (2016). *PNAS*

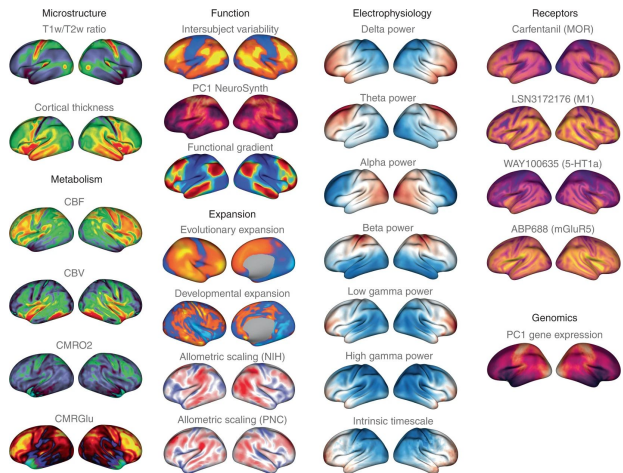
Neuromaps



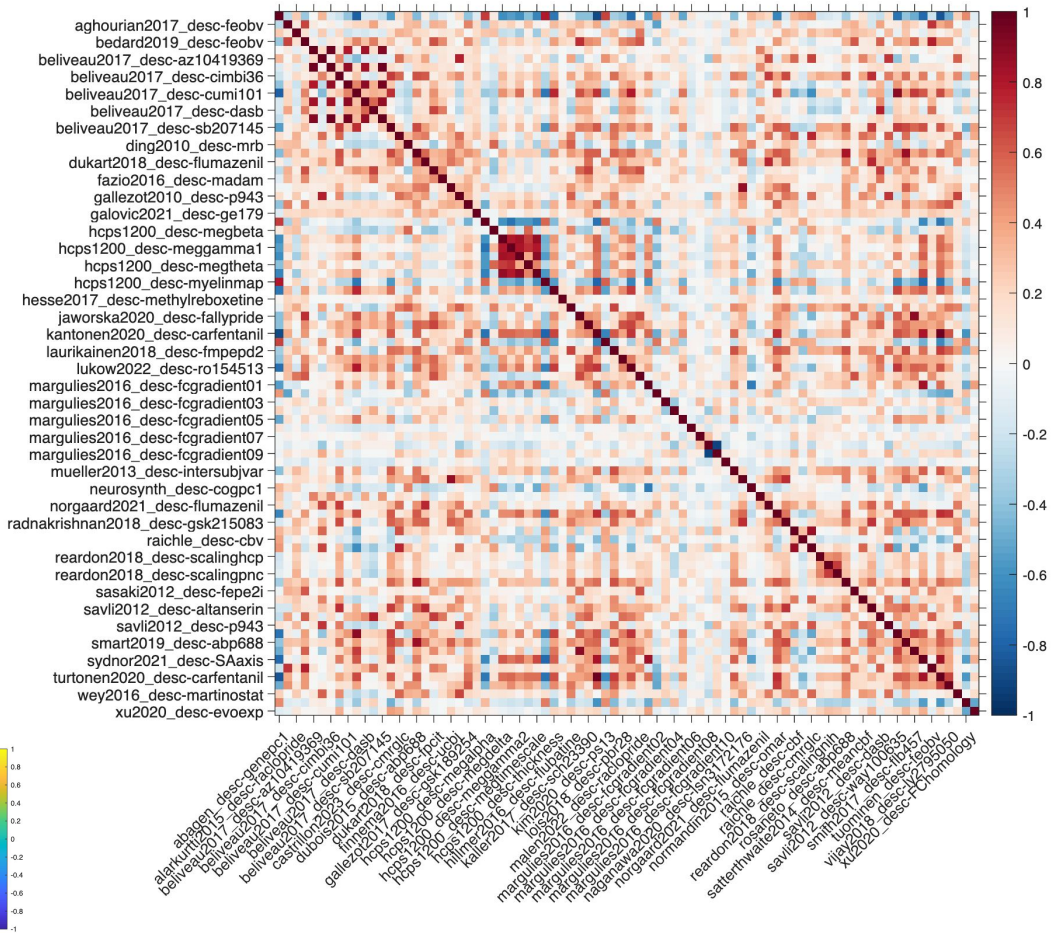
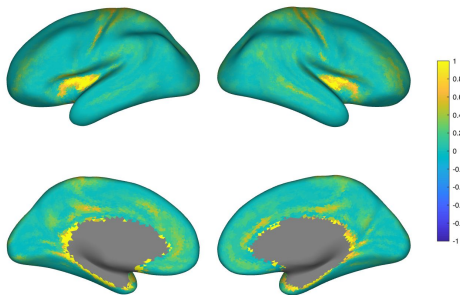
A toolbox that makes
accessing canonical group
average maps easy

Can be used in many different
contexts, to add extra
information or contextualize!

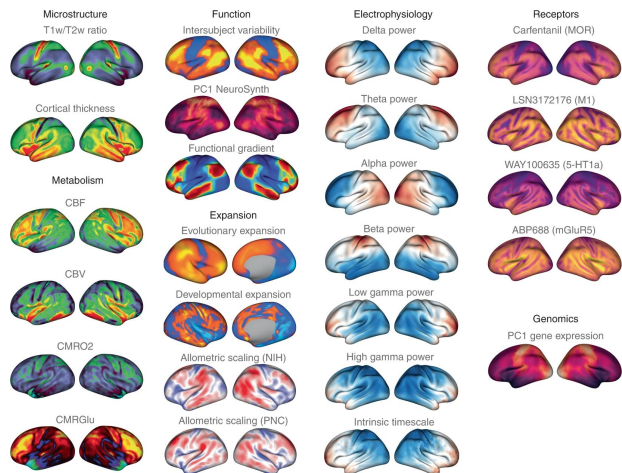
Neuromaps



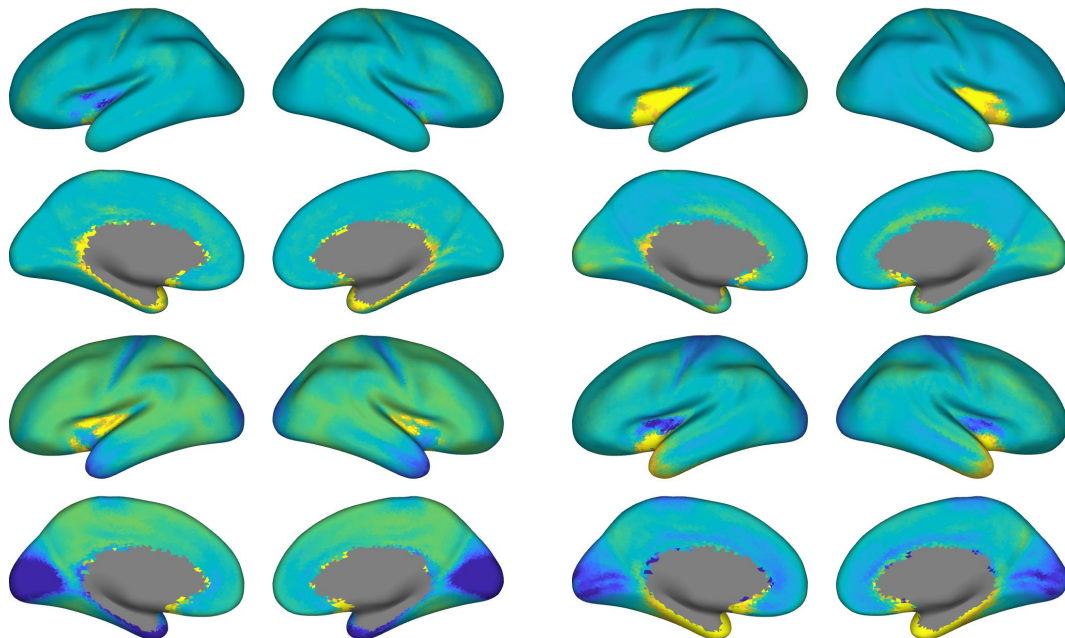
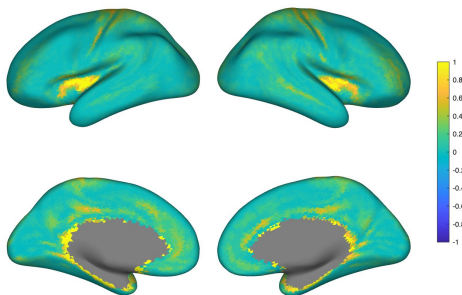
How do all these atlas maps interrelate?



Neuromaps



How do all these atlas maps interrelate?

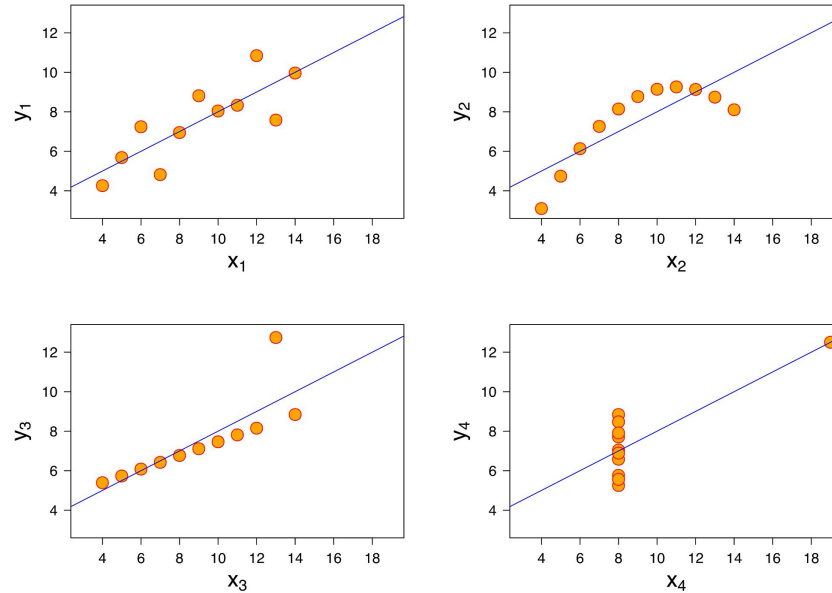


Orthogonal patterns of similarity across the 3321 comparisons

(might better be done with clustering / non-negative matrix factorization)

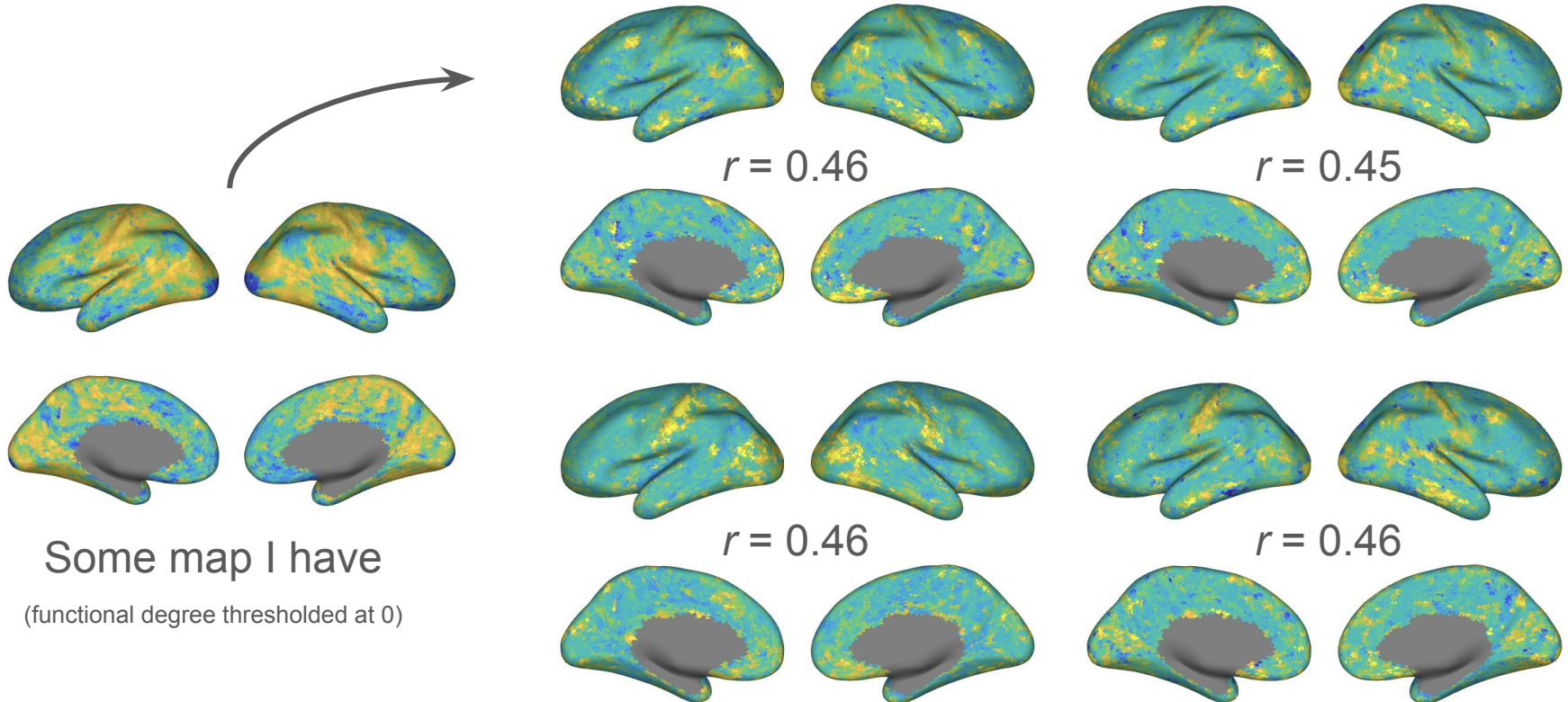
Wouldn't it be nice to know *how* maps correlate?

Anscombe's quartet emphasizes that correlation can be arrived upon in different manners

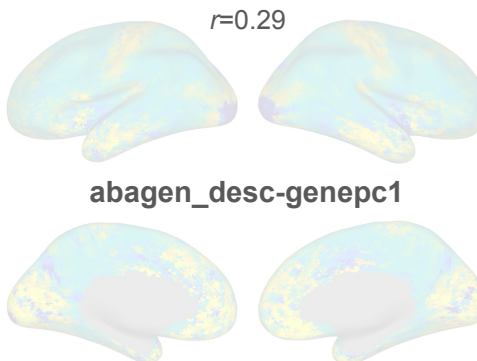
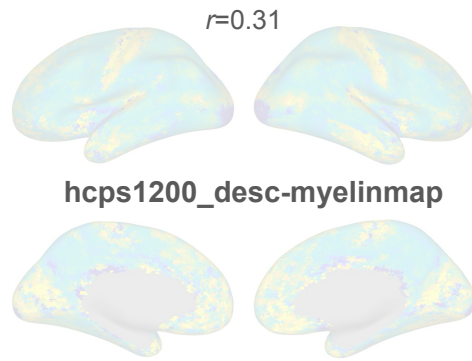
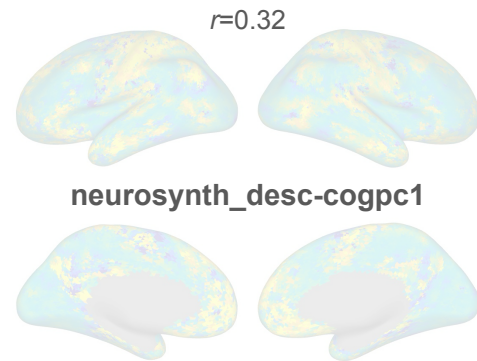
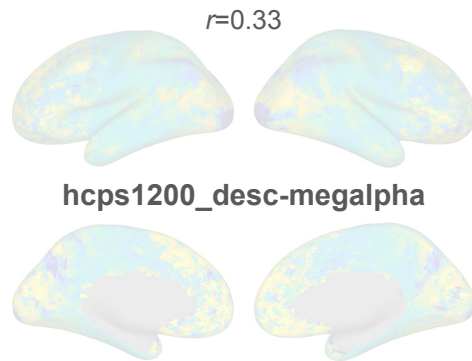
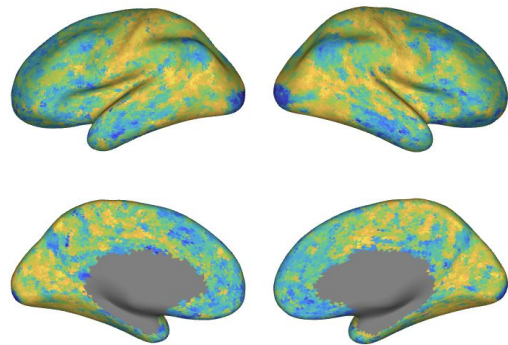
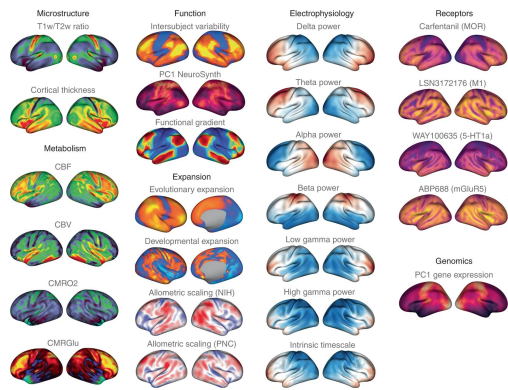


And that you need to visually inspect data

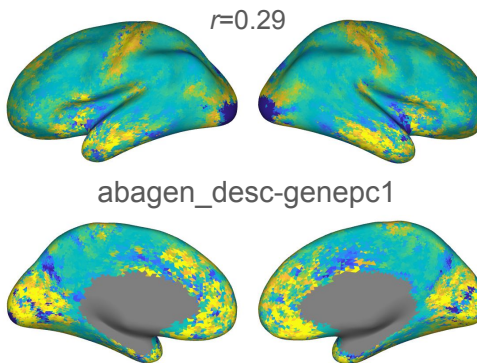
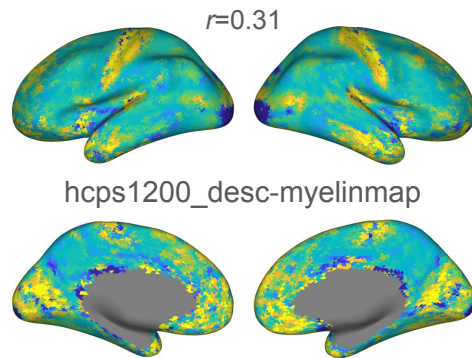
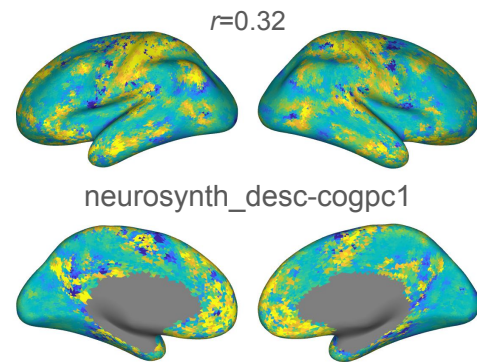
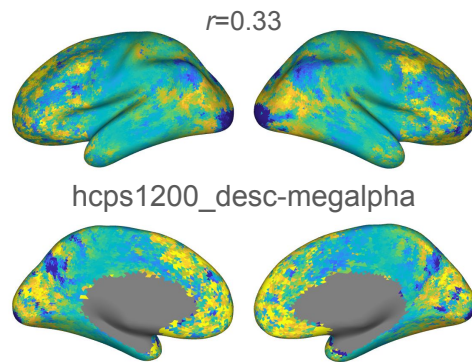
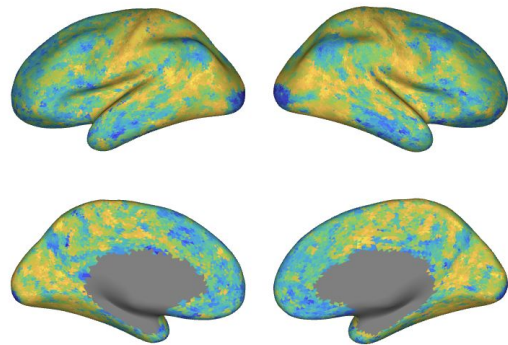
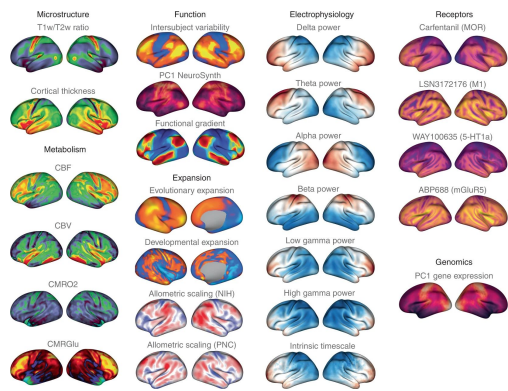
Wouldn't it be nice to know *how* maps correlate?



Wouldn't it be nice to know *how* maps correlate?



Wouldn't it be nice to know *how* maps correlate?



Spatial similarity map, which tells you which regions disproportionately influence similarity

Pinpoint areas of the brain that are more similar within-subj. rather than between-subj.

Anscombe's quartet for neuroimaging

Intercompare neuro-maps templates

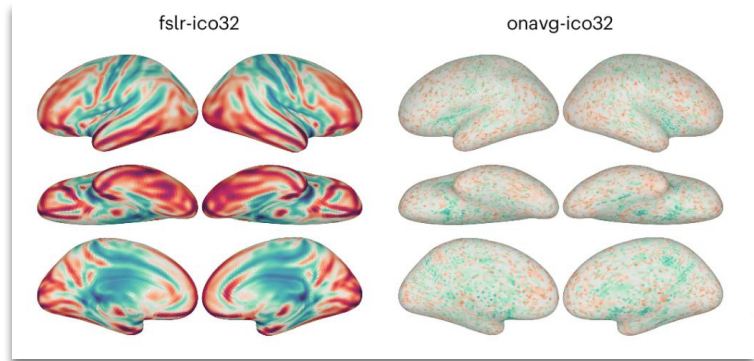
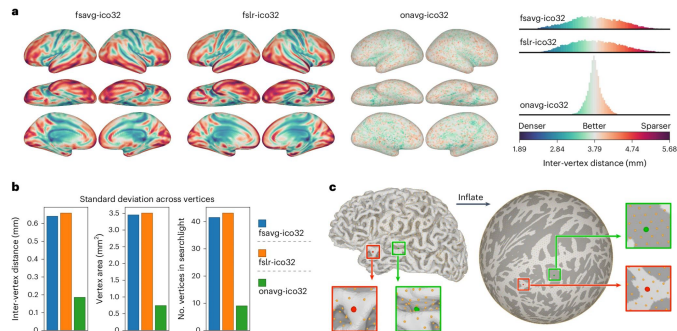
Compare relationship of subject (meylin) maps to canonical template map

Evaluate the structure function relationship across the brain?

HCP dataset

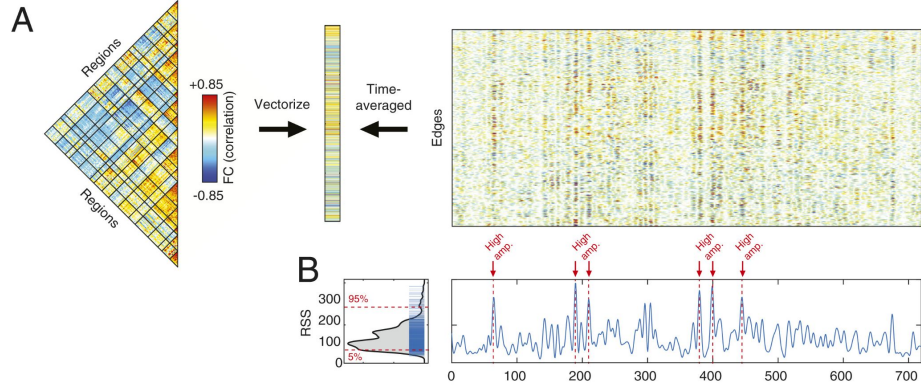
- 176 quality-controlled subjects
 - Low motion, no reported artifacts, no twins
- Data resampled from fs_LR (cifti) space to the on-avg surface using weighted mean in spherical projection space
- Mapped data obtained for
 - Structural features (e.g. myelin),
 - Functional features (e.g. reho, func. degree)
 - Features averaged across 15-minute runs for each scanning day (2 days)

Feilong et al. (2024).
Nat. Meth.

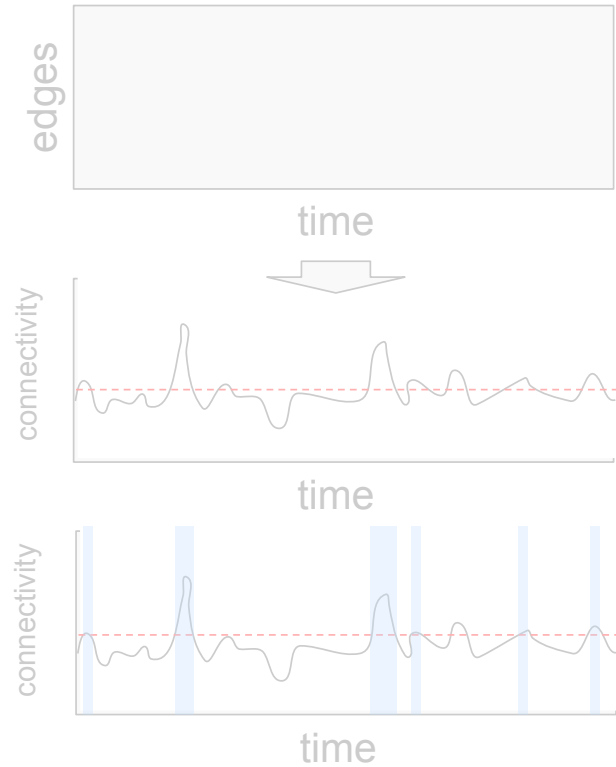
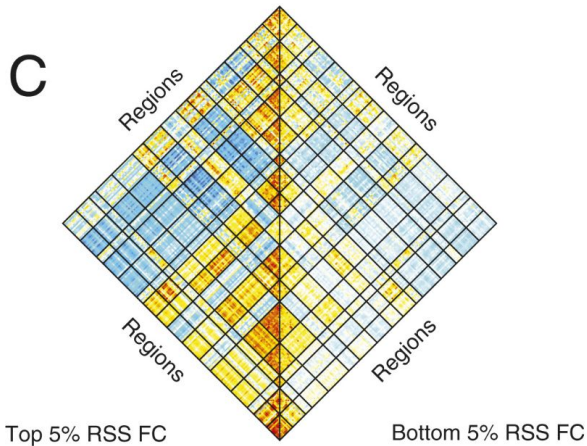


Individual specific features in brain maps

Finding where the “info” resides



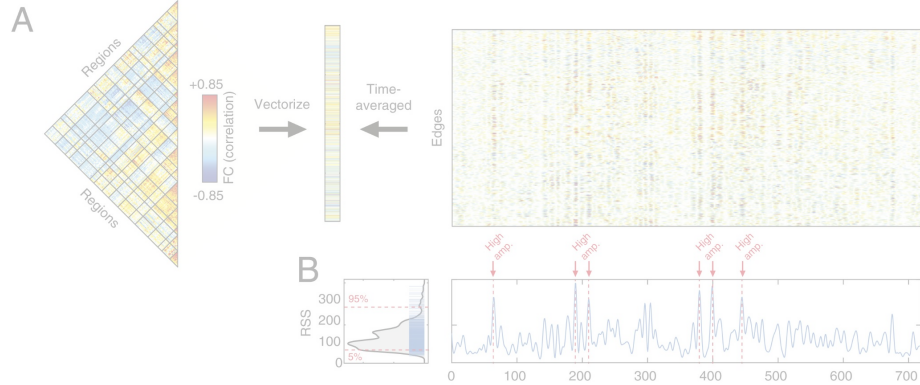
Suggests that the connectivity can be distilled (or compressed) using specific points in time



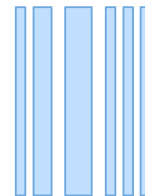
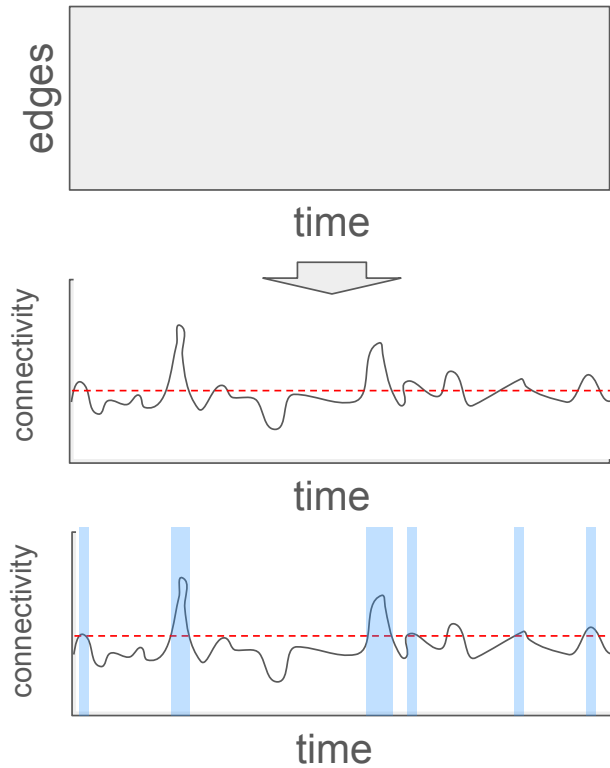
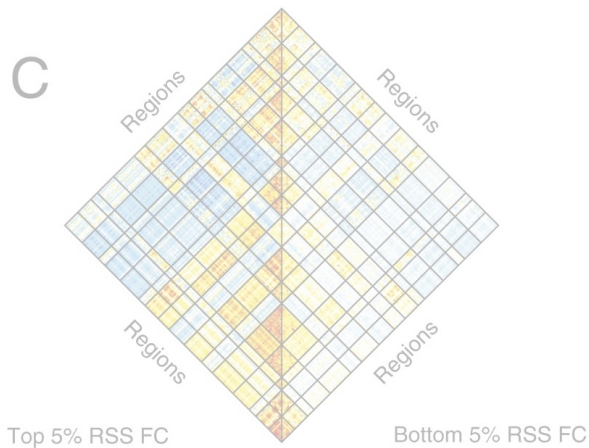
Slices of time contain disproportionate information about time-averaged FC



Finding where the “info” resides



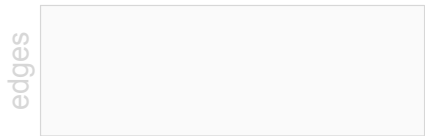
Suggests that the connectivity can be distilled (or compressed) using specific points in time



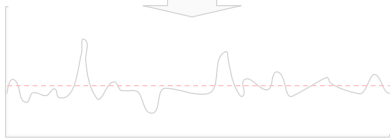
Slices of time contain disproportionate information about time-averaged FC



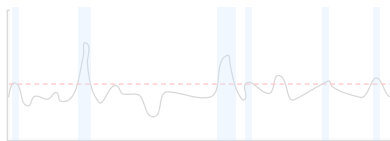
What is the spatial analogue of this process?



time



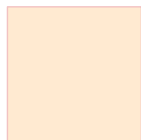
time



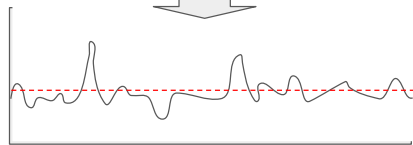
time



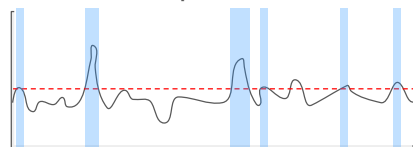
Slices of time contain disproportionate information about time-averaged FC



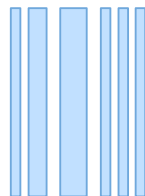
Where each row is a subject's self spatial similarity map (i.e., test-retest similarity)



space

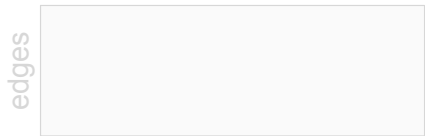


space

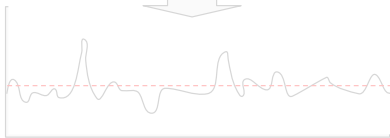


Points in space that exceed self-similarity threshold

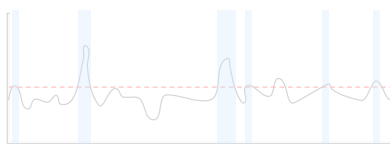
What matrix to reconstruct ?



time



time



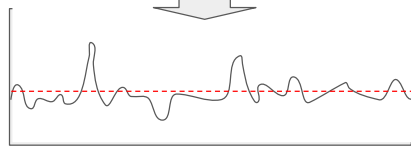
time



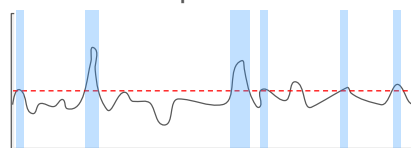
Slices of time contain disproportionate information about time-averaged FC



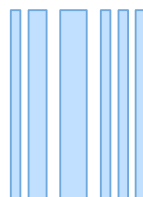
Where each row is a subject's self spatial similarity map (i.e., test-retest similarity)



space



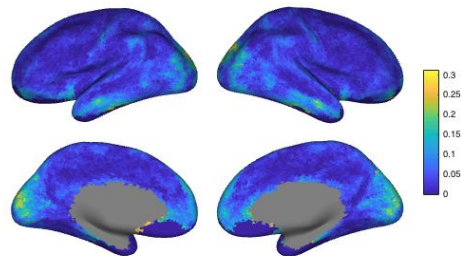
space



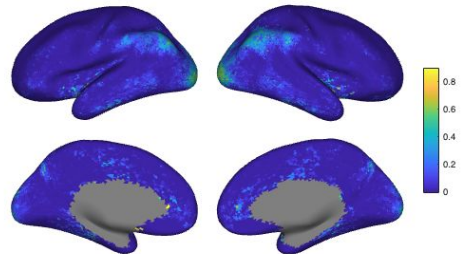
Points in space that exceed self-similarity threshold

What matrix to reconstruct ?

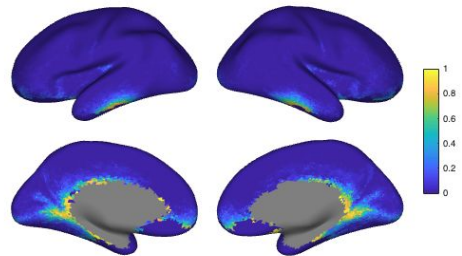
funcsum

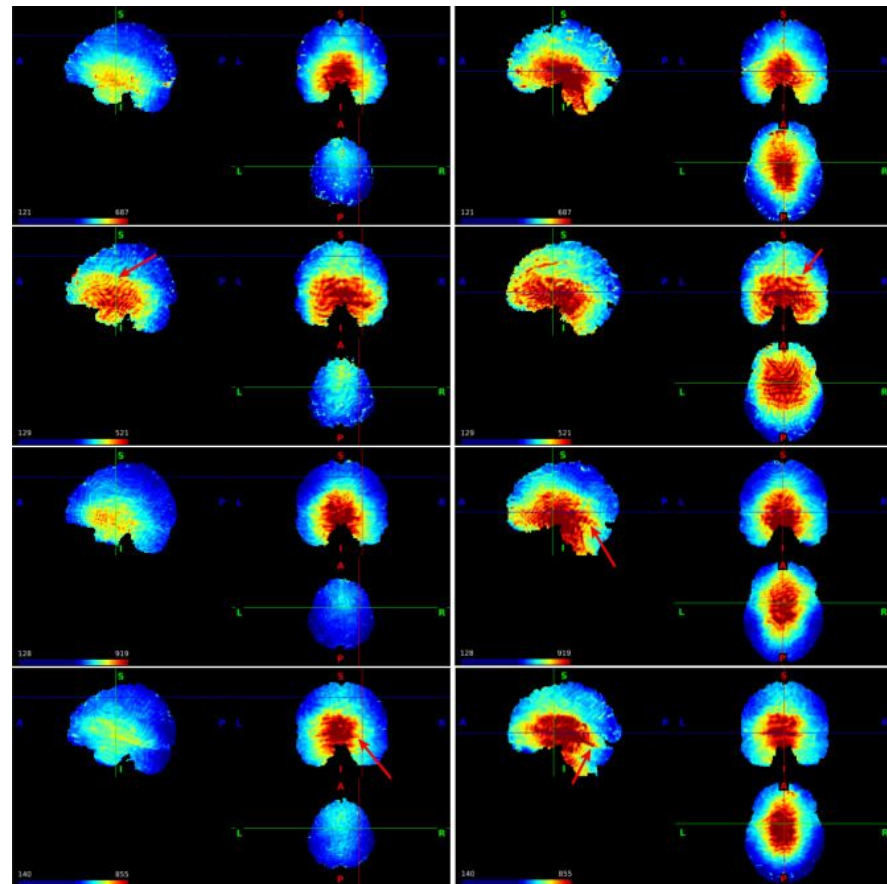
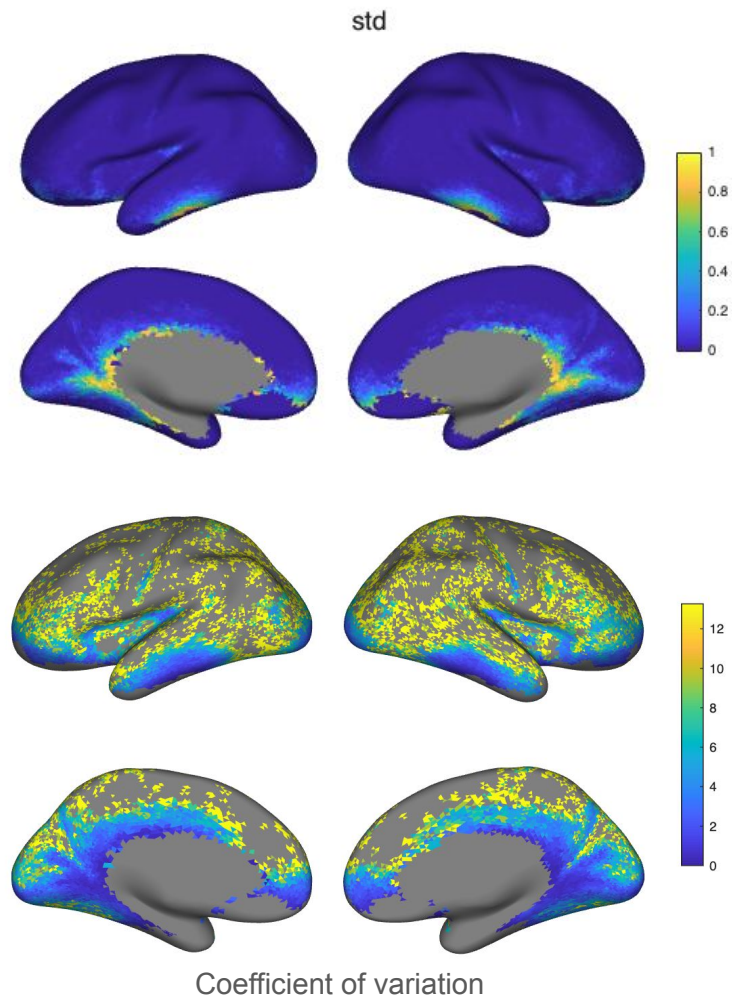


reho

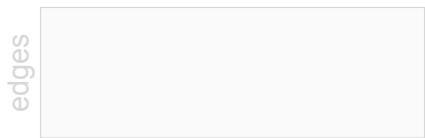


std

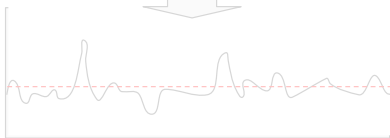




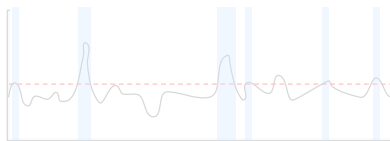
Risk et al. (2018). *NeuroImage*



time



time



time

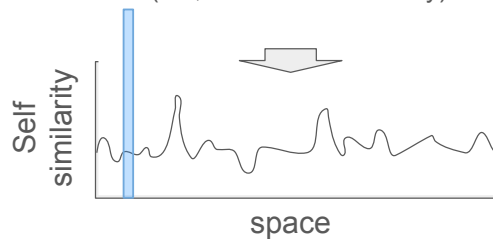


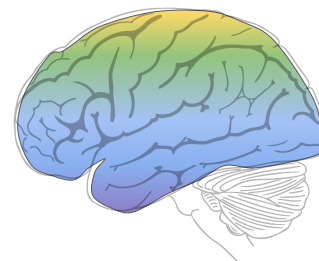
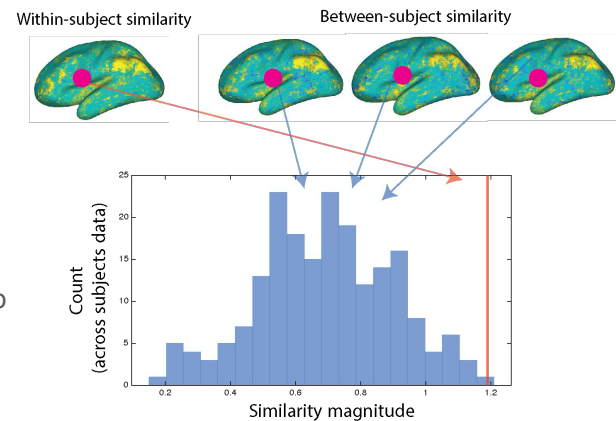
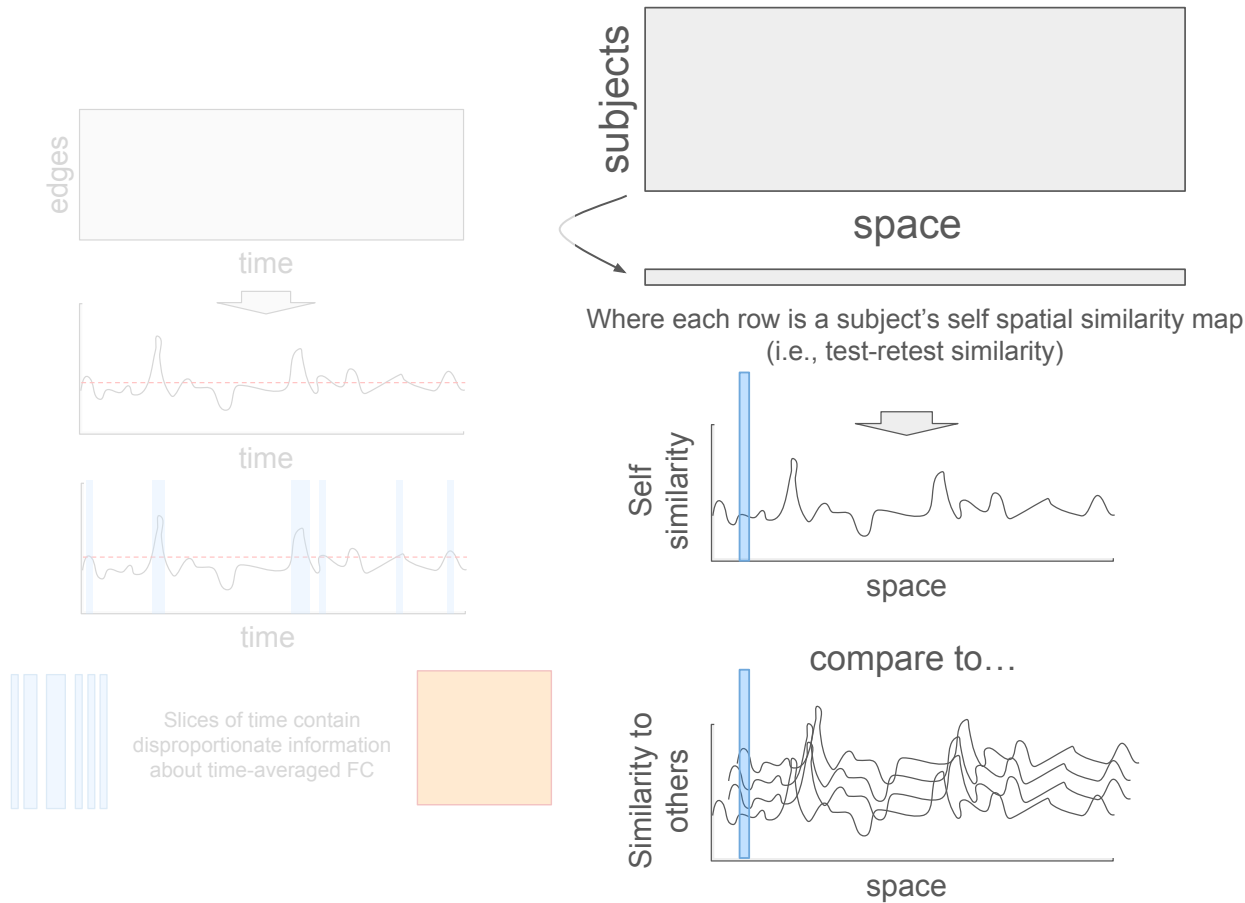
Slices of time contain
disproportionate information
about time-averaged FC



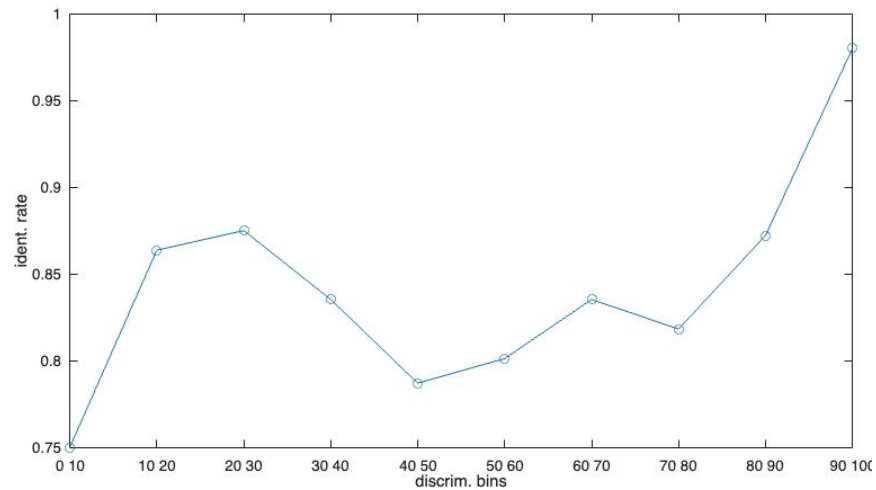
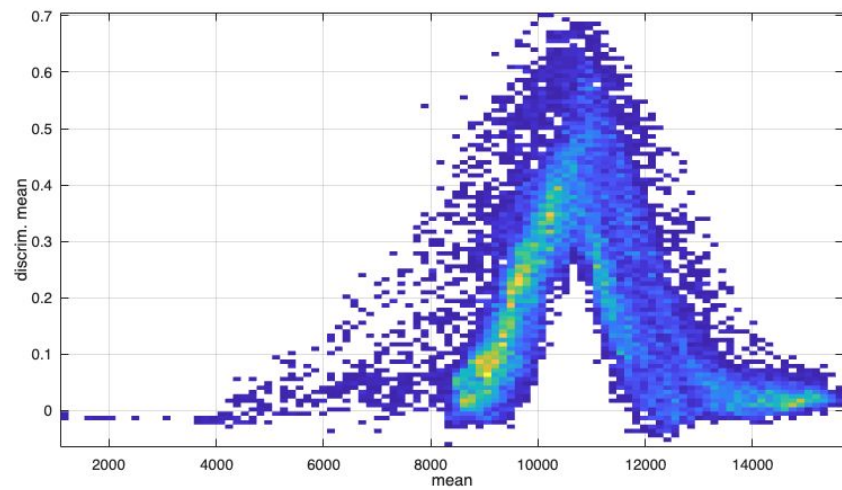
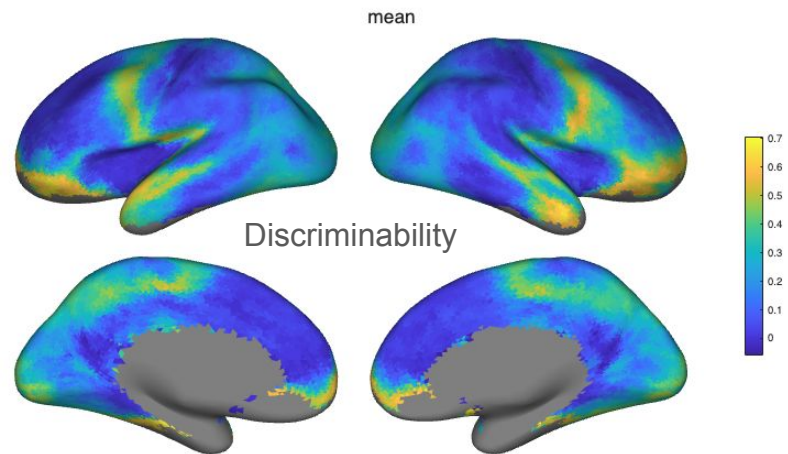
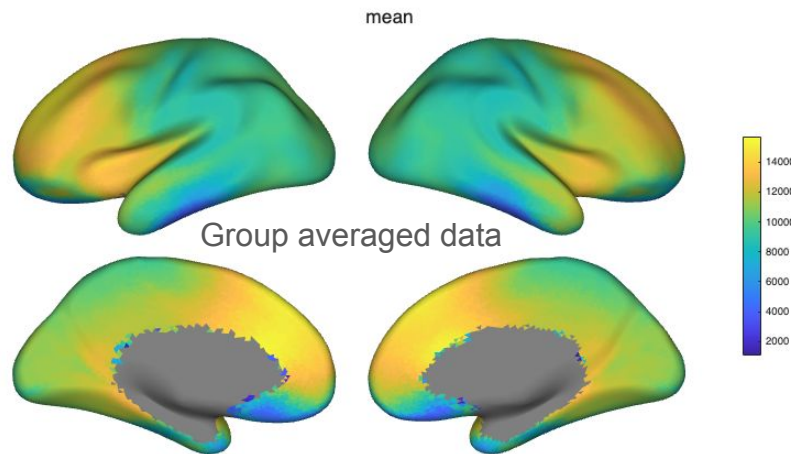
space

Where each row is a subject's self spatial similarity map
(i.e., test-retest similarity)

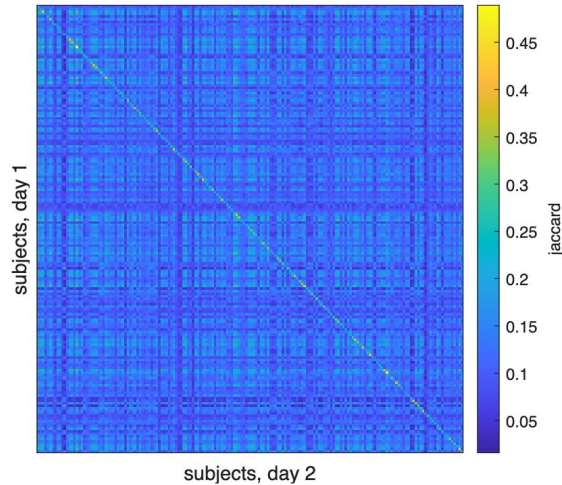




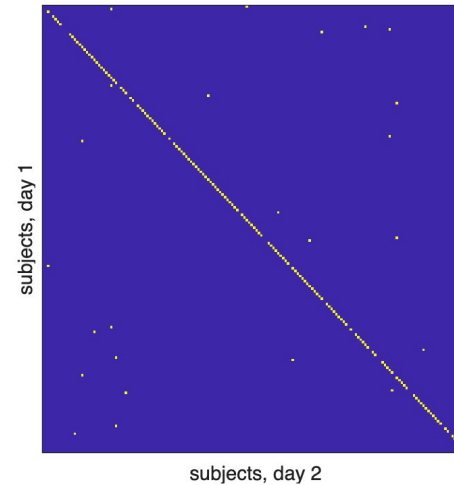
Discriminability map, where each value is the z-score of the self-similarity, relative to the distribution of inter-similarities



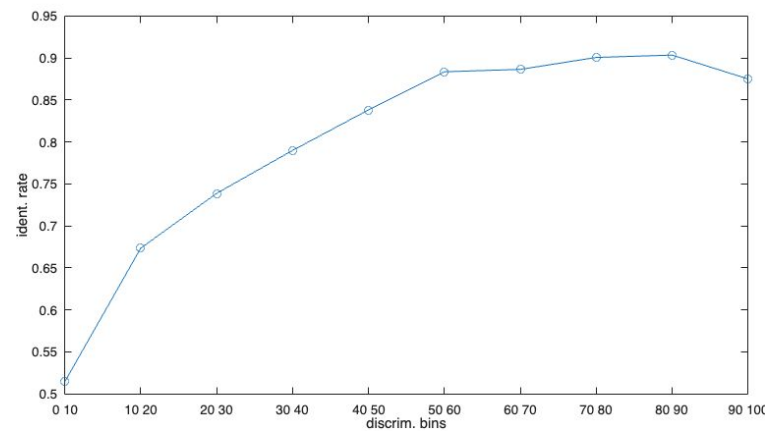
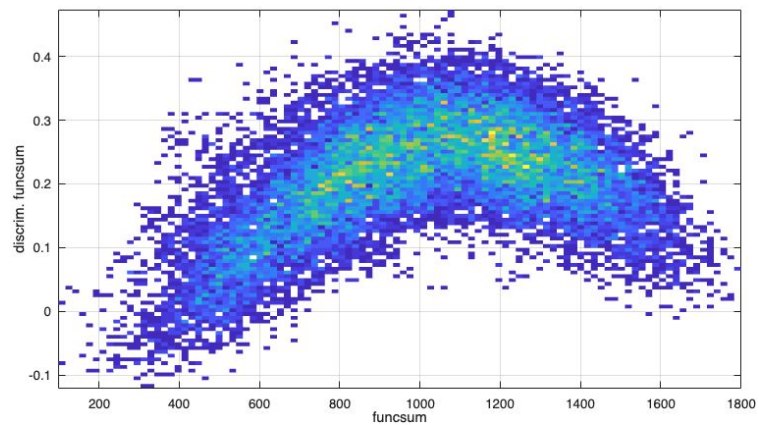
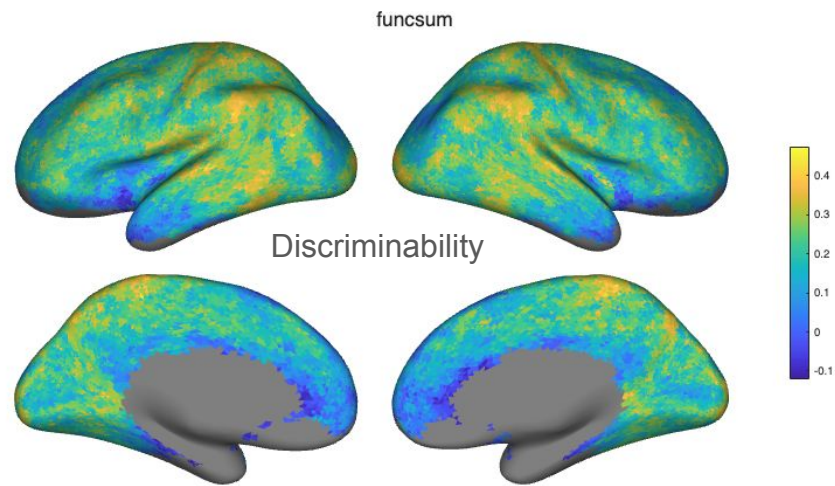
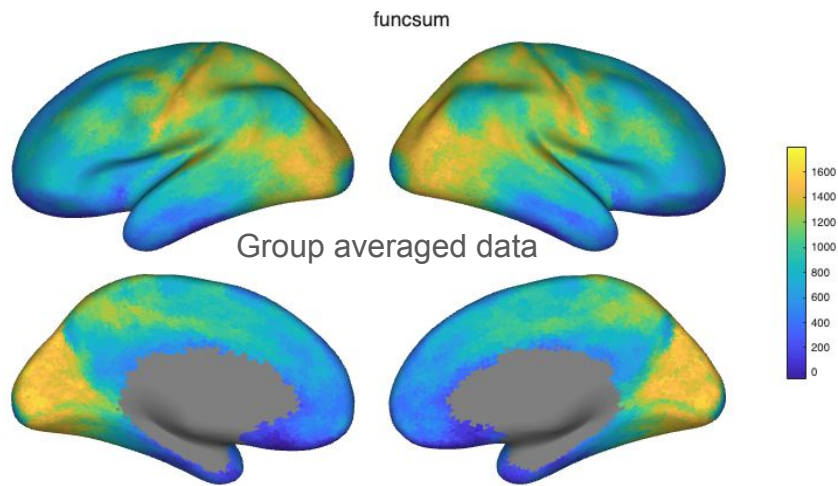
The identifiability metric

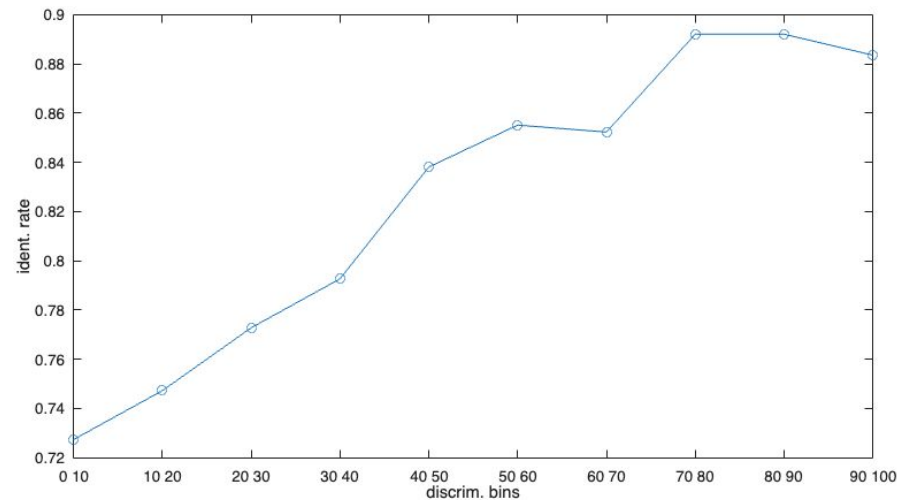
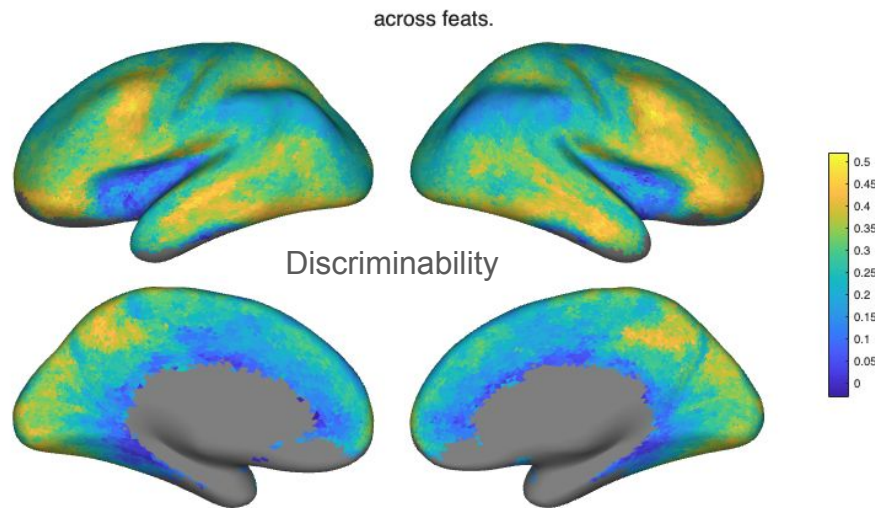


Subject comparison matrix, where each row is day 1 to day 2 similarity

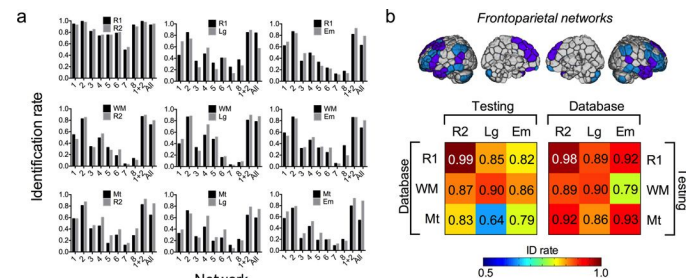


The maximum value for each row; perfect data will have pure on-diagonal pattern

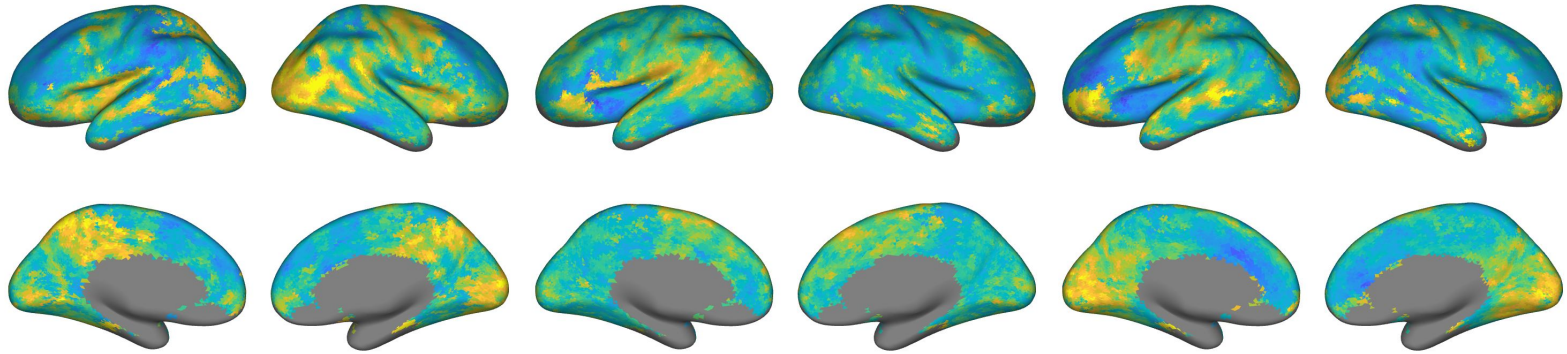




- The ranking of the spatial similarity can outline areas of the cortex that contain ‘more identifiable’ information
- These percentile areas contain way ~1700 vertices



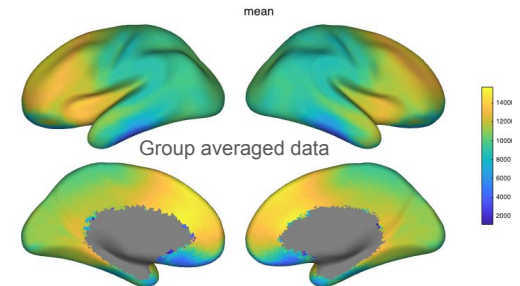
Group averaged discriminability is not the whole story



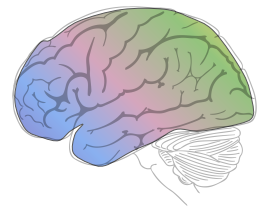
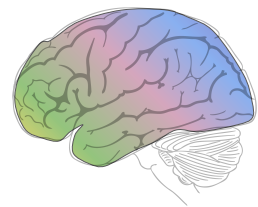
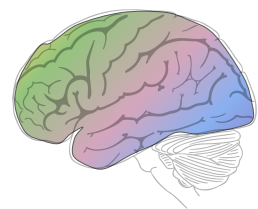
Subject 42

Subject 43

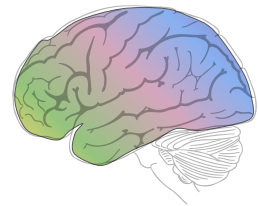
Subject 44



Comparing subject maps to canonical templates



...



Spatially
correlate!

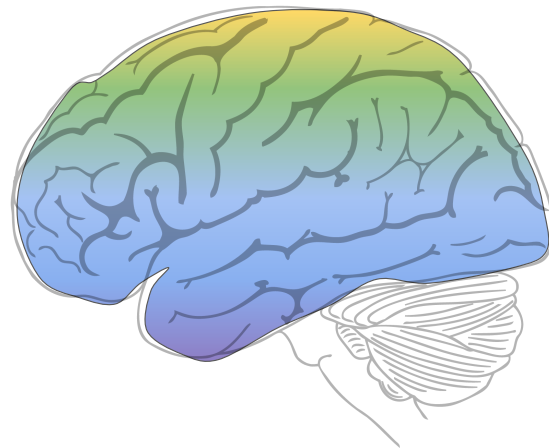
0.5

0.45

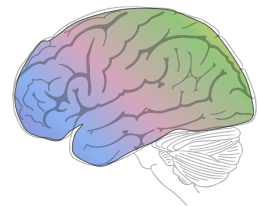
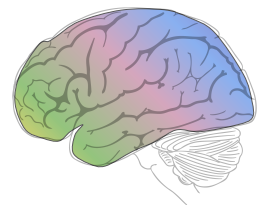
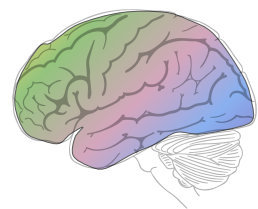
-0.2

0.48

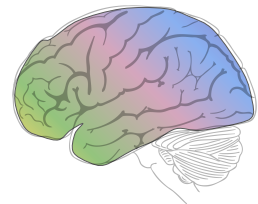
Reference information that
validates a theory or makes a
story from your data



Margulies et al. 2016. *PNAS*



...



Spatially
correlate!

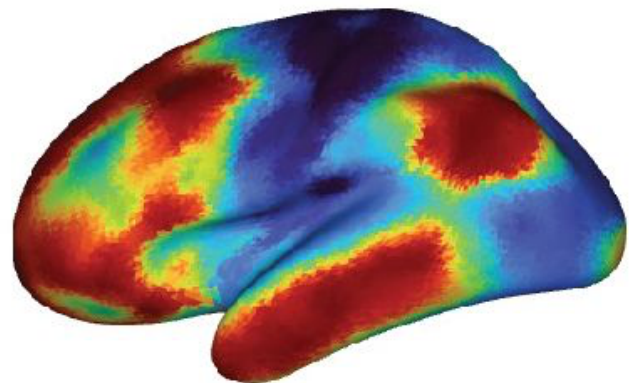
0.5

0.45

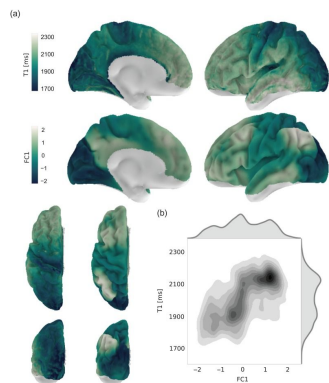
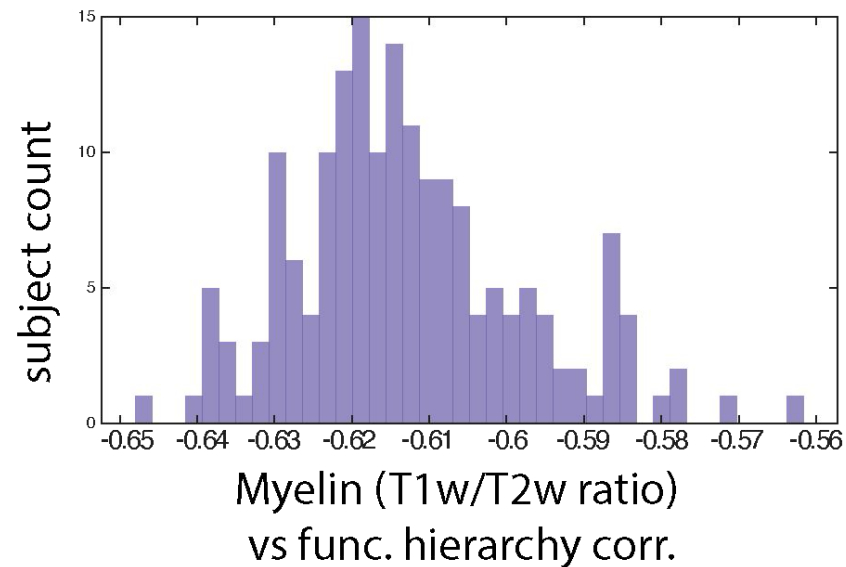
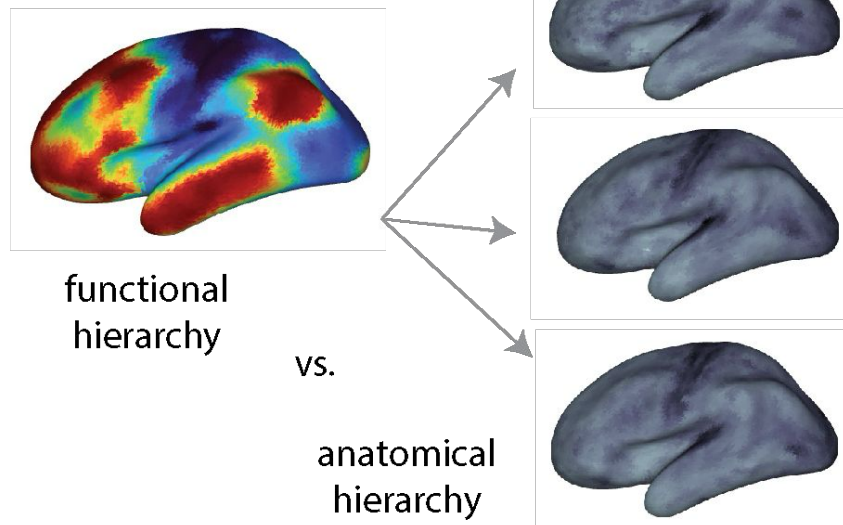
-0.2

0.48

Reference information that
validates a theory or makes a
story from your data

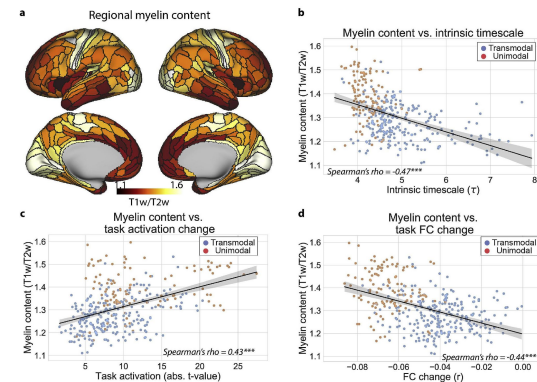


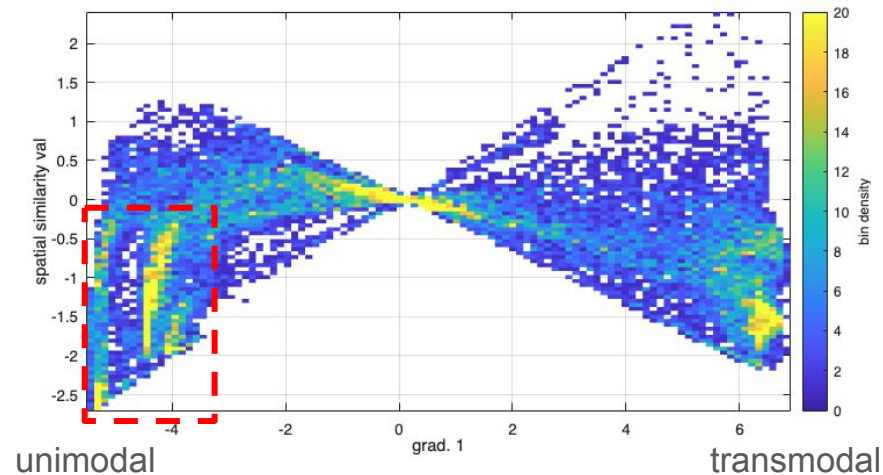
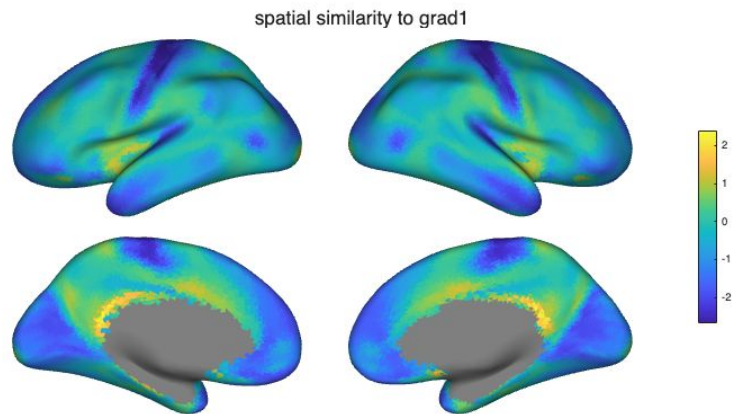
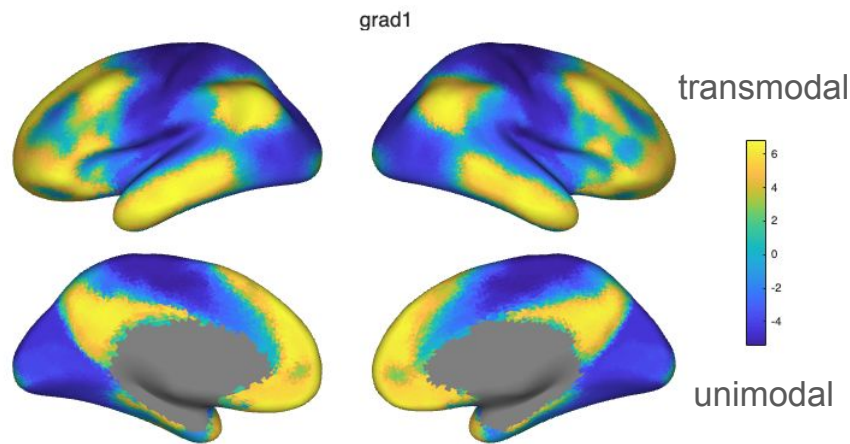
Margulies et al. 2016. *PNAS*



Ito et al. (2020).
NeuroImage

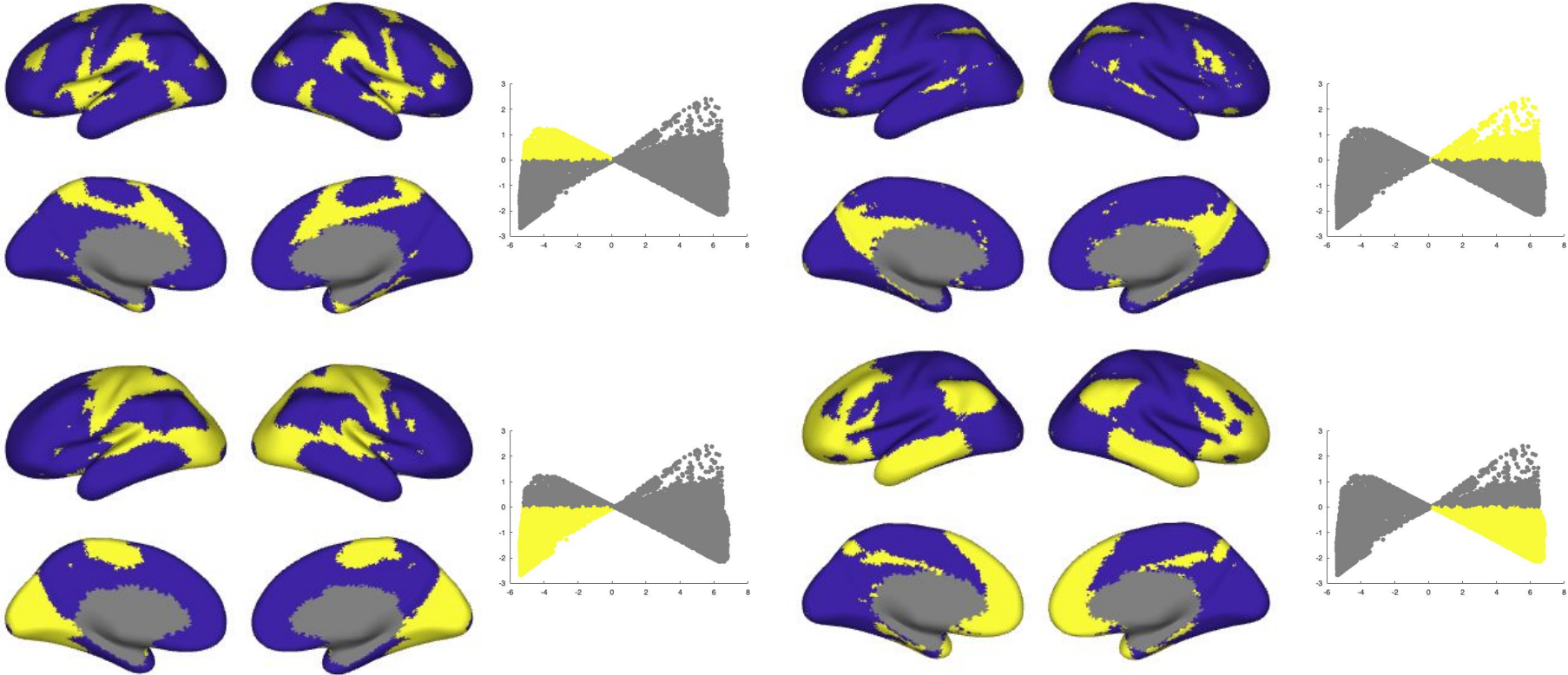
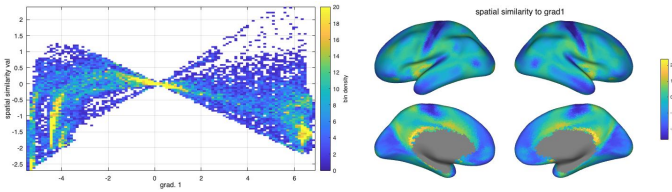
Huntenburg et al. (2017). *Cereb. Cortex*





The (negative) relationship of myelin to the principle Margulies gradient is driven by unimodal areas

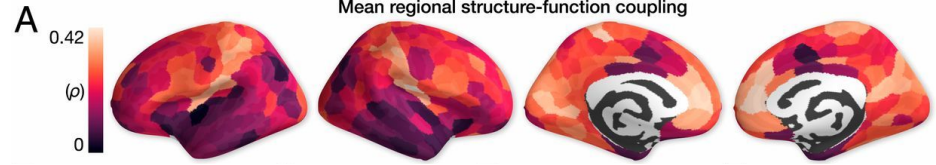
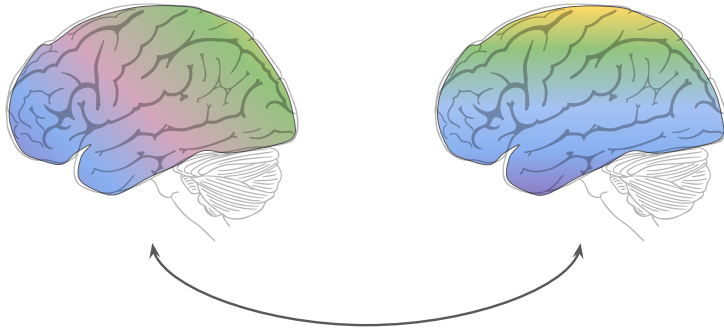
Can further parse the relationship and spatially map it to the cortex



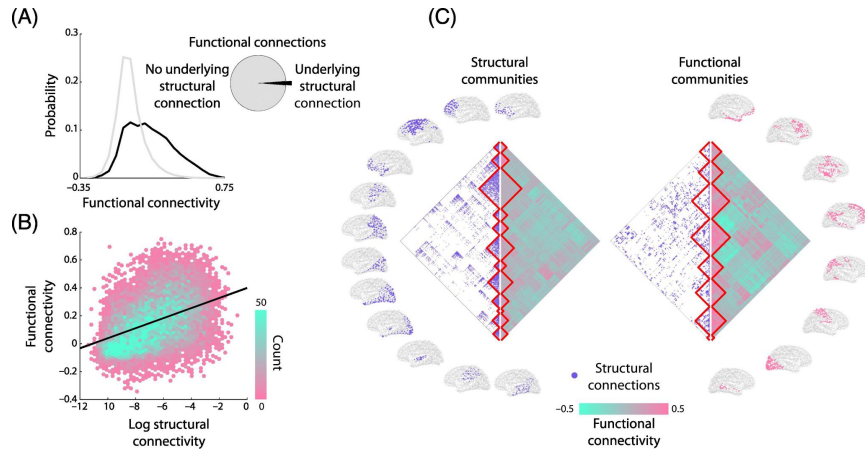
Structure function relationship

structure

function

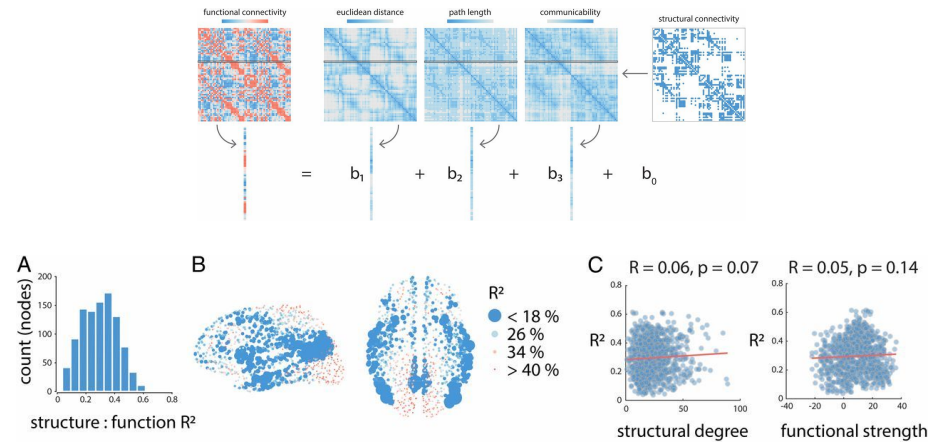


Baum et al. (2019). *PNAS*

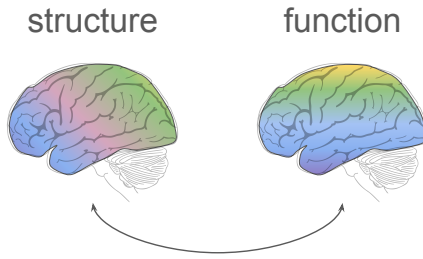


Trends In Cognitive Sciences

Suárez et al (2020). *TICS*

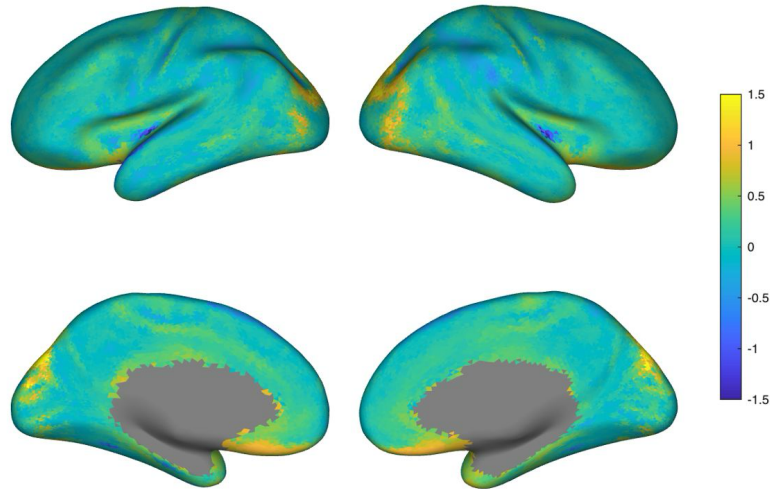


Vázquez-Rodríguez et al. (2019). *PNAS*

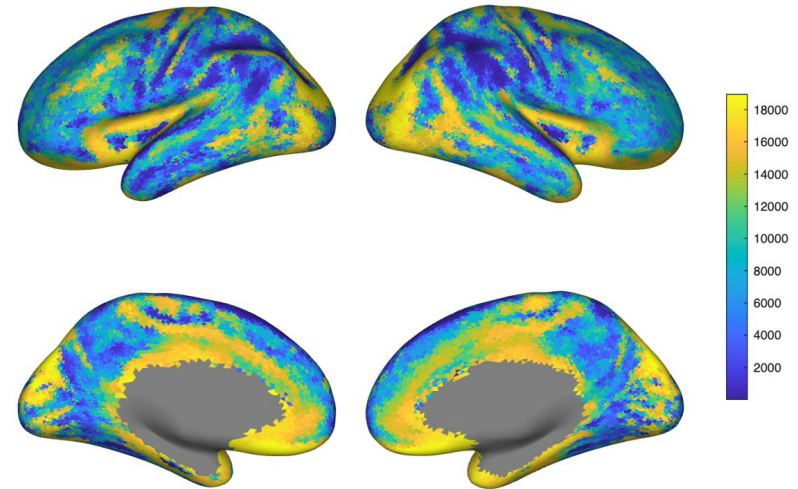


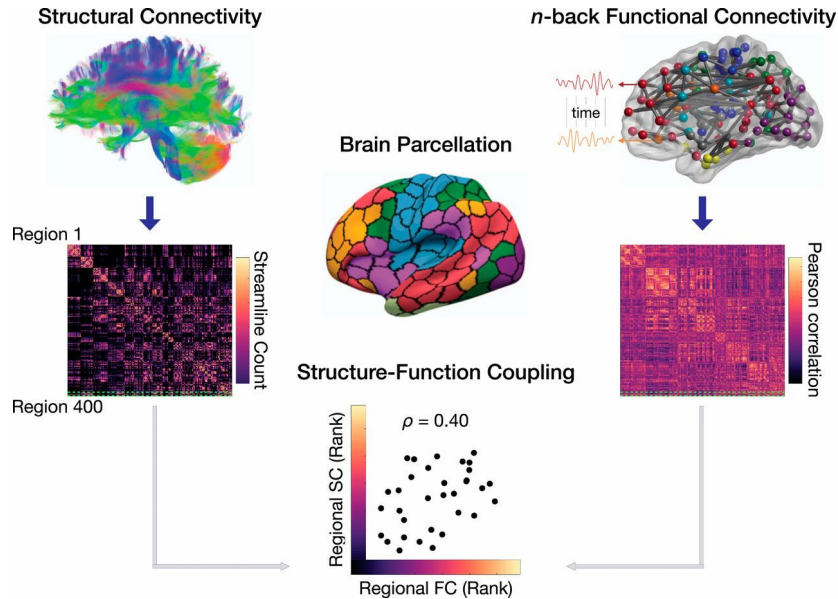
- Compare the vertex-wise functional and structural degree maps within subjects, to obtain a spatial similarity map per subject (then average)

struct-func coupling

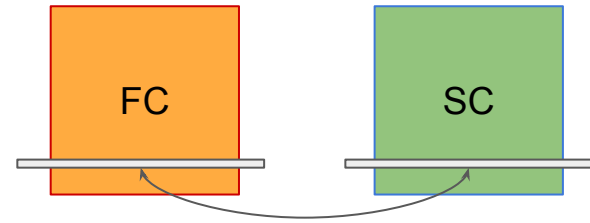
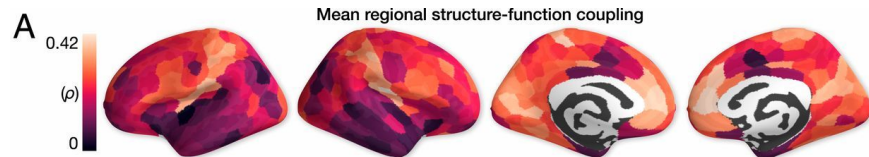


struct-func coupling rank



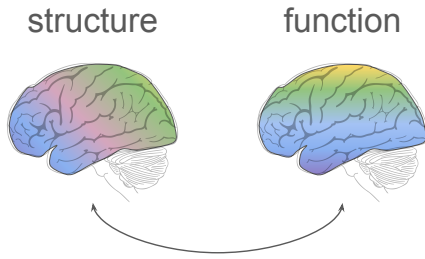


Baum et al. (2019). *PNAS*



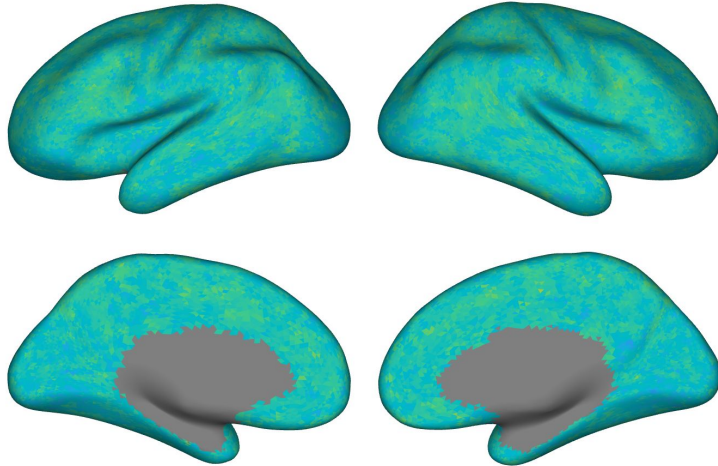
FC-SC correlation
for each row yields a
single coupling map
for your dataset



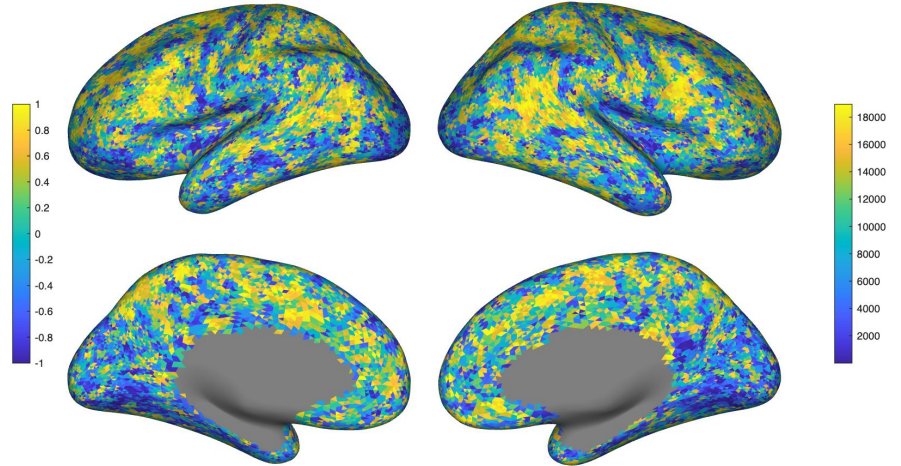


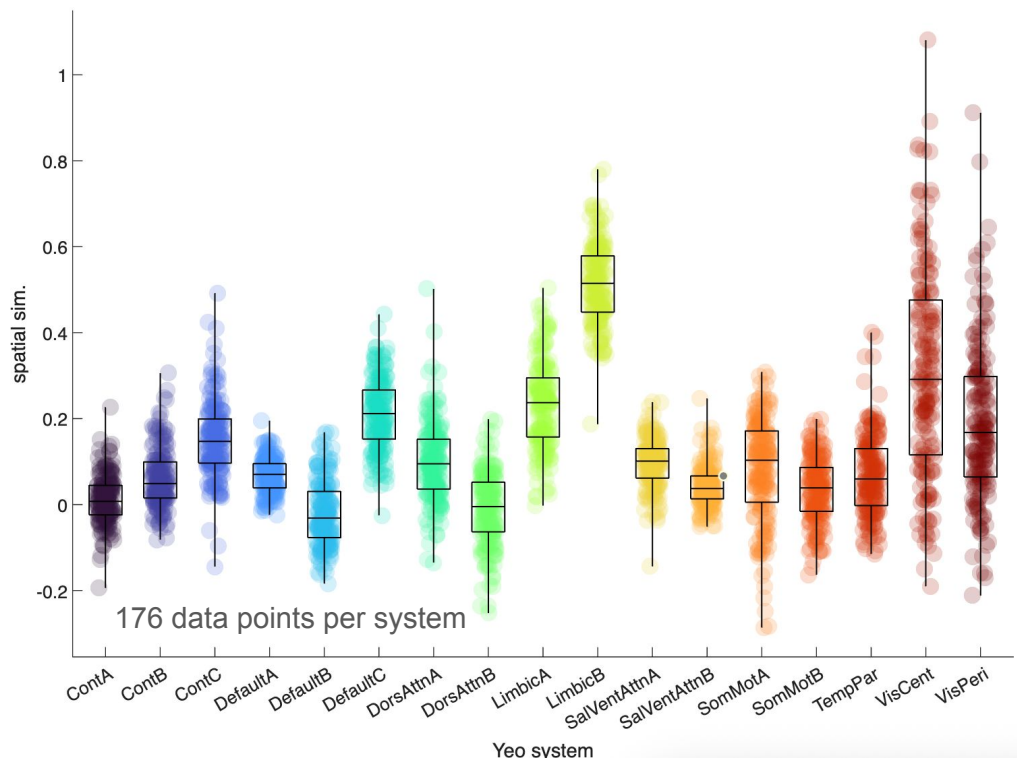
- Compare the vertex-wise functional and structural degree maps across subjects, like people have done before

struct-func coupling across subj.

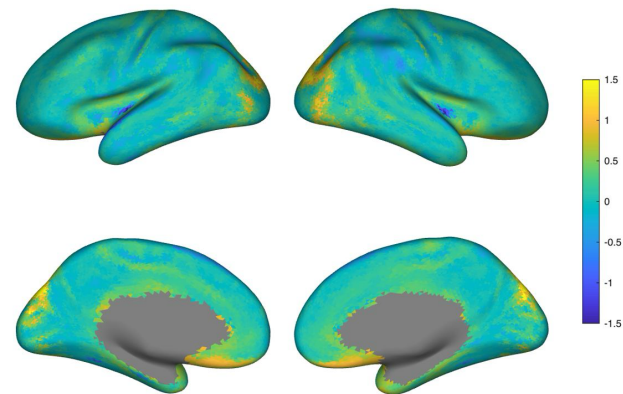


struct-func coupling across subj. rank



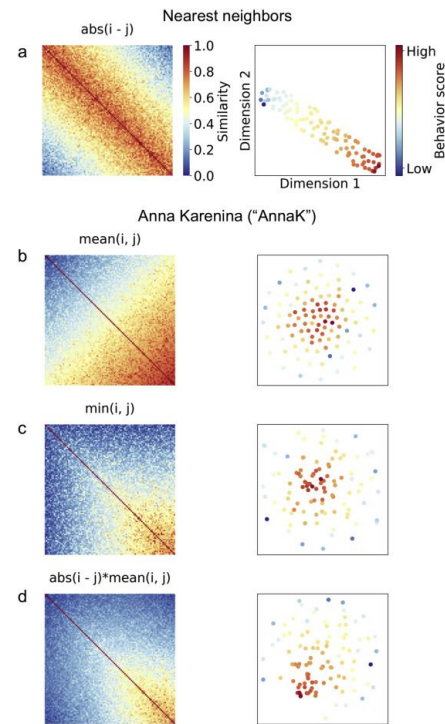
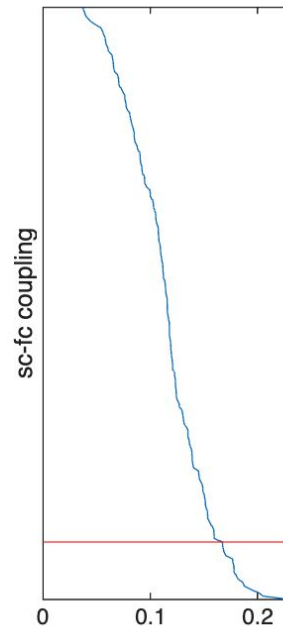
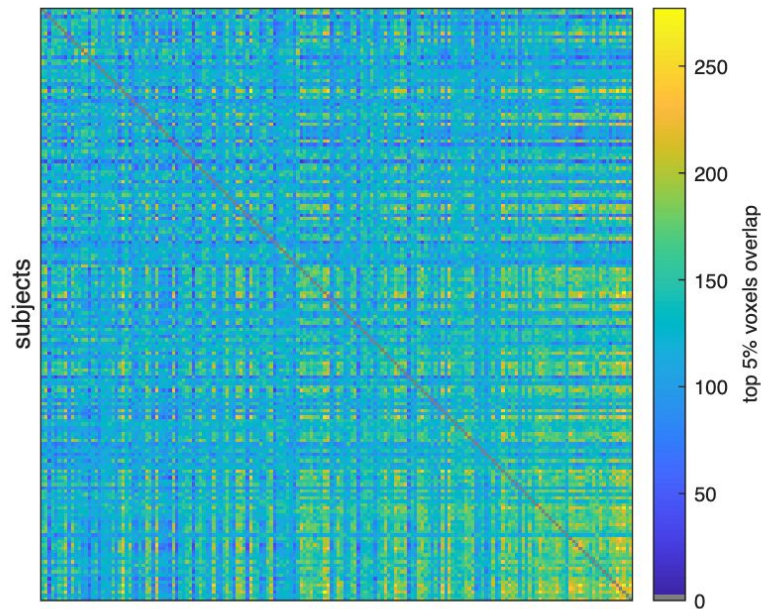


struct-func coupling



Where does the similarly commonly aggregate across subjects?

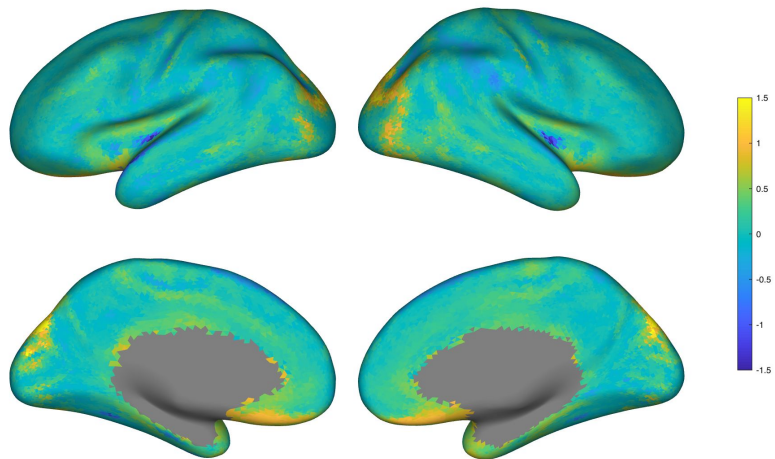
Matrix showing the similarity of each subjects sc-fc similarity map, via the # of top voxels overlapping



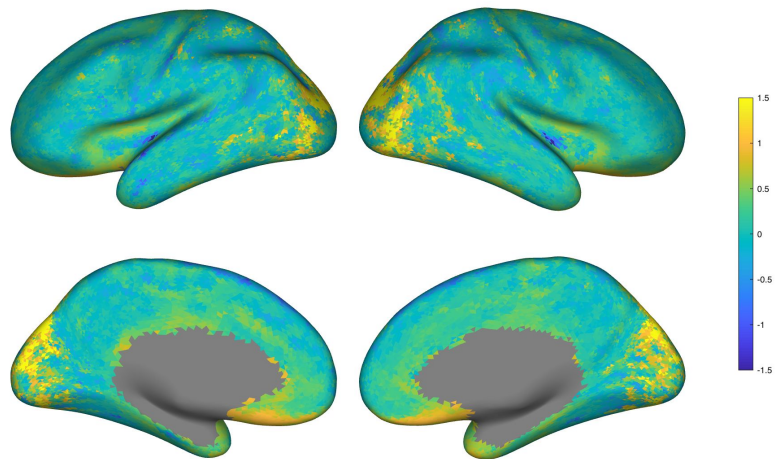
Finn et al. (2019). *NeuroImage*

Sort subjects X subjects matrix by overall sc-fc coupling value to a view of between subject similarity

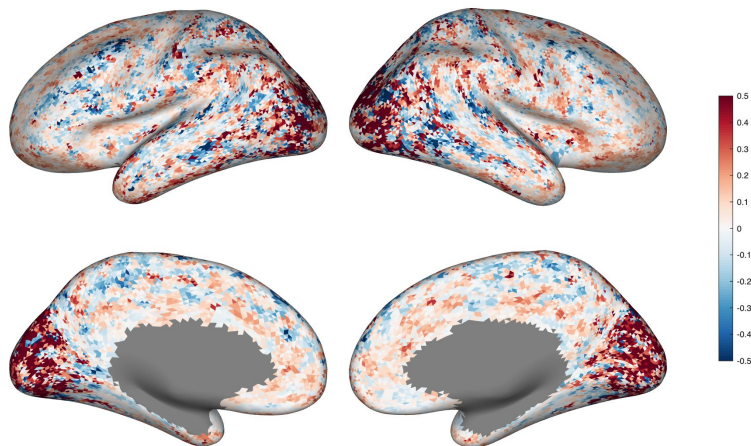
bottom 90% sc-fc subjects



top 10% sc-fc subjects



diff



Spatial similarity map, which tells you which regions disproportionately influence similarity

Pinpoint areas of the brain that are more similar within-subj. rather than between-subj.

Anscombe's quartet for neuroimaging

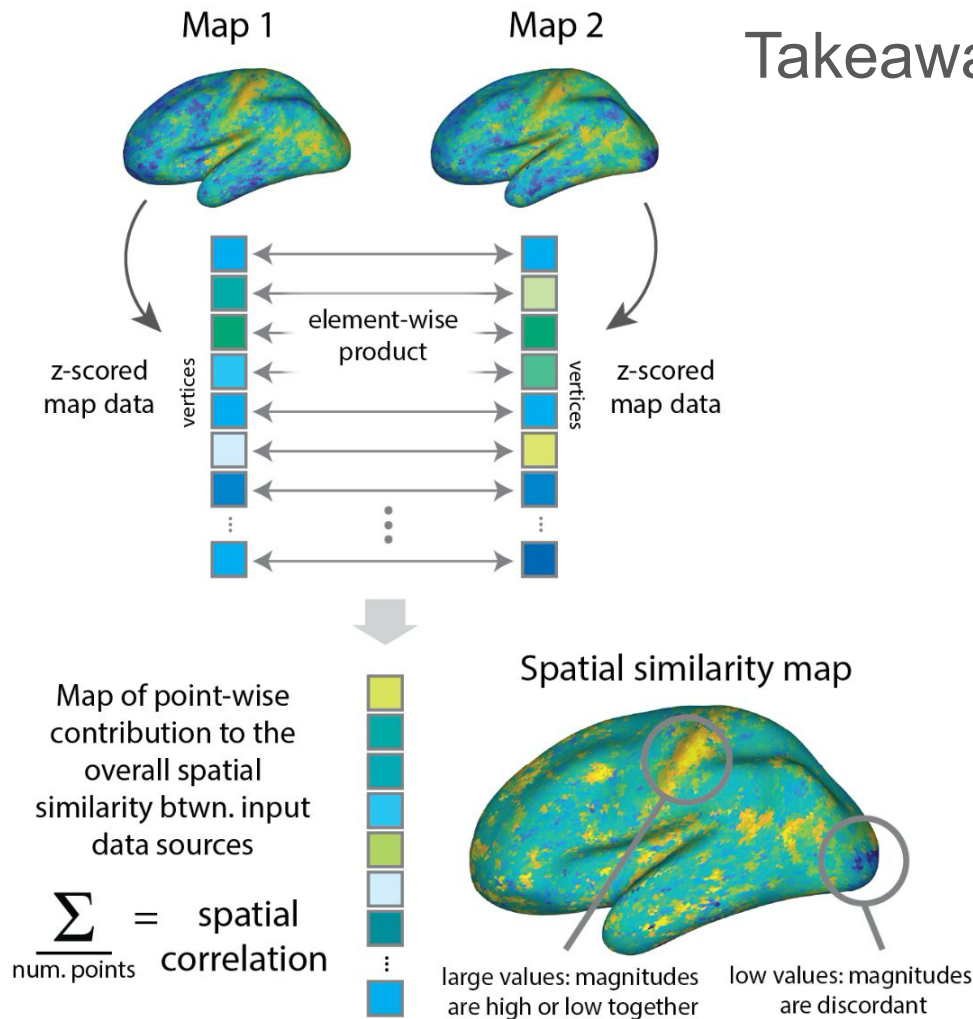
Intercompare neuro-maps templates

Compare relationship of subject (meylin) maps to canonical template map

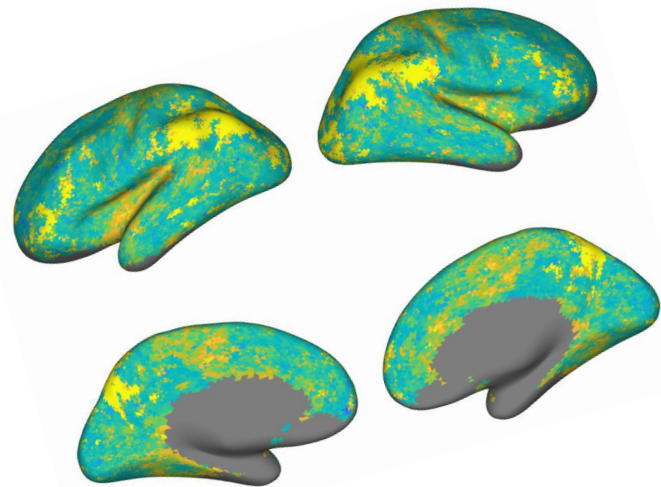
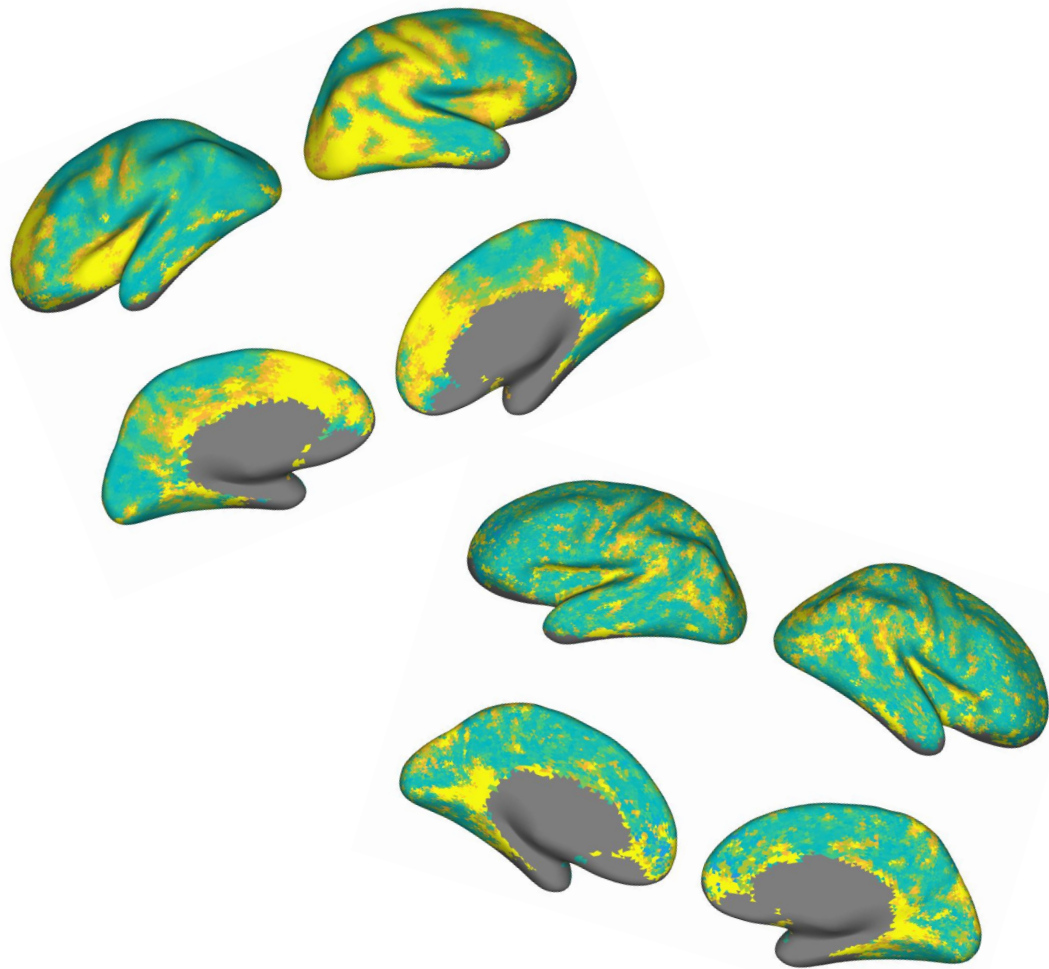
Evaluate the structure function relationship across the brain?

When have you correlated spatially mapped data, and could you benefit from looking at how that relationship plays out across space?

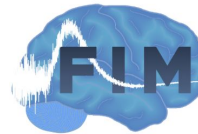
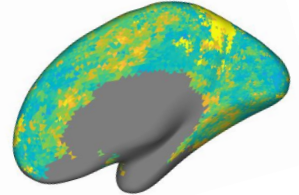
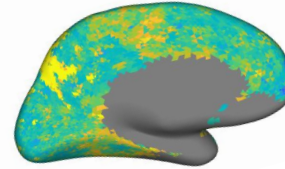
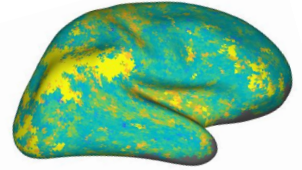
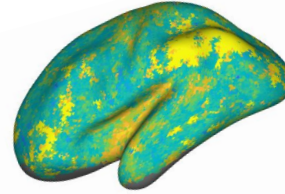
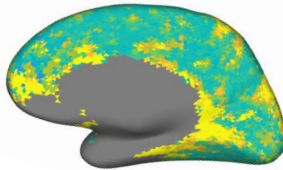
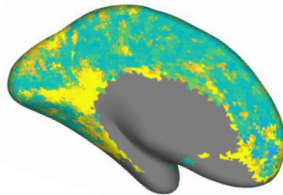
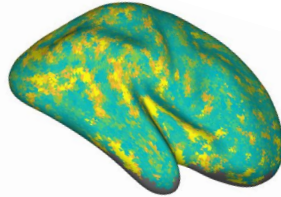
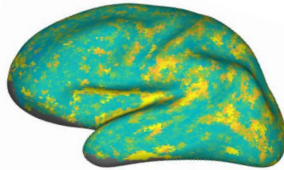
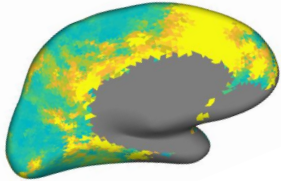
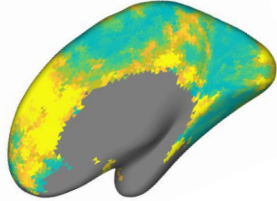
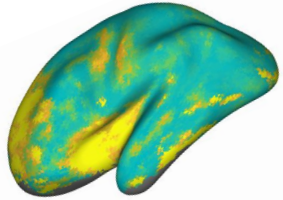
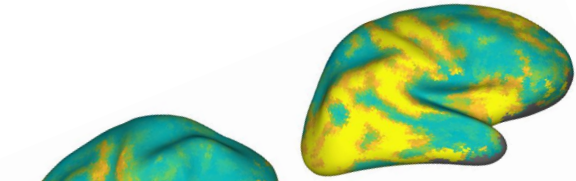
Takeaways



- Spatially-resolved similarity
 - Think analogously to time-varying correlation
 - Or think about a searchlight with a window of 1
- Is this a thing already?
 - Well kind of... in the image registration world they employ point-wise similarity
- Future directions
 - Behavioral relationship
 - Statistical map comparisons
 - Permutation statistical validations



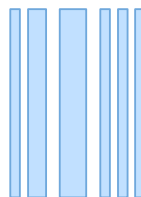
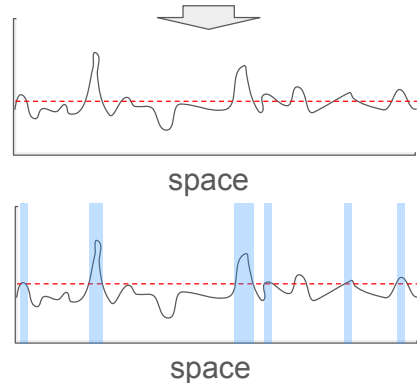
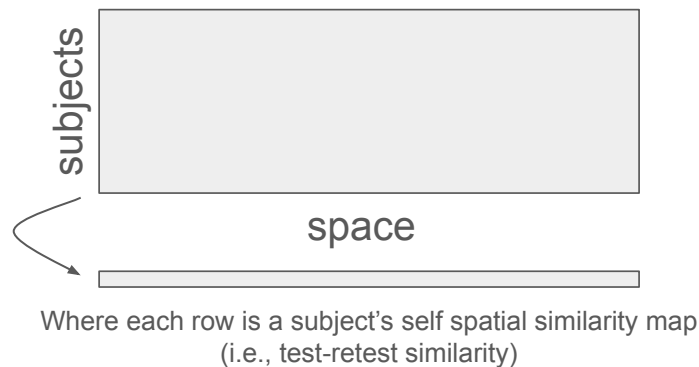
Thanks to SFIM for support!
And thanks for your attention



Section on Functional Imaging Methods

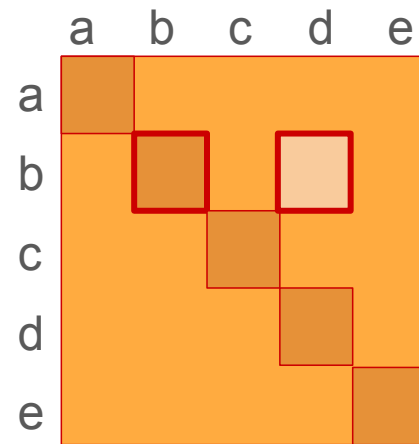


Slices of time contain disproportionate information about time-averaged FC



Points in space that exceed self-similarity threshold

What matrix to reconstruct ?

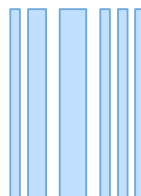
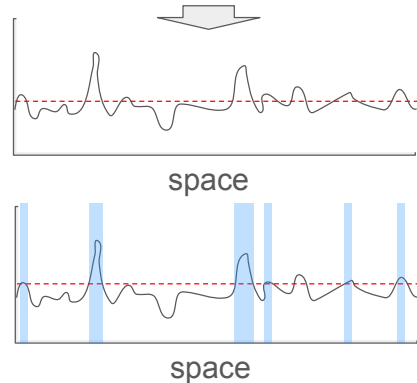
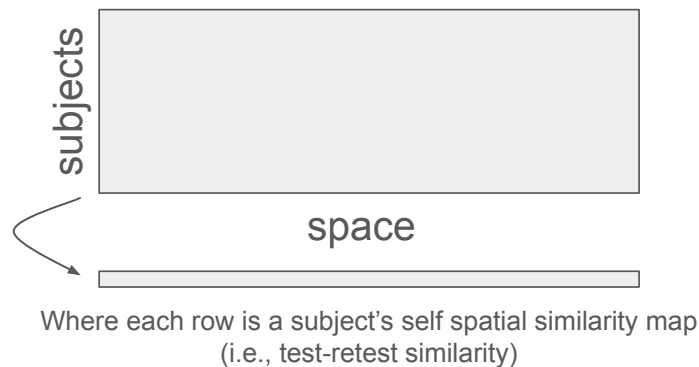


Subject-subject comparison (overlap) matrix

Which similarity thresholds in space lead to better self- than between similarity. Can be measured with "identifiability" or "discriminability"

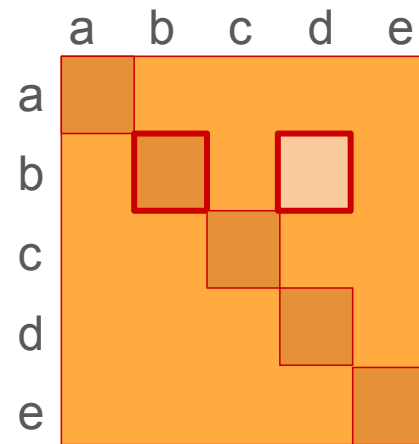


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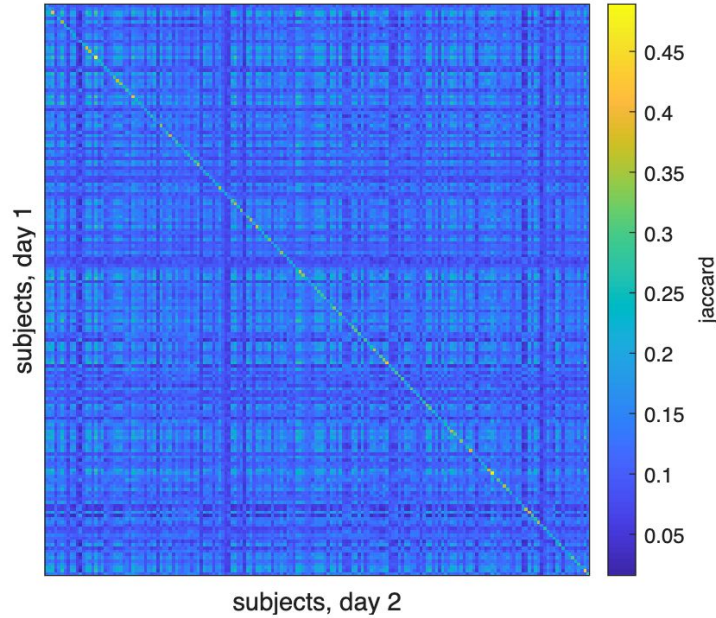
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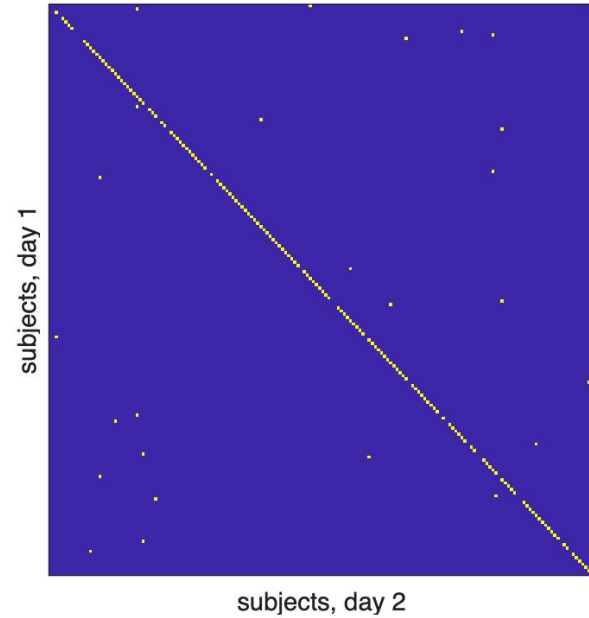


Subject-subject comparison (overlap) matrix

Which similarity thresholds in space lead to better self- than between similarity. Can be measured with "identifiability" or "discriminability"



Subject comparison matrix, where each row is day 1 to day 2 jaccard for a measure



The maximum value for each row; perfect data will have pure on-diagonal pattern

