

Connectome Coding

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Please interrupt and ask questions!

- what is connectome coding
- applications

what is connectome coding?

Neural coding: characterizing the relationship between the **ongoing environment** and **neuronal activity**

Connectome Coding: characterizing the relationship between the **past environment** and the **neural connectivity**

Neural Encoding: $P[r | s]$

Connectome Encoding: $P[g | s]$

Neural Decoding: $P[s | r]$

Connectome Decoding: $P[s | g]$

Neural Code: $P[s,r]$

Connectome Code: $P[s,g]$

We need the joint distribution of brain stuff & external stuff:

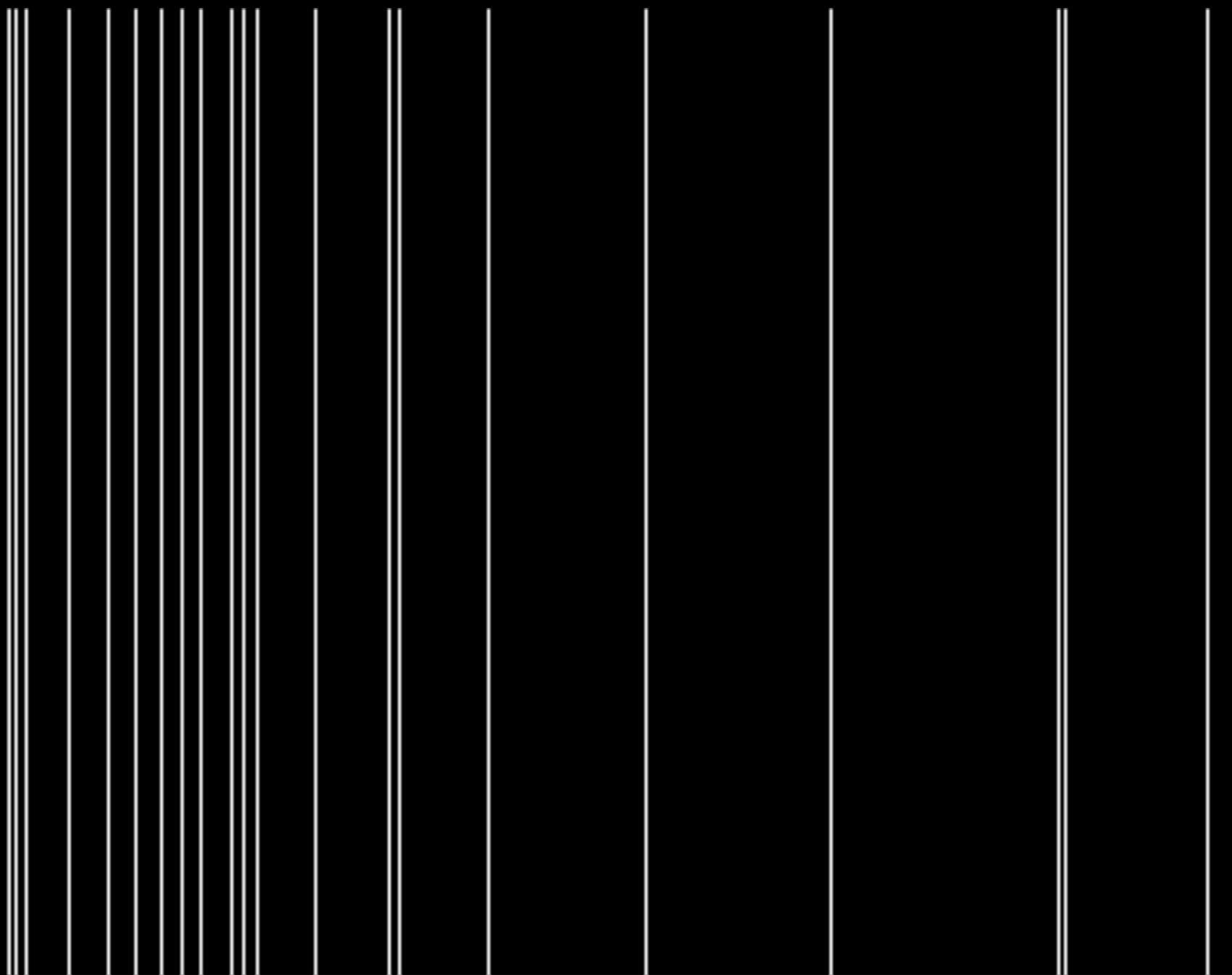
- Joint distribution: $P[s,r] = P[s | r] P[r]$
- Joint distribution: $P[s,r] = P[r | s] P[s]$
- So, we need $P[s|r]$, $P[r|s]$, $P[r]$, $P[s]$
- Let's start with $P[r]$

Principles of Data Science

- Look at it
- Keep it simple

Let's do it for the response, $P[r]$

Look at it



Keep it Simple

- Each spike is independent
- Probability of a spike at any time is λ
- $P[r] = \text{Poisson}(\lambda)$

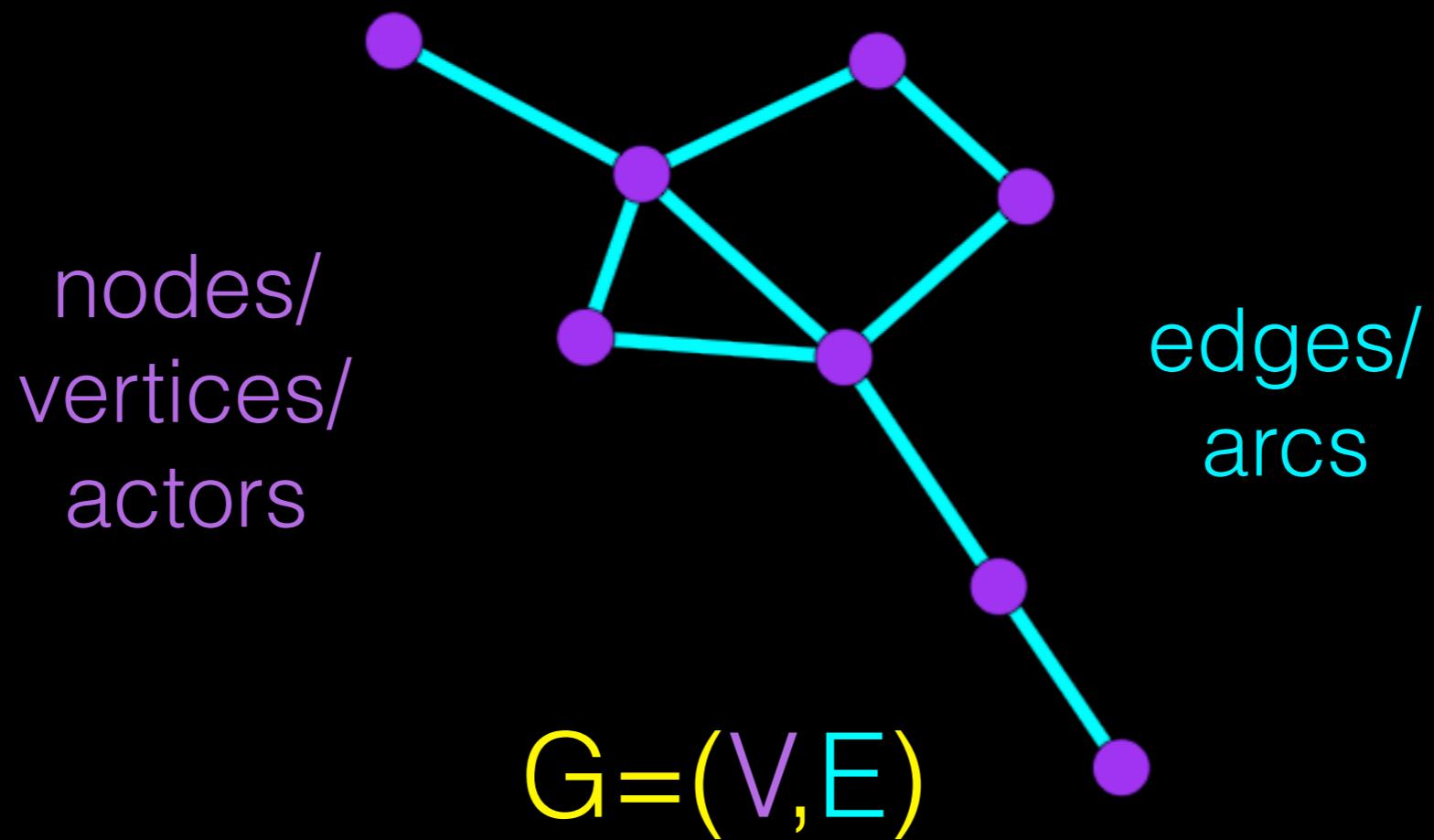
Principles of Data Science

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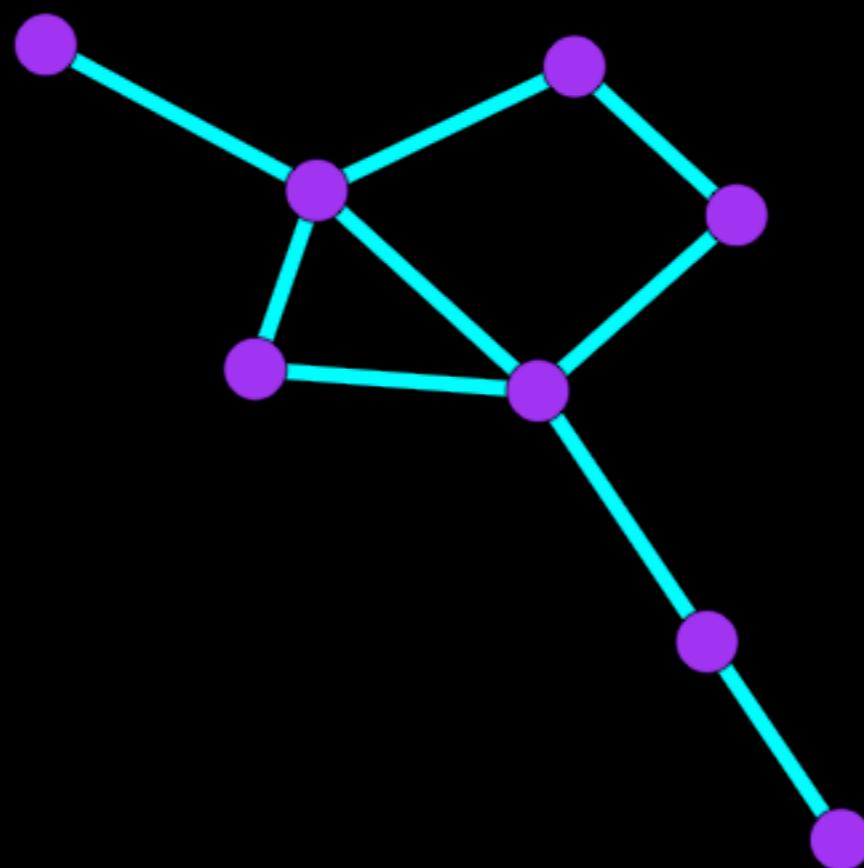
Let's do it for networks now, $P[g]$

Look at it

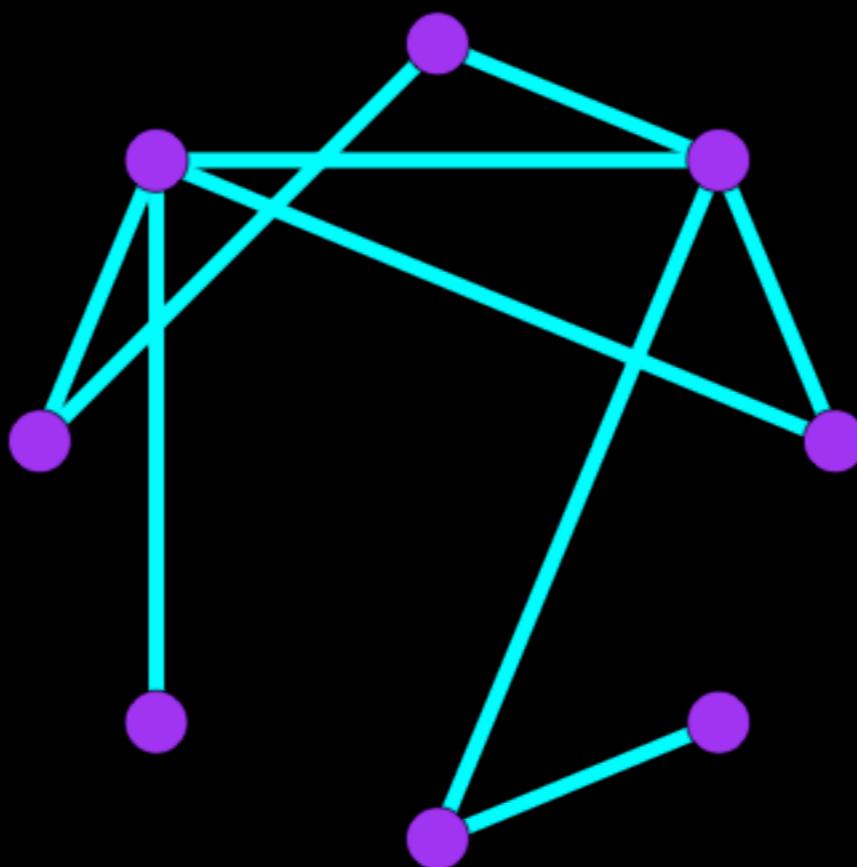
a simple graph



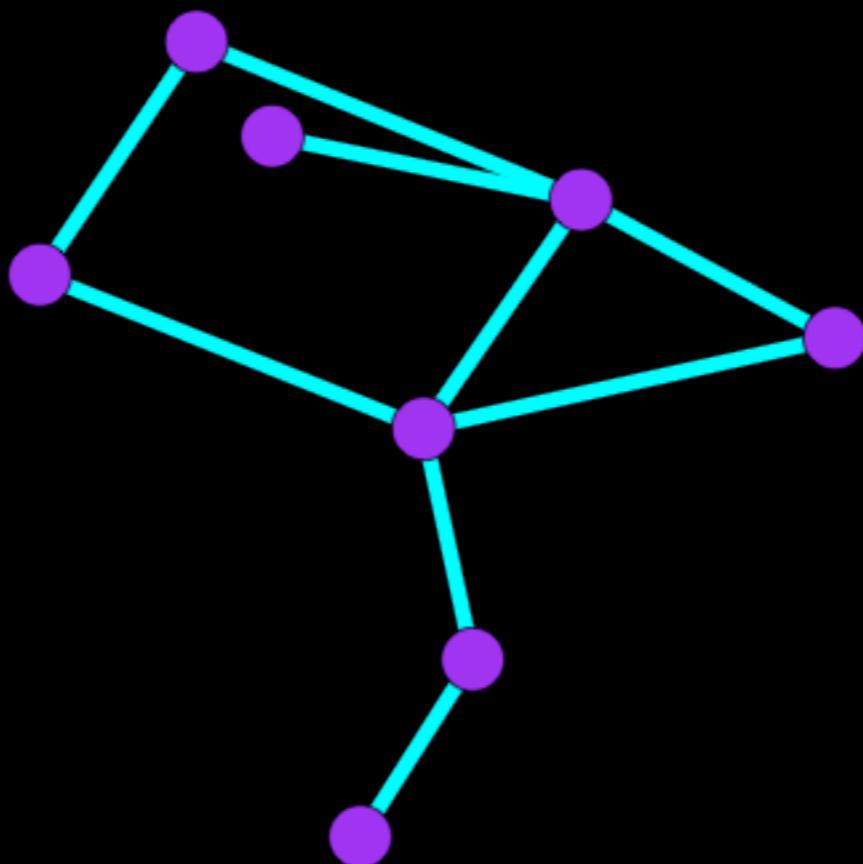
the same graph



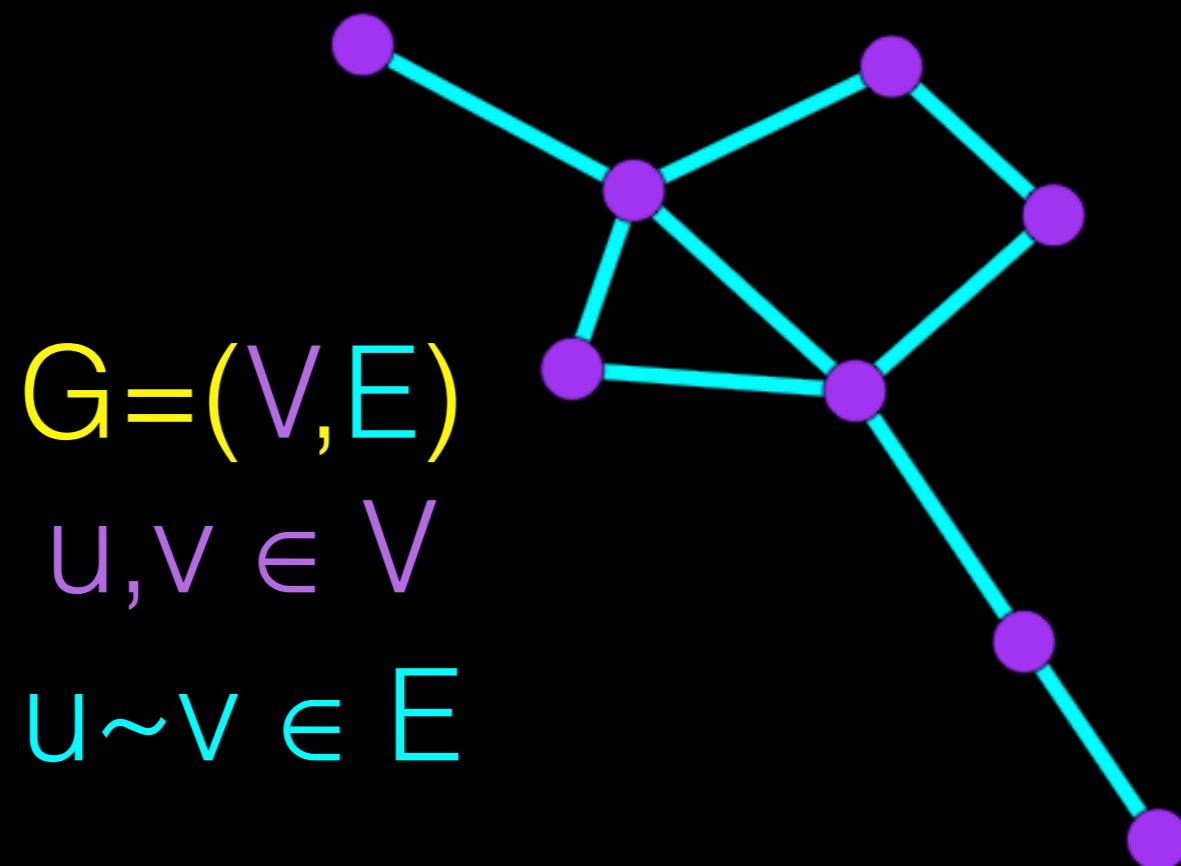
the same graph



the same graph

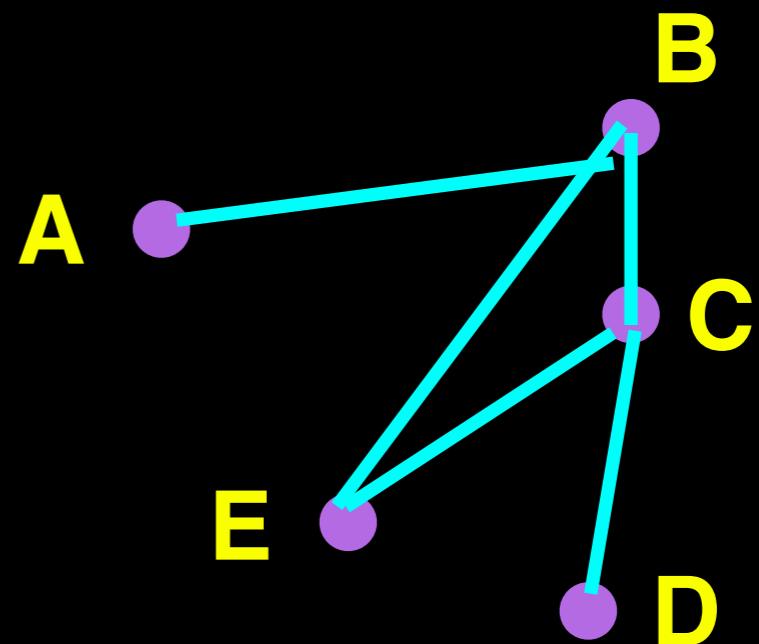


the same graph

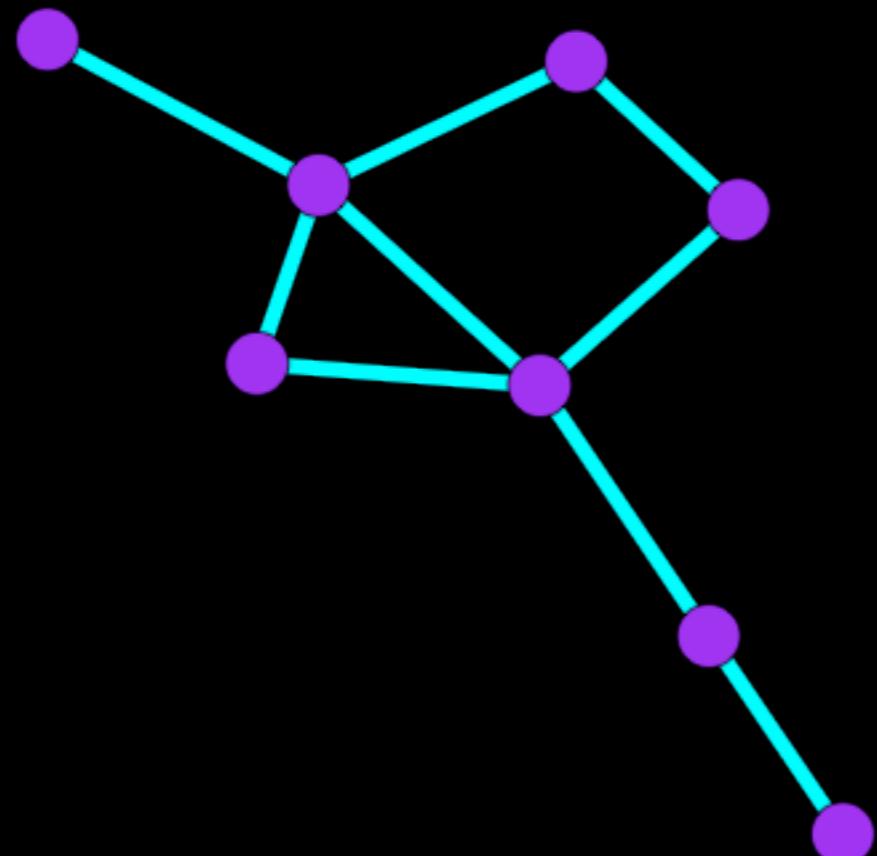


labeled graph

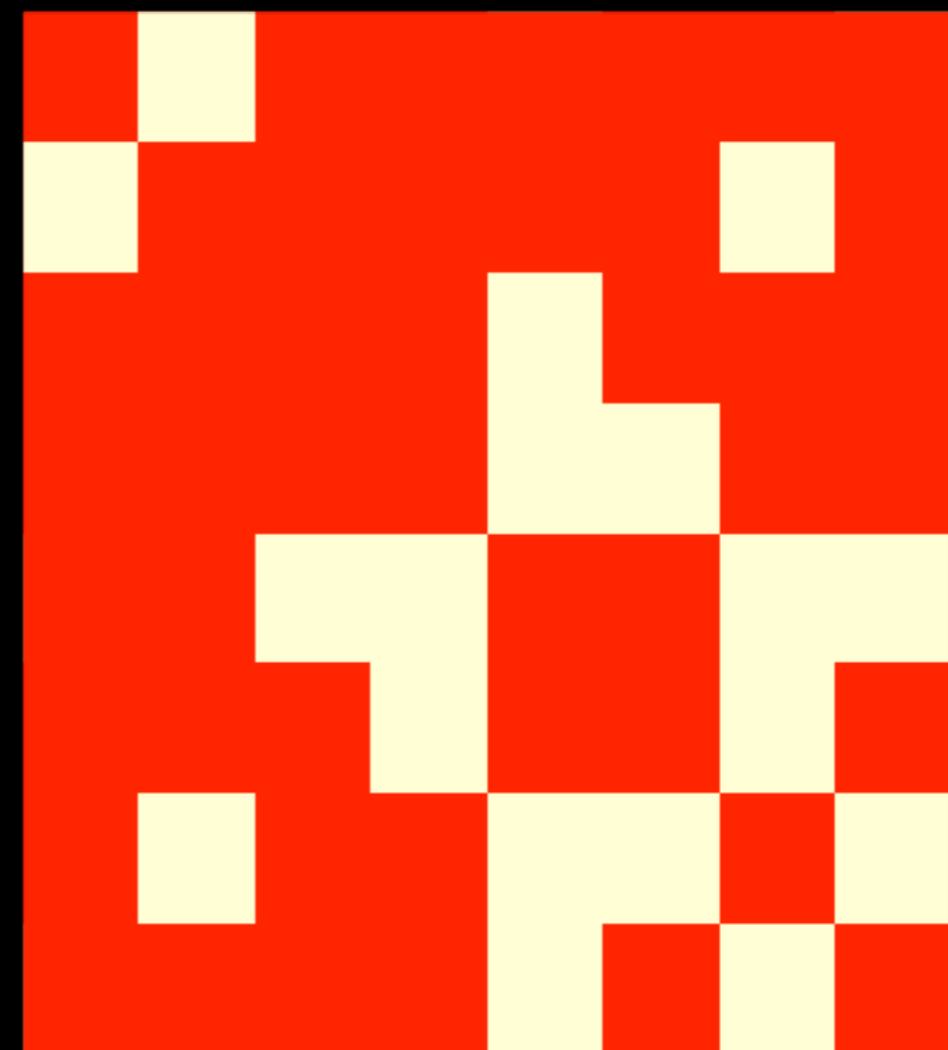
- uv means there is an edge between u & v
- e.g., in this graph AB , but not AE



same graph
(2D layout)

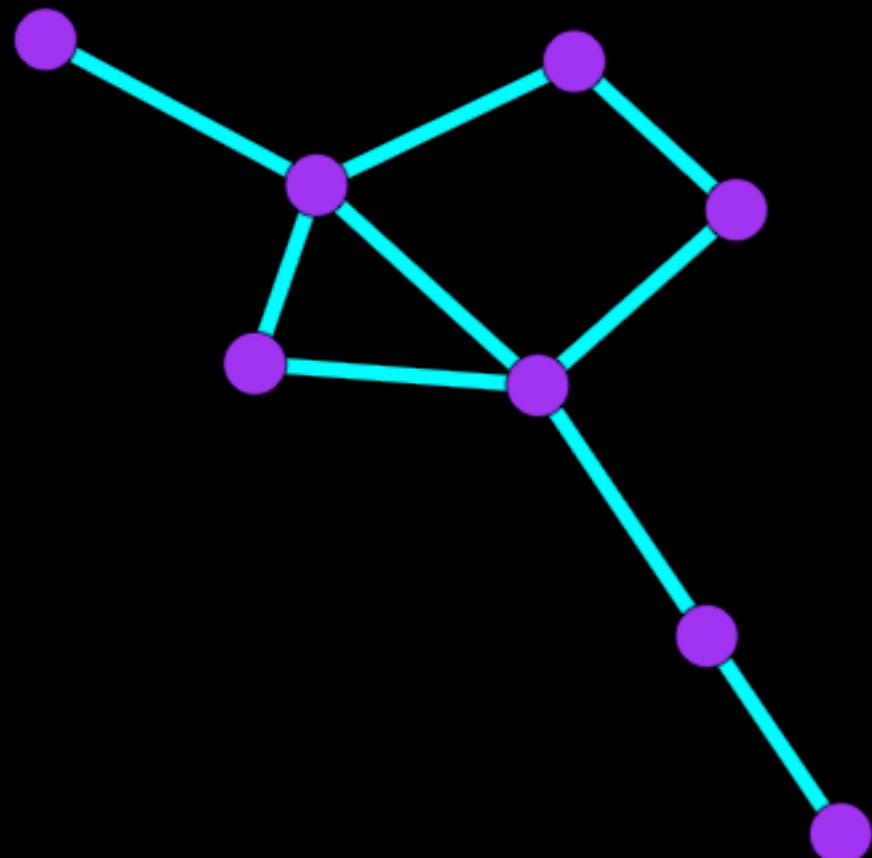


same graph
(adjacency matrix)

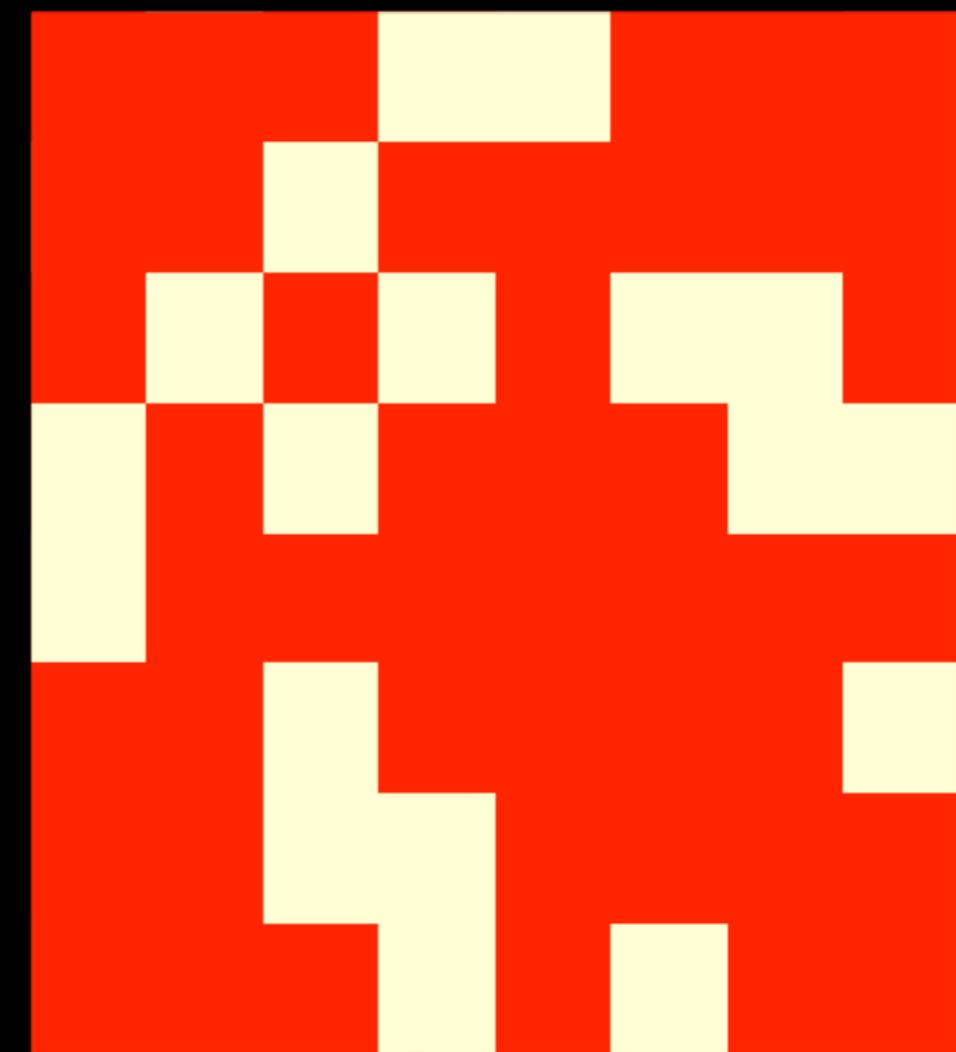


- A is the adjacency matrix
- $A(u,v) = 1$ iff $u \sim v$

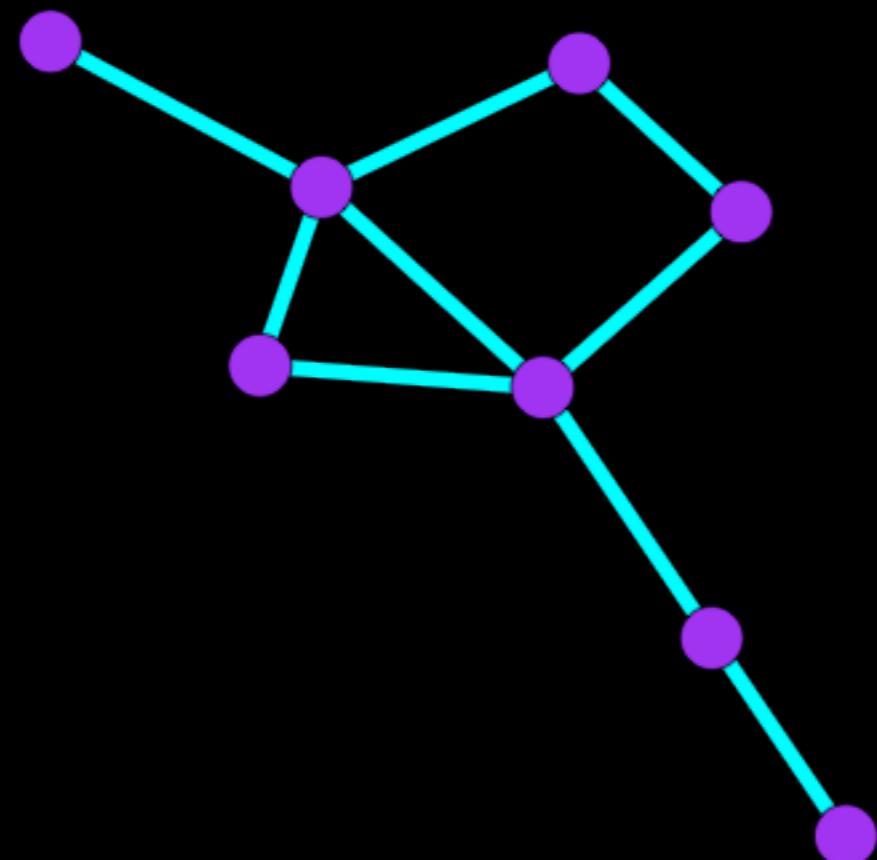
same graph
(2D layout)



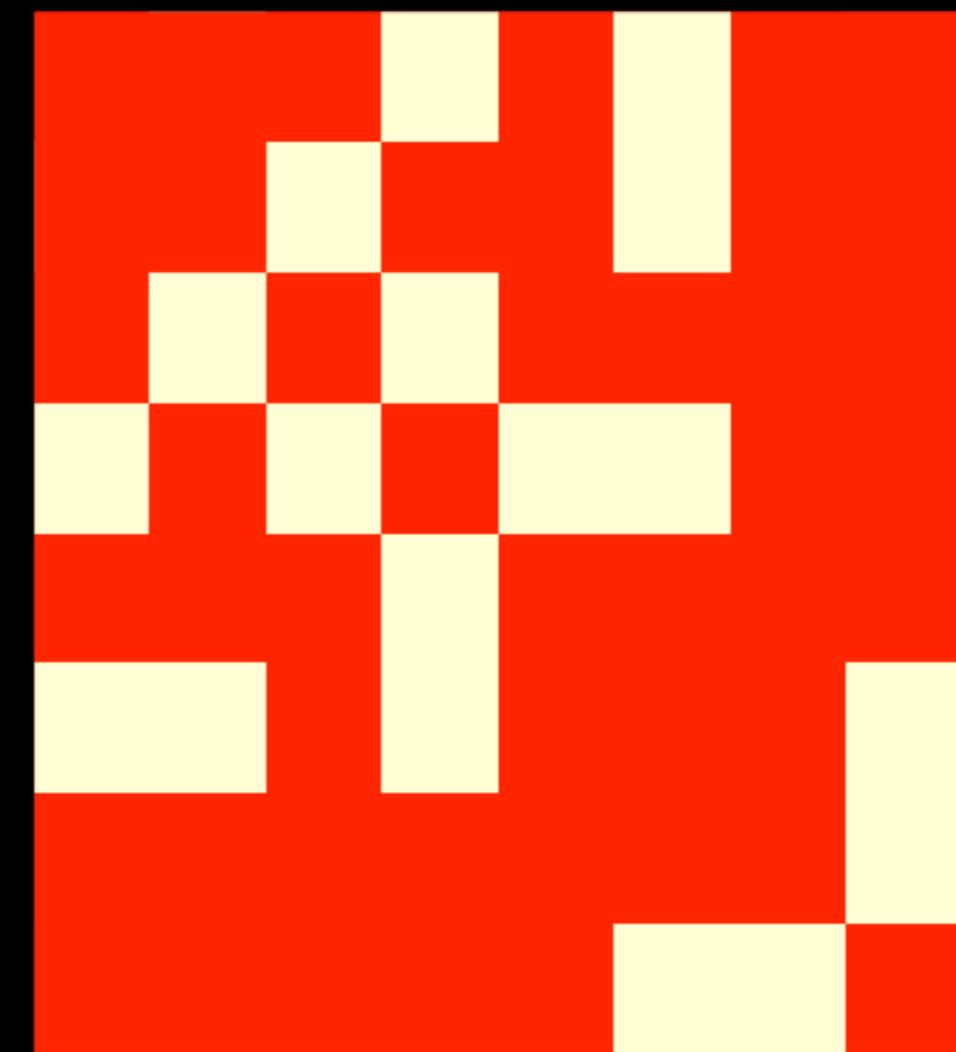
same graph
(adjacency matrix)



same graph
(2D layout)



same graph
(adjacency matrix)

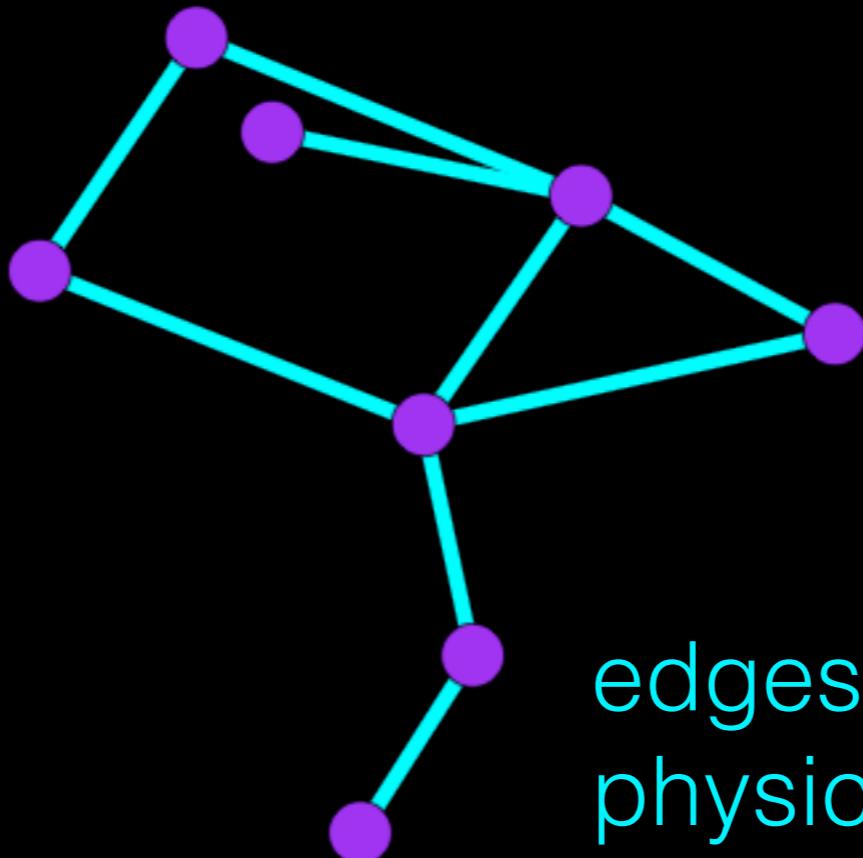


Keep it Simple

- Each **edge** is independent
- Probability of a edge between any pair of vertices is p
- $P[a_{uv}] = \text{Bernoulli}(p)$

What's a connectome?

connectome = brain-graph



vertices =
brain regions
or voxels
or electrodes
or neurons
or even compartments

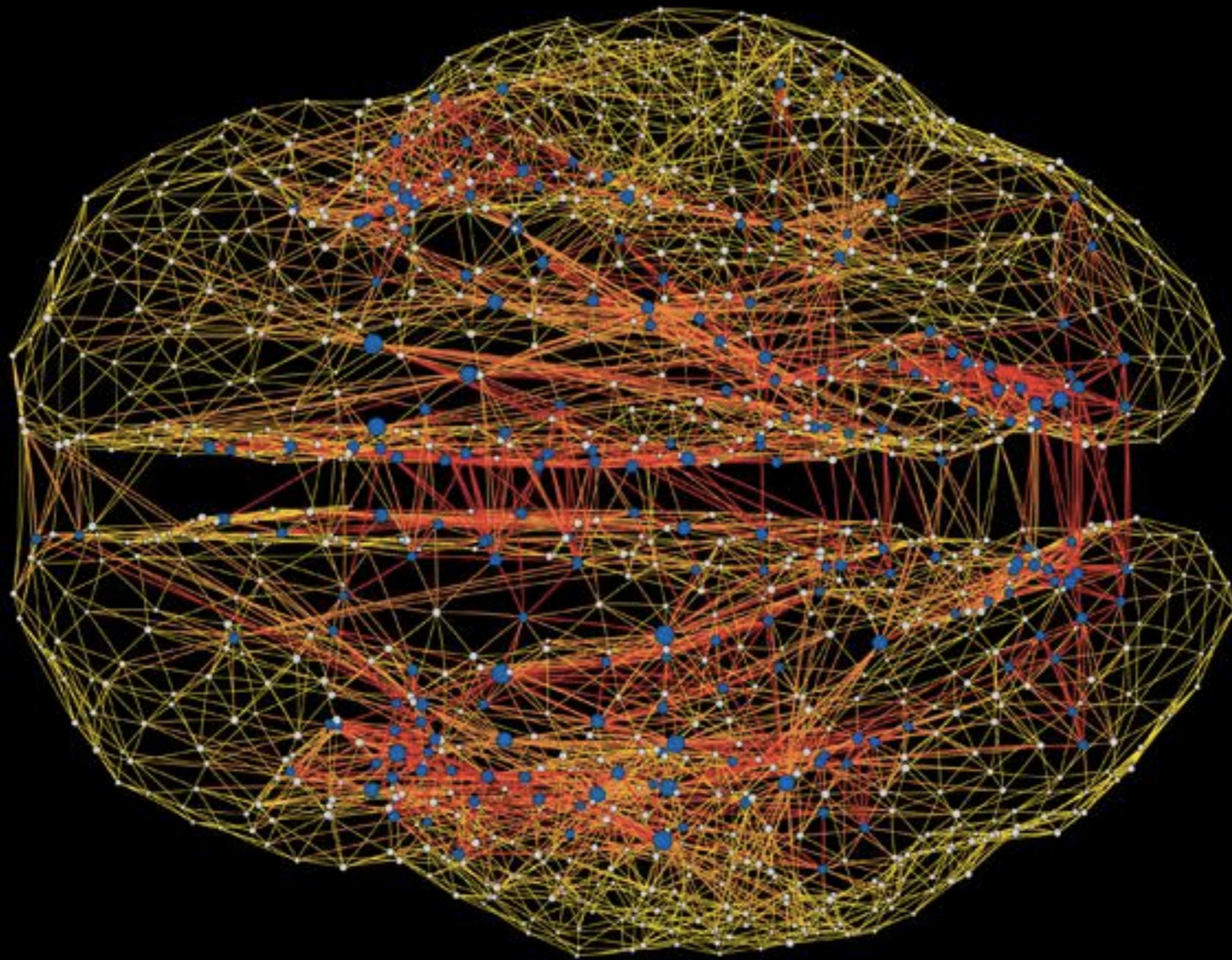
edges =
physical connections
or functional connections
or correlations

Principles of Data Science

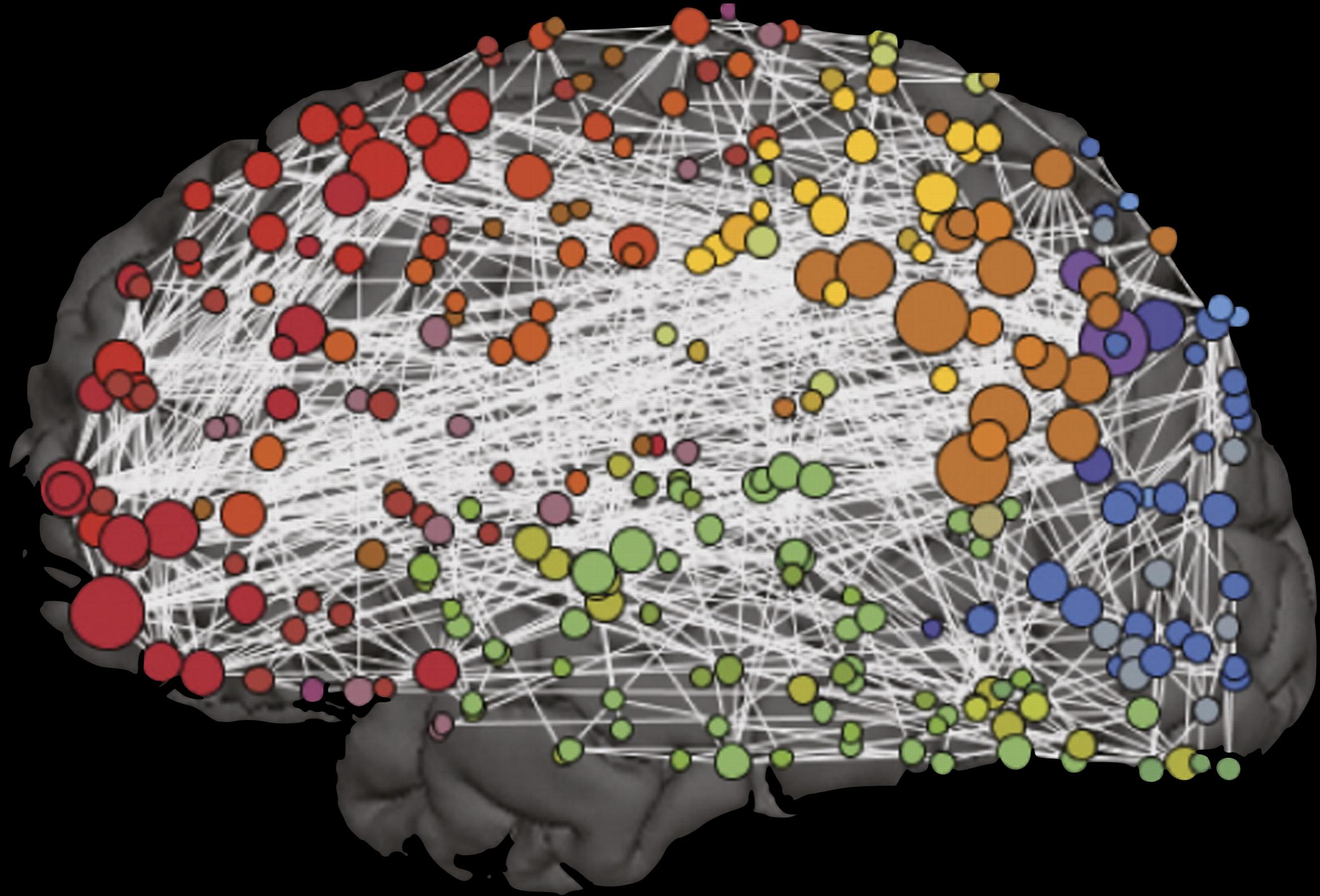
- Look at it
- Keep it simple

Let's do it for connectome coding now

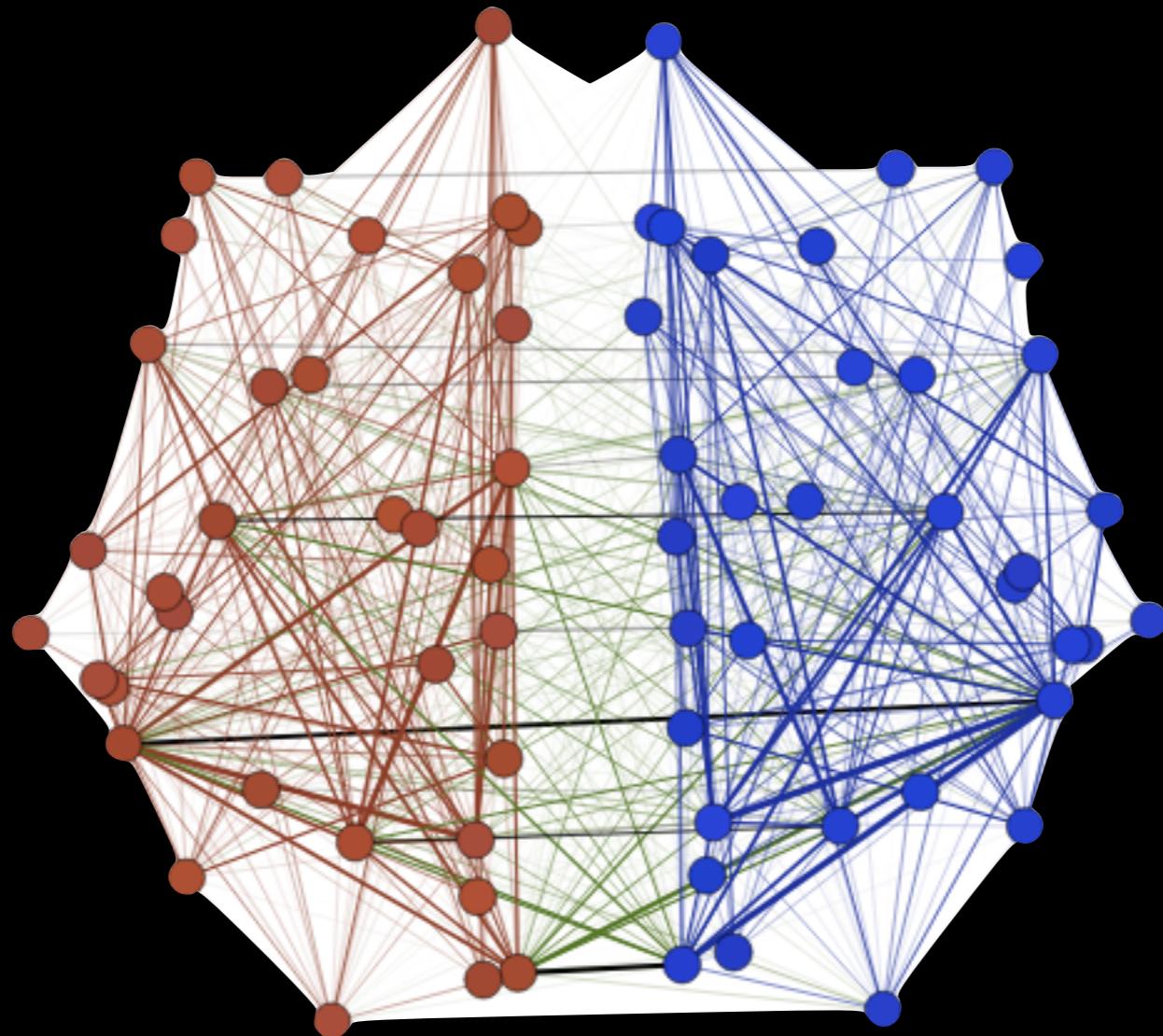
connectome



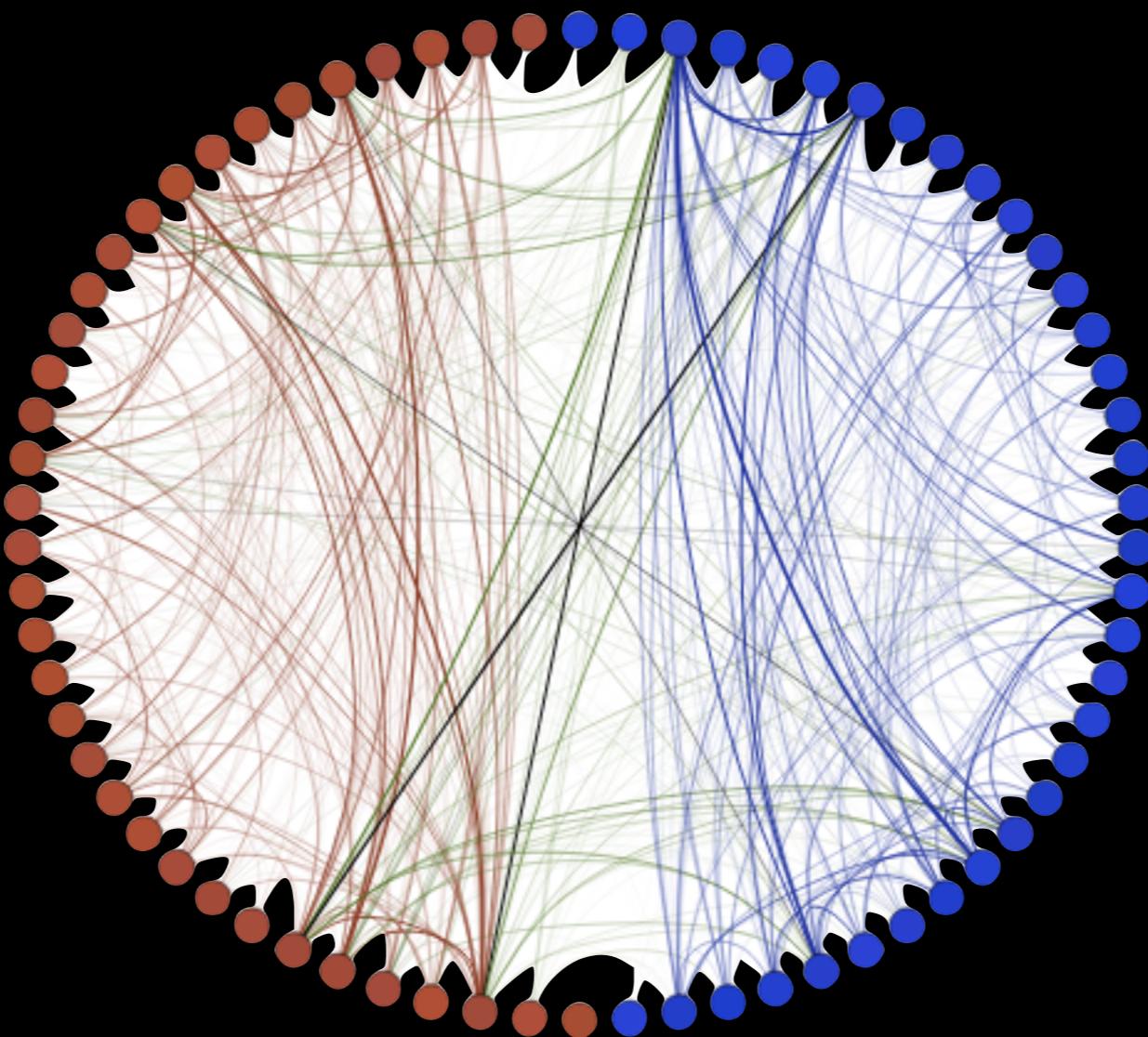
connectome



connectome



connectome



Keep it Simple

- Each **edge** is independent
- Probability of a edge between any pair of vertices is p
- $P[a_{uv}] = \text{Bernoulli}(p)$

What else do we need?

We need the joint distribution of brain stuff & external stuff:

- Joint distribution: $P[s,r] = P[s | r] P[r]$
- Joint distribution: $P[s,r] = P[r | s] P[s]$
- So, we need $P[s|r]$, $P[r|s]$, $P[r]$, $P[s]$
- Let's start with $P[r]$
- Now let's do $P[r|s]$

Principles of Data Science

- Look at it
- Keep it simple

Let's do it for the conditional response, $P[r|s]$



Keep it Simple

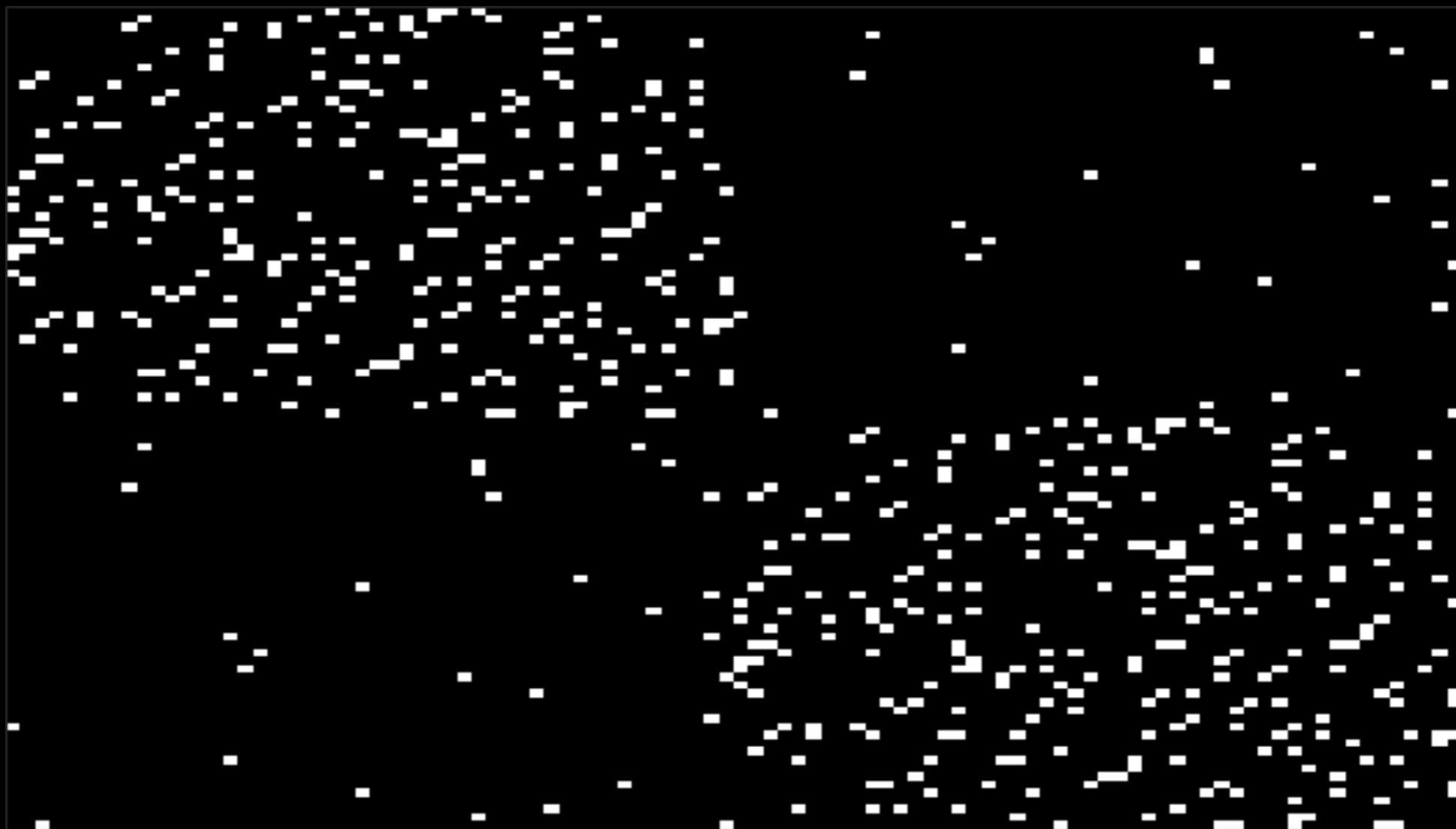
- Each spike is independent
- Probability of a spike at any time is λ_i
- $P[r|s] = \text{Poisson}(\lambda_s)$

Principles of Data Science

- Look at it
- Keep it simple

Let's do it for the conditional response, $P[g|s]$

Look at it



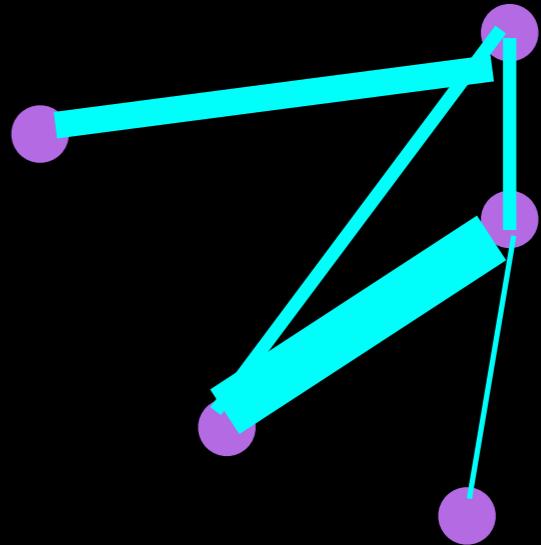
Keep it Simple

- Each edge is independent
- Probability of an edge within a hemisphere is p_w
- Probability of an edge between hemisphere is p_b
- $B=[p_w \ p_b; \ p_b \ p_w]$
- $P[g|s] = \text{SBM}(B \mid \tau)$

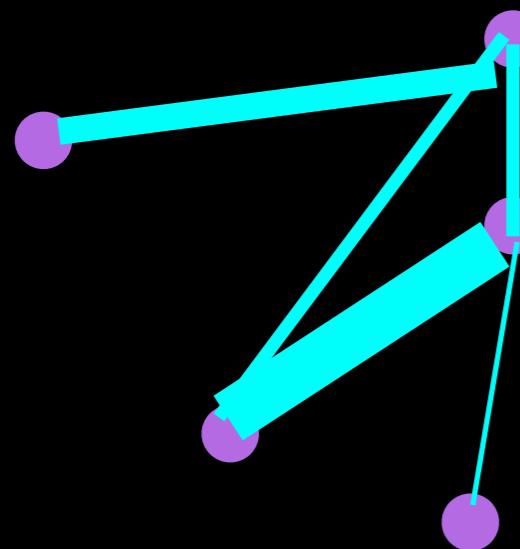
but are these models
too simple?

weighted graph

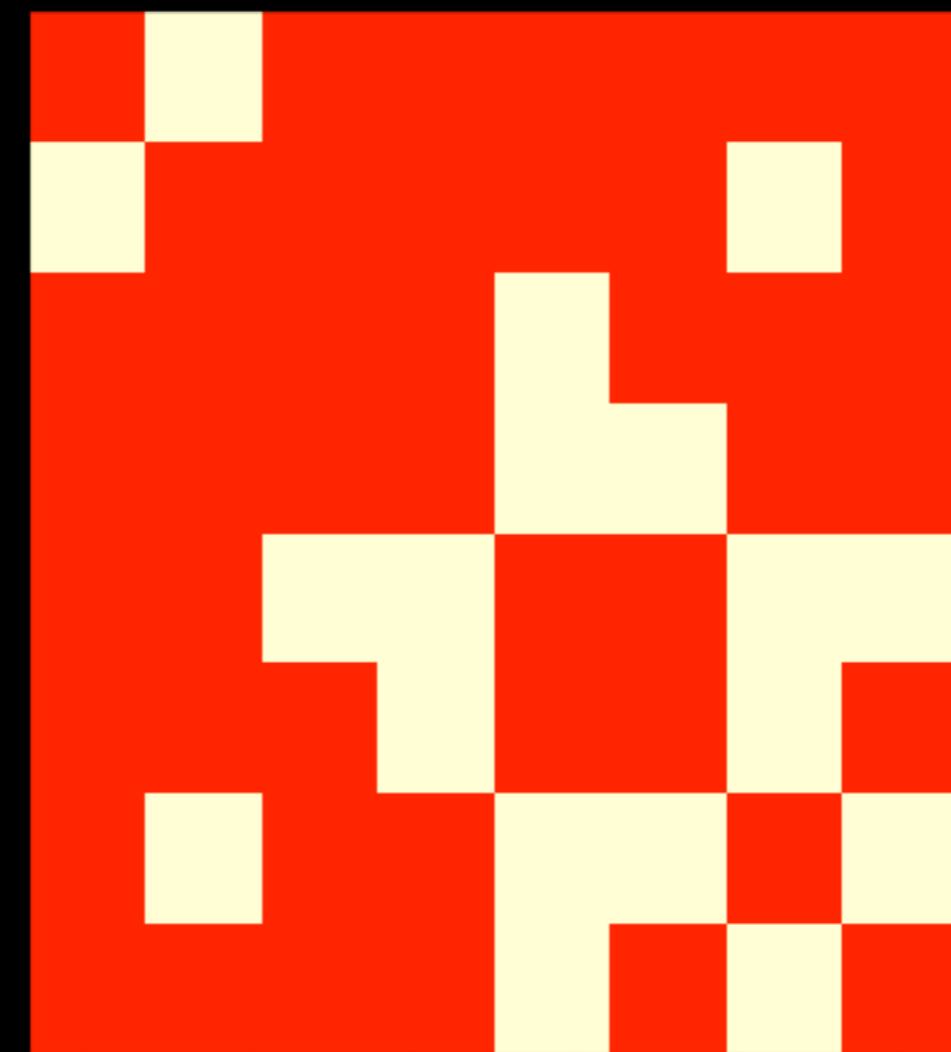
- each edge has a weight
- weights can be positive,
negative, integer, zero, etc.



weighted graph
(2D layout)

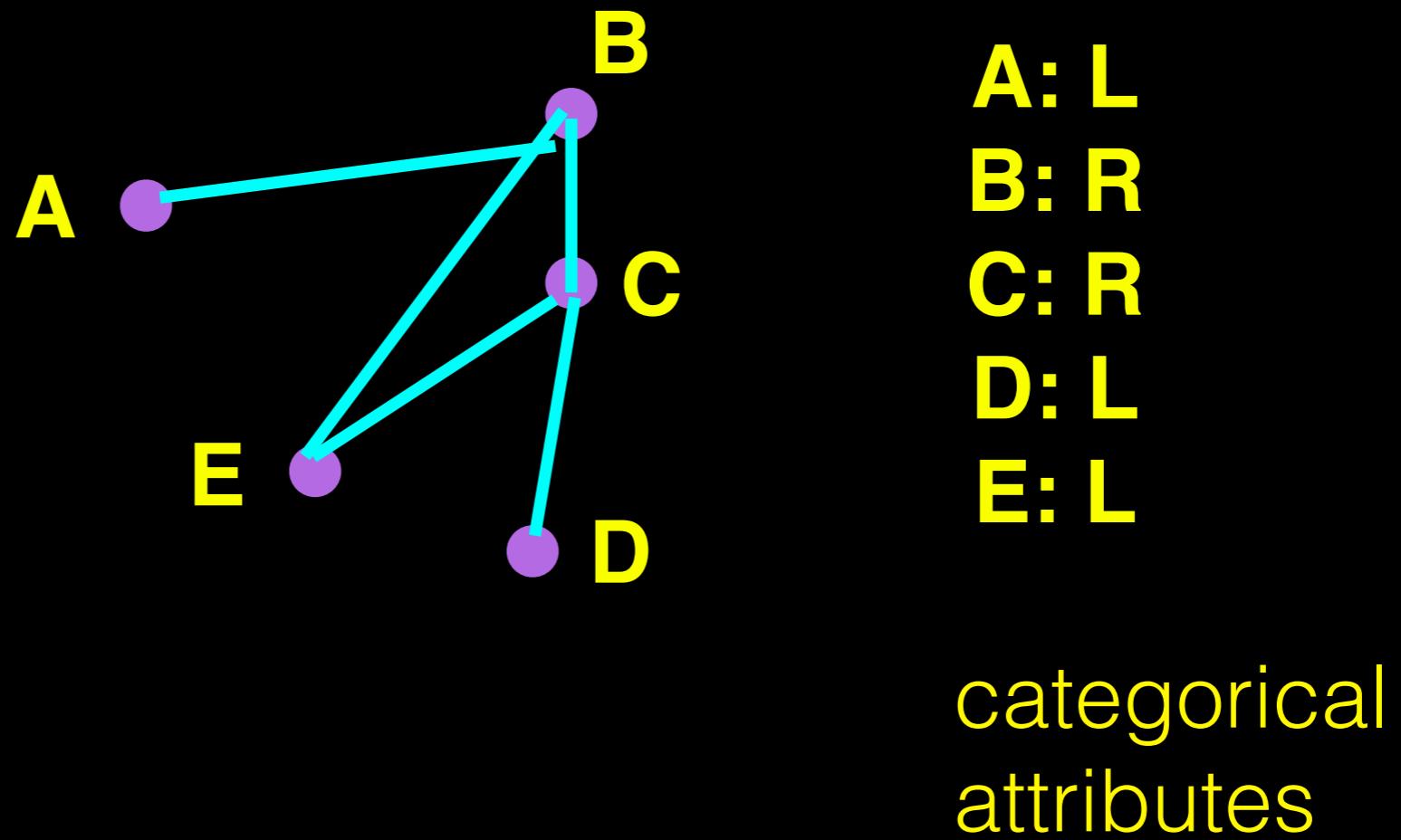


weighted graph
(adjacency matrix)

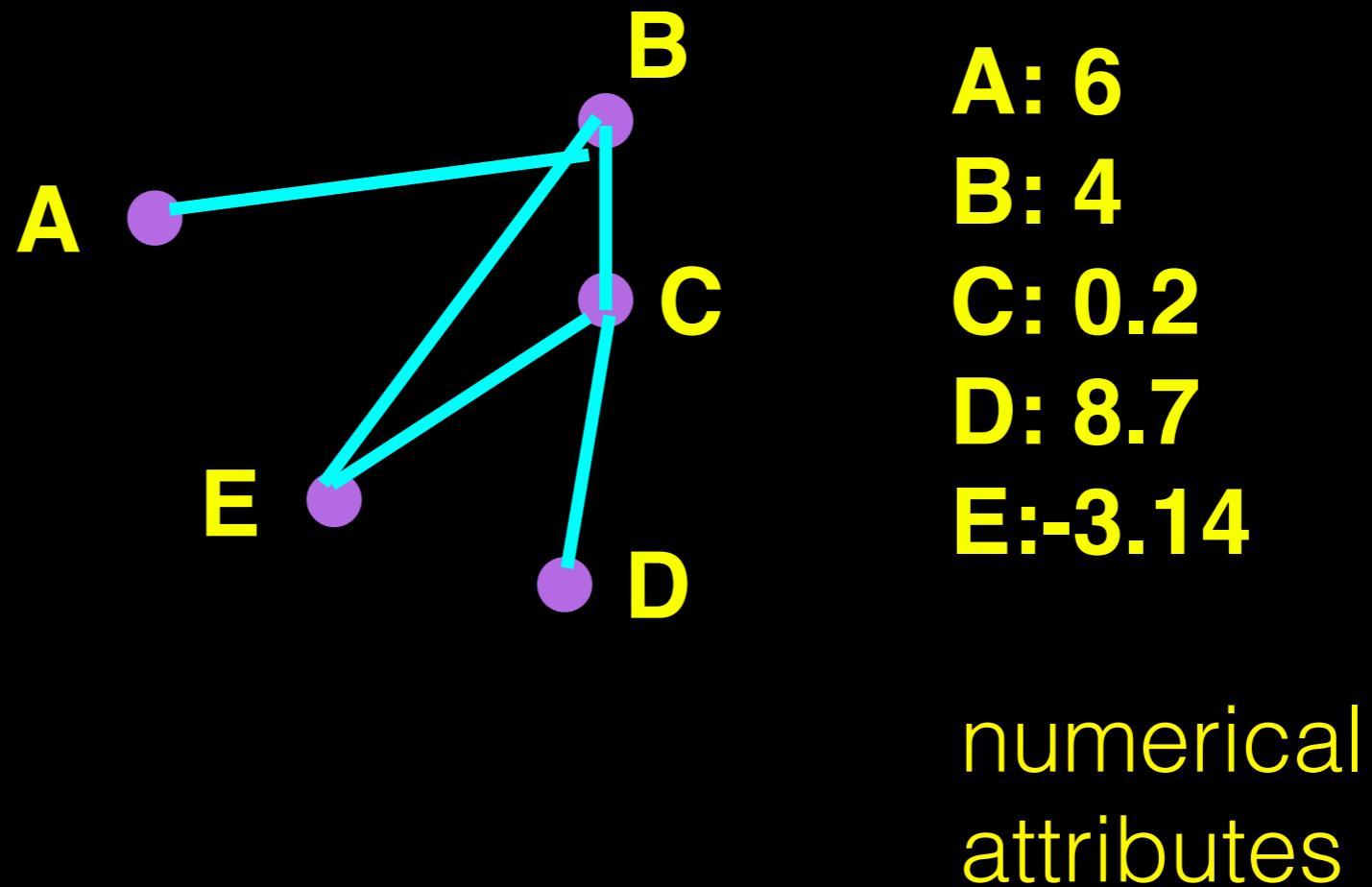


elements of A can take any value

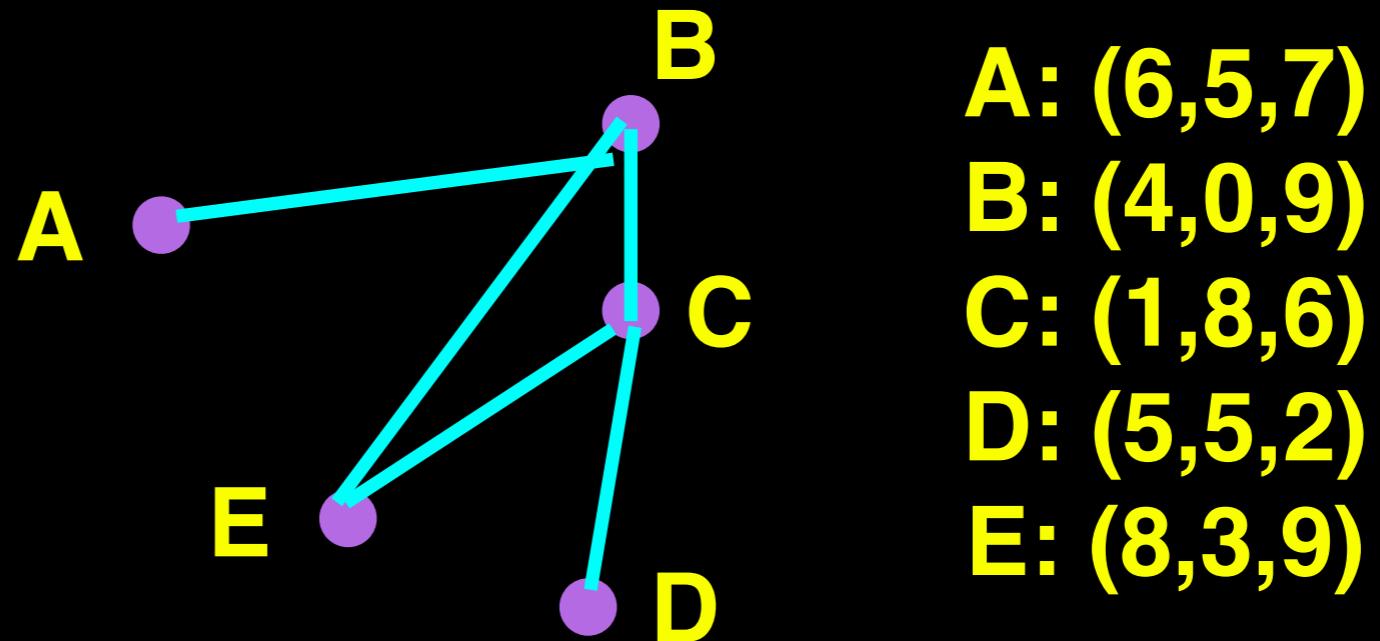
vertex attributed graph



vertex attributed graph

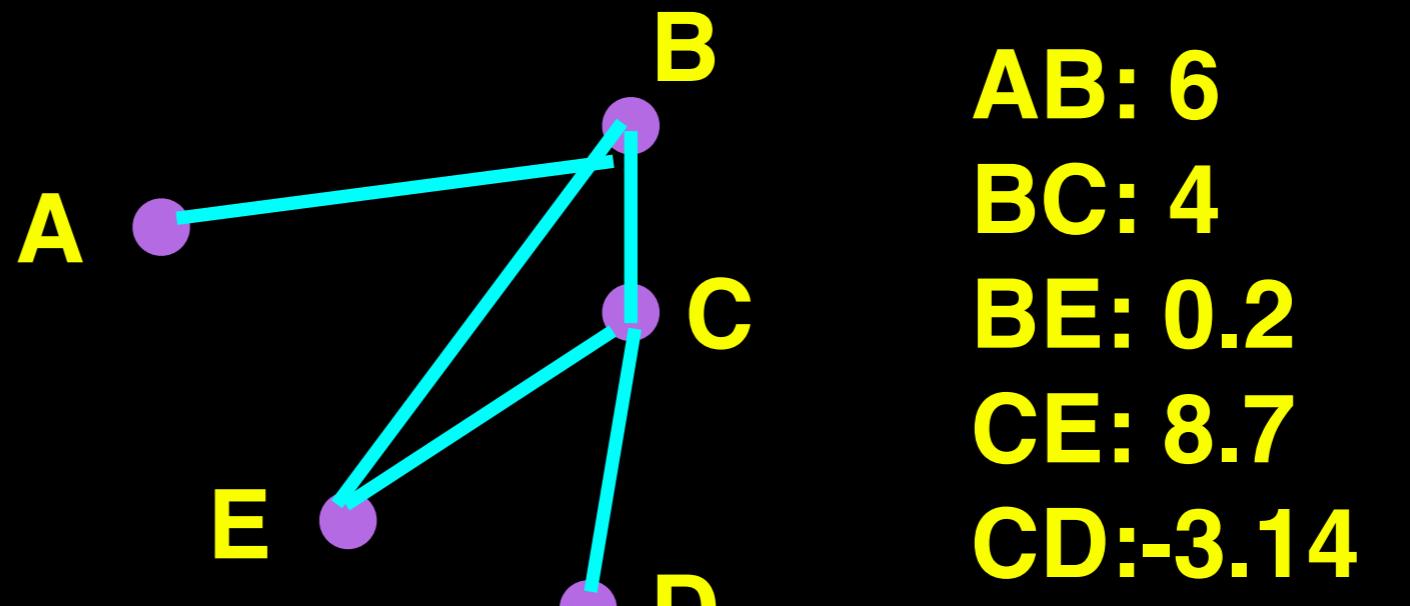


vertex attributed graph



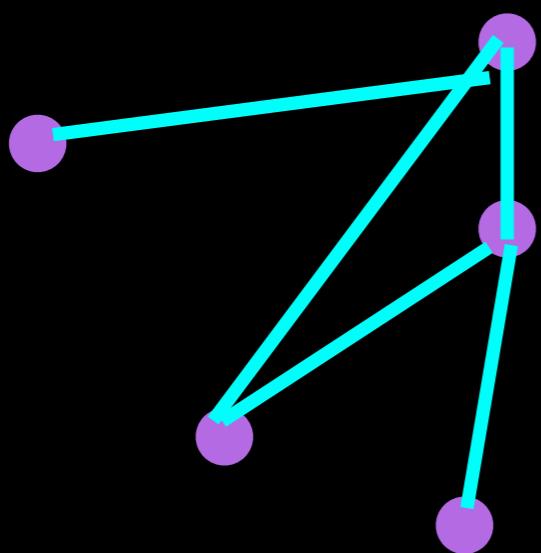
multi-dimensional
attributes

edge attributed graph

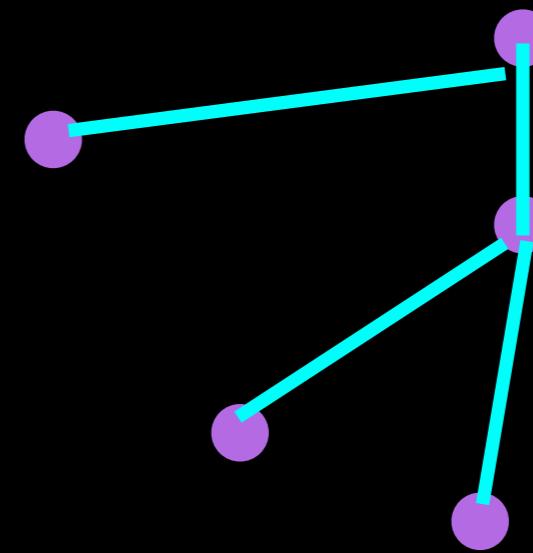


numerical
attributes

graph attributed graphs

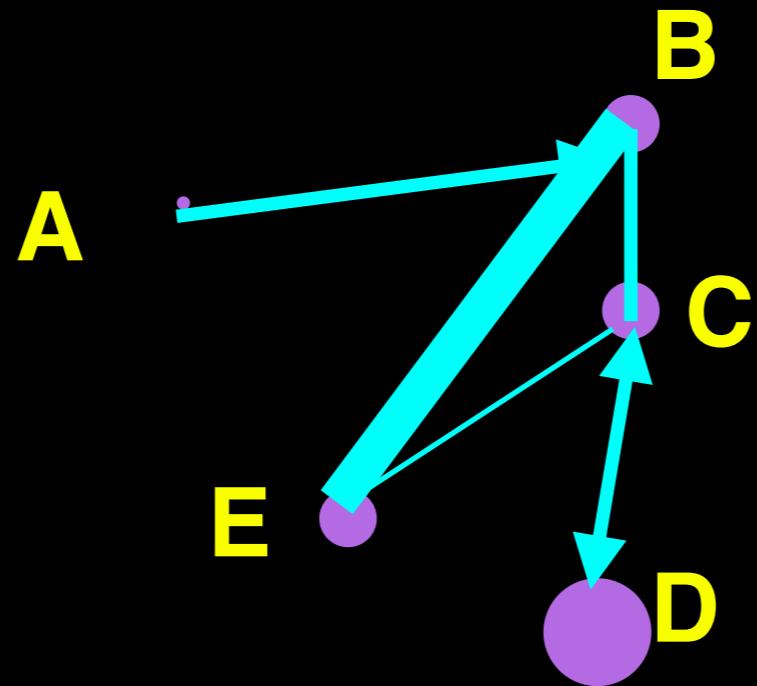


subject 1



scan 2

Graphs with Rich attriUTEs (Grutes)



A: 6, L	AB: 6
B: 4, R	BC: 4
C: 1, L	BE: 0.2
D: 0, L	CE: 8.7
E: 8, R	CD:-3.14

Latent Structure Model

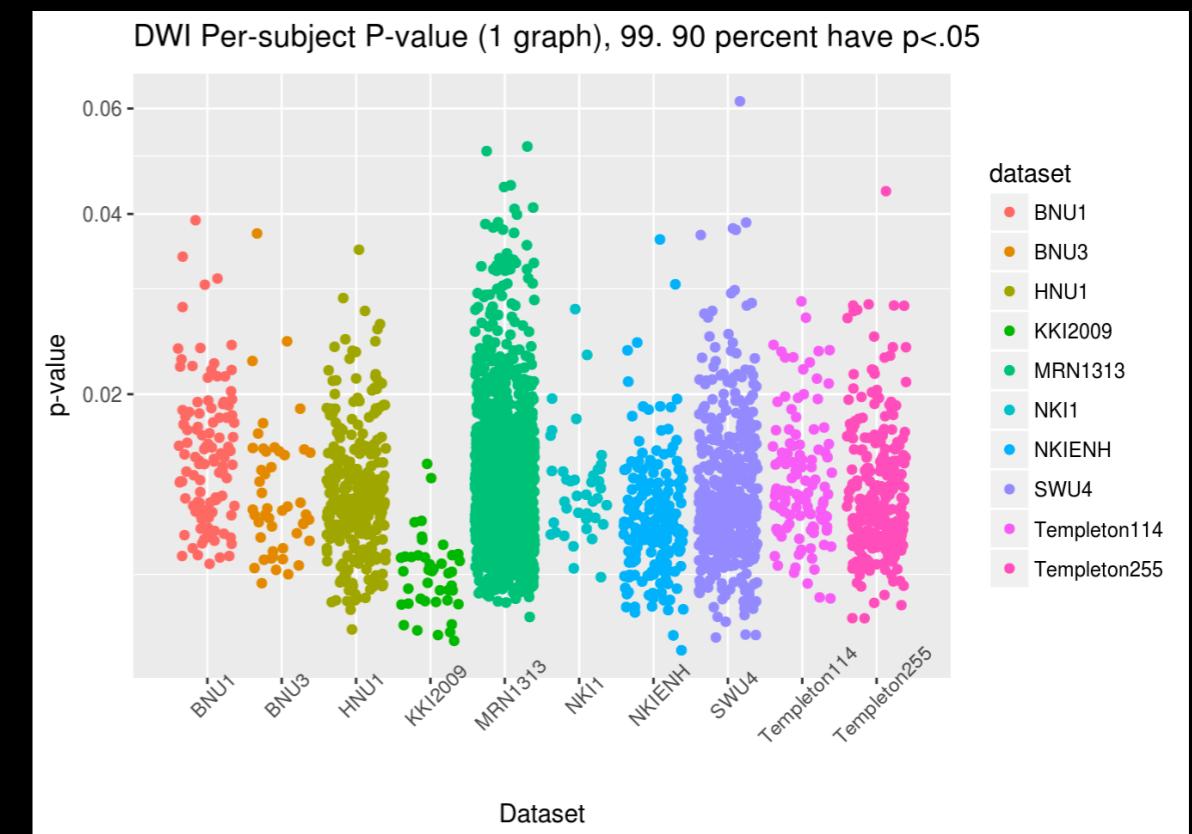
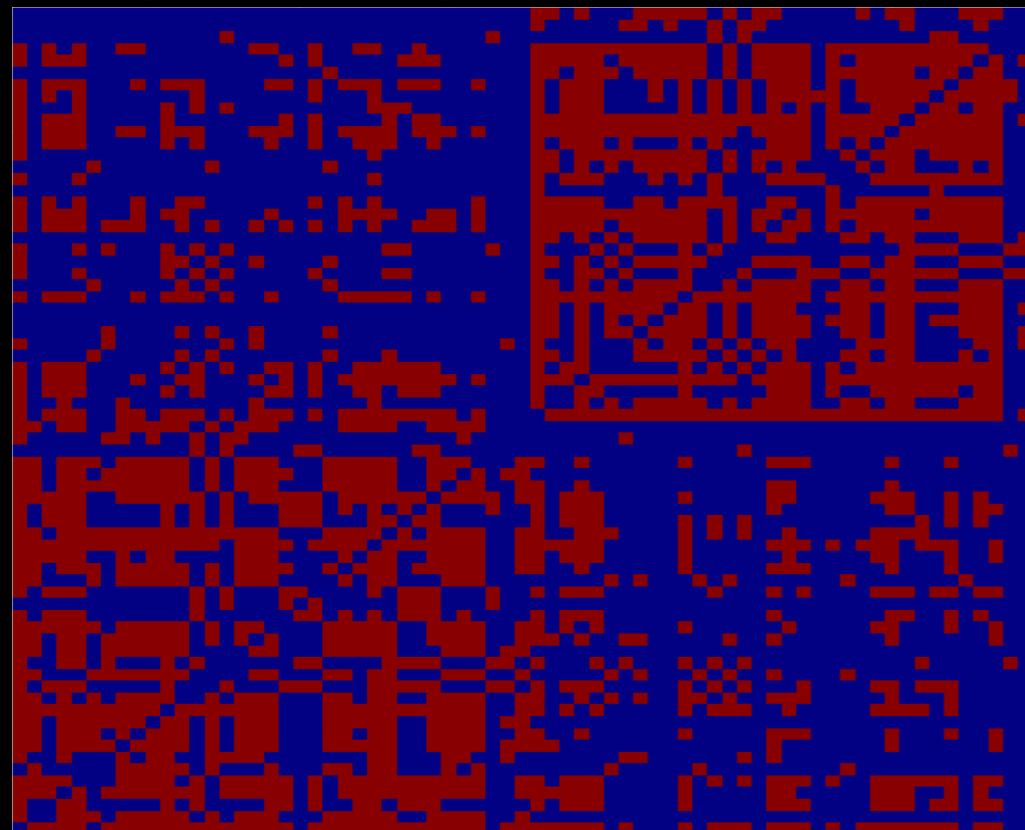
Latent Structure Model

- Each vertex can have **latent** & observed variable
 - can be categorical, numerical, vectors, etc.
- The latent variables have **structure**
 - can be cluster, nonlinear relationships, hierarchy, etc.

applications

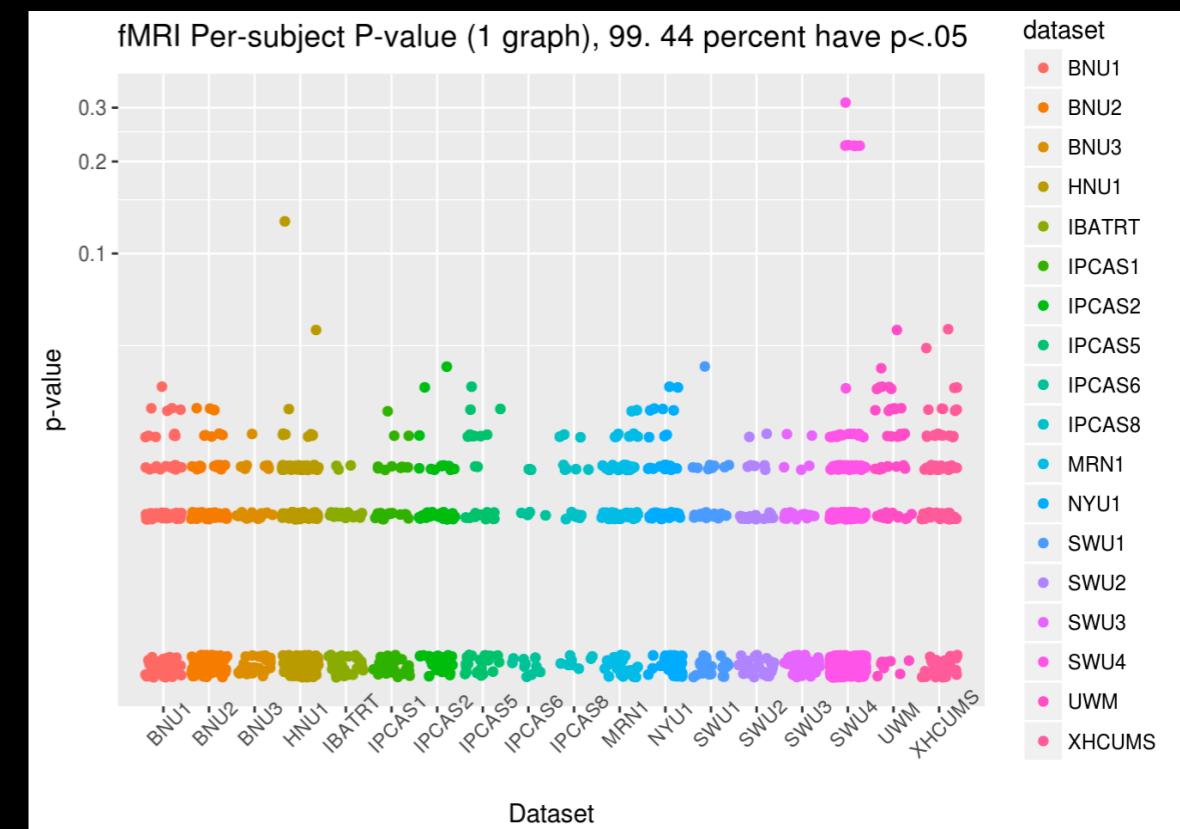
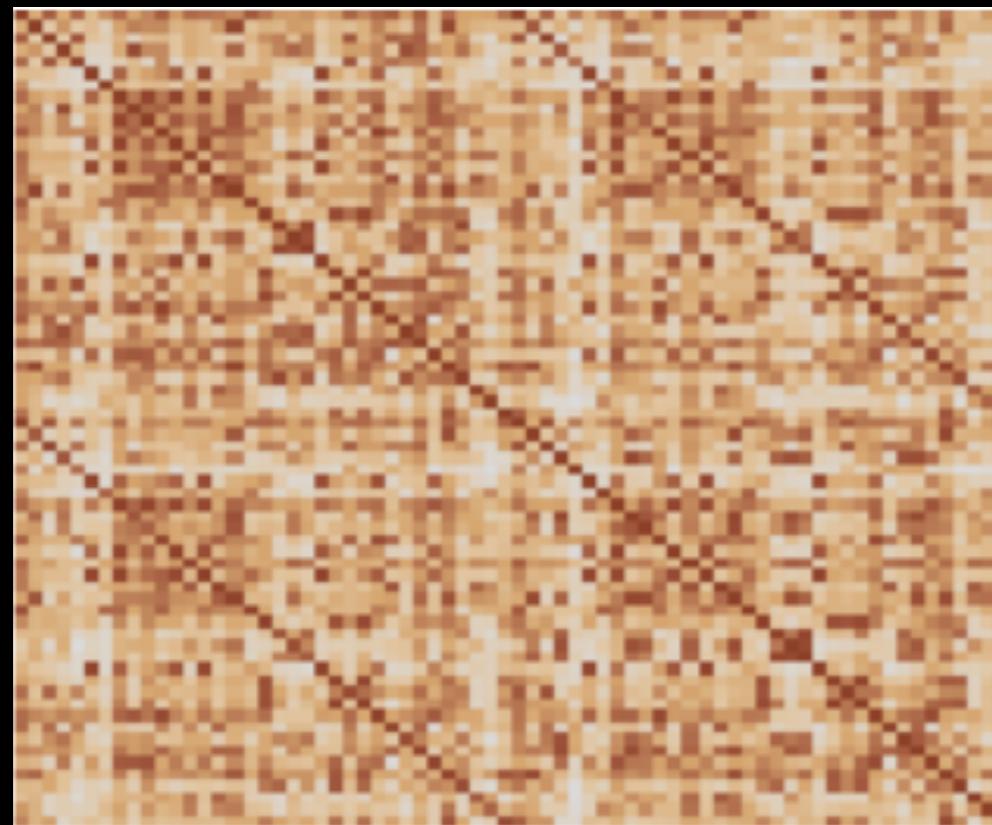
Human DTI Connectome Code

ipsilateral connections are stronger than contralateral

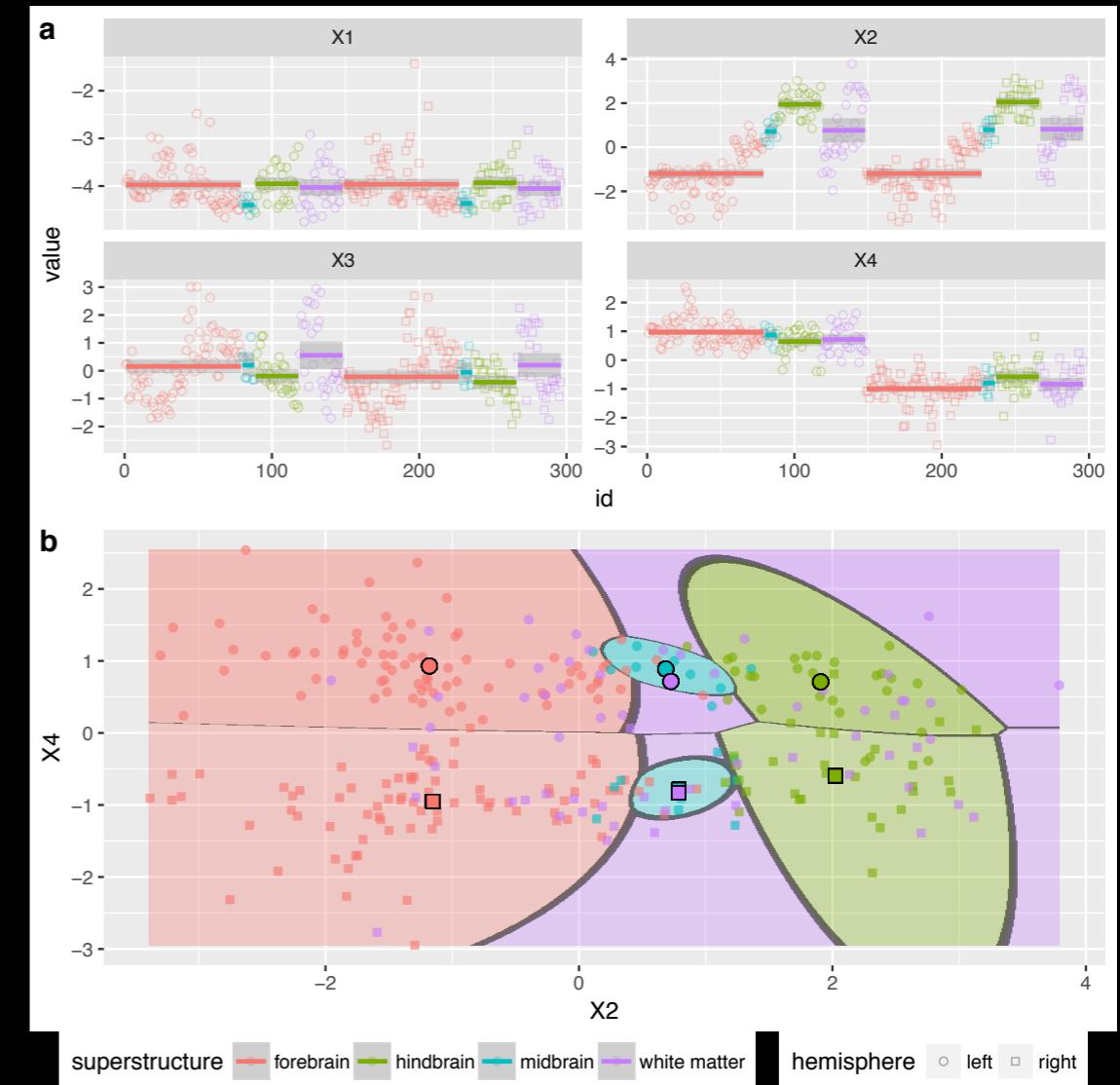
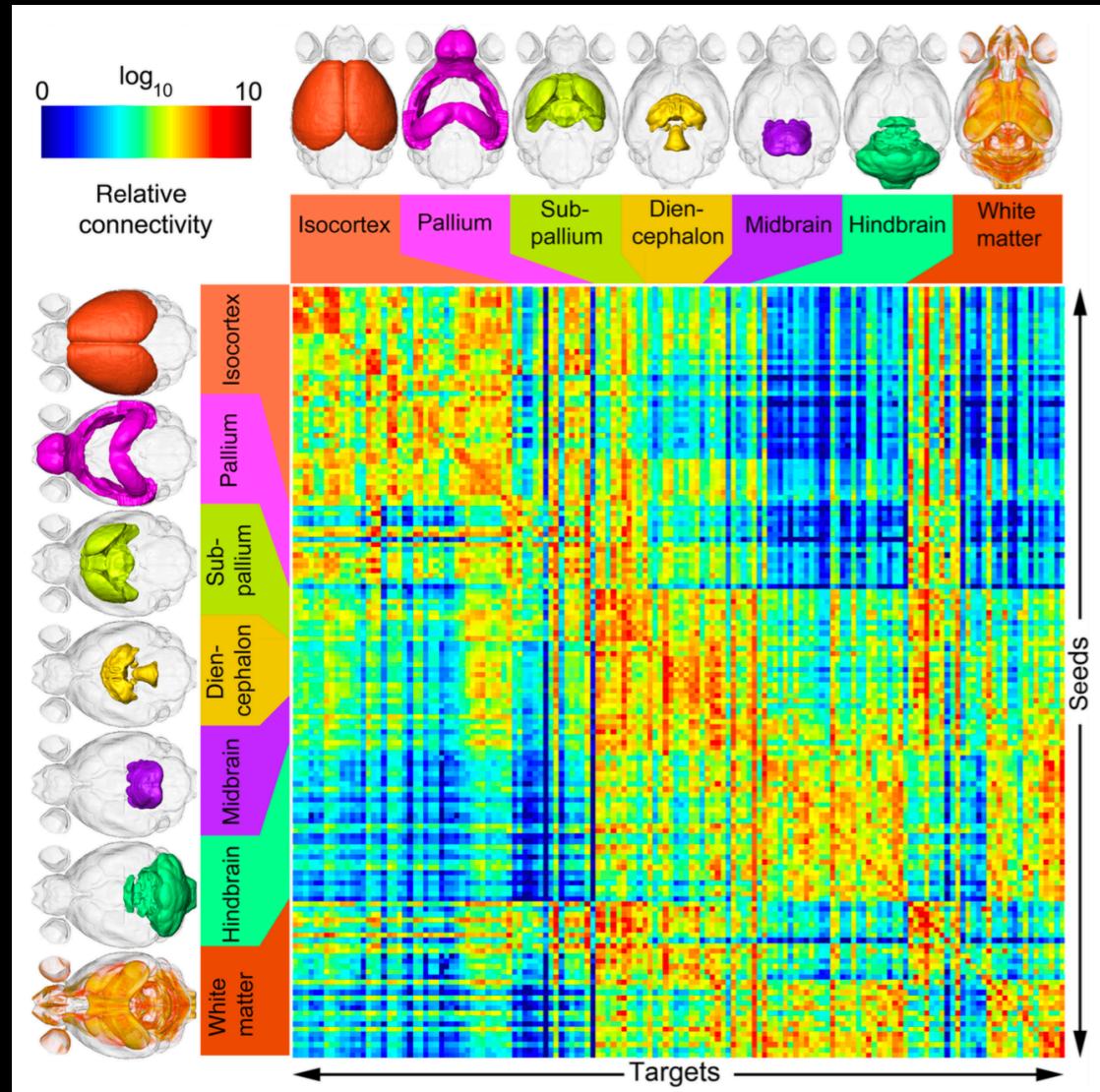


Human fMRI Connectome Code

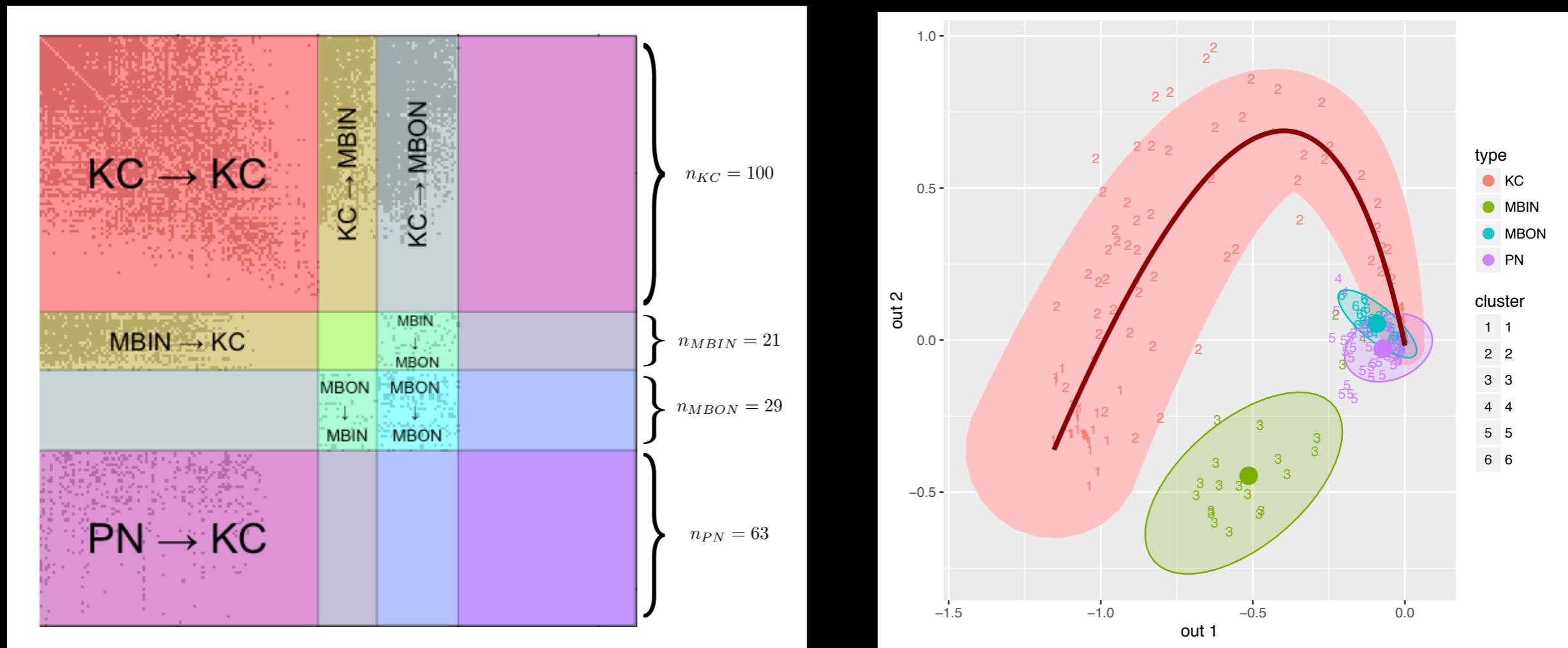
bilateral connections are stronger than non-bilateral



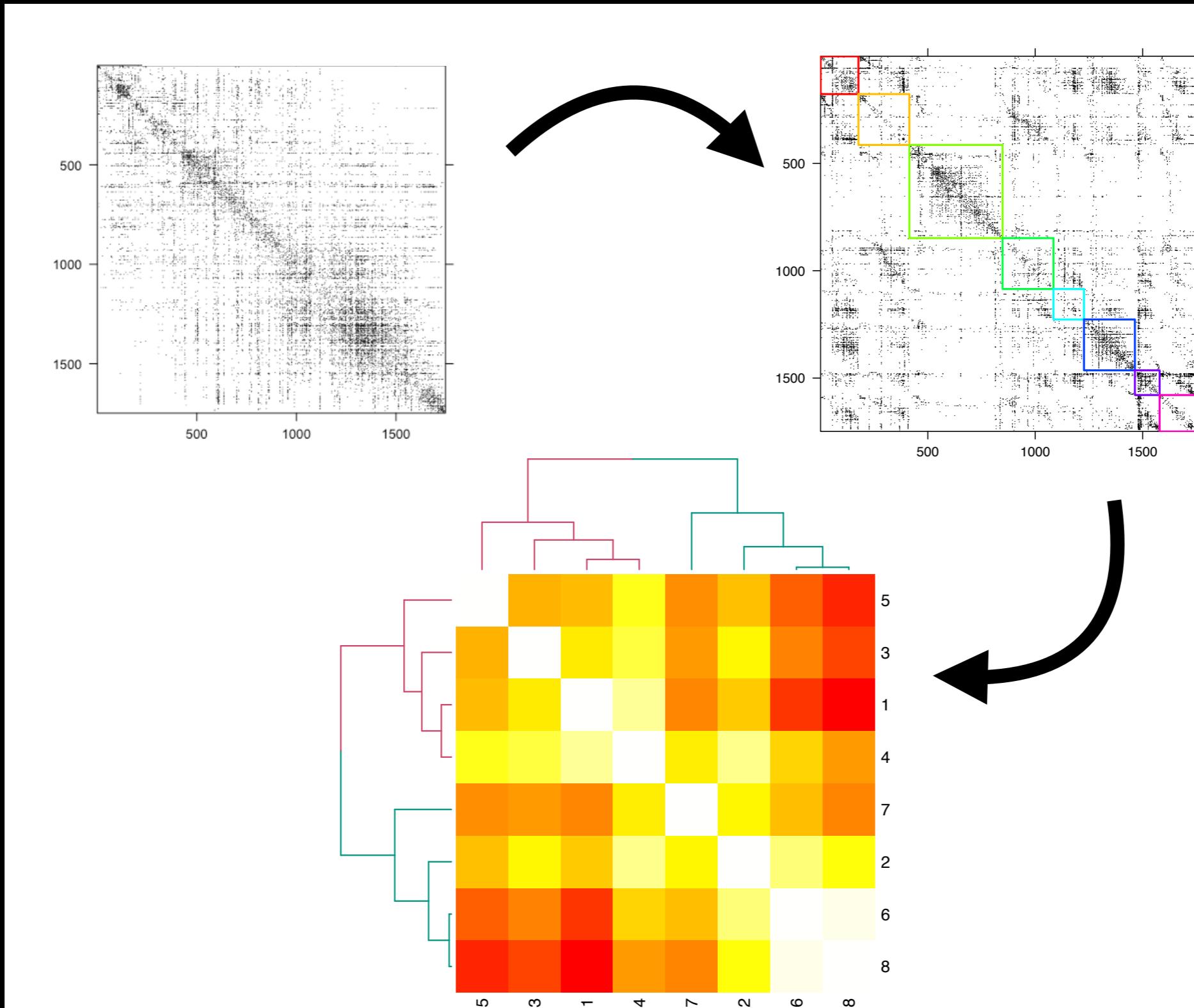
Mouse Connectome Code



Larval Drosophila Mushroom Body Connectome Code



Drosophila Optic Medulla Connectome Code



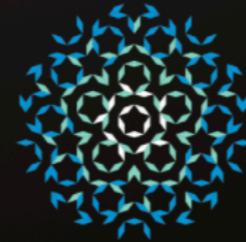
References

- Statistical inference on random dot product graphs: a survey
- Law of Large Graphs for Statistical Connectomics
- A Principled Approach to Human Connectome Estimation and Meganalysis
- Community Detection and Classification in Hierarchical Stochastic Blockmodels

Questions?

Joshua T. Vogelstein, Dept BME, JHU

Co-founder: NeuroData Lab, Gigantum



Kavli
NDI

