

Connectome Coding

Joshua Vogelstein

Dept of BME, Johns Hopkins university

w: jovo.me e: jovo@jhu.edu s:brainx.io/sfn17

Please interrupt and ask questions!

- what is connectome coding
- applications of connectome coding

what is connectome coding?

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

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

Ongoing environment: stimulus, movements, rewards, etc.

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

Ongoing environment: stimulus, movements, rewards, etc.

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

Ongoing environment: stimulus, movements, rewards, etc.

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

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

Ongoing environment: stimulus, movements, rewards, etc.

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

Past environment: genome, psychiatric condition, memory, location, etc.

Principles of Data Science

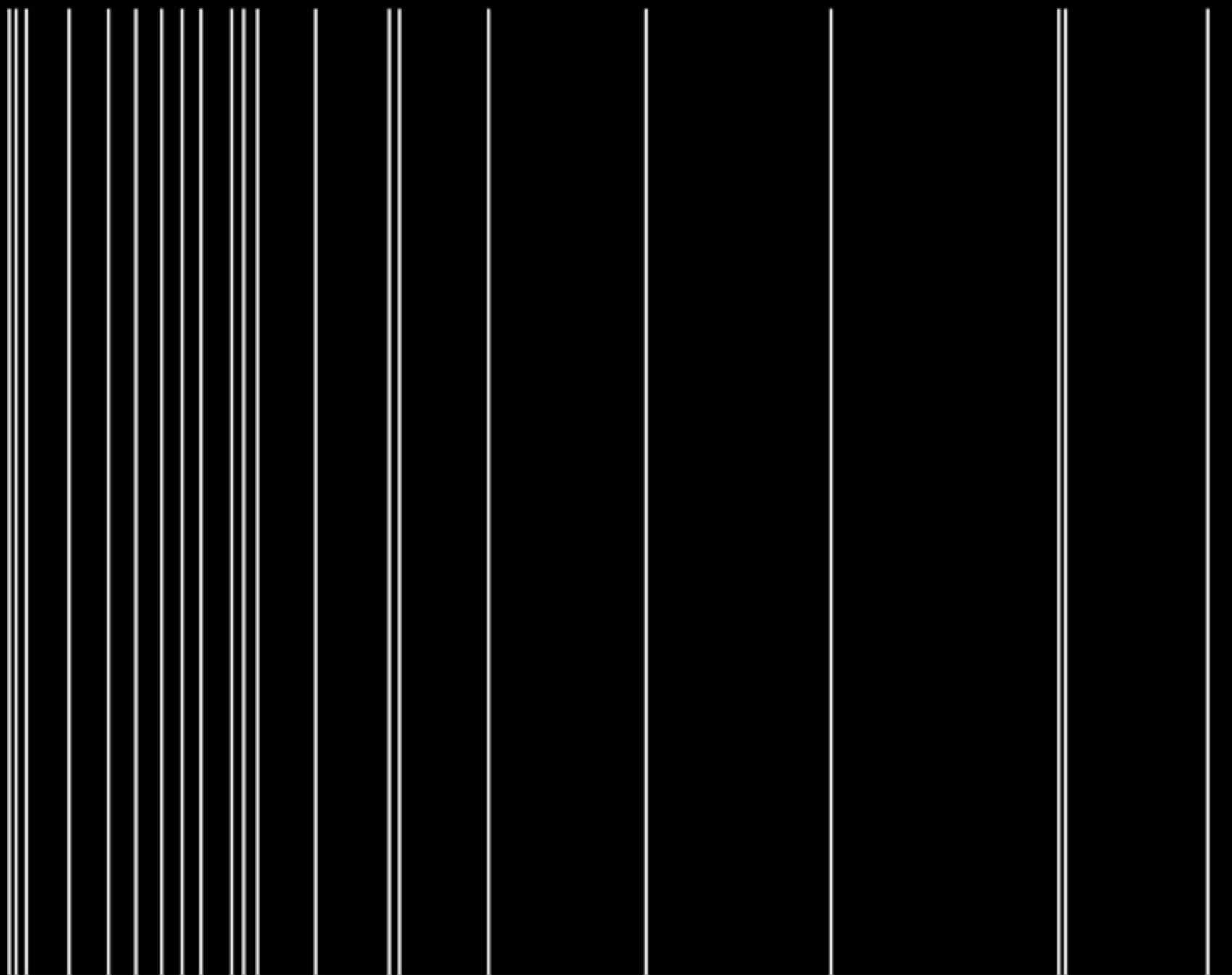
- Look at it
- Keep it simple

Principles of Data Science

- Look at it
- Keep it simple

Let's do it for the **neural coding**

Look at it



Keep it Simple

Neural Encoding: $P[r | s]$

Neural Decoding: $P[s | r]$

Neural Code: $P[s, r]$

Keep it Simple

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

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

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

- Look at it
- Keep it simple

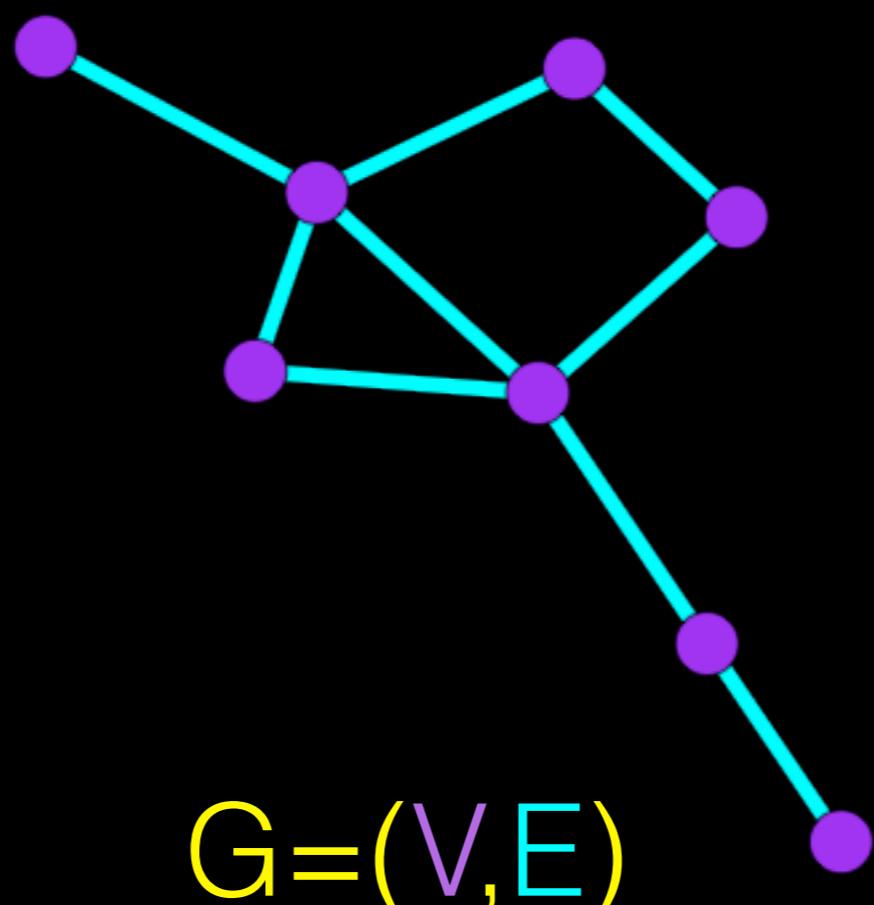
Principles of Data Science

- Look at it
- Keep it simple

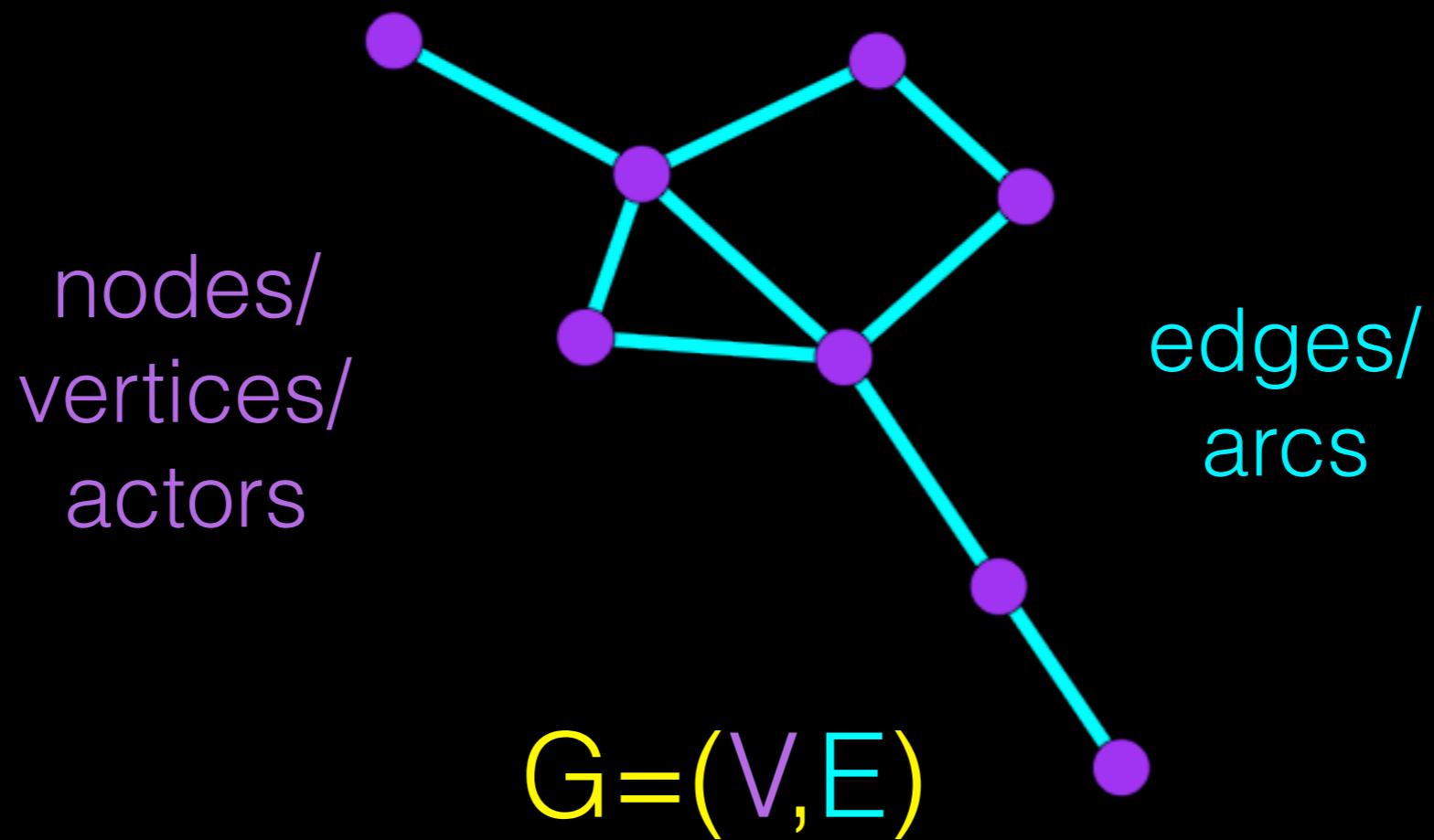
Let's do it for networks, $P[g]$

Look at it

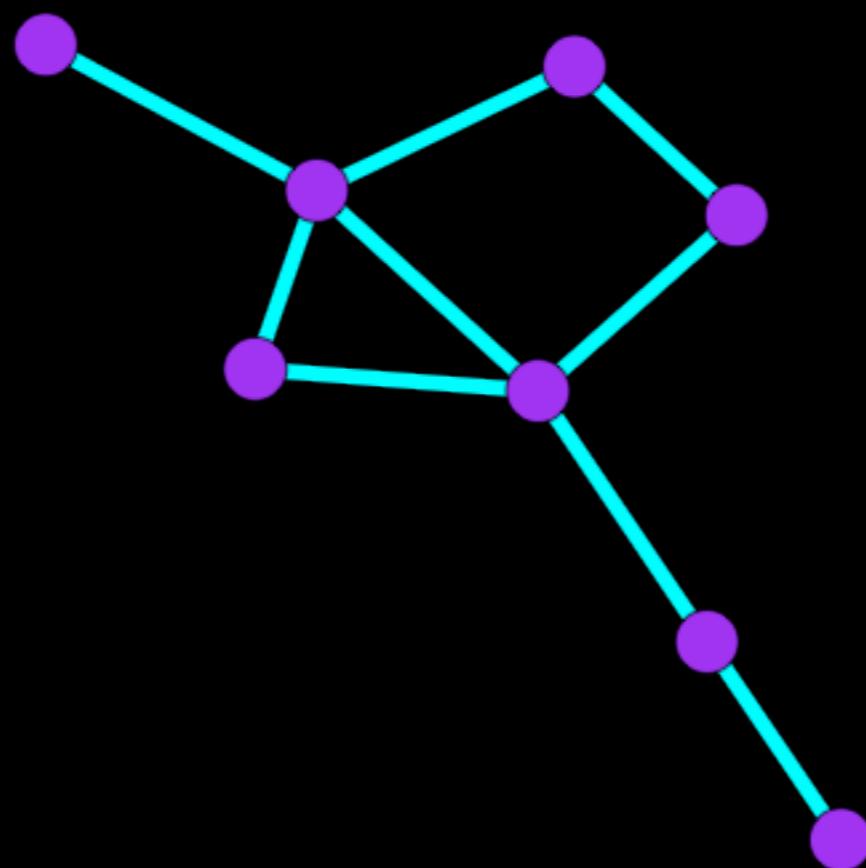
a simple graph



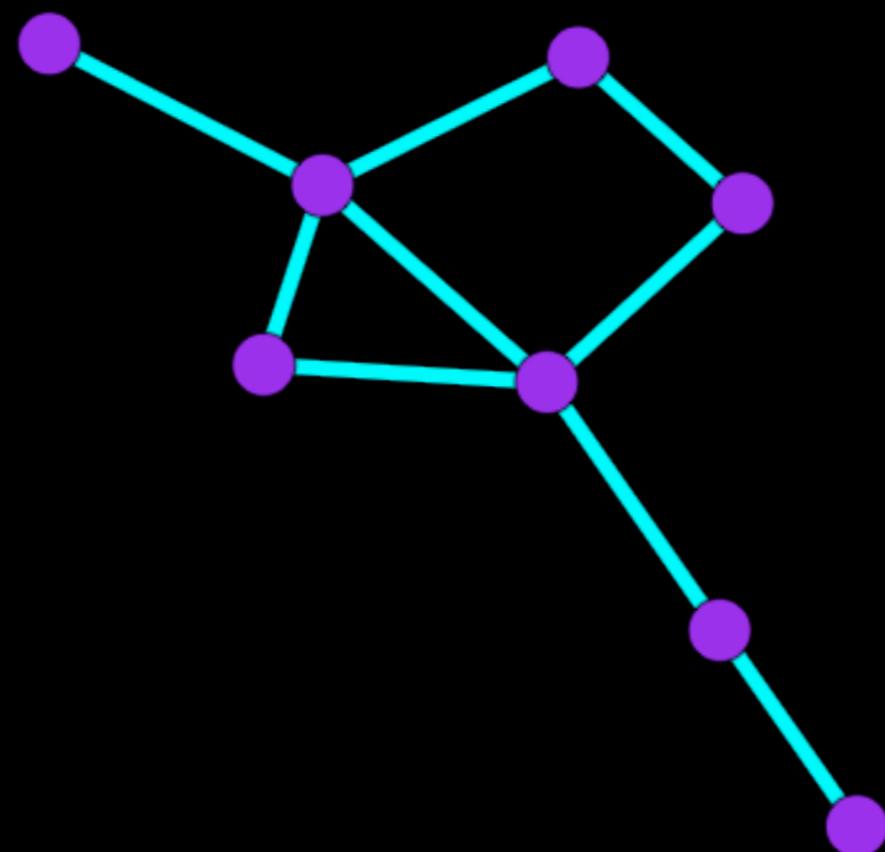
a simple graph



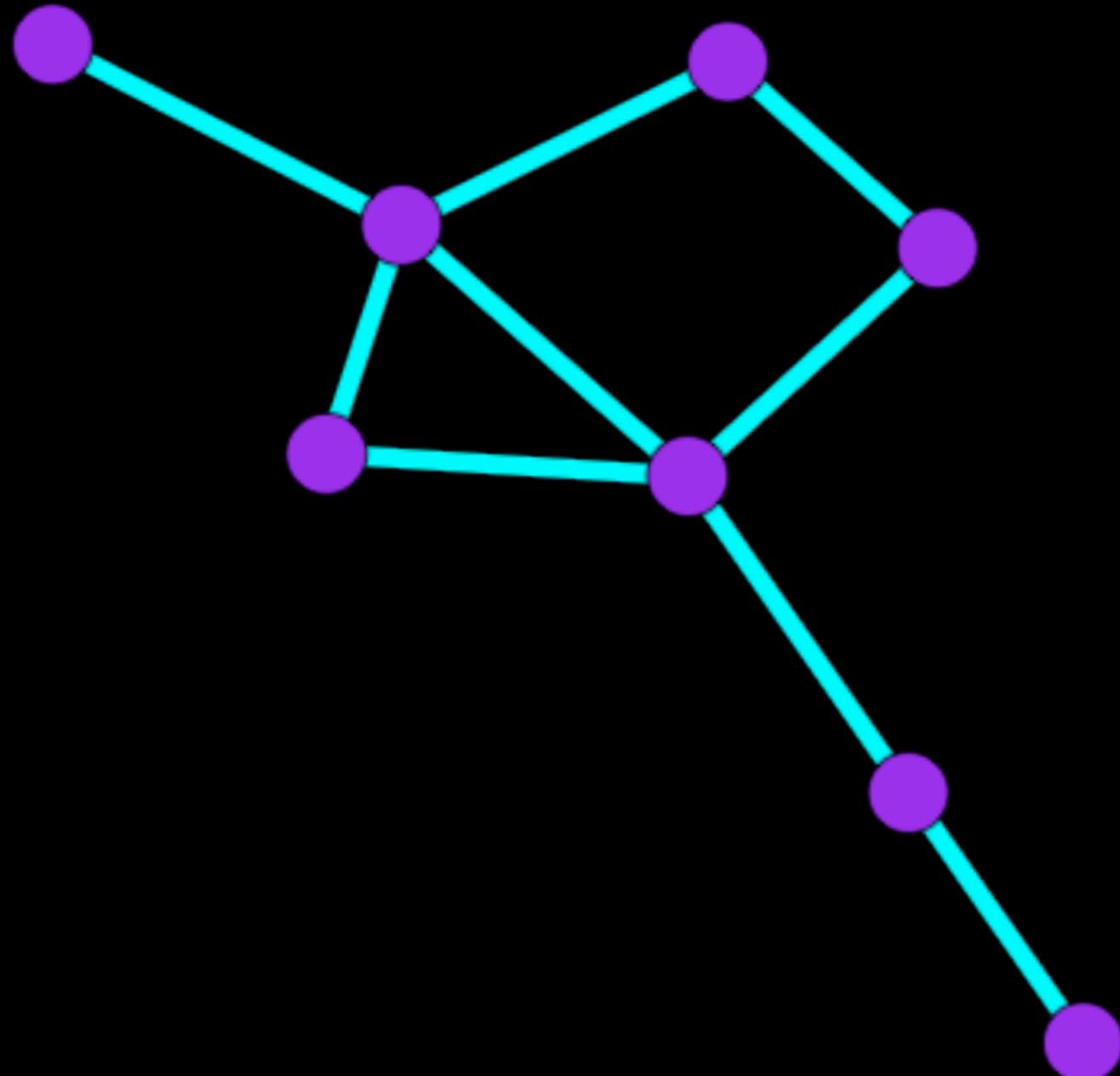
the same graph



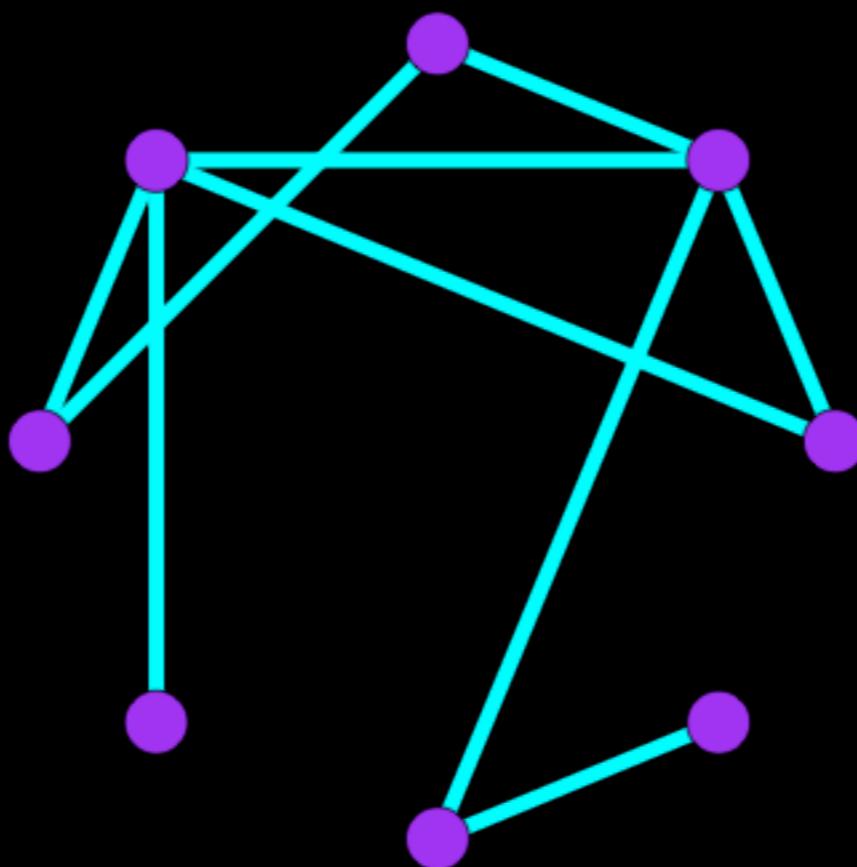
the same graph



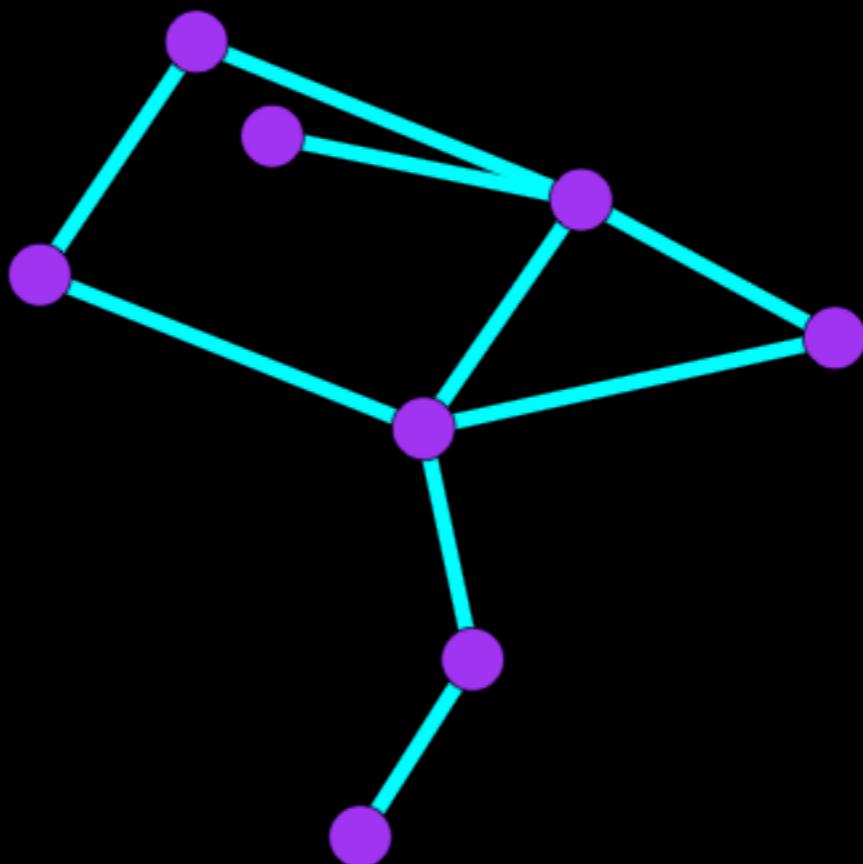
the same graph



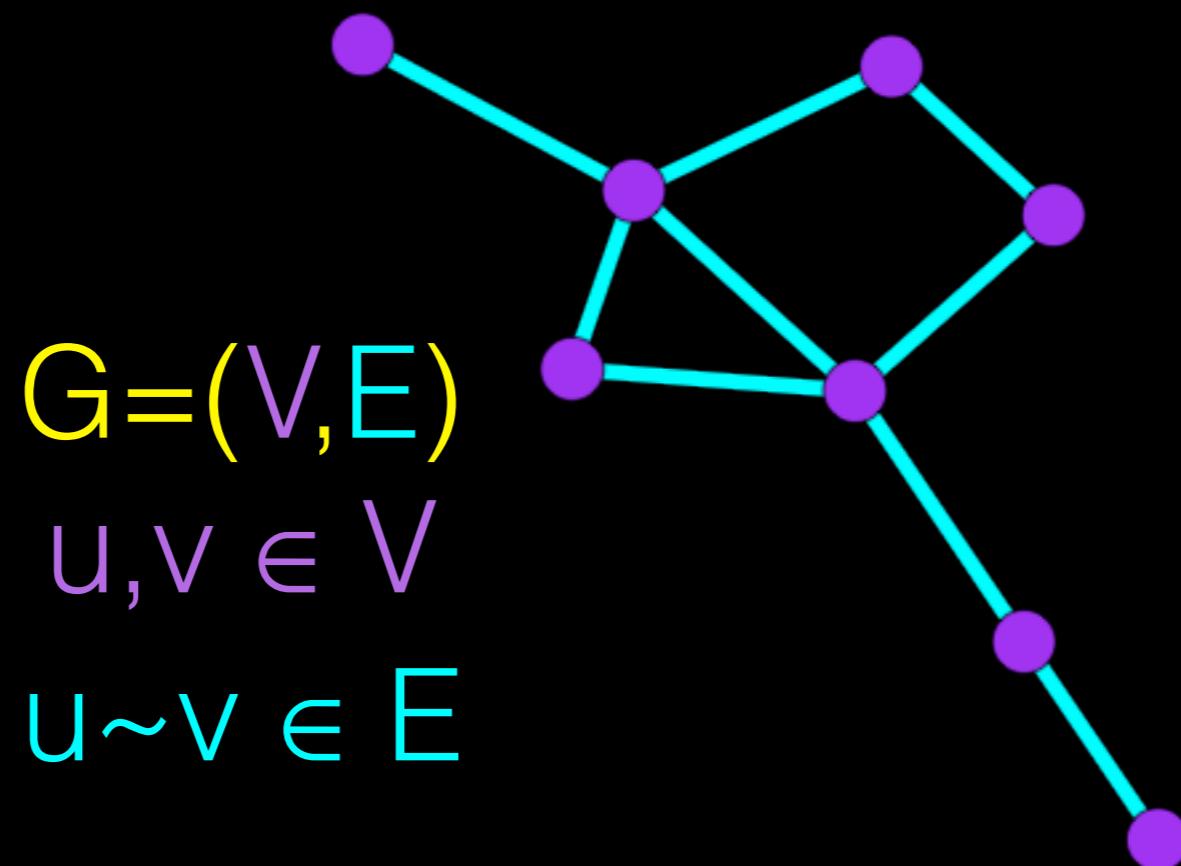
the same graph



the same graph

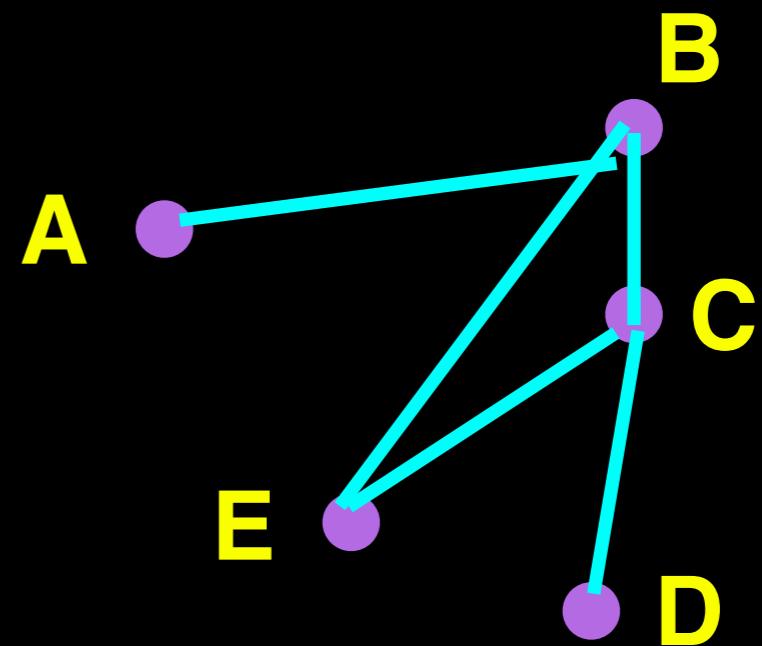


the same graph

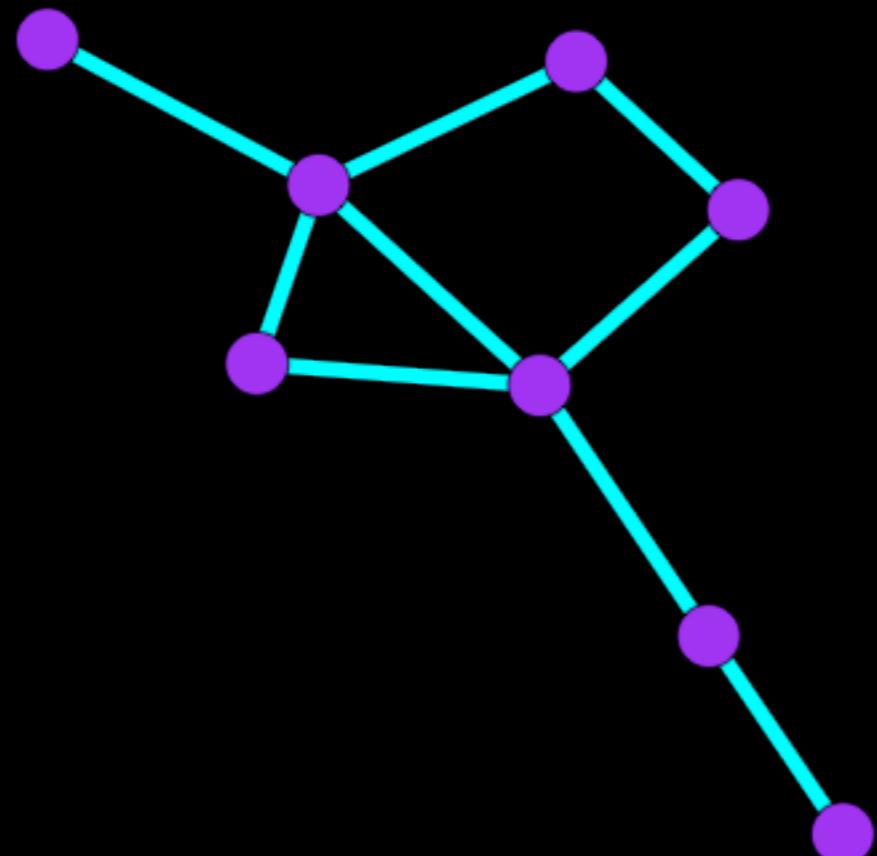


labeled graph

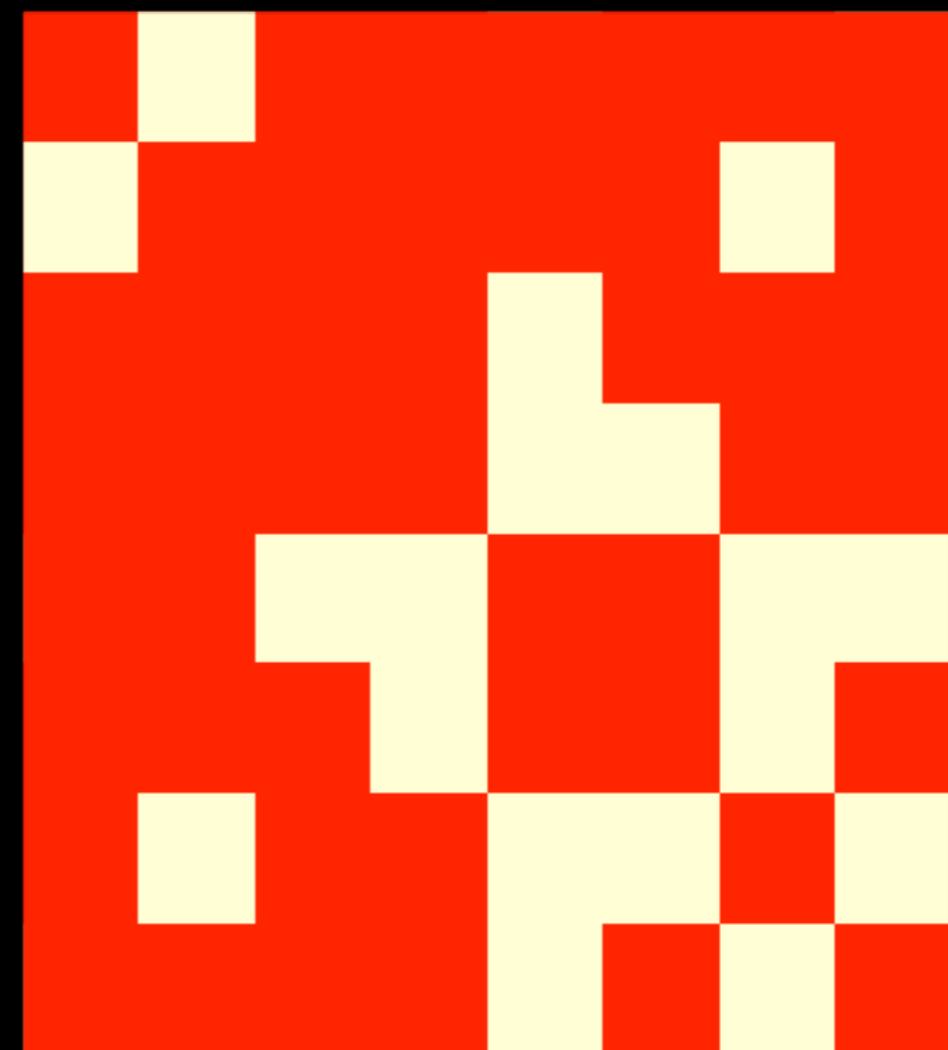
- uv means there is an edge between u & v
- e.g., in this graph AB , but not AE



same graph
(2D layout)

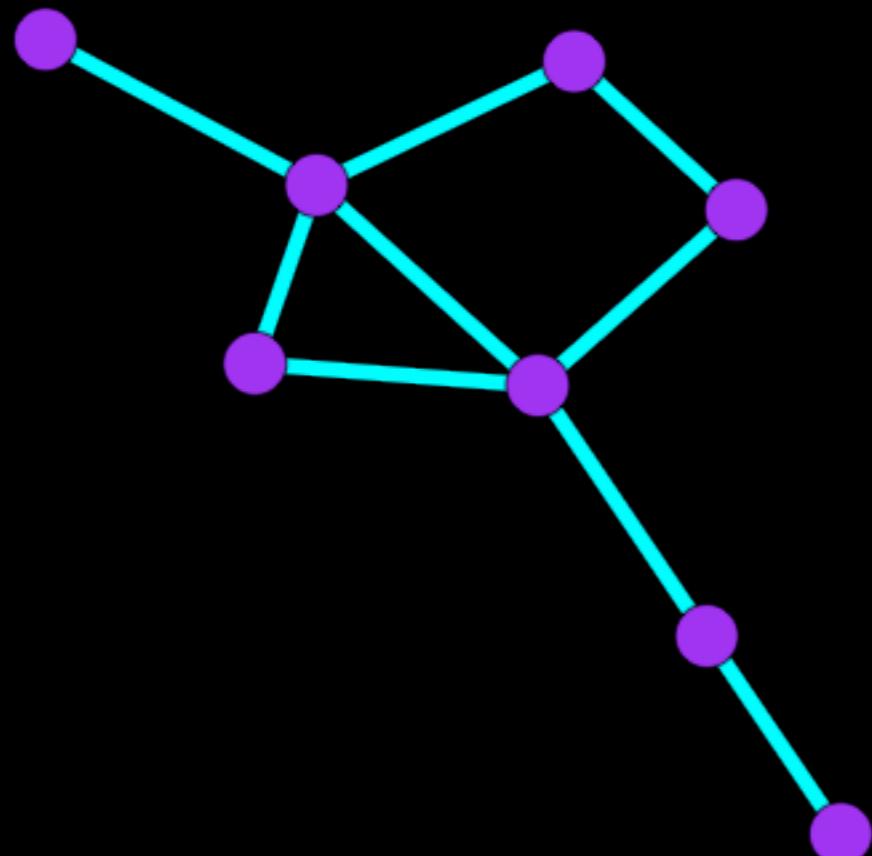


same graph
(adjacency matrix)

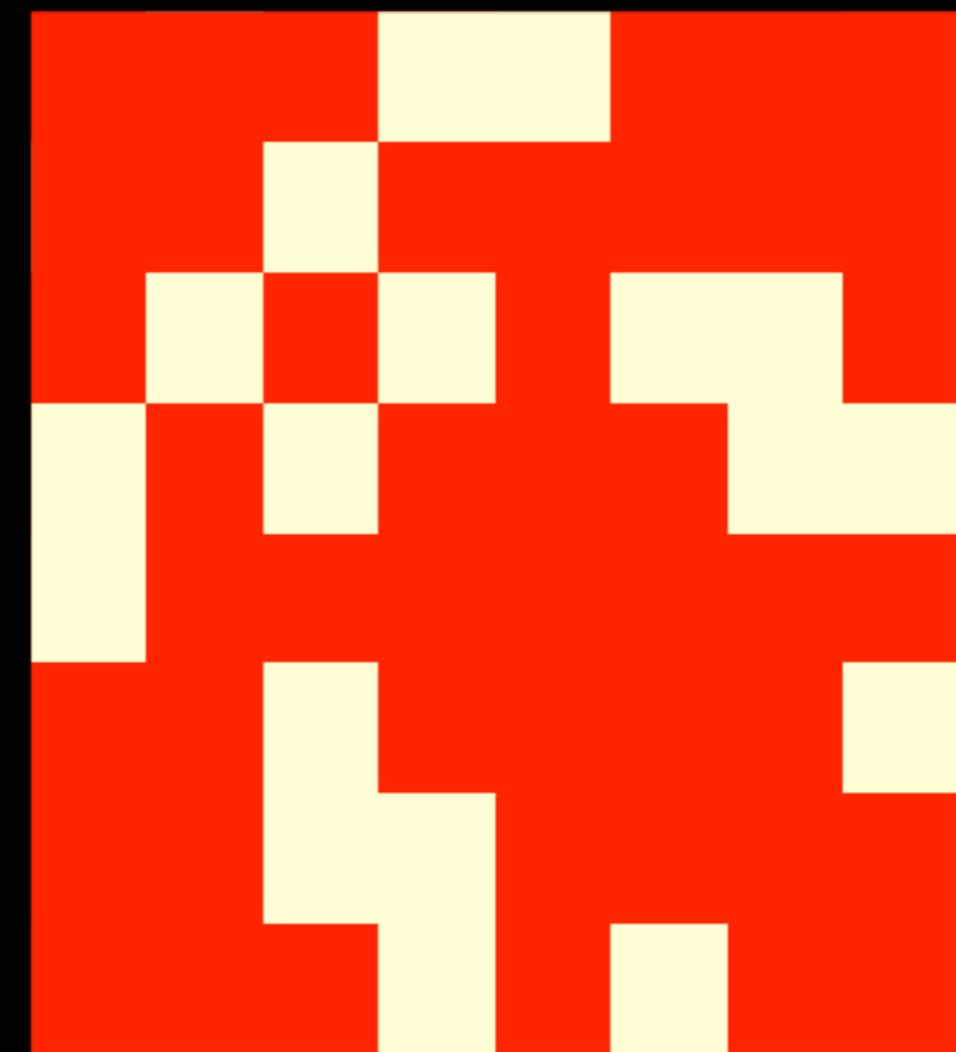


- A is the adjacency matrix
- $A(u,v) = 1$ iff $u \sim v$

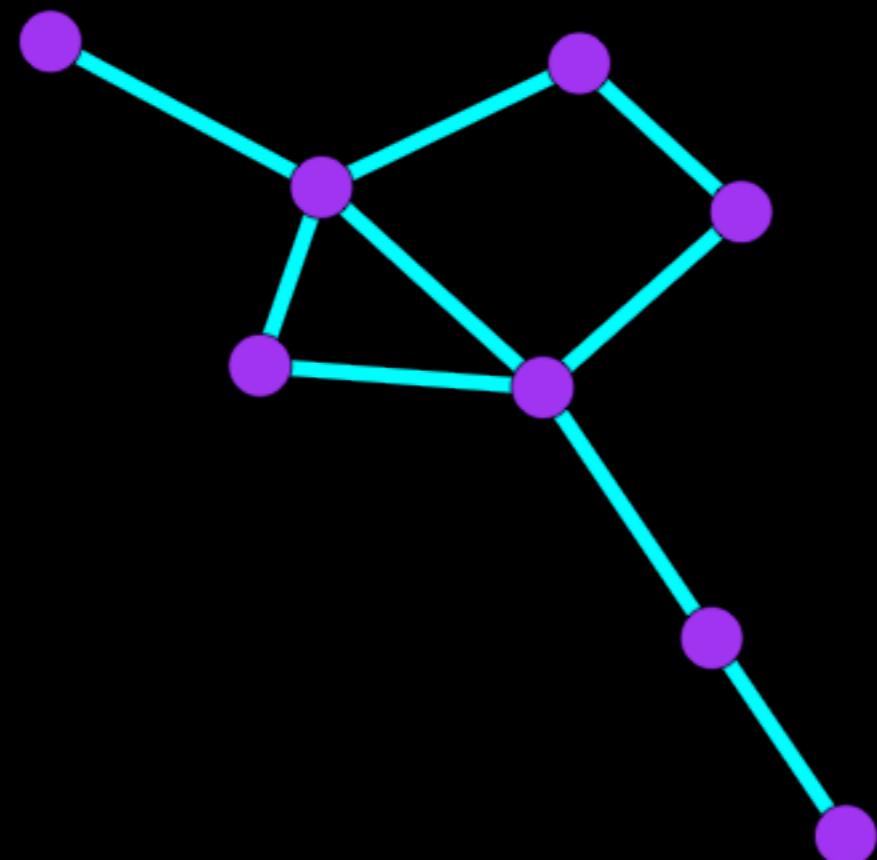
same graph
(2D layout)



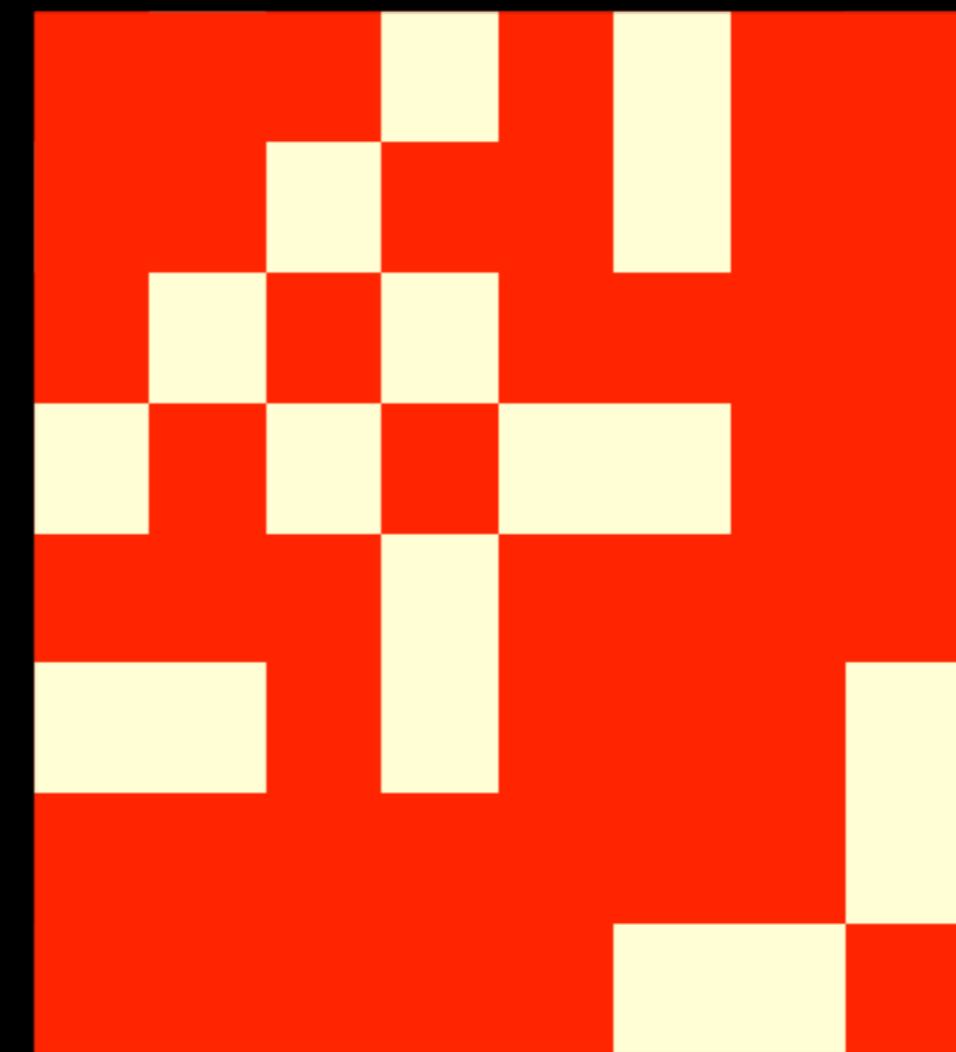
same graph
(adjacency matrix)



same graph
(2D layout)



same graph
(adjacency matrix)



Look at it

- *c. elegans*: $\sim 10^2$
- larval drosophila: $\sim 10^4$
- larval zebrafish, adult drosophila: $\sim 10^5$
- DTI-derived human connectome: $\sim 10^6$
- adult zebrafish, mouse: $\sim 10^7$
- monkey: $\sim 10^9$
- human: $\sim 10^{11}$

Keep it Simple

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

Keep it Simple

Neural Encoding: $P[r | s]$

Neural Decoding: $P[s | r]$

Neural Code: $P[s, r]$

Keep it Simple

Neural Encoding: $P[r | s]$

Connectome Encoding: $P[g | s]$

Neural Decoding: $P[s | r]$

Neural Code: $P[s, r]$

Keep it Simple

Neural Encoding: $P[r | s]$

Neural Decoding: $P[s | r]$

Neural Code: $P[s, r]$

Connectome Encoding: $P[g | s]$

Connectome Decoding: $P[s | g]$

Keep it Simple

Neural Encoding: $P[r | s]$

Neural Decoding: $P[s | r]$

Neural Code: $P[s,r]$

Connectome Encoding: $P[g | s]$

Connectome Decoding: $P[s | g]$

Connectome Code: $P[s,g]$

What's a connectome?

Principles of Data Science

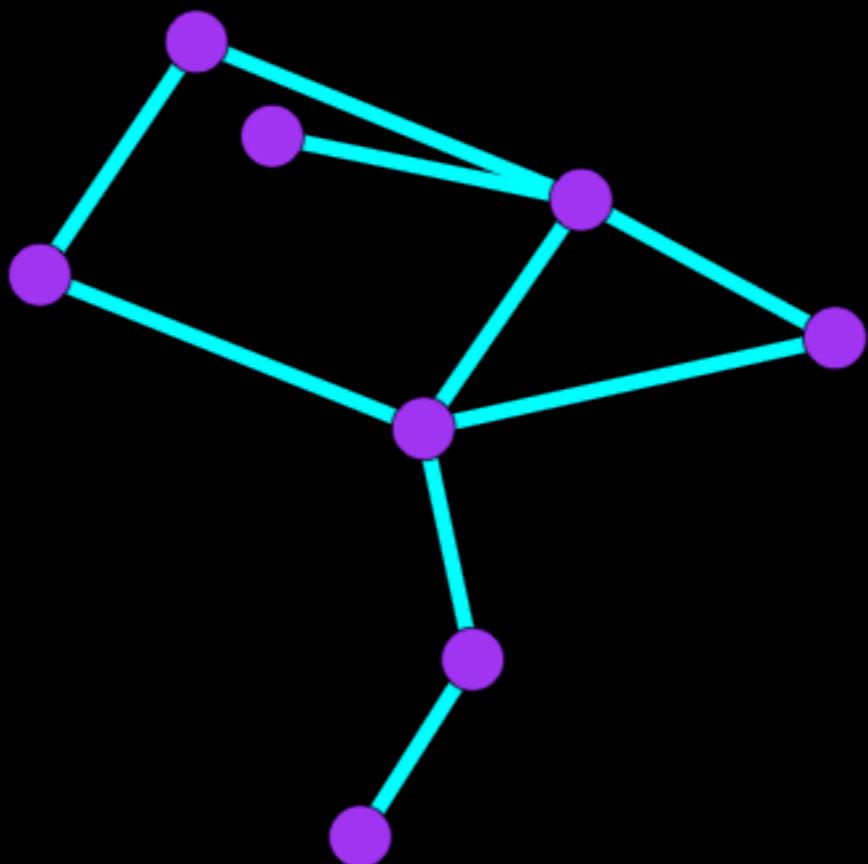
- Look at it
- Keep it simple

Principles of Data Science

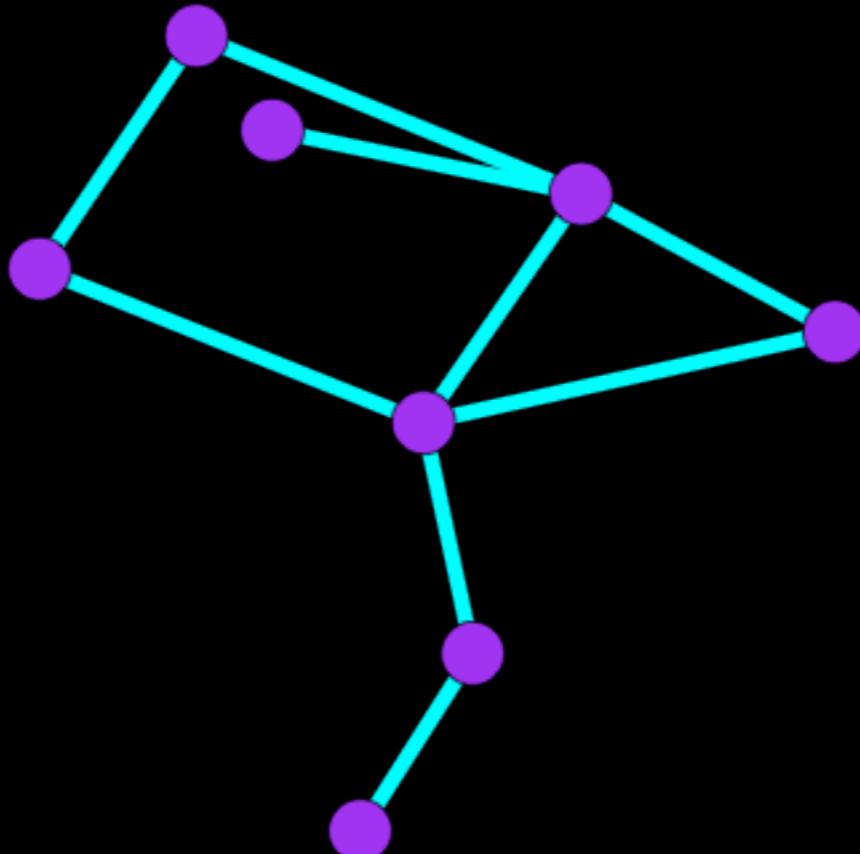
- Look at it
- Keep it simple

Let's do it for connectome coding now

connectome = brain-graph

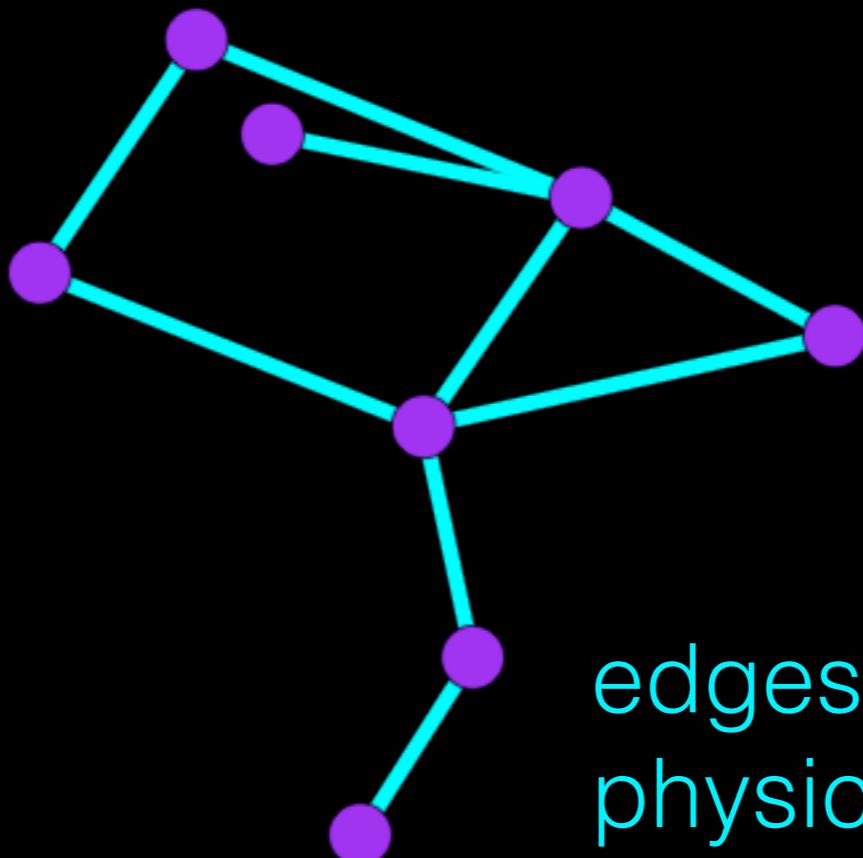


connectome = brain-graph



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

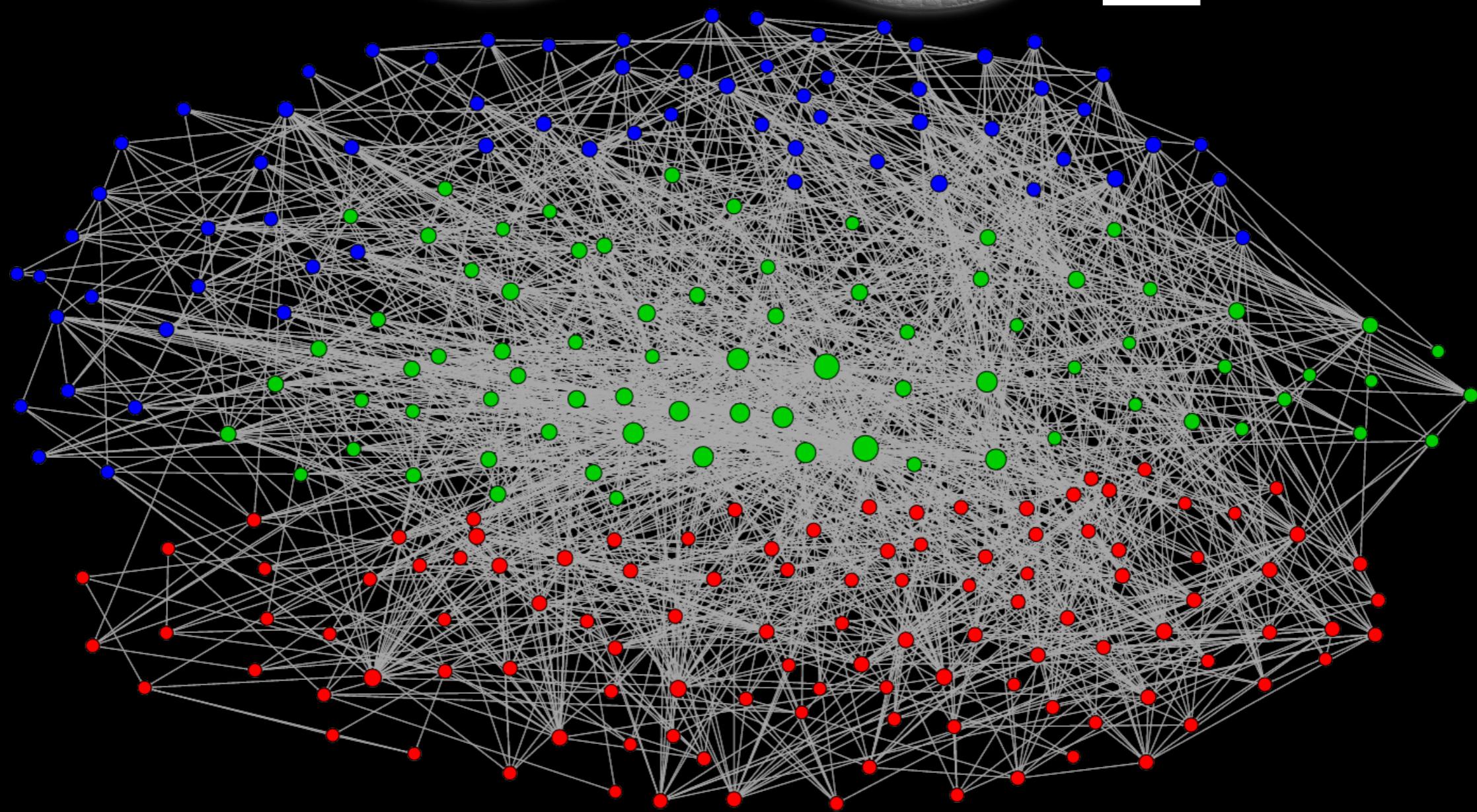
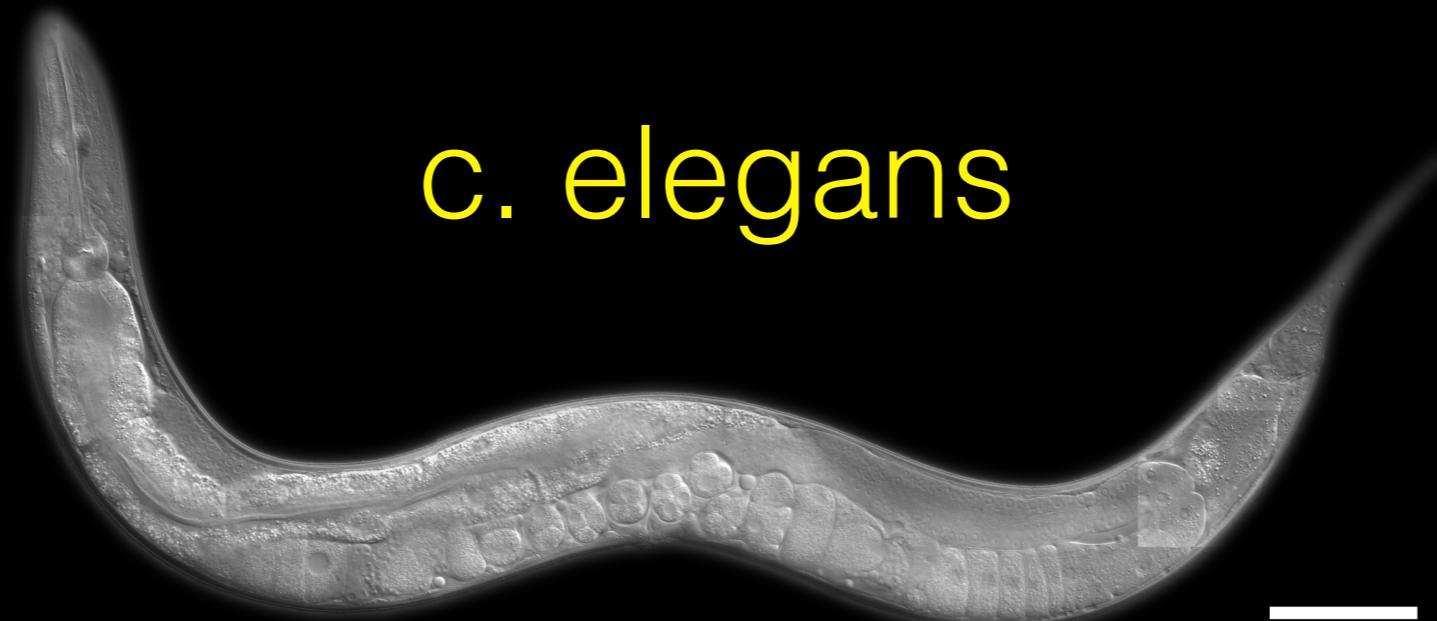
connectome = brain-graph



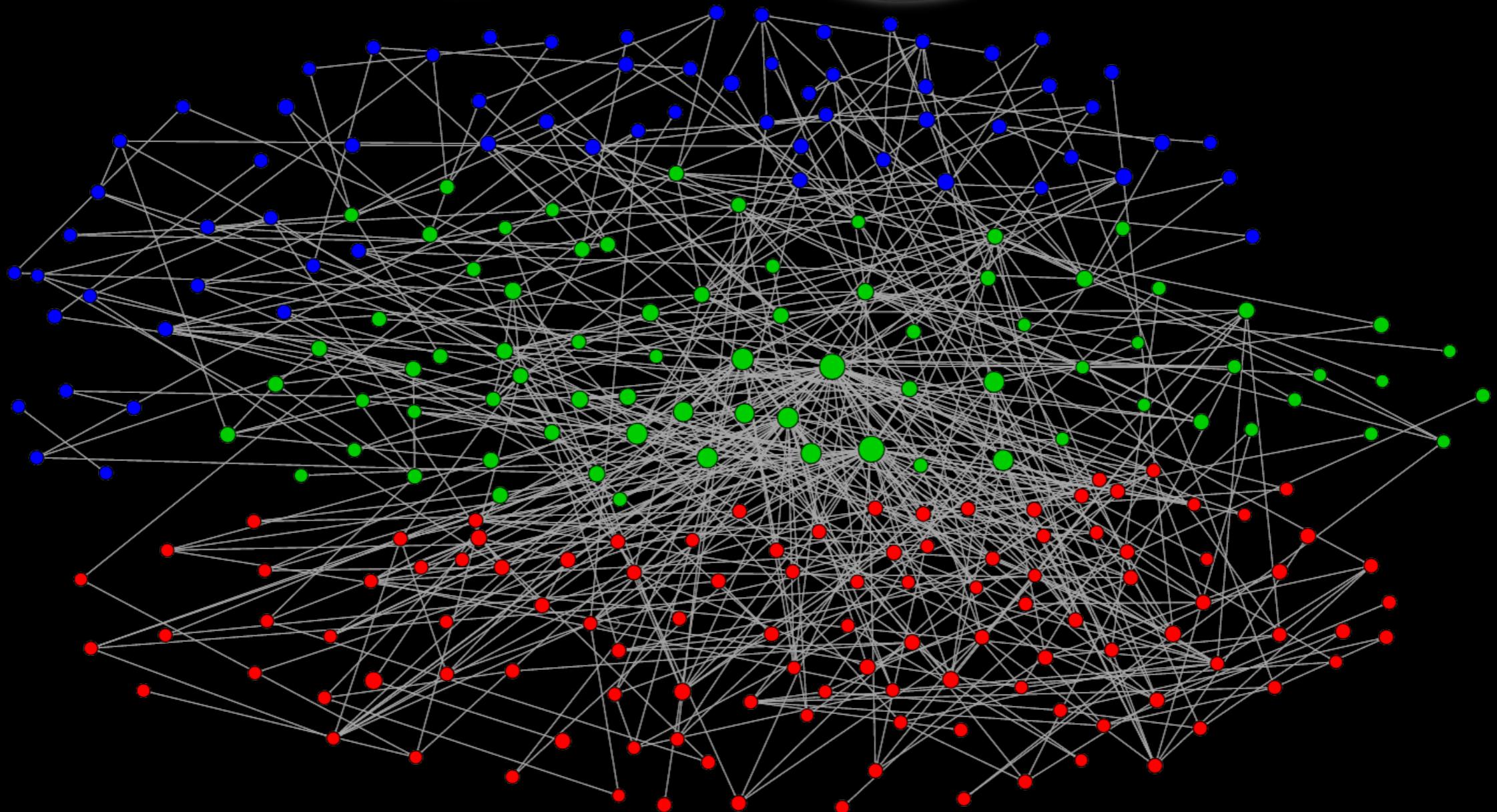
vertices:
brain regions
or voxels
or electrodes
or neurons
or even compartments

edges:
physical connections
or functional connections
or correlations

c. elegans



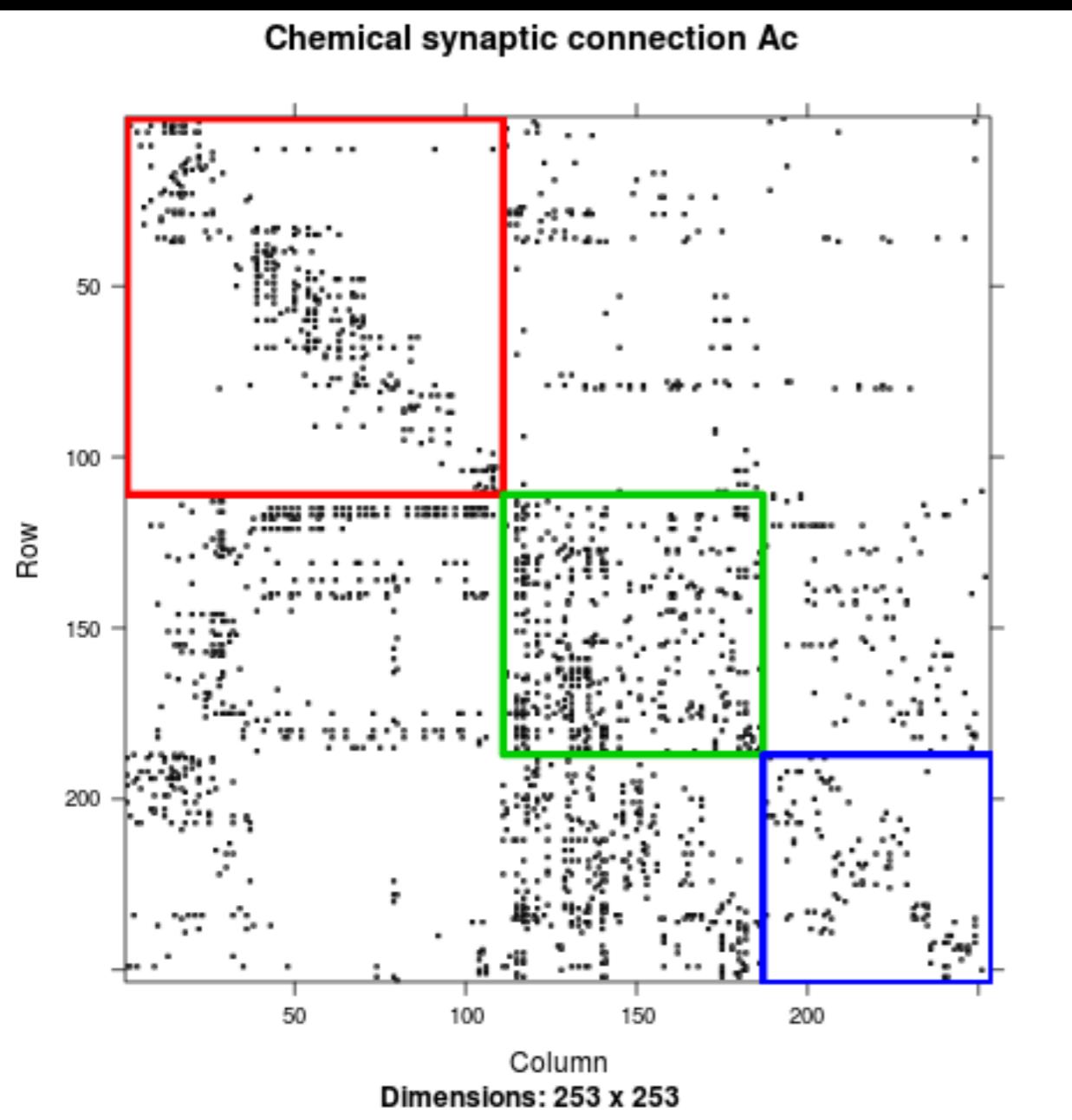
c. elegans



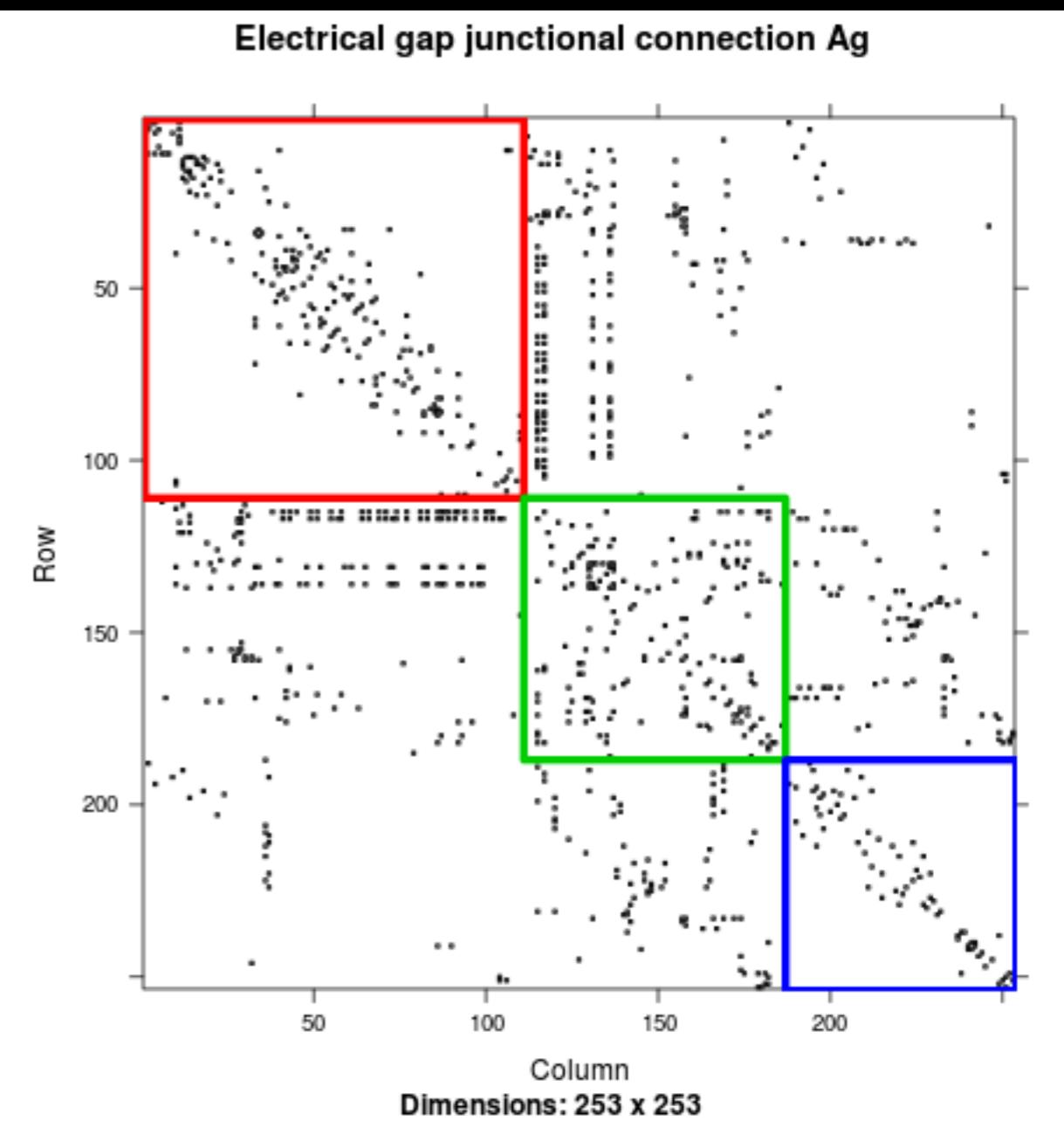
c. elegans



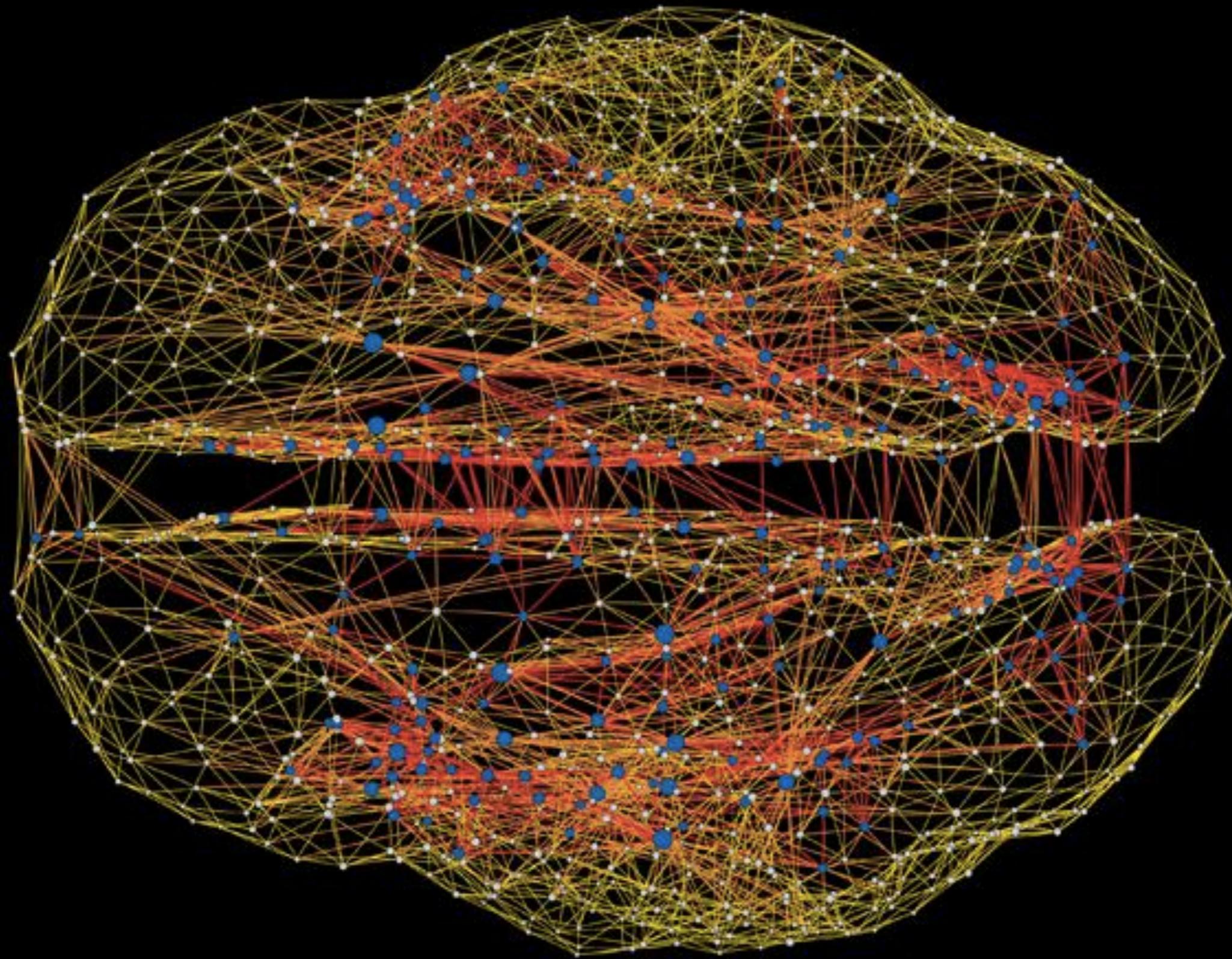
Chemical synaptic connection Ac



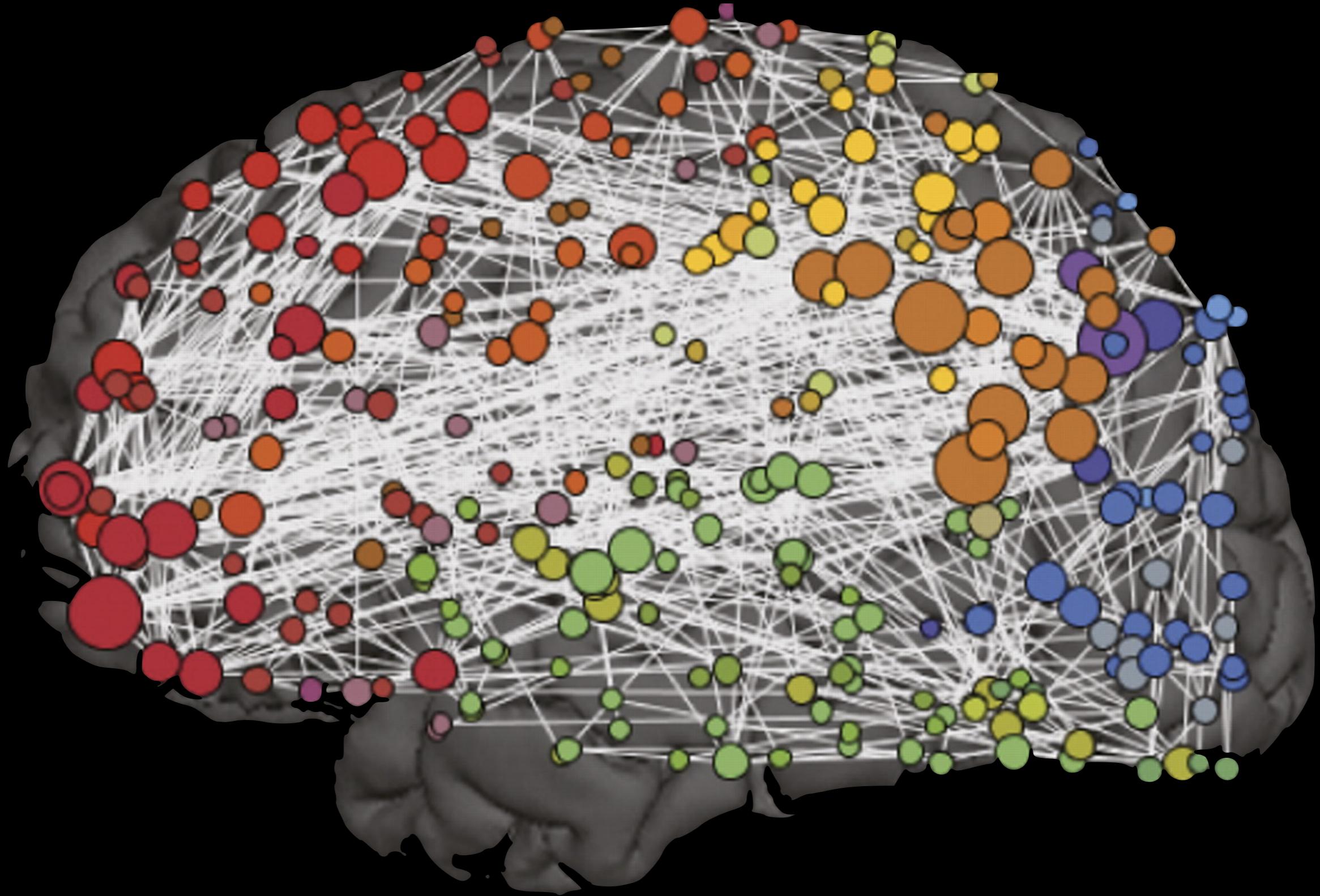
Electrical gap junctional connection Ag



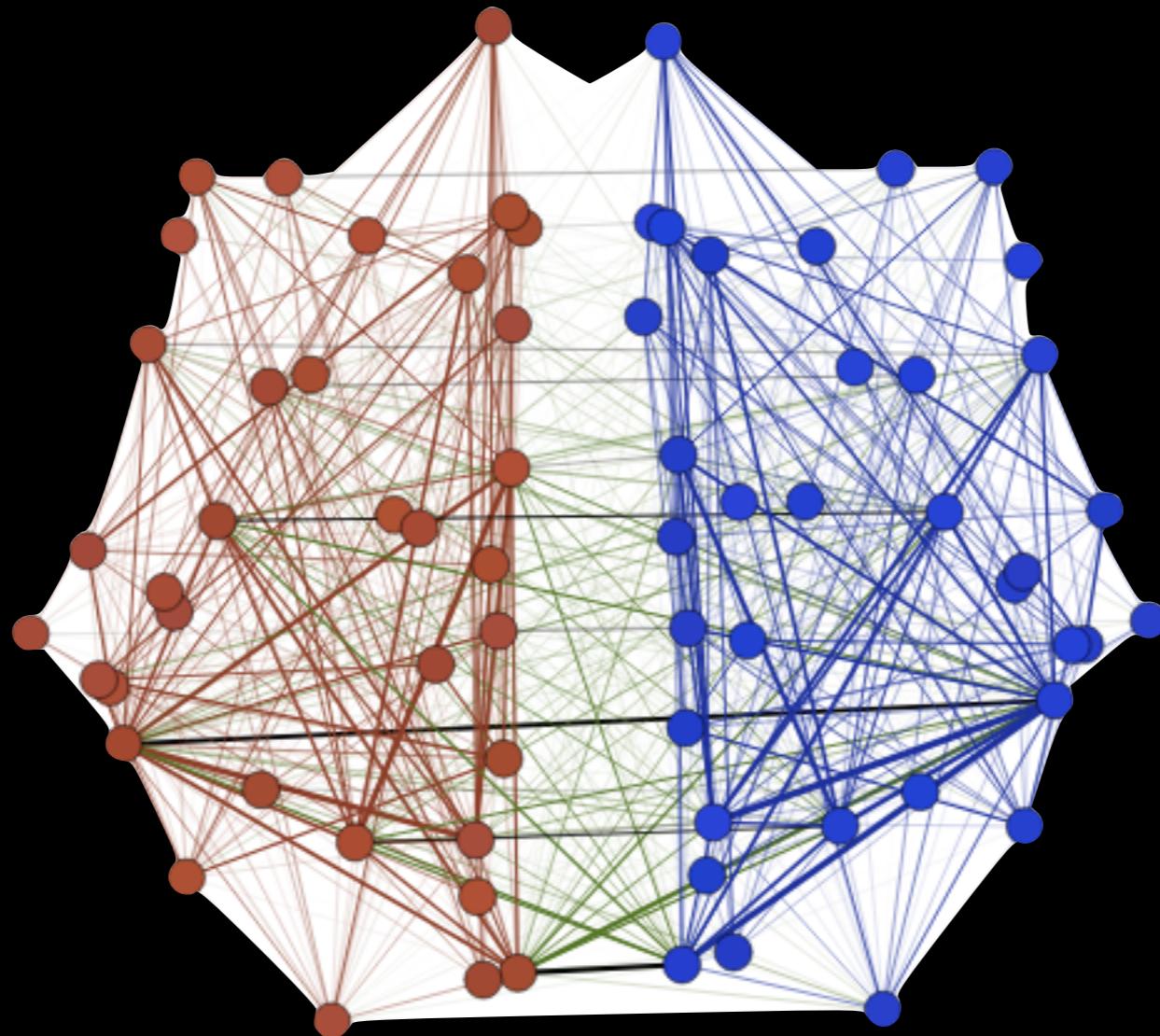
human connectome



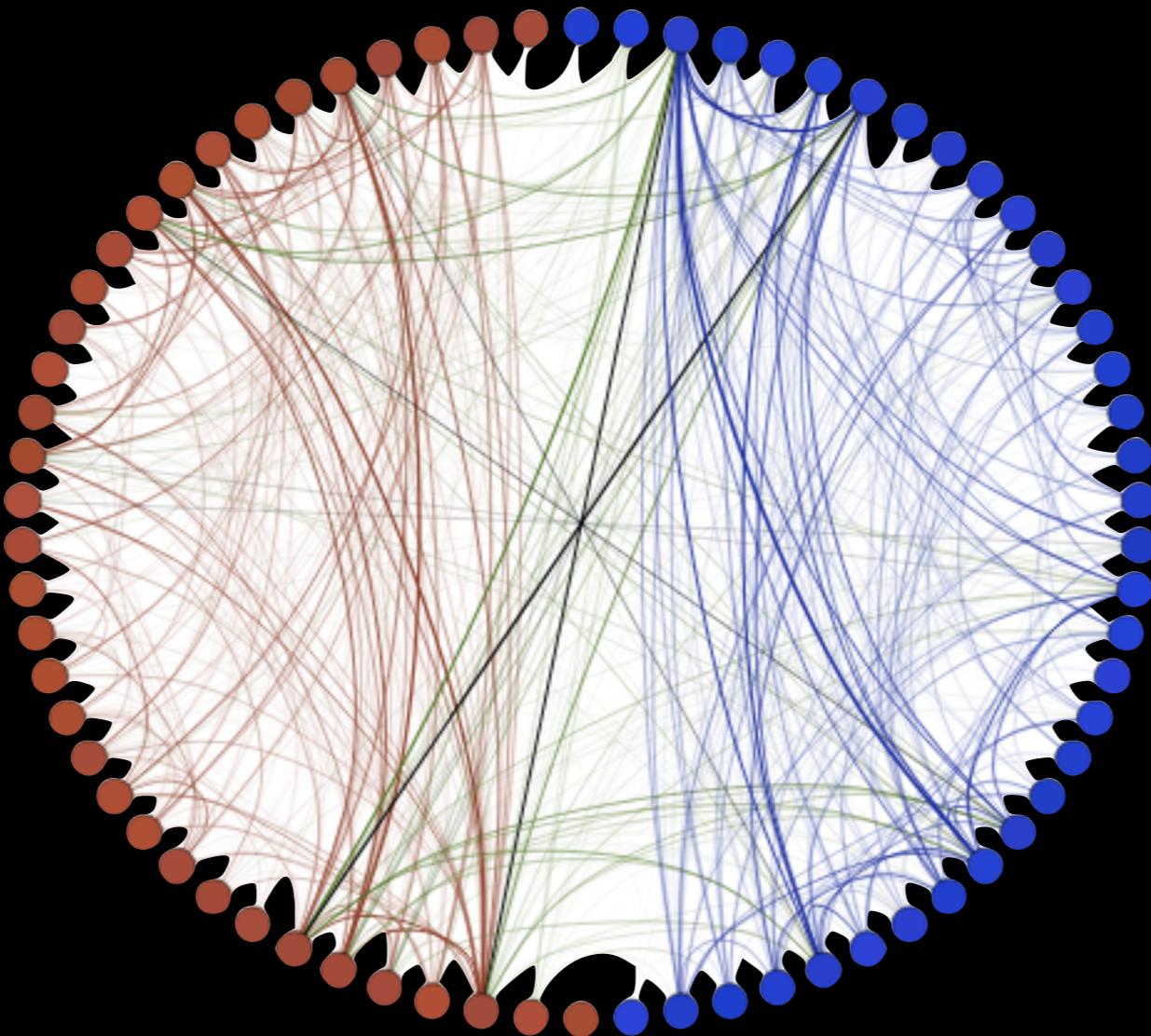
human connectome



human connectome



human connectome



Keep it Simple

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

Principles of Data Science

- Look at it
- Keep it simple

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



Keep it Simple

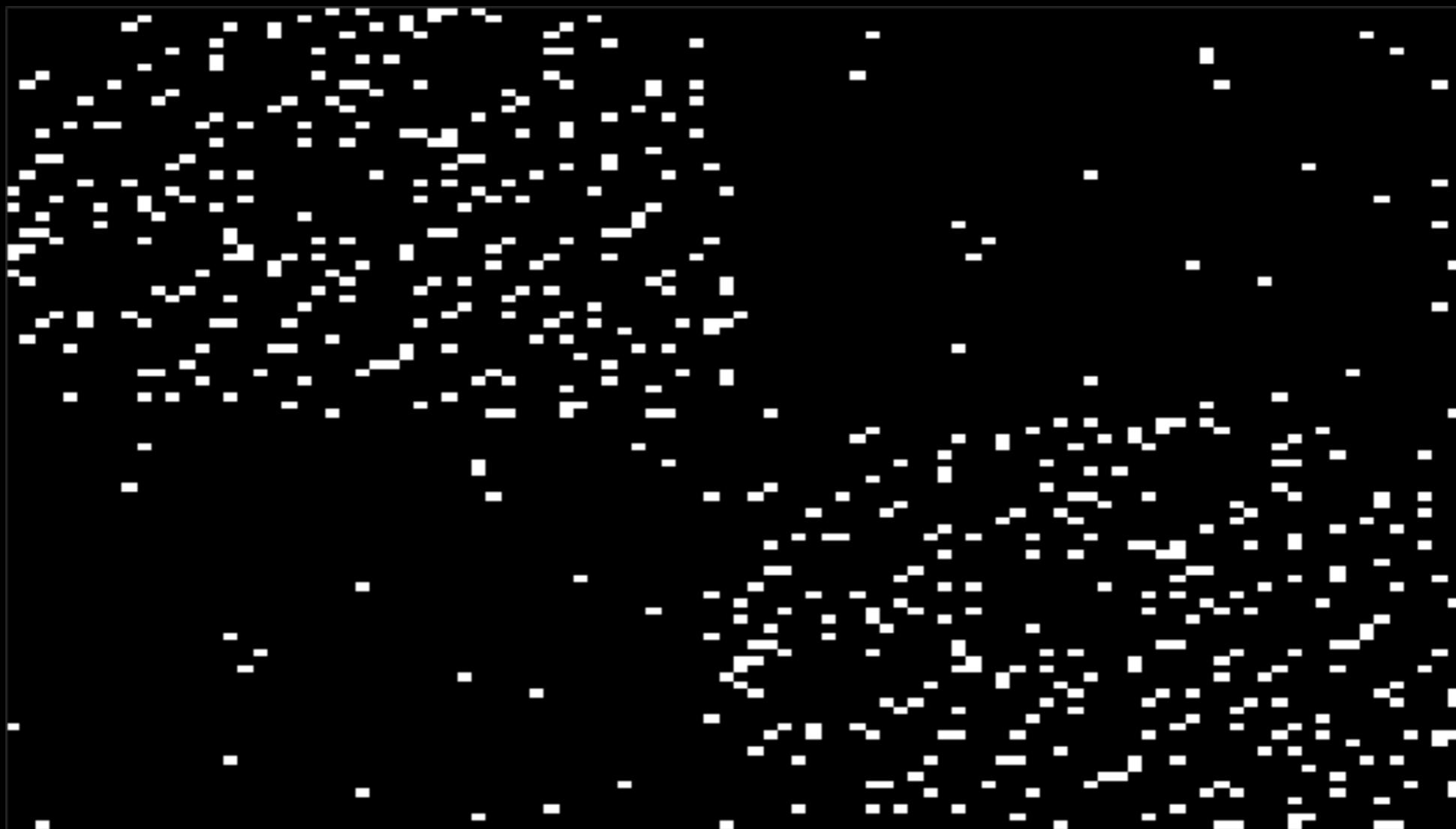
- Each spike is independent
- Probability of a spike at any time is λ_i
- $P[r|s] = \text{Poisson}(\lambda_s)$

Principles of Data Science

- Look at it
- Keep it simple

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

Look at it



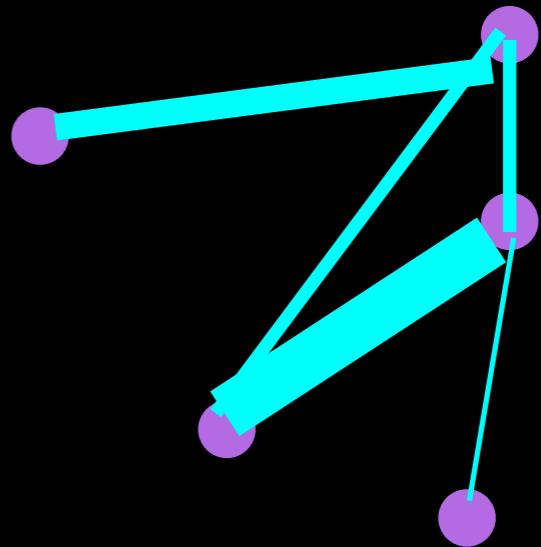
Keep it Simple

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

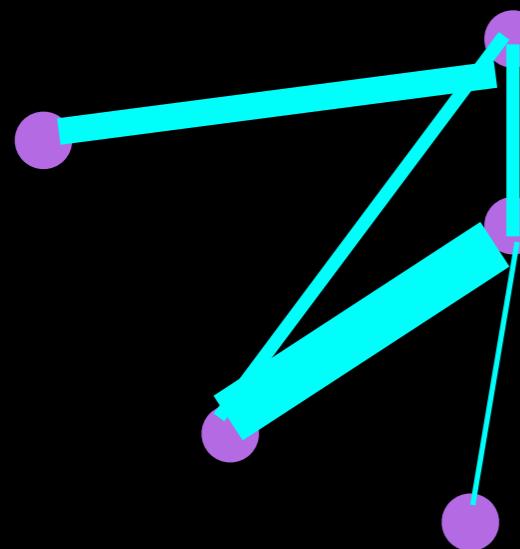
let's do it for a little bit more
complex models

weighted graph

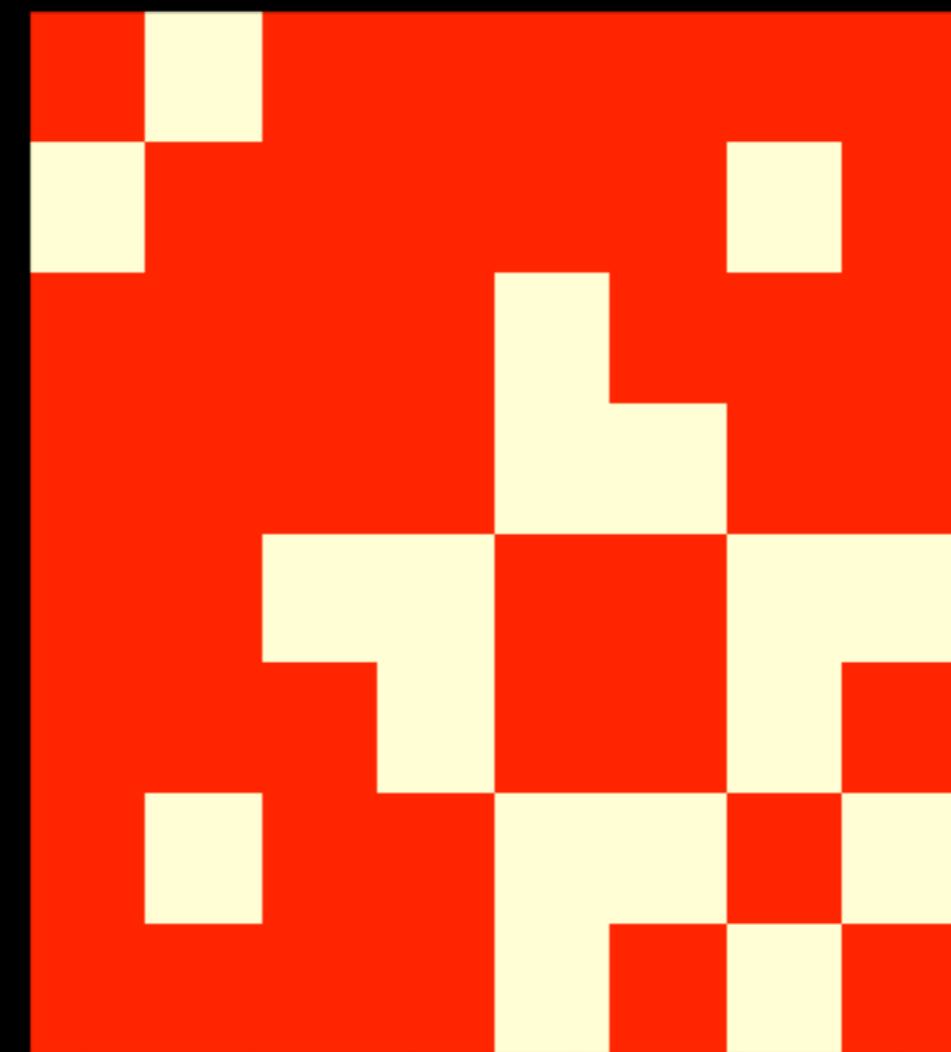
- each edge has a weight
- weights can be positive,
negative, integer, zero, etc.



weighted graph
(2D layout)

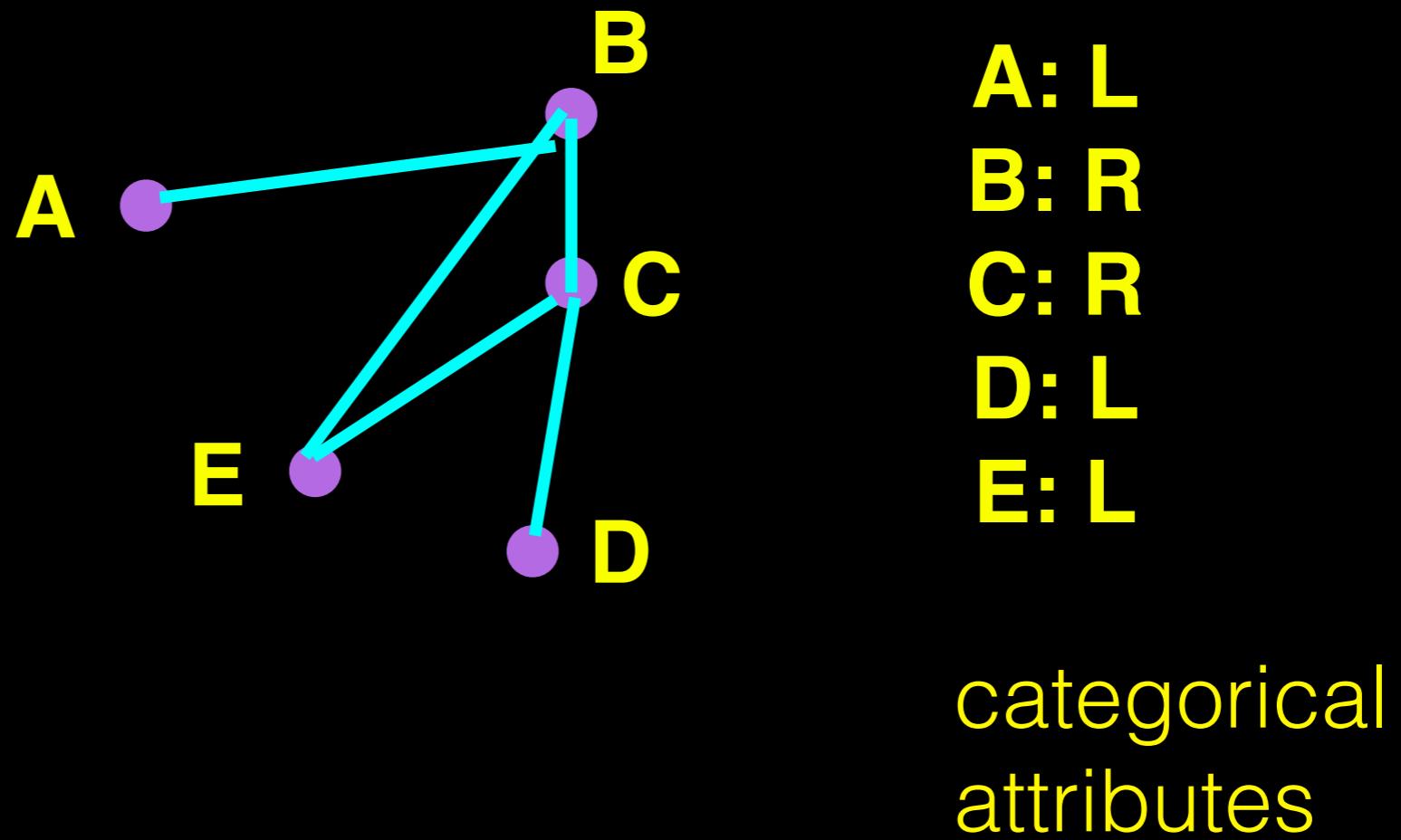


weighted graph
(adjacency matrix)

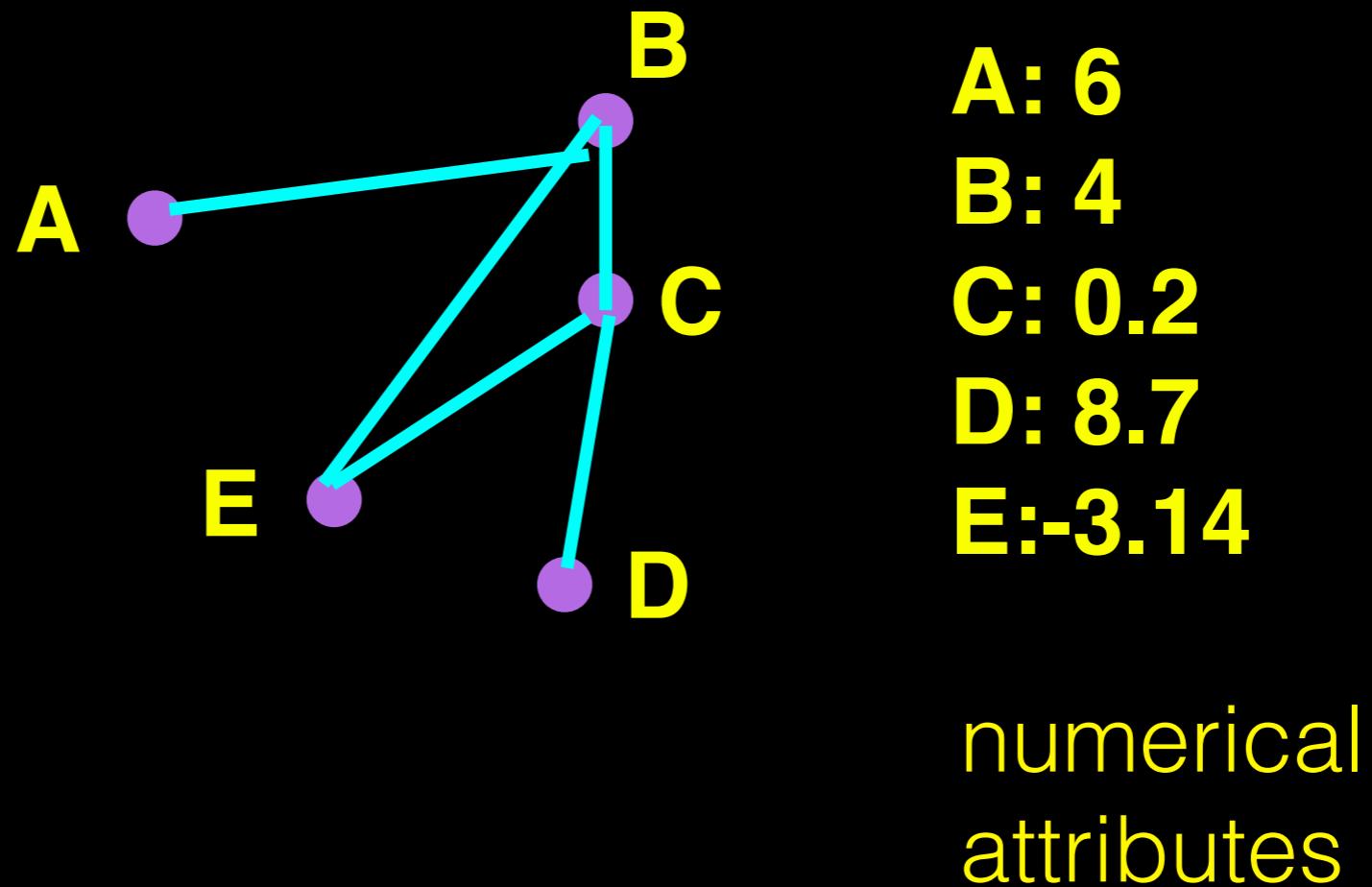


elements of A can take any value

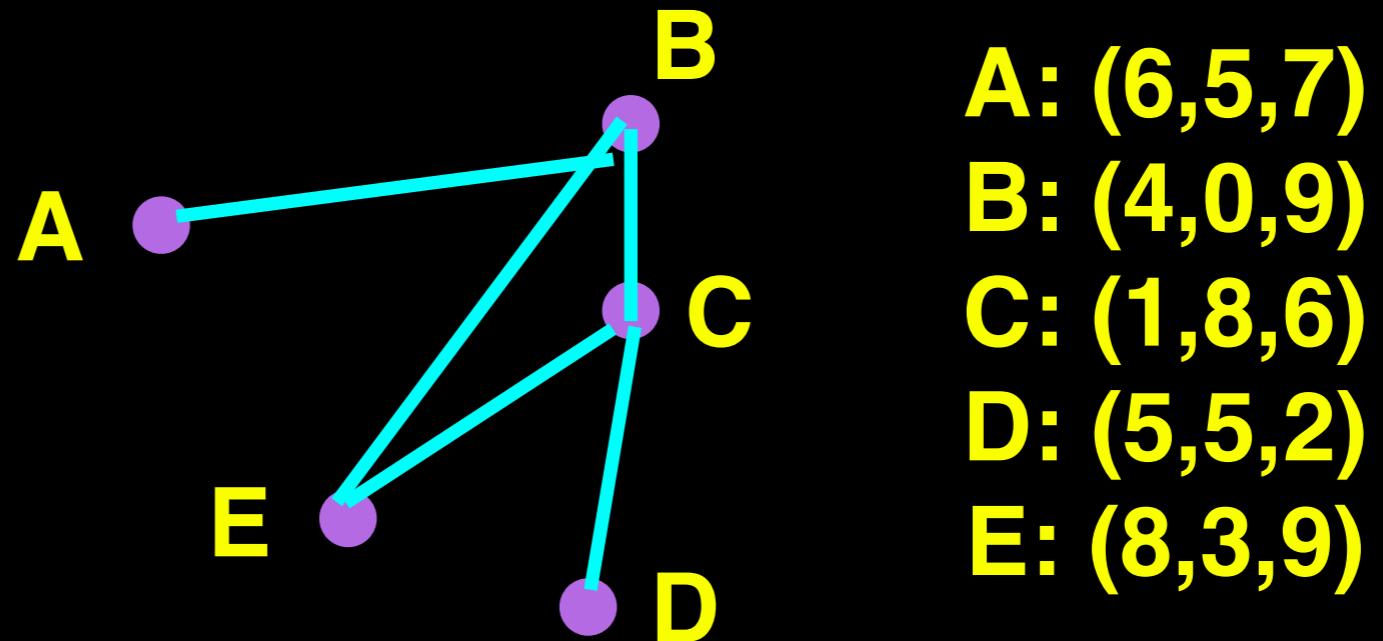
vertex attributed graph



vertex attributed graph

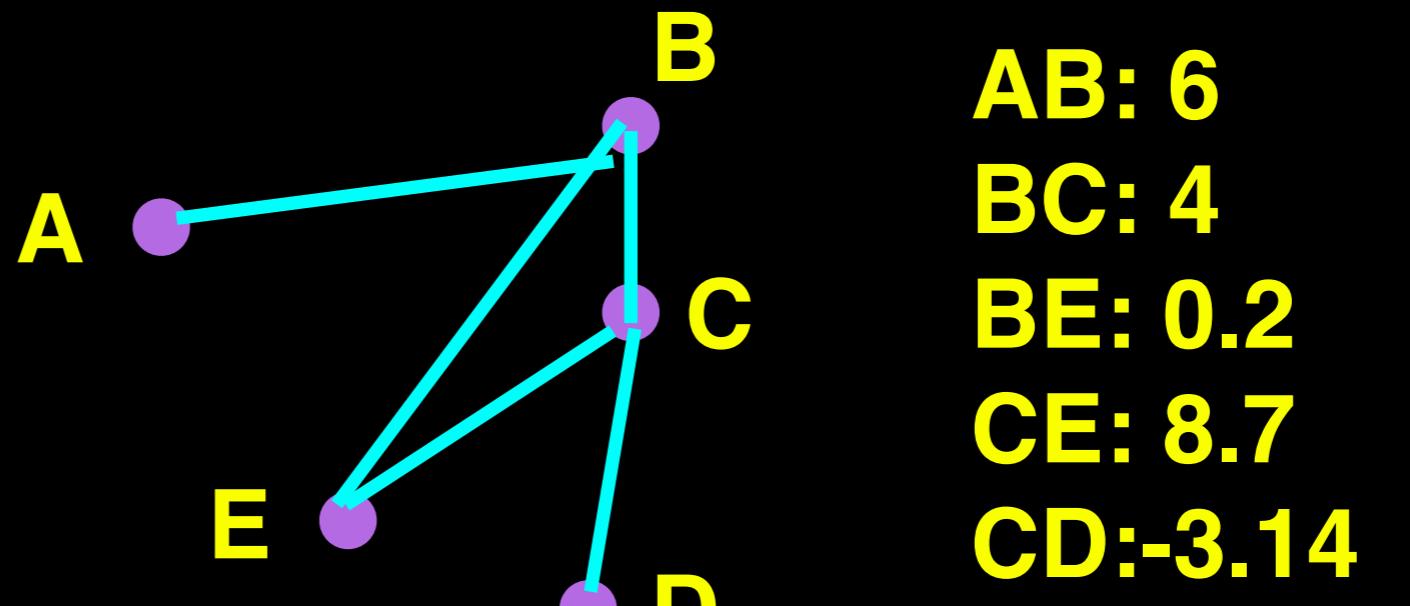


vertex attributed graph



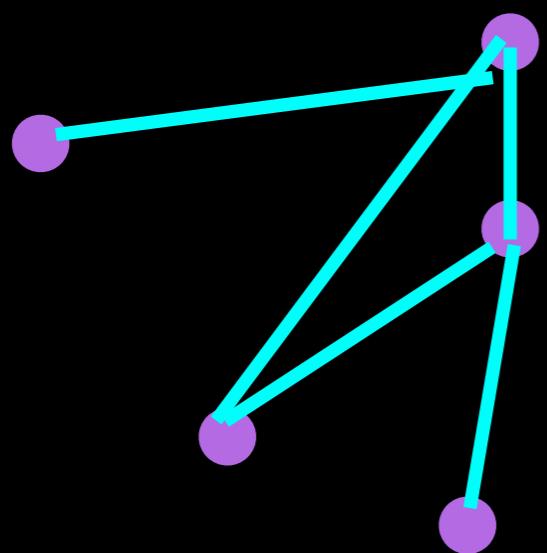
multi-dimensional
attributes

edge attributed graph

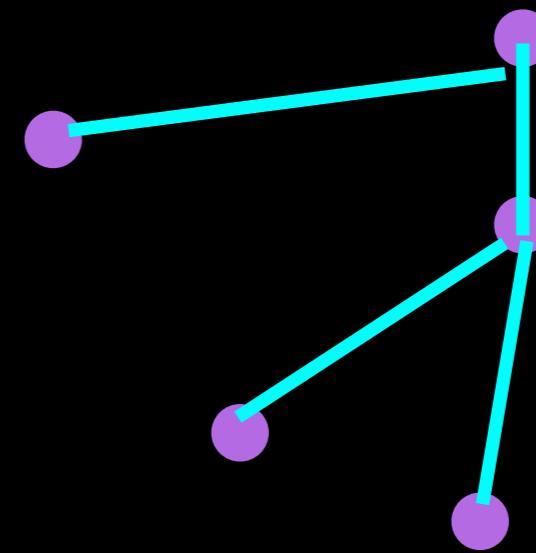


numerical
attributes

graph attributed graphs

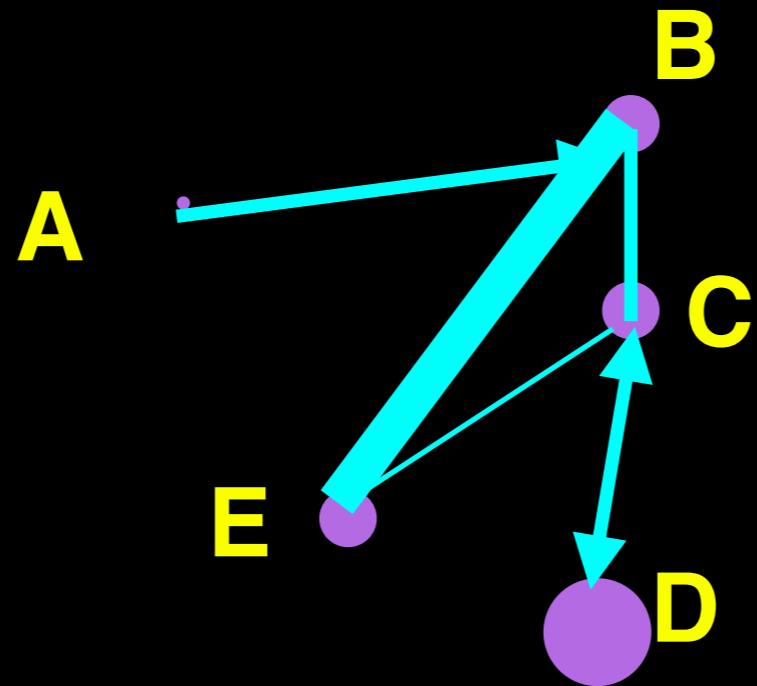


subject 1



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 |

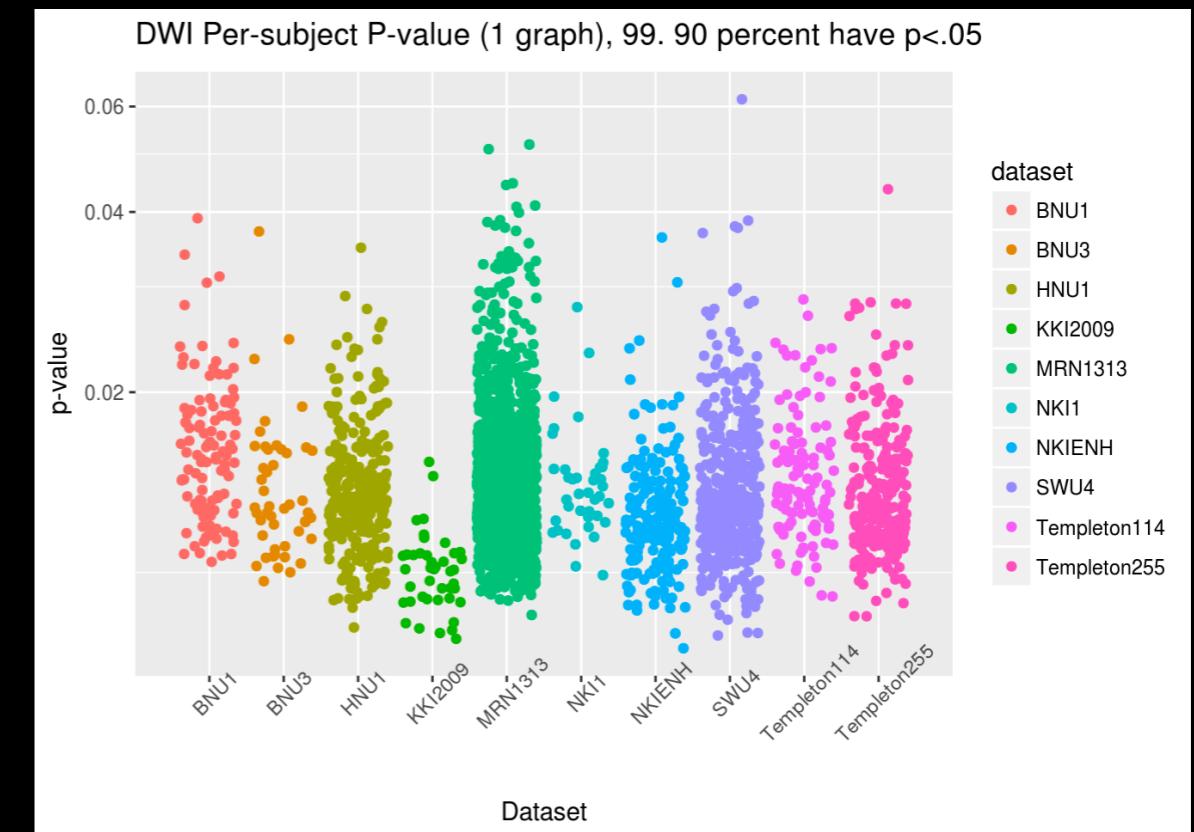
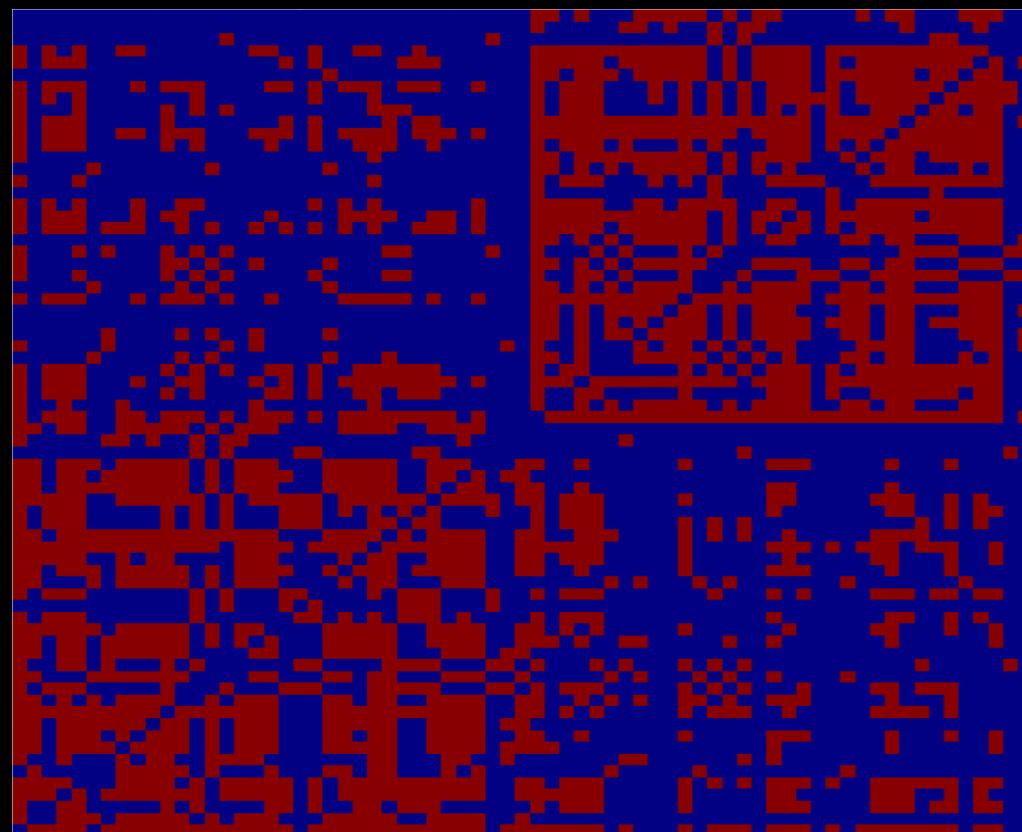
Latent Structure Model

- 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

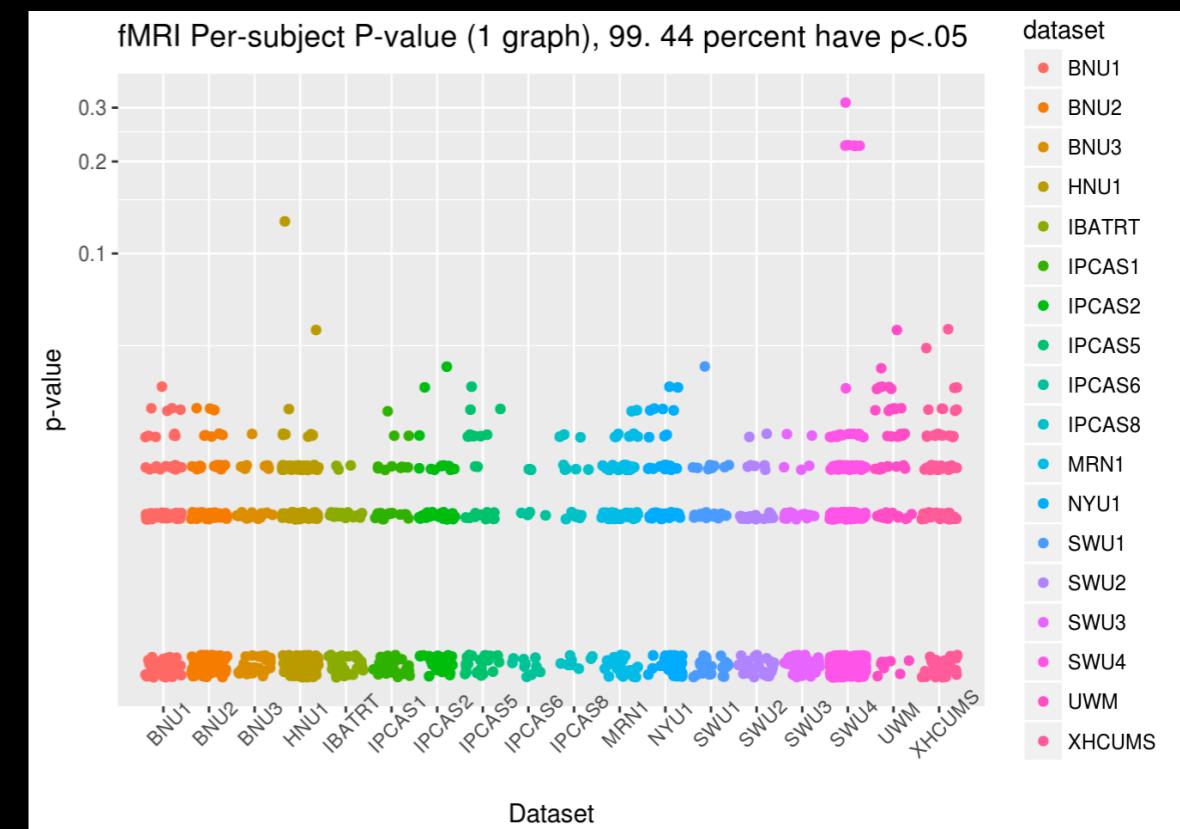
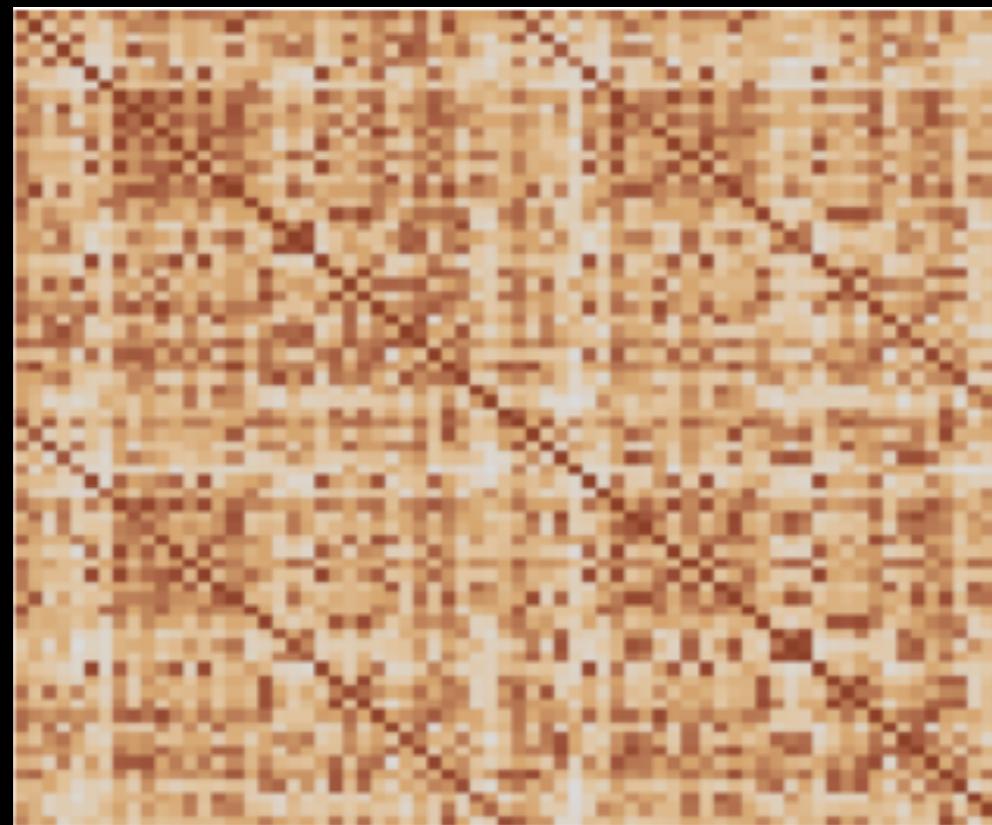
Human DTI Connectome Code

ipsilateral connections are stronger than contralateral

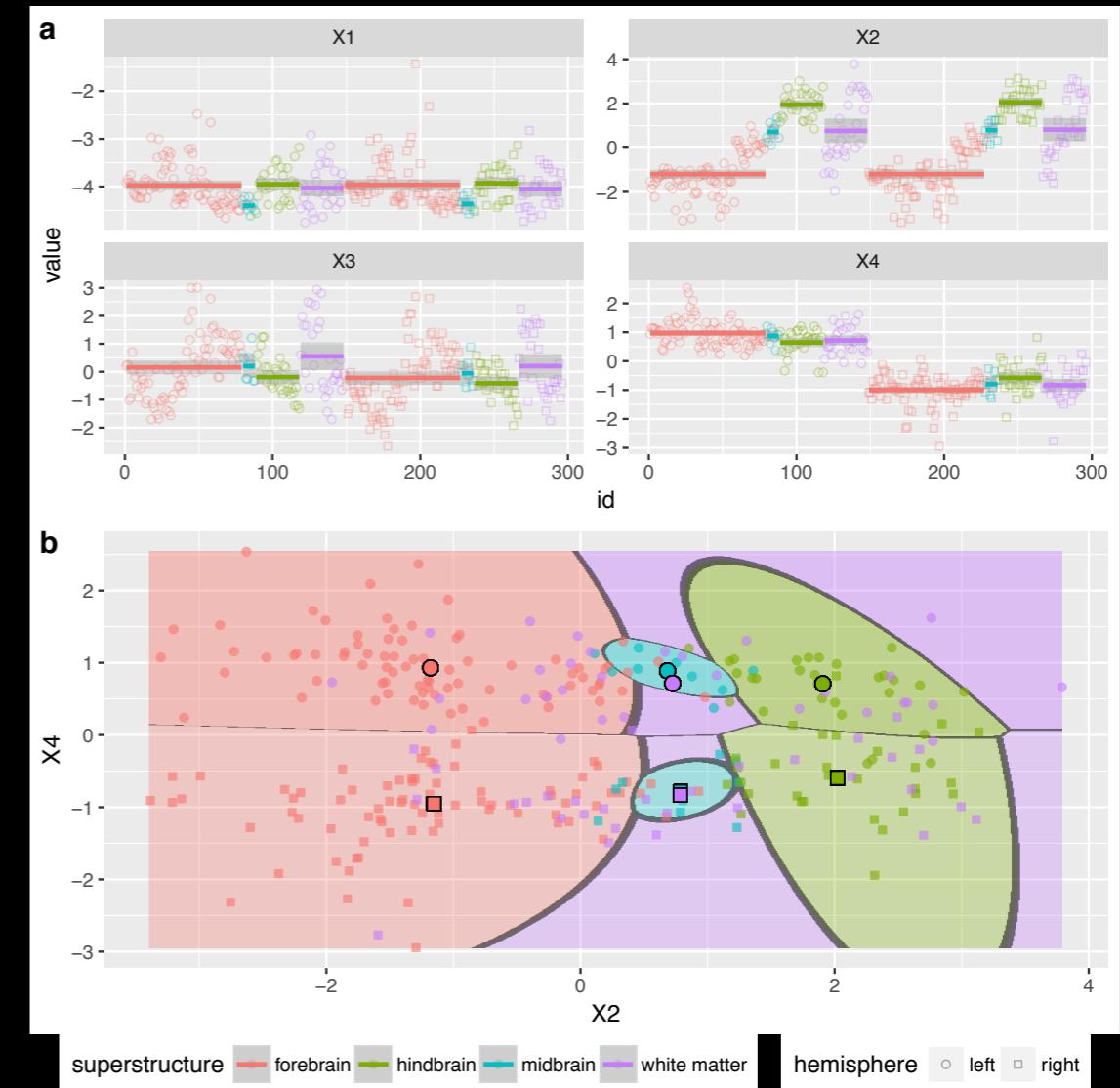
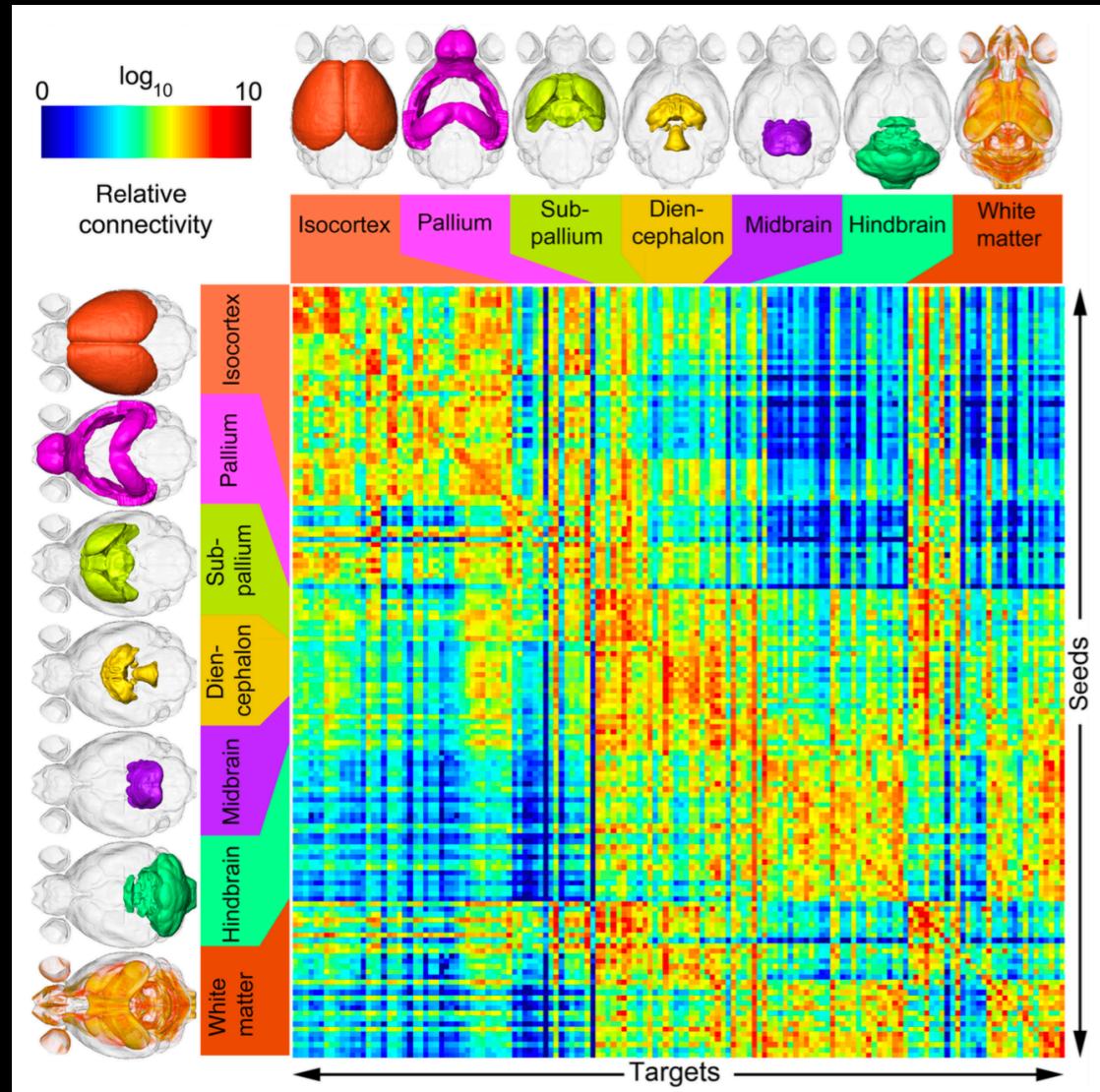


Human fMRI Connectome Code

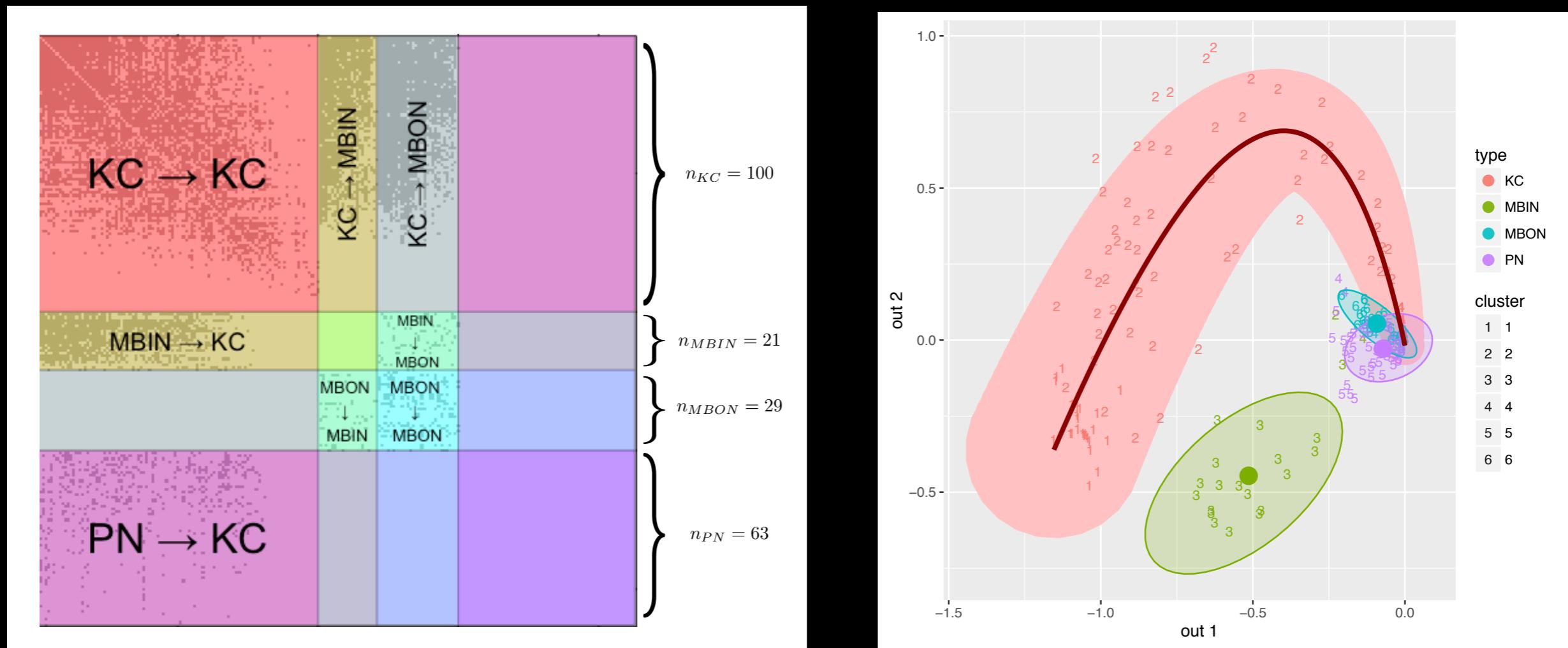
bilateral connections are stronger than non-bilateral



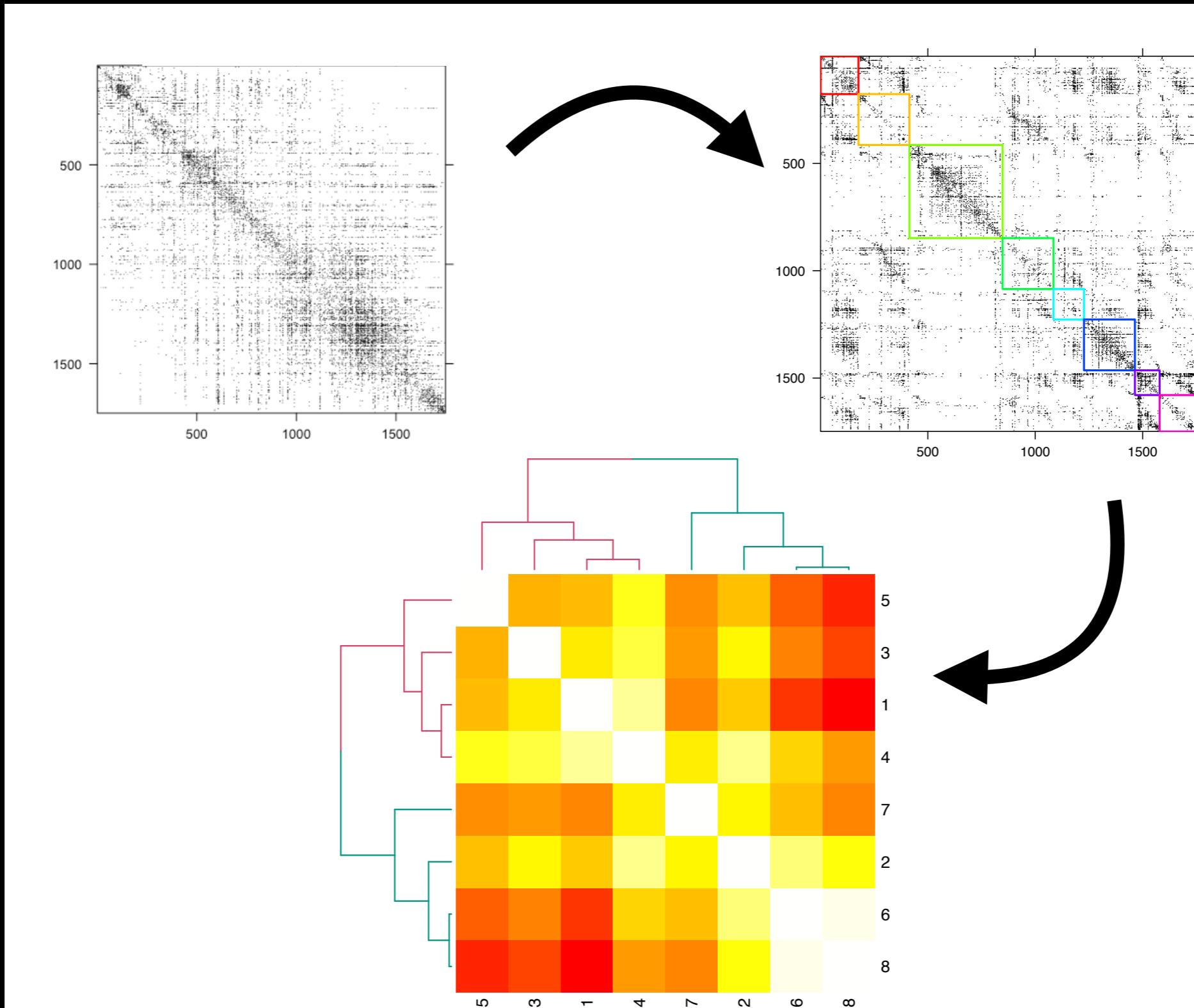
Mouse Connectome Code



Larval Drosophila Mushroom Body Connectome Code



Drosophila Optic Medulla Connectome Code



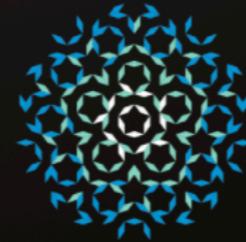
References

- 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



$$\Pr[\mathbf{A}|\mathbf{X}] = \prod_{i < j} (\mathbf{X}_i^\top \mathbf{X}_j)^{\mathbf{A}_{ij}} (1 - \mathbf{X}_i^\top \mathbf{X}_j)^{1 - \mathbf{A}_{ij}}$$

$$\Pr[\mathbf{A}|\mathbf{X}] = \prod_{i < j} \mathbf{P}_{ij}^{\mathbf{A}_{ij}} (1 - \mathbf{P}_{ij})^{1 - \mathbf{A}_{ij}}$$

$$\mathbf{A}\sim\text{SBM}(\tau,\{\mathbf{X}_{(i)}\}_{i=1}^K)$$

$$\mathbf{A}\sim\text{SBM}(\pi,\{X_{(i)}\}).$$

$$\mathbf{P}_{ij}=\mathbf{B}_{\tau(i),\tau(j)},$$

$$\mathbb{P}\left(\|\mathbf{A}-\mathbf{P}\| \leq 2\sqrt{\delta(\mathbf{P})} + C\delta^{1/4}(\mathbf{P})\ln n\right) \geq 1-n^{-c}.$$

$$\max_i \|(\hat{\mathbf{X}}_n)_i - \mathbf{W}_n(\mathbf{X}_n)_i\| \leq \frac{Cd^{1/2}\log^2 n}{\delta^{1/2}(\mathbf{P}_n)}$$

$$\lim_{n\rightarrow\infty}\Pr\left[n^{1/2}\left(\hat{\mathbf{X}}_n\mathbf{W}_n-\mathbf{X}_n\right)_i\leq z\right]=\int_{\mathrm{supp}\, F}\Phi\left(z,\Sigma(\mathbf{x})\right)dF(\mathbf{x}),$$