Connectome Coding

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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**

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Ongoing environment: stimulus, movements, rewards, etc.

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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

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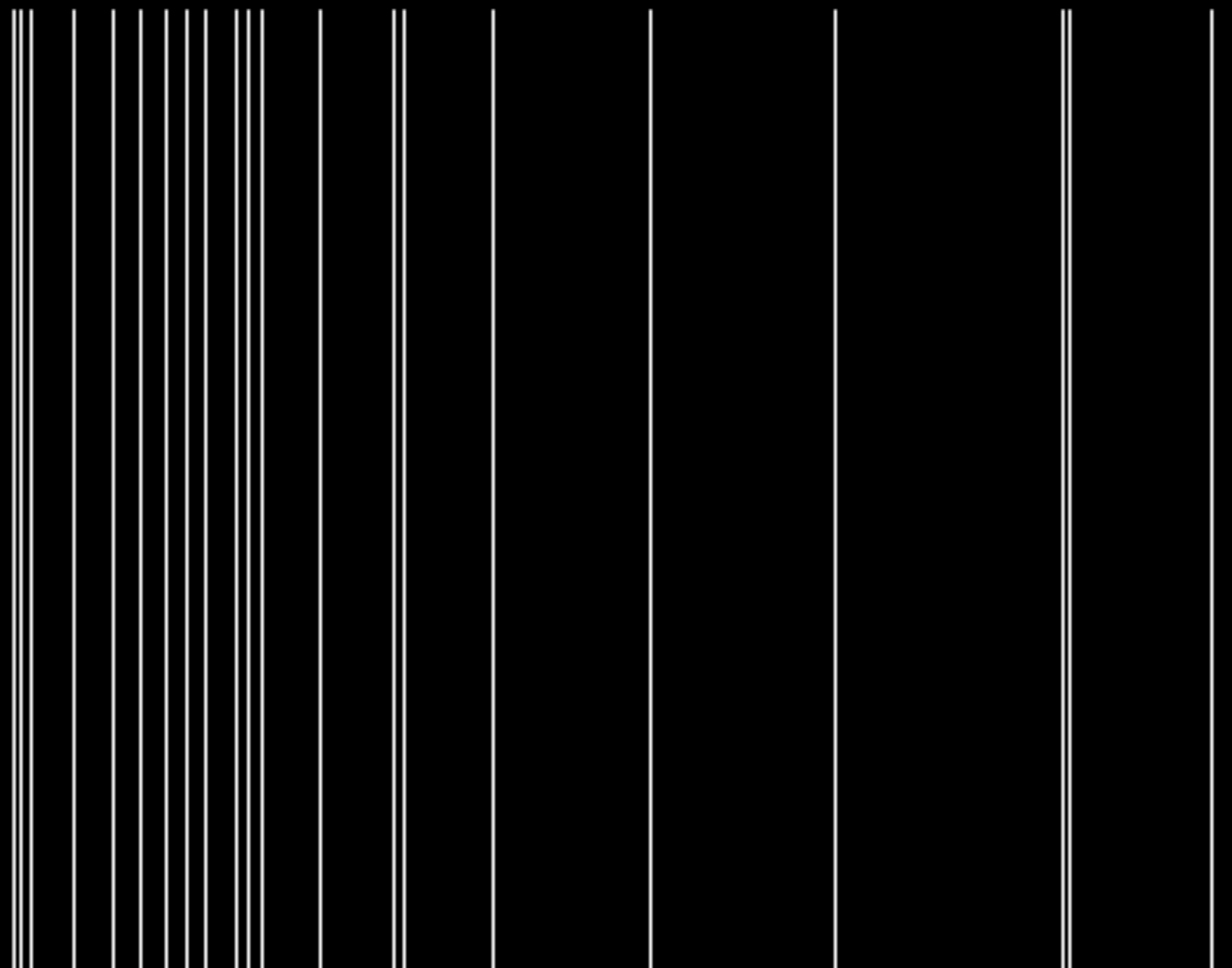
Let’s do it for the **neural coding**

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

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Principles of Data Science

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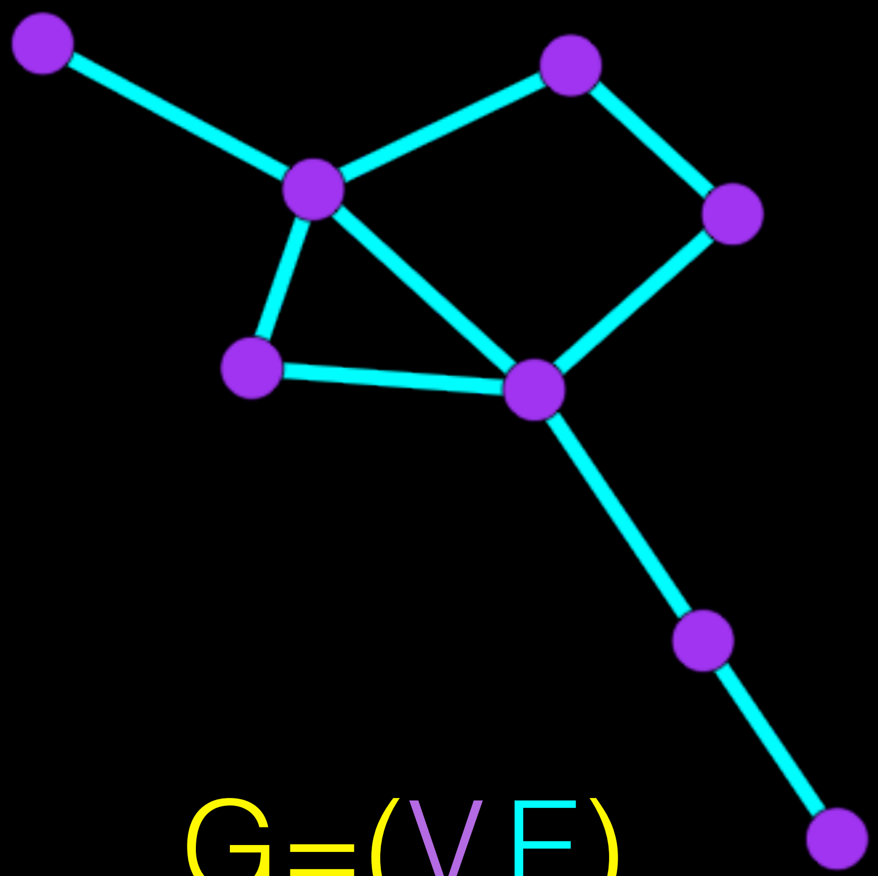
Let’s do it for networks, P[g]

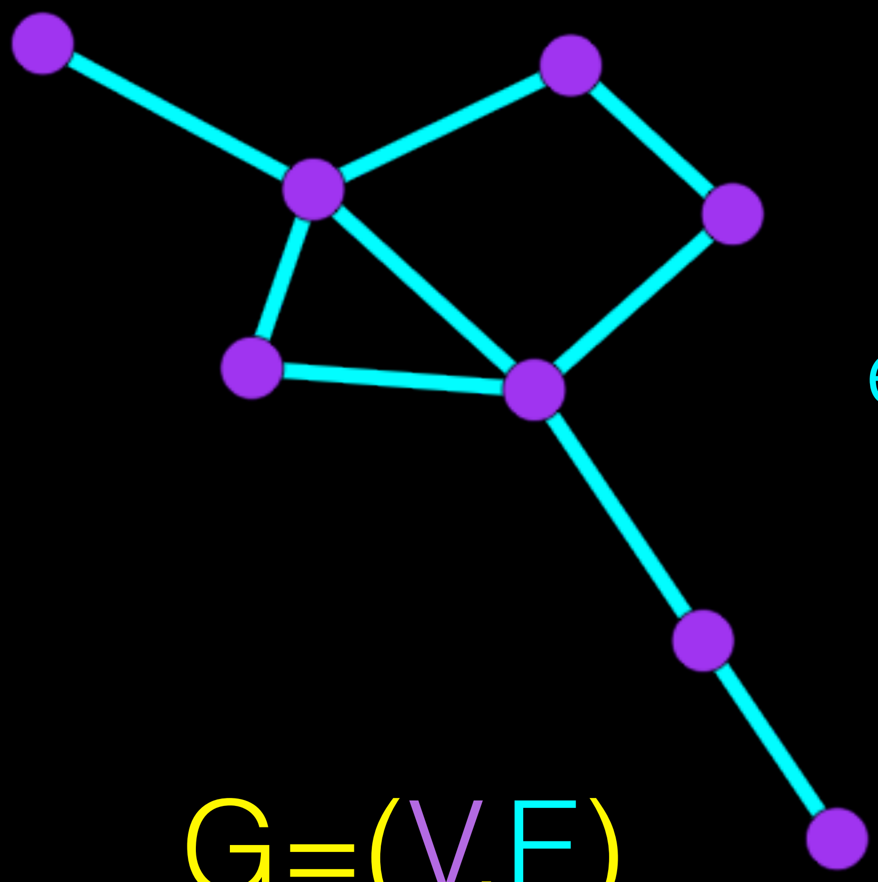
Look at it

a simple graph



$G=(V,E)$

a simple graph

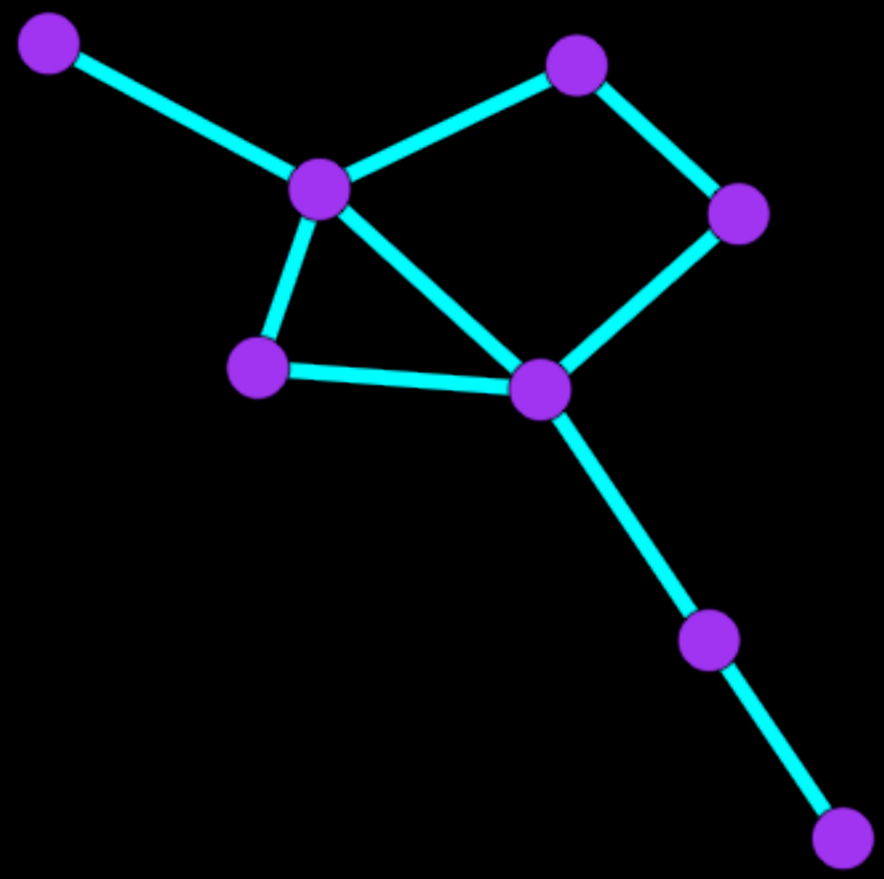


nodes/
vertices/
actors

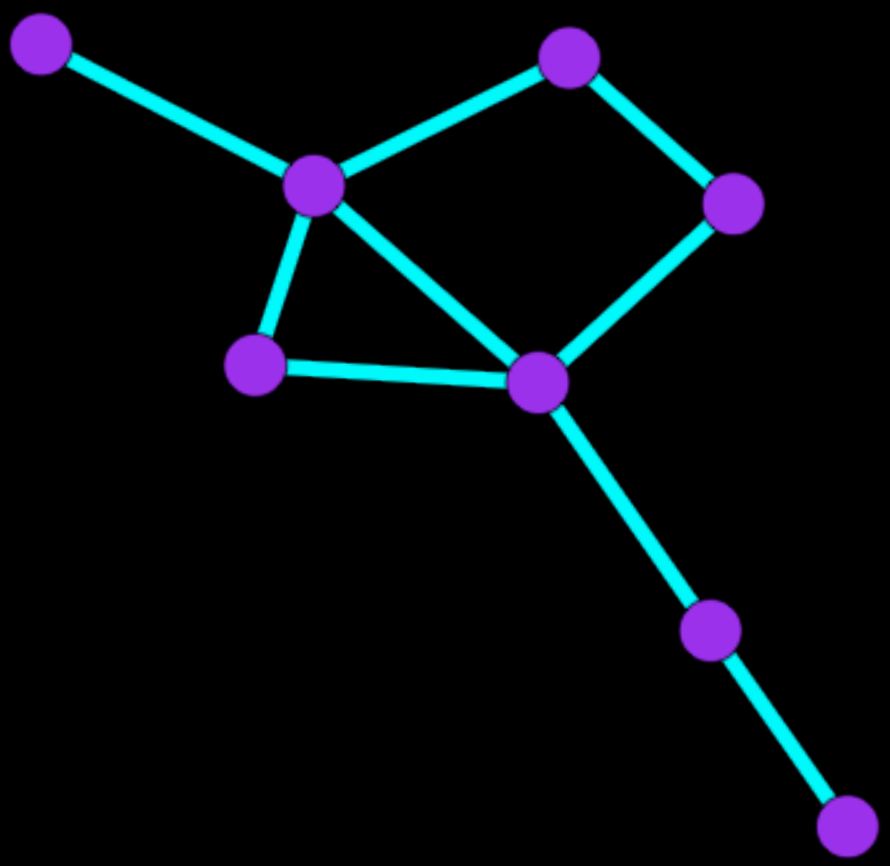
edges/
arcs

$G=(V,E)$

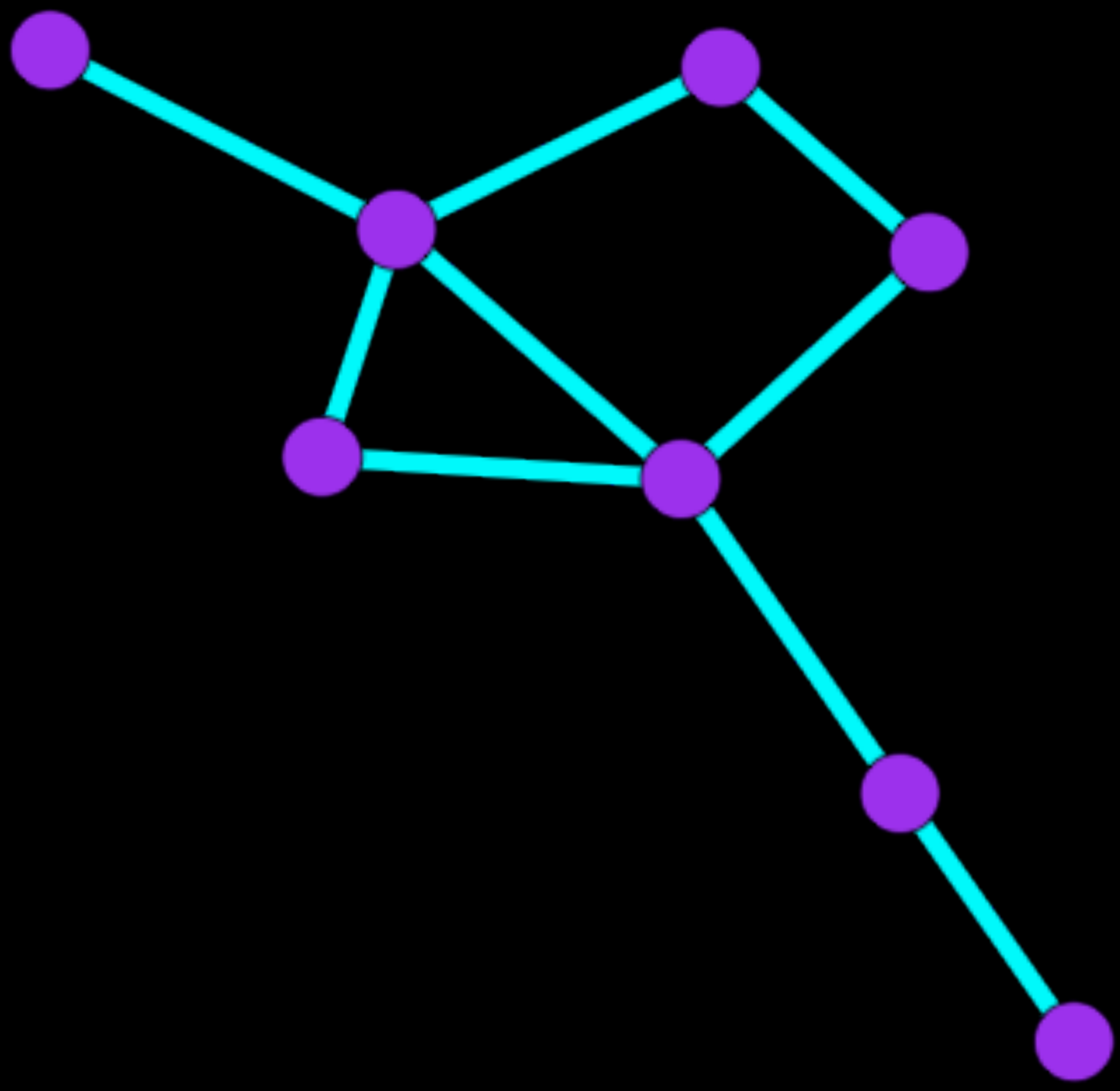
the same graph



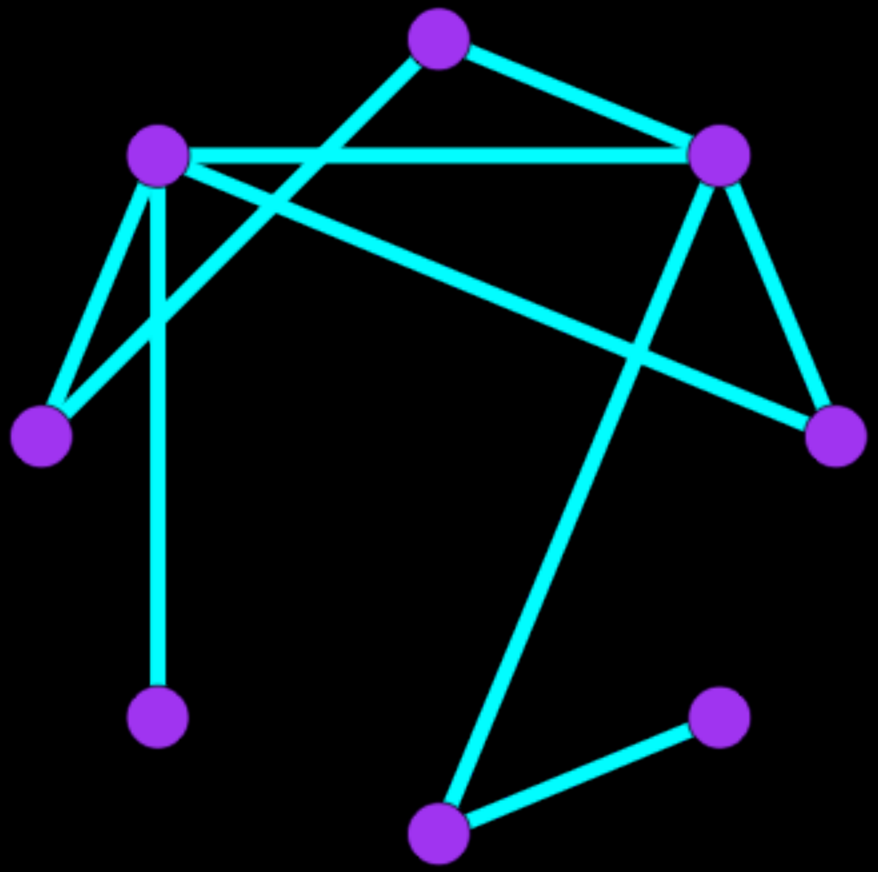
the same graph



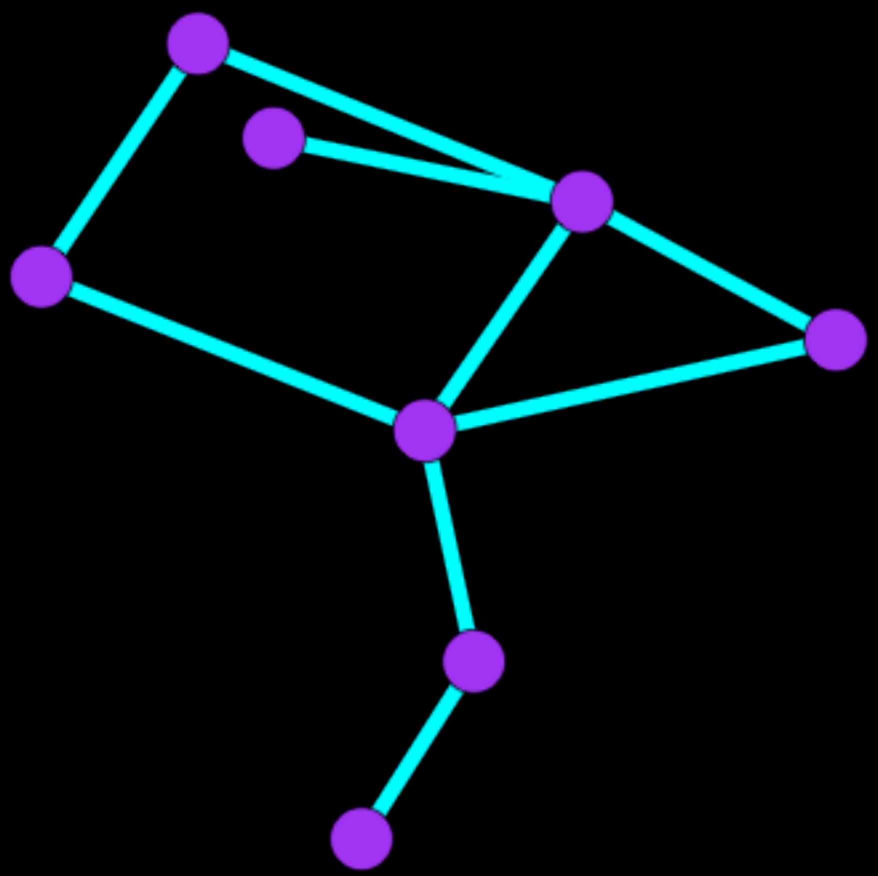
the same graph



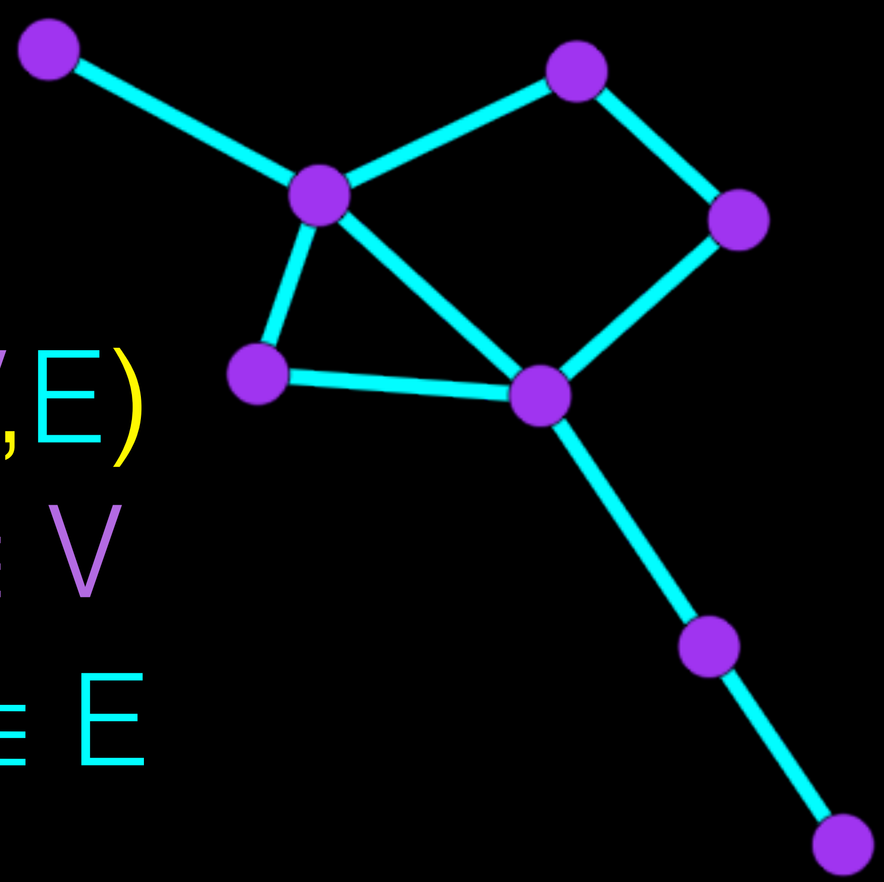
the same graph



the same graph



the same graph



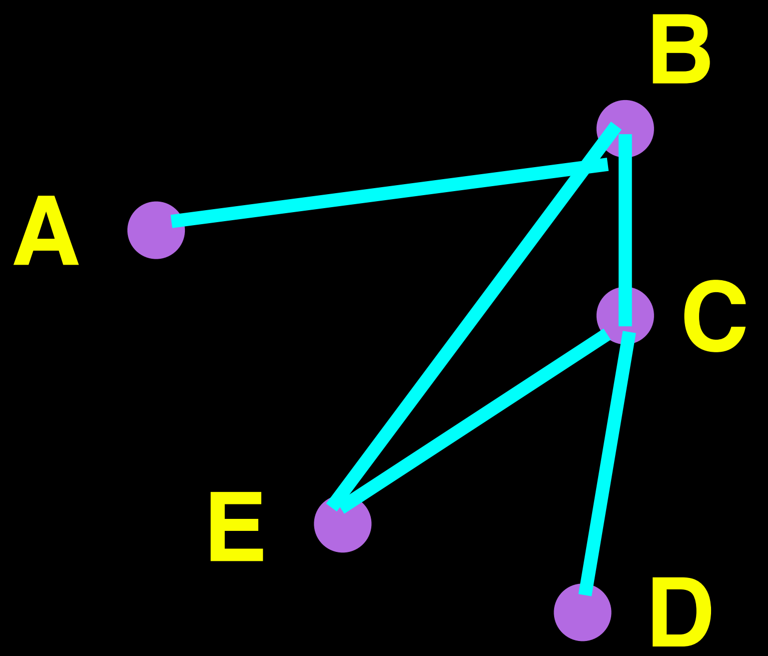
$G=(V,E)$

$u,v \in V$

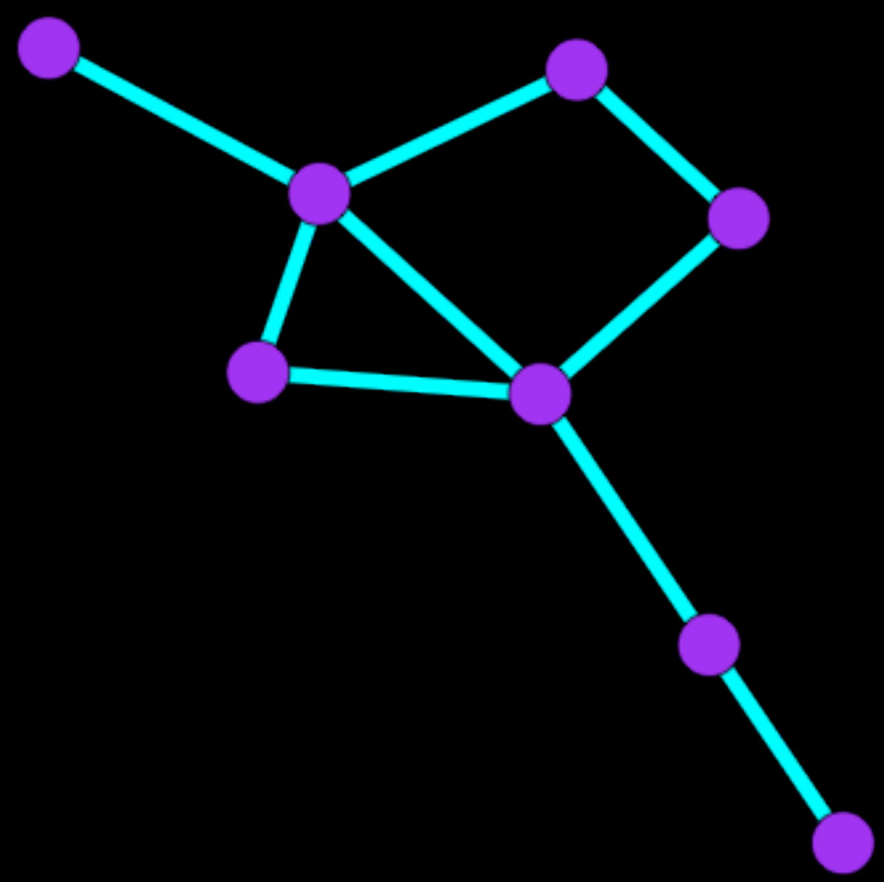
$u \sim v \in E$

labeled graph

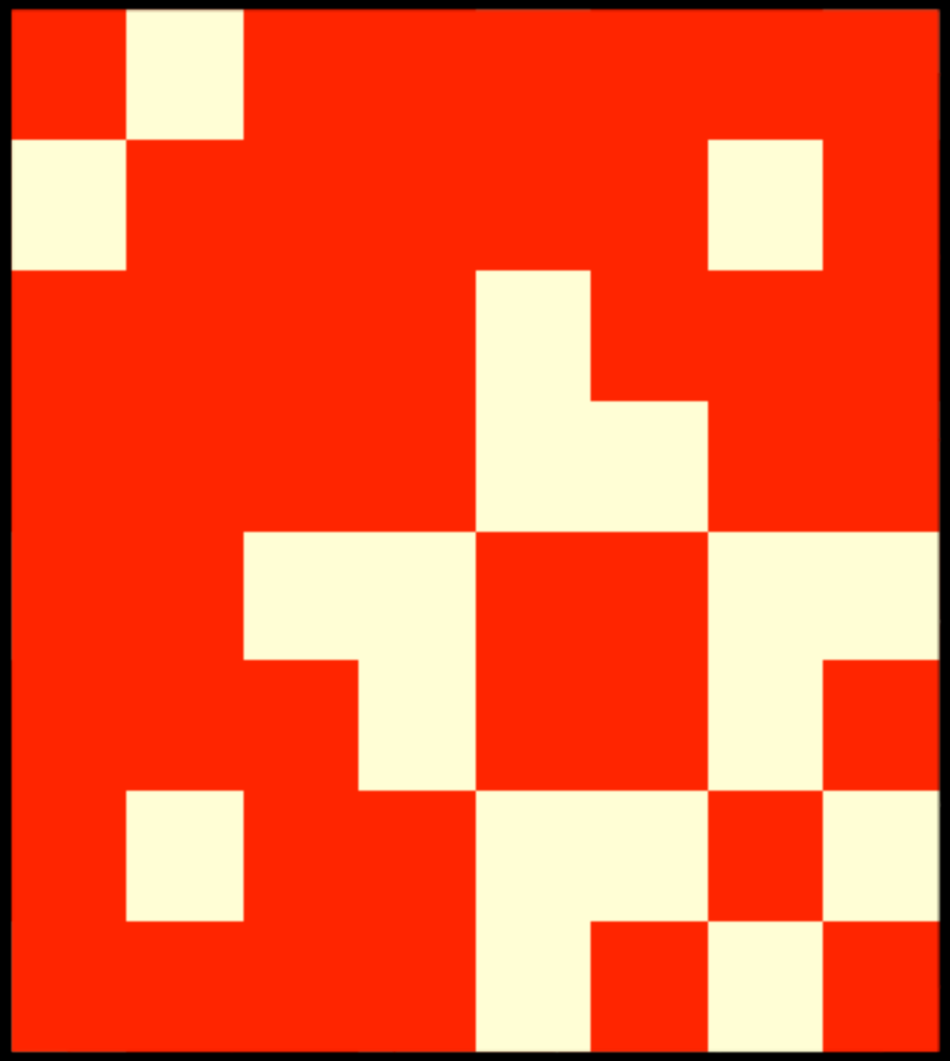
- uv means there is an edge between u & v
- e.g., in this graph AB, but not AE



same graph
(2D layout)

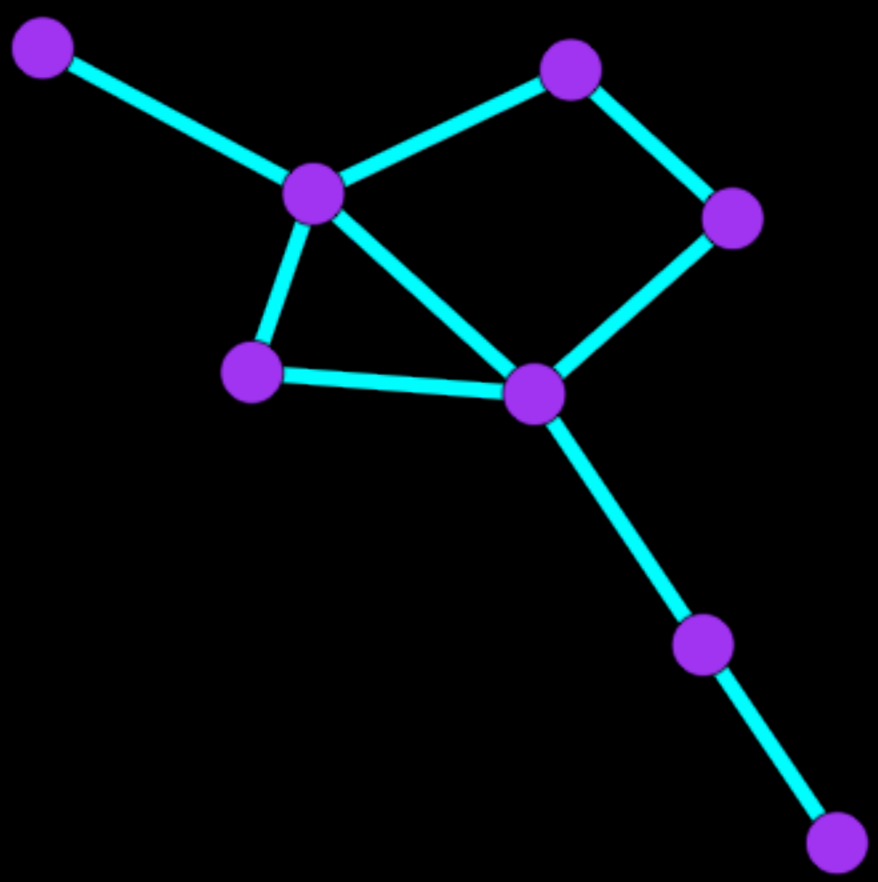


same graph
(adjacency matrix)

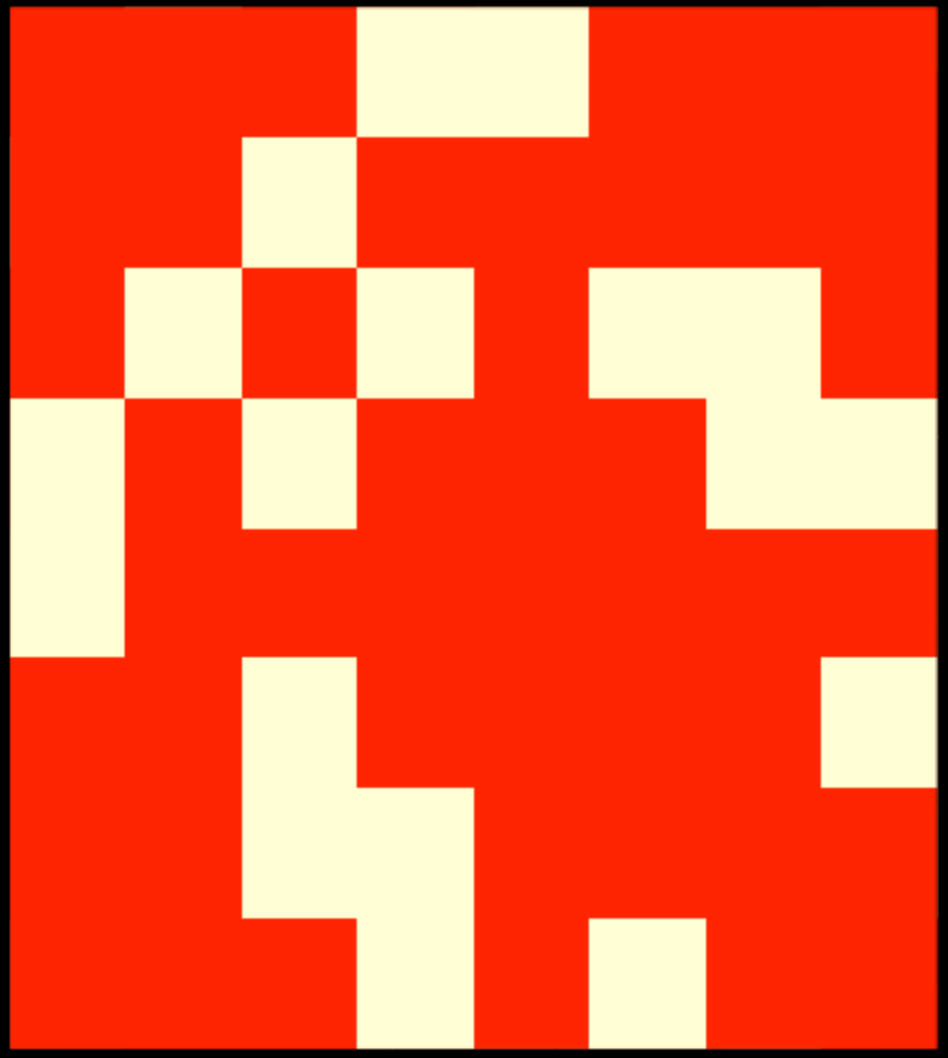


- A is the adjacency matrix
- A(u,v) = 1 iff u~v

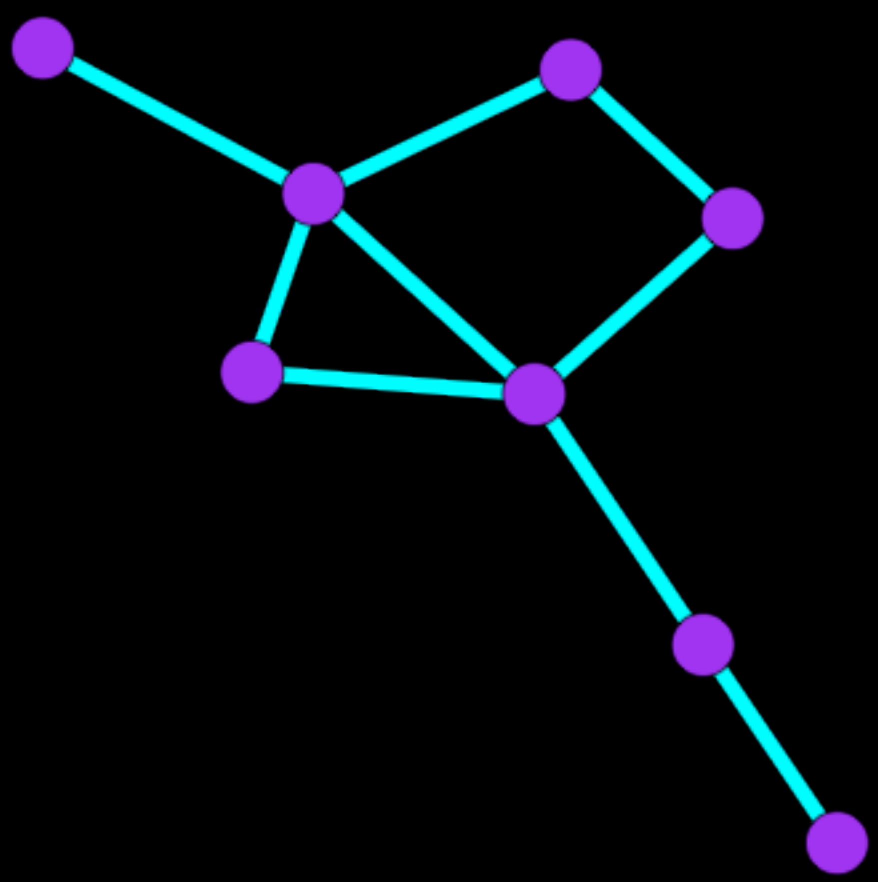
same graph
(2D layout)



same graph
(adjacency matrix)



same graph
(2D layout)



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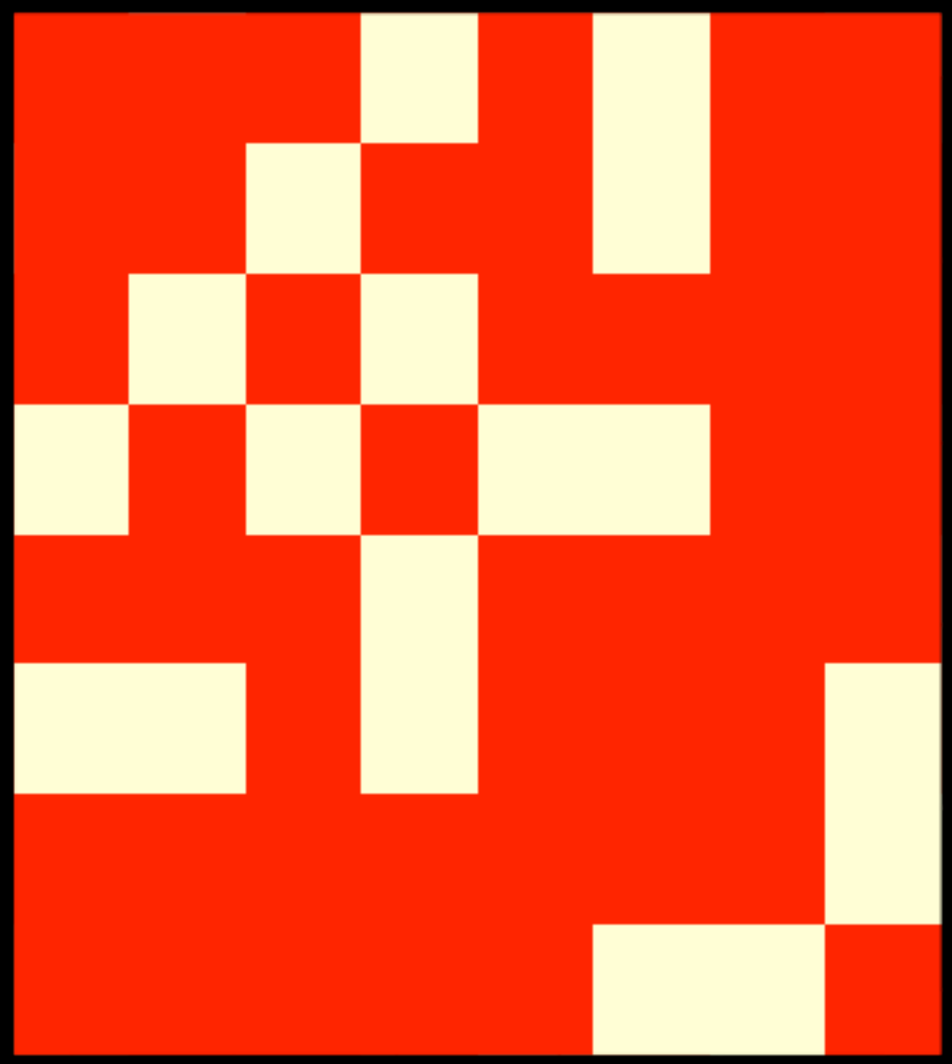

Look at it

- c. elegans: ~10^2
- larval drosophila: ~10^4
- larval zebrafish, adult drosophila: ~10^5
- DTI-derived human connectome: ~10^6
- adult zebrafish, mouse: ~10^7
- monkey: ~10^9
- human: ~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]

Neural Decoding: P[s | r]

Neural Code: P[s,r]

Connectome Encoding: P[g | s]

Keep it Simple

Neural Encoding: $P[r \mid s]$

Neural Decoding: $P[s \mid r]$

Neural Code: $P[s,r]$

Connectome Encoding: $P[g \mid s]$

Connectome Decoding: $P[s \mid g]$

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?

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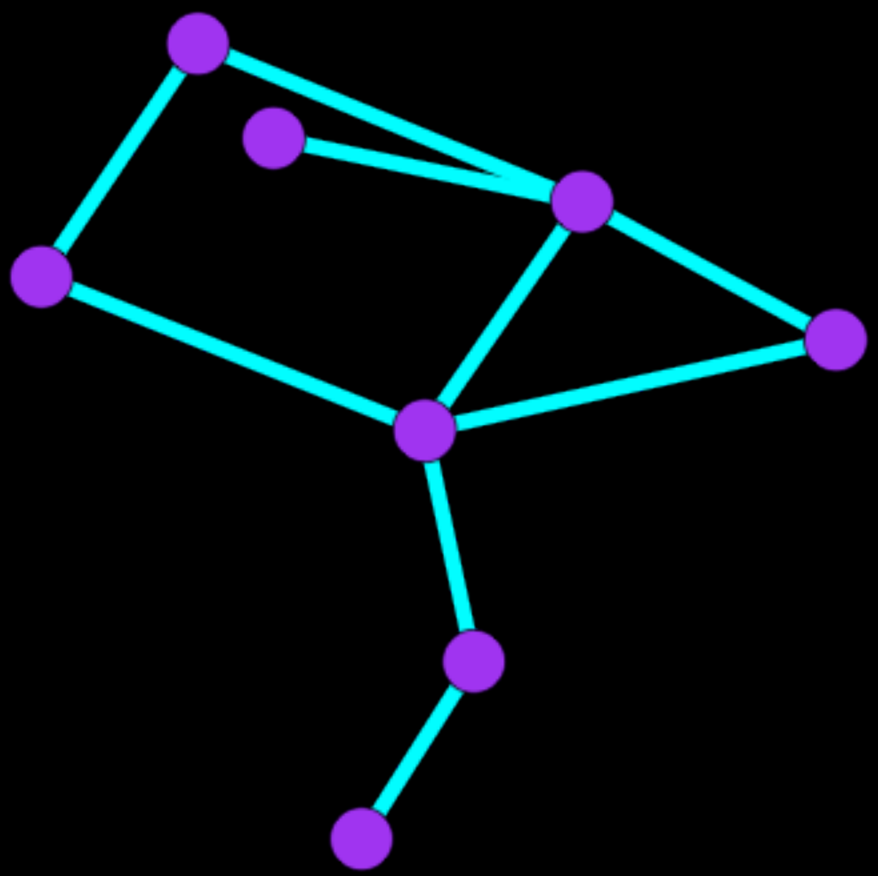
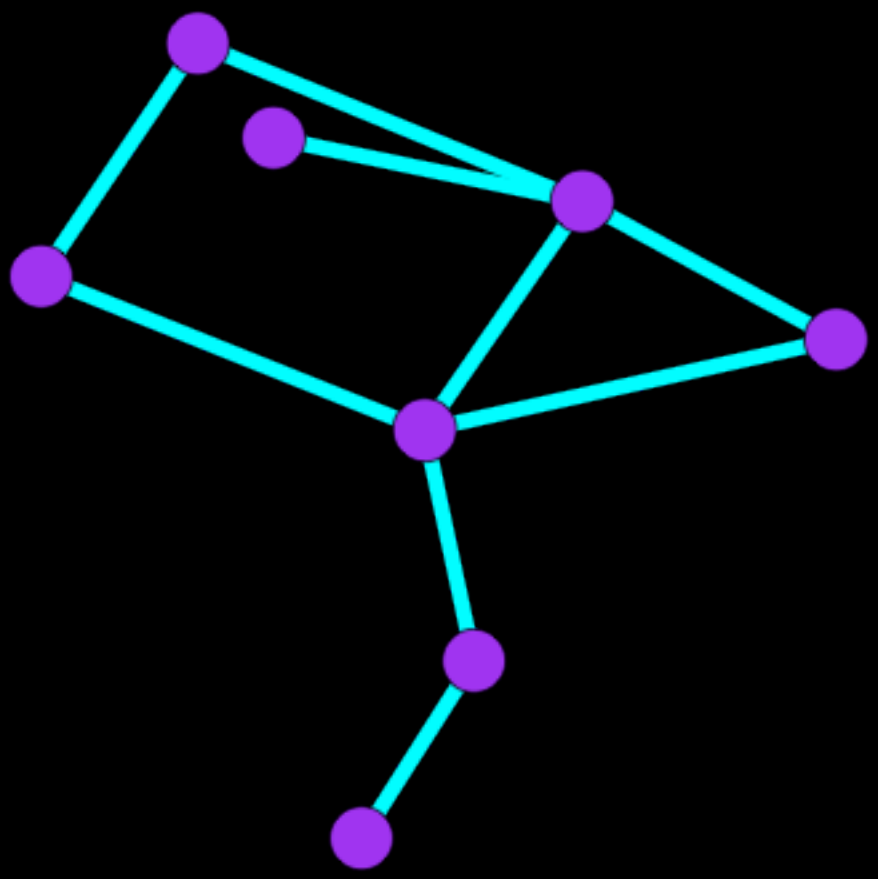
Let’s do it for connectome coding now

connectome = brain-graph

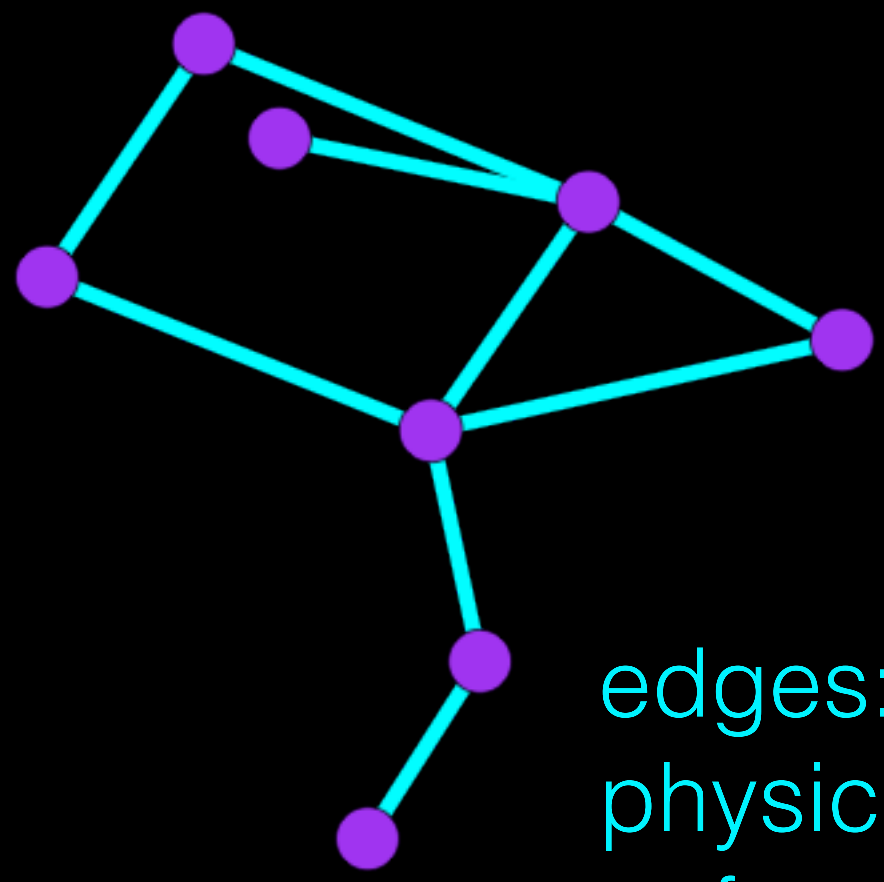


connectome = brain-graph



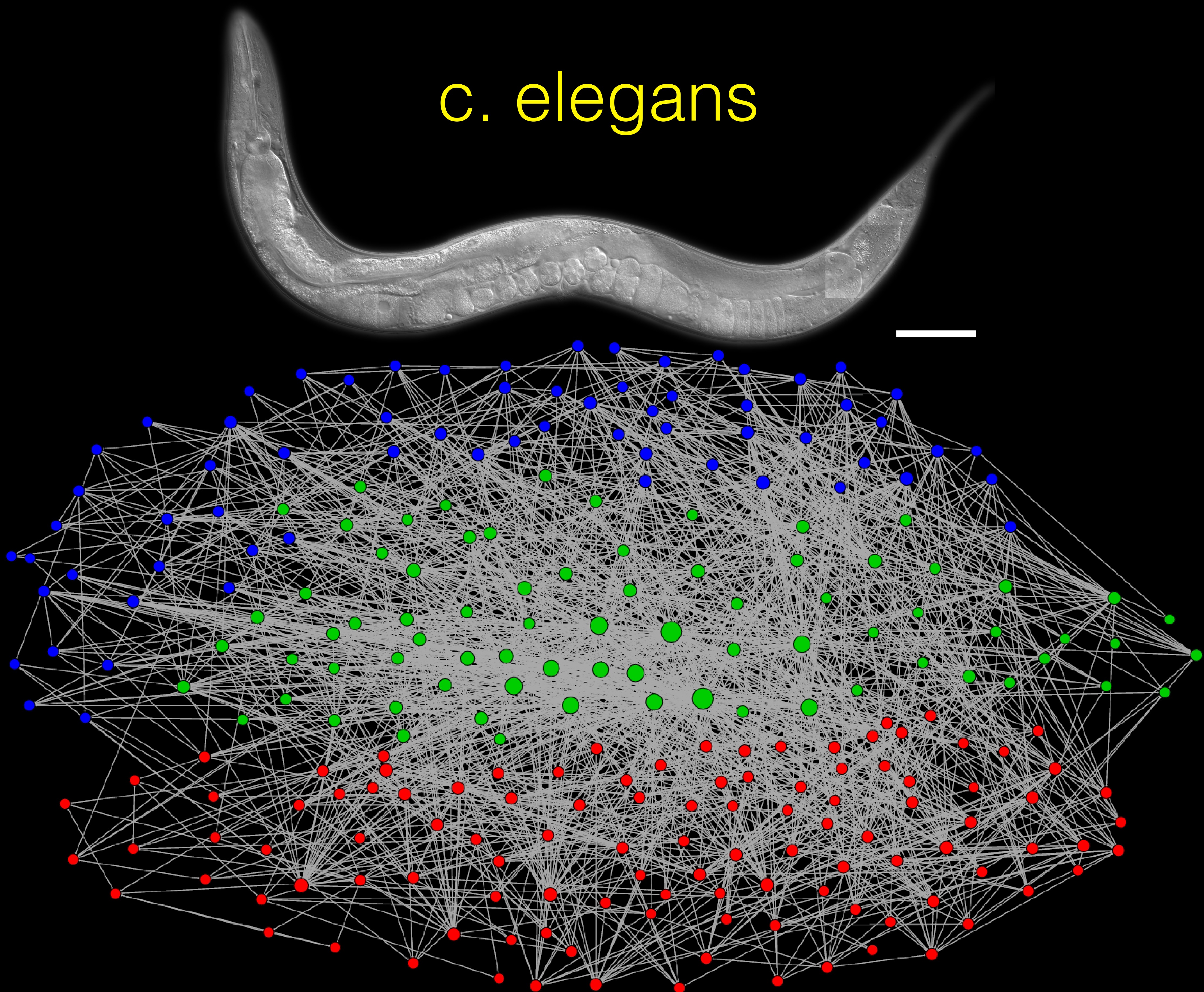
vertices:
brain regions
or voxels
or electrodes
or neurons
or even compartments

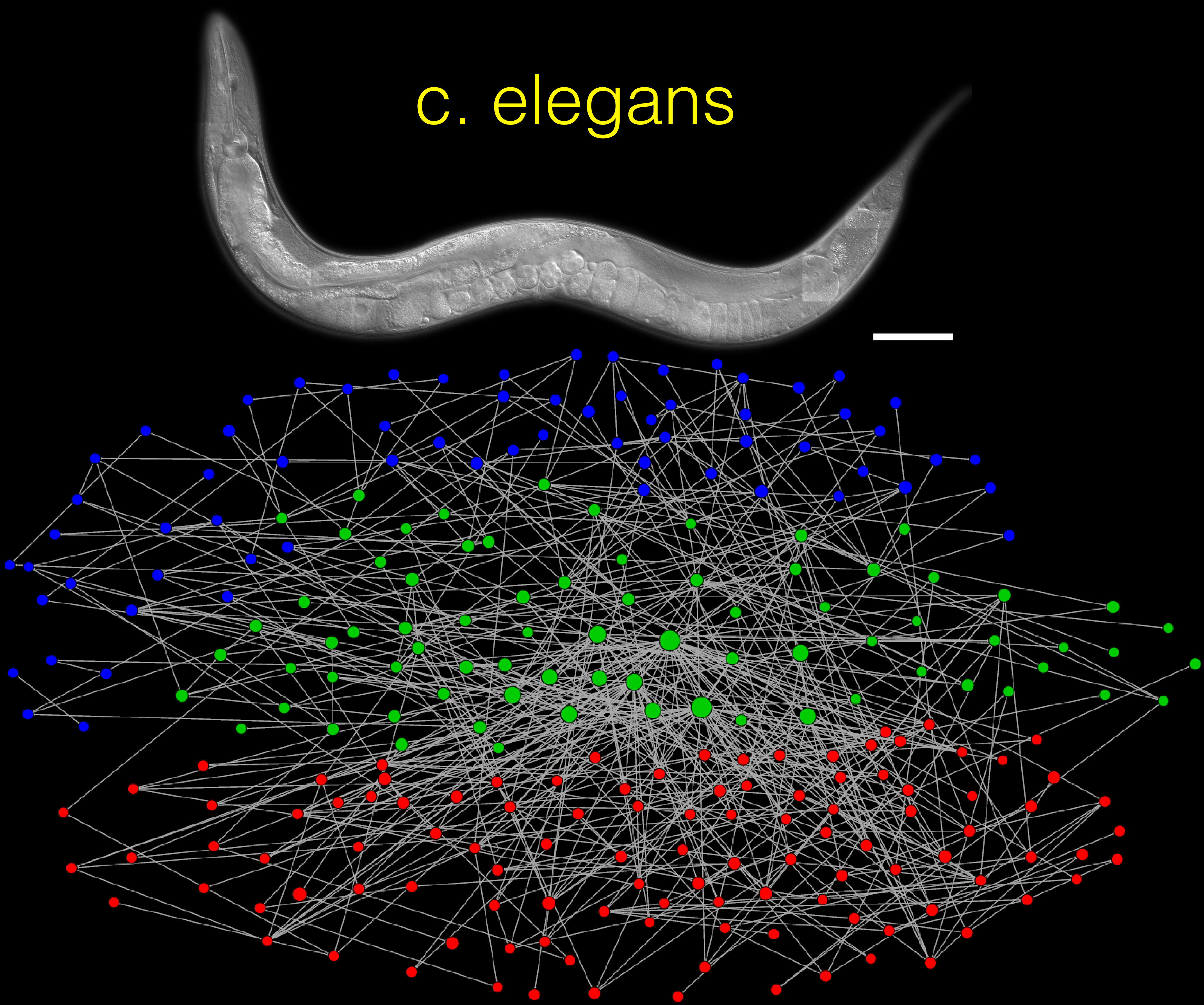
connectome = brain-graph



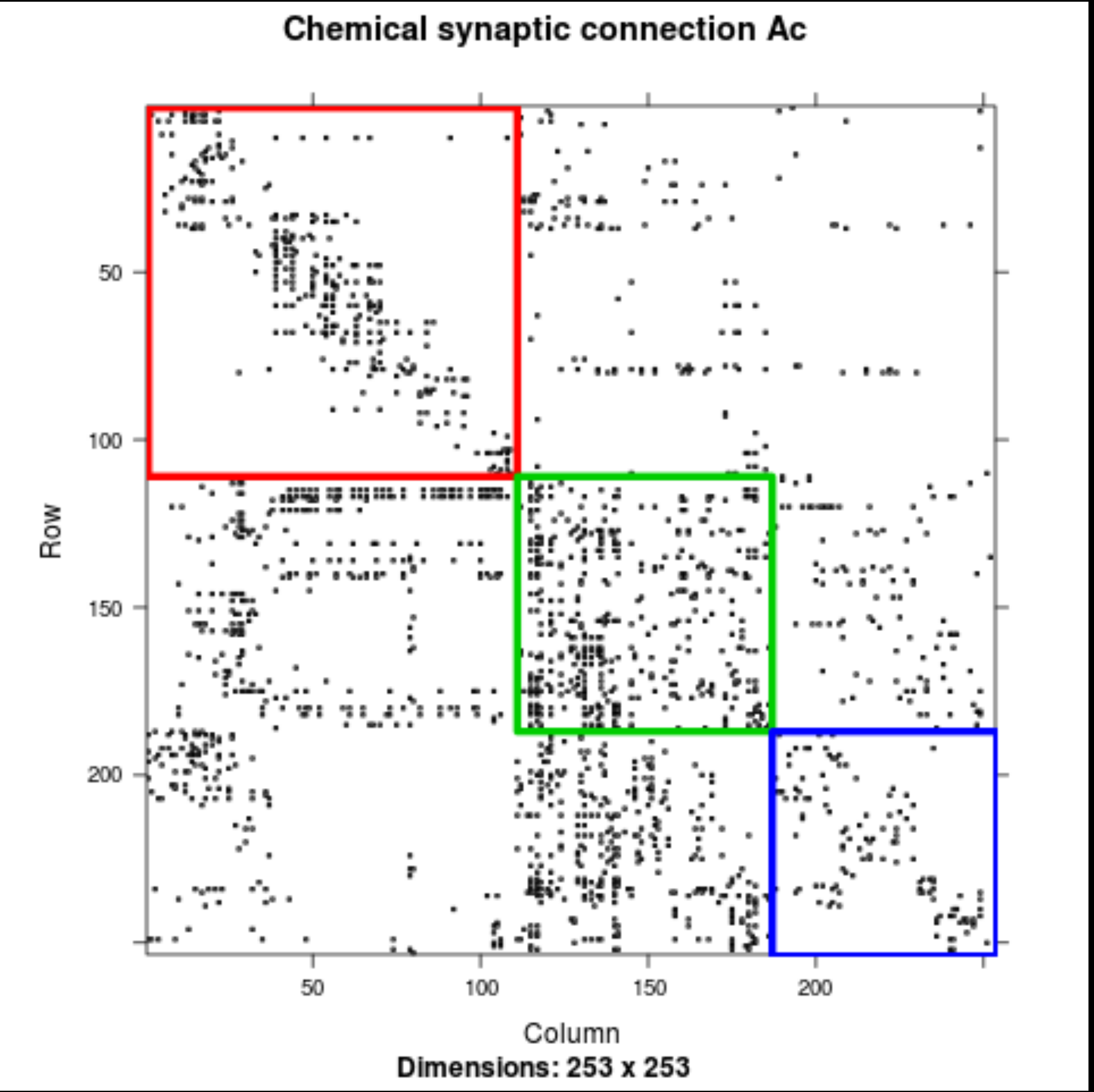
vertices:
brain regions
or voxels
or electrodes
or neurons
or even compartments

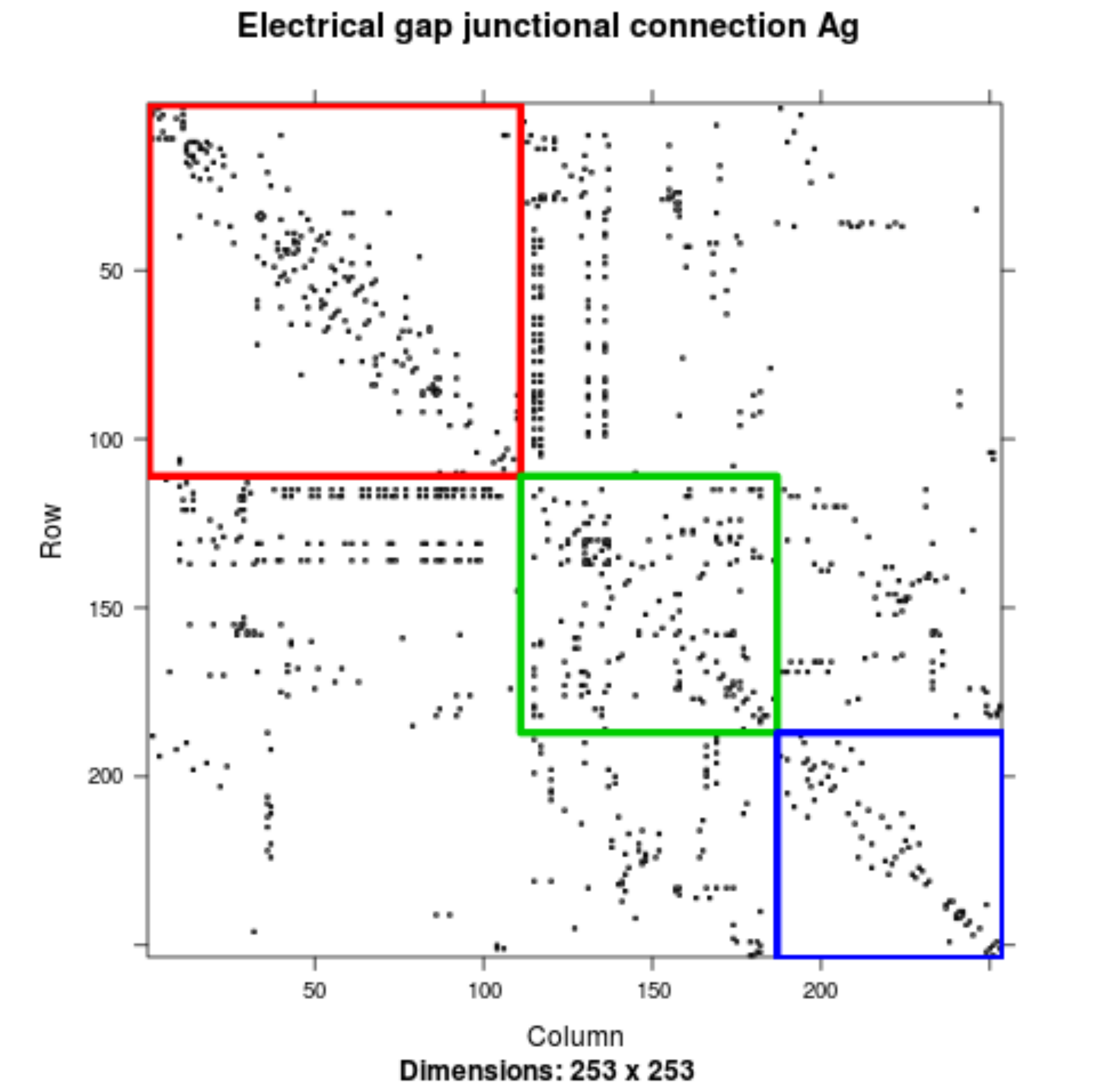
edges:
physical connections
or functional connections
or correlations


c. elegans

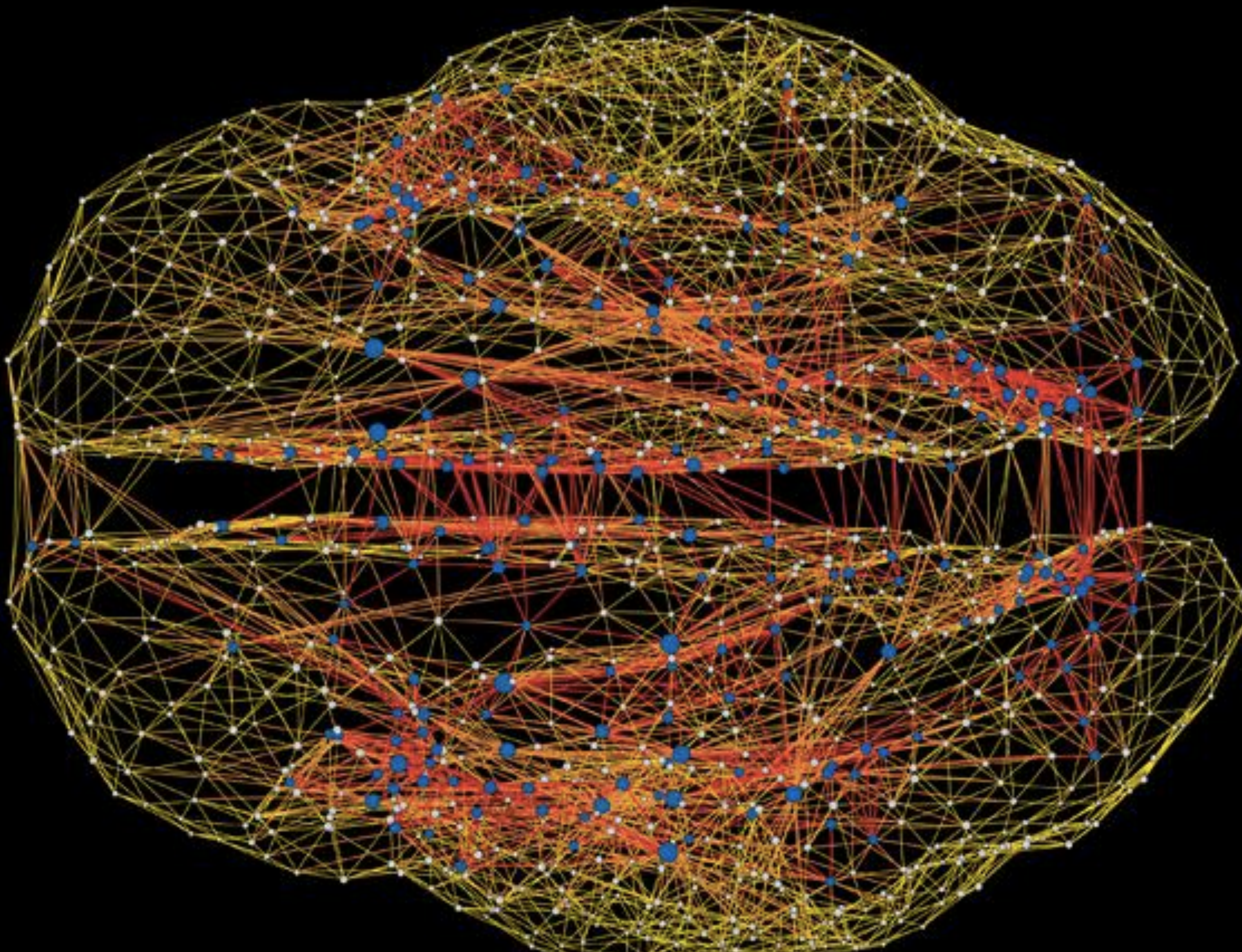

c. elegans

c. elegans

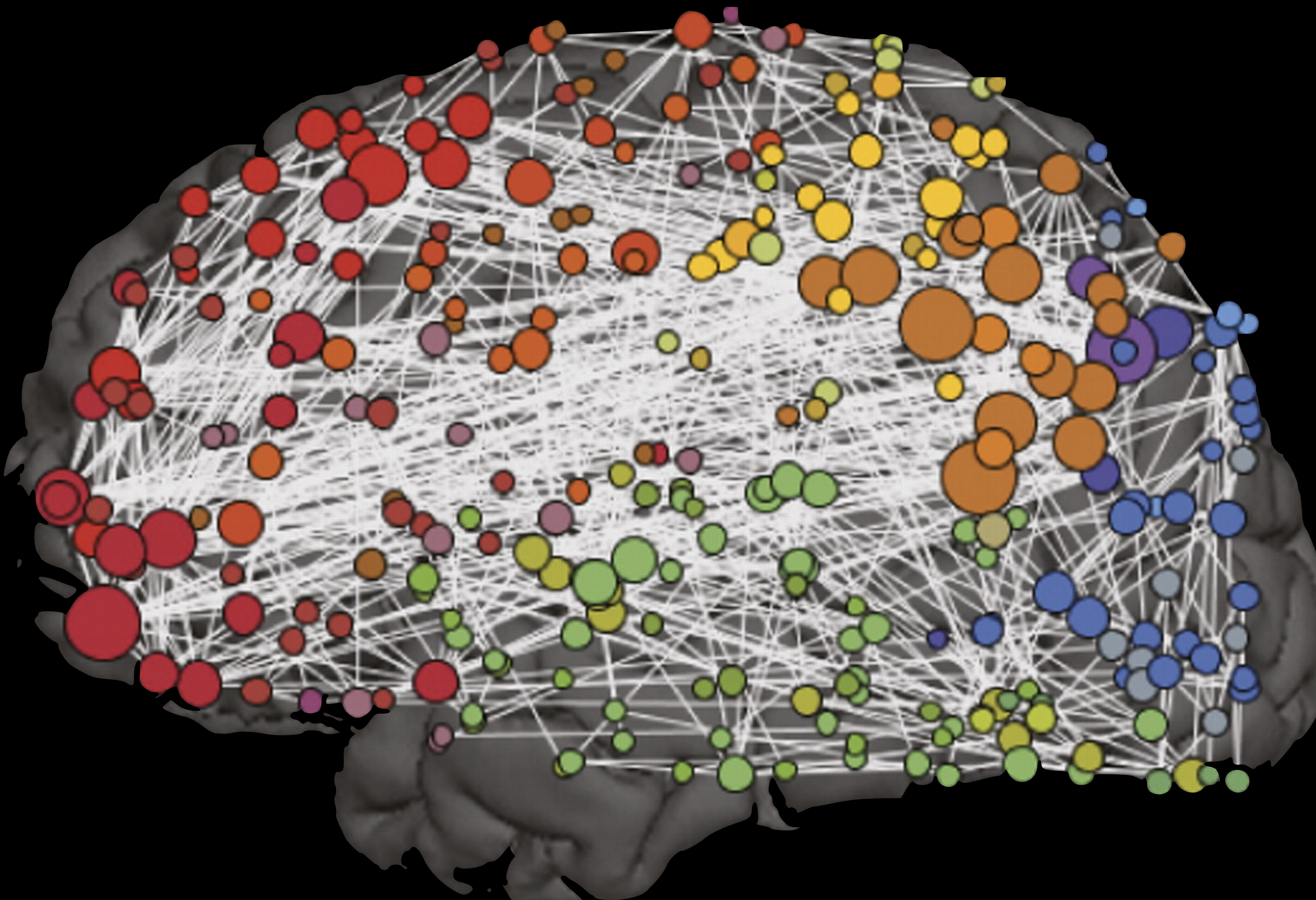

Chemical synaptic connection Ac
50
100
150
200
Row
Column
Dimensions: 253 x 253


Electrical gap junctional connection Ag
50
100
150
200
Row
Column
Dimensions: 253 x 253

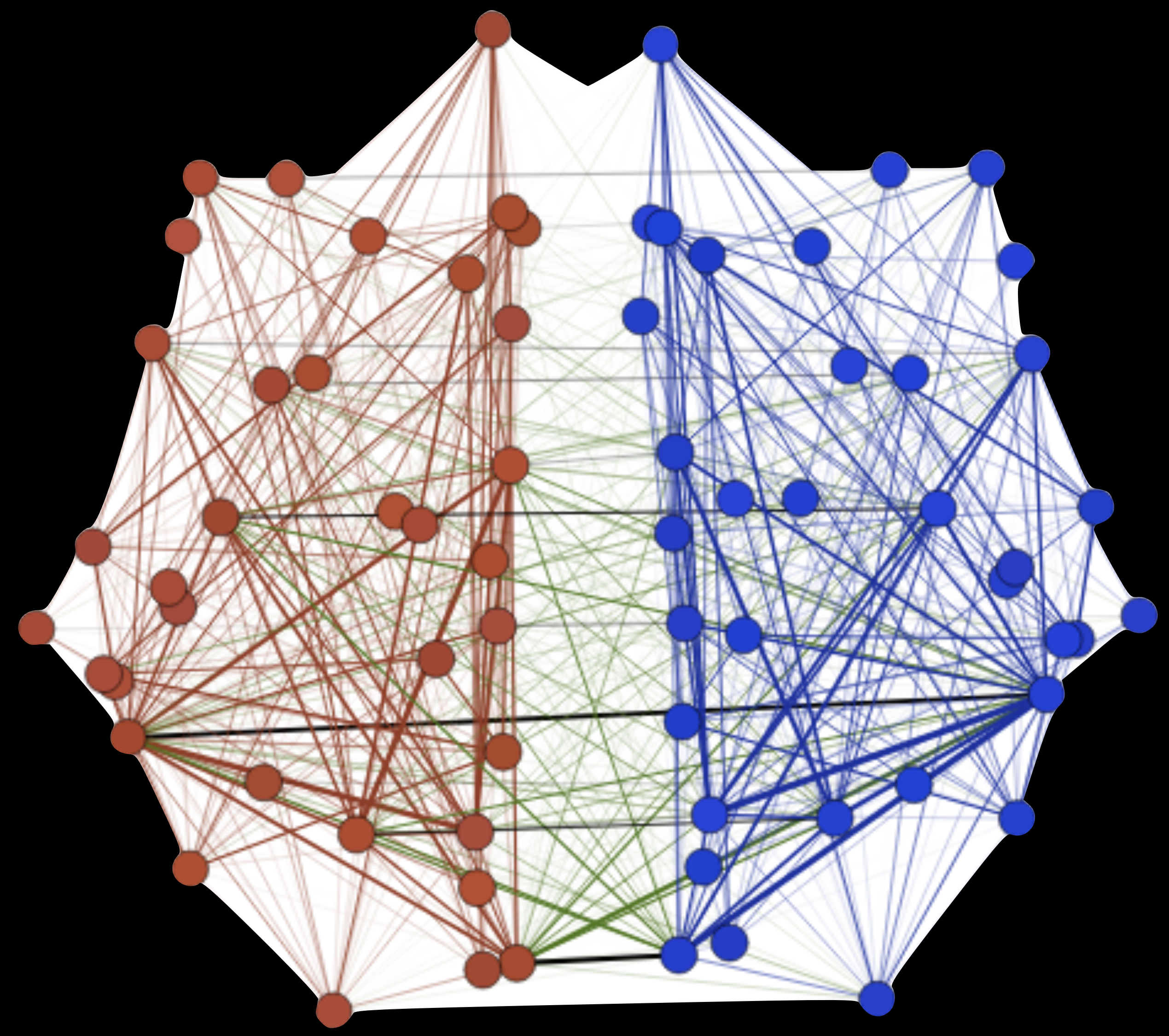
human connectome



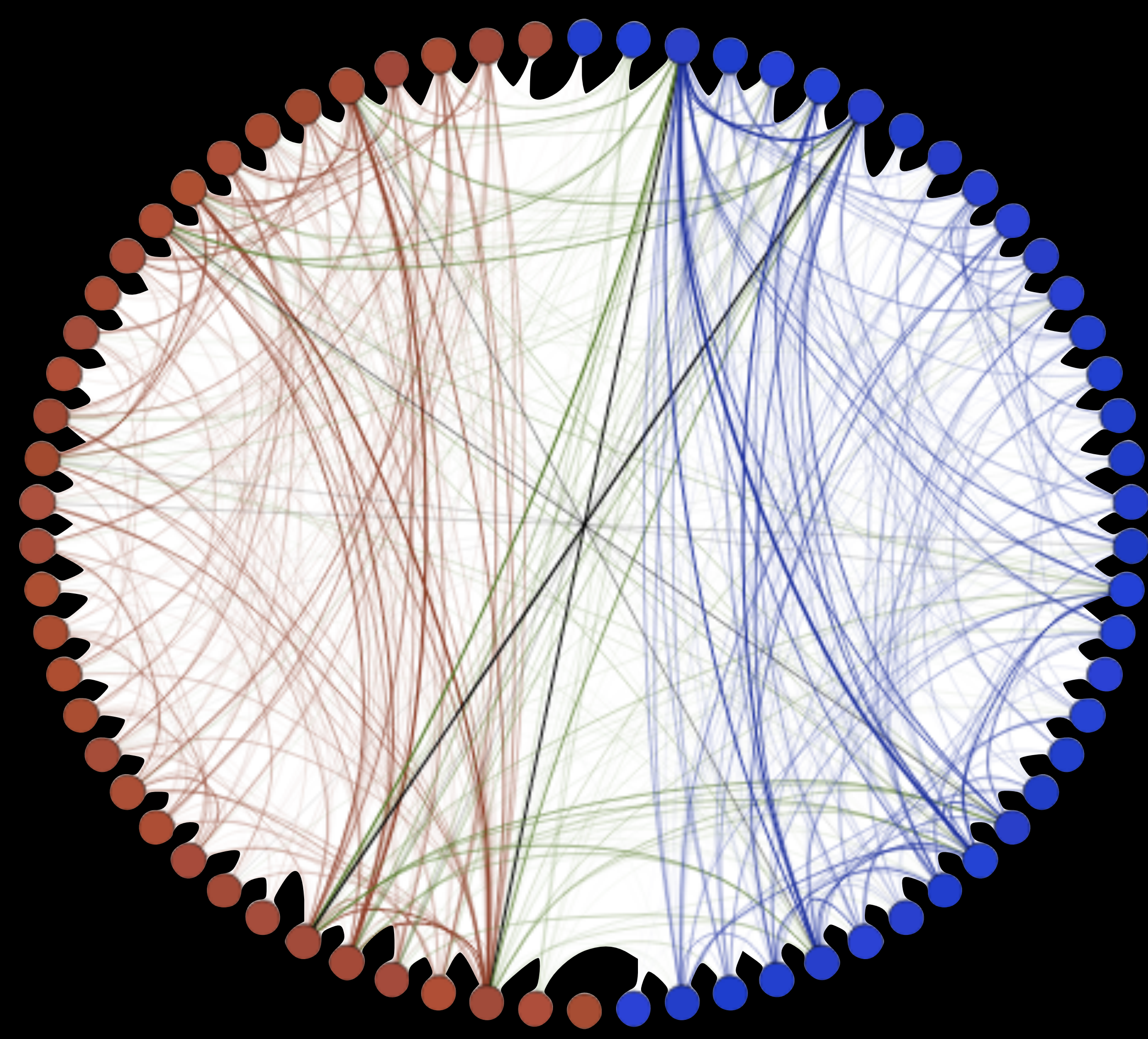
human connectome



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

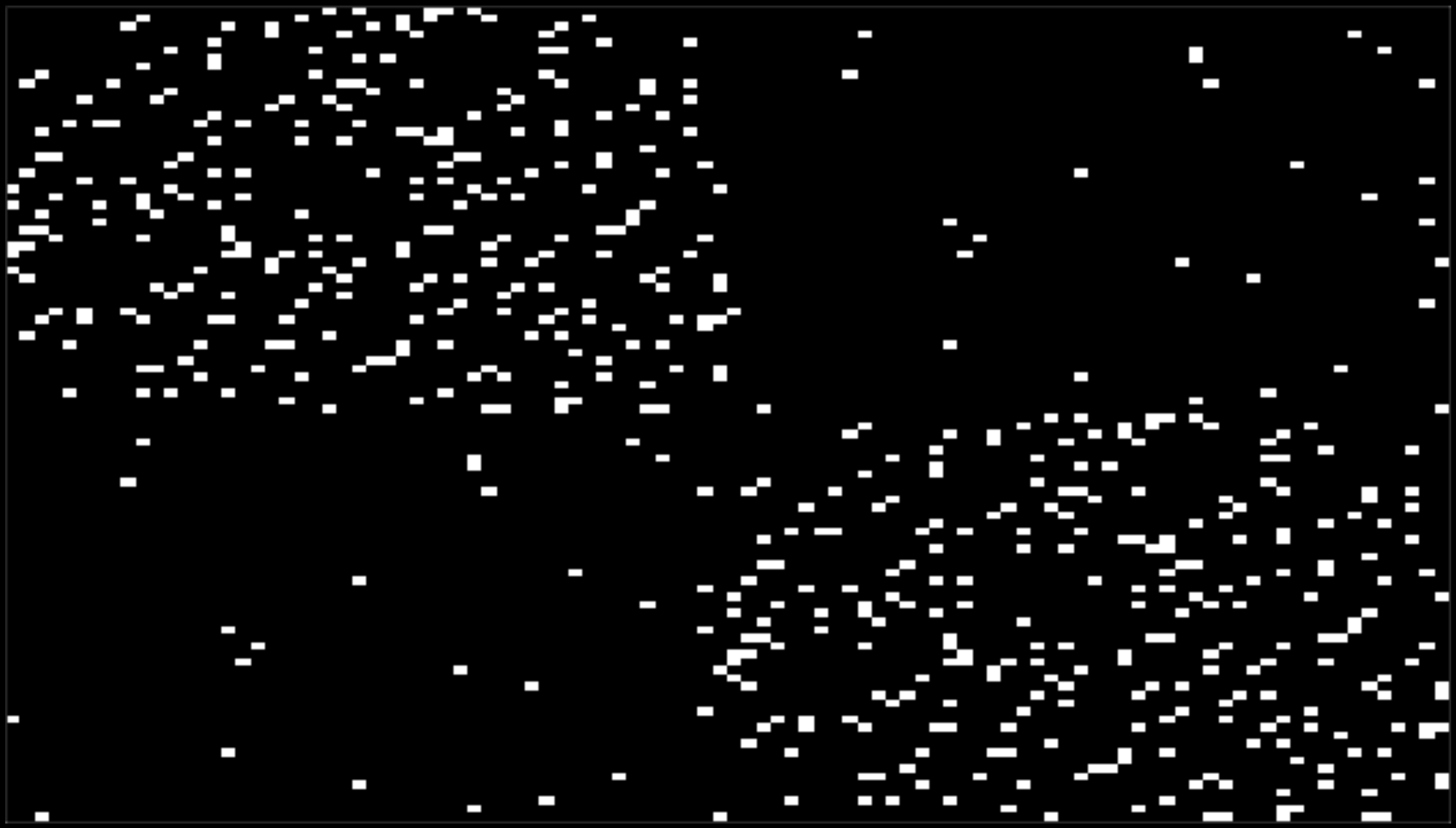
- Each spike is independent
- Probability of a spike at any time is λ_i
- $P[r|s] = \text{Poisson}(\lambda_s)$

Principles of Data Science

- Look at it
- Keep it simple

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

Look at it



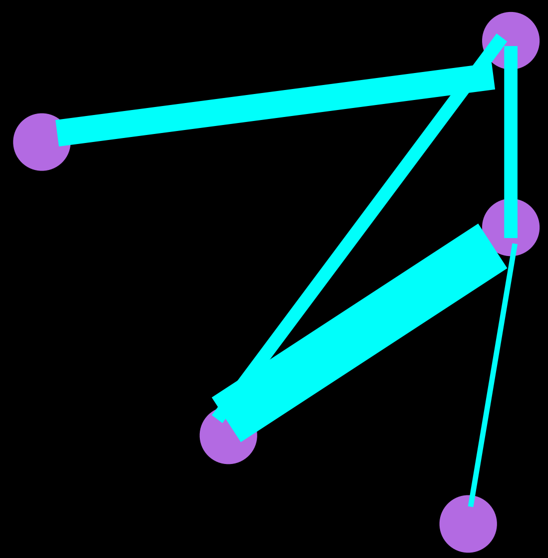
Keep it Simple

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

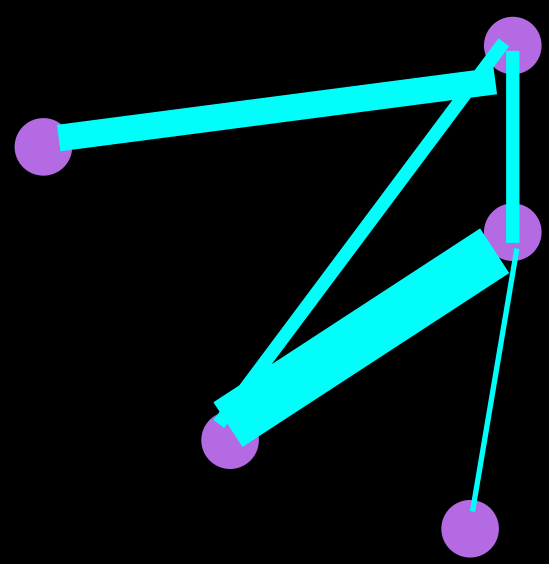
let’s do it for a little bit more complex models

weighted graph

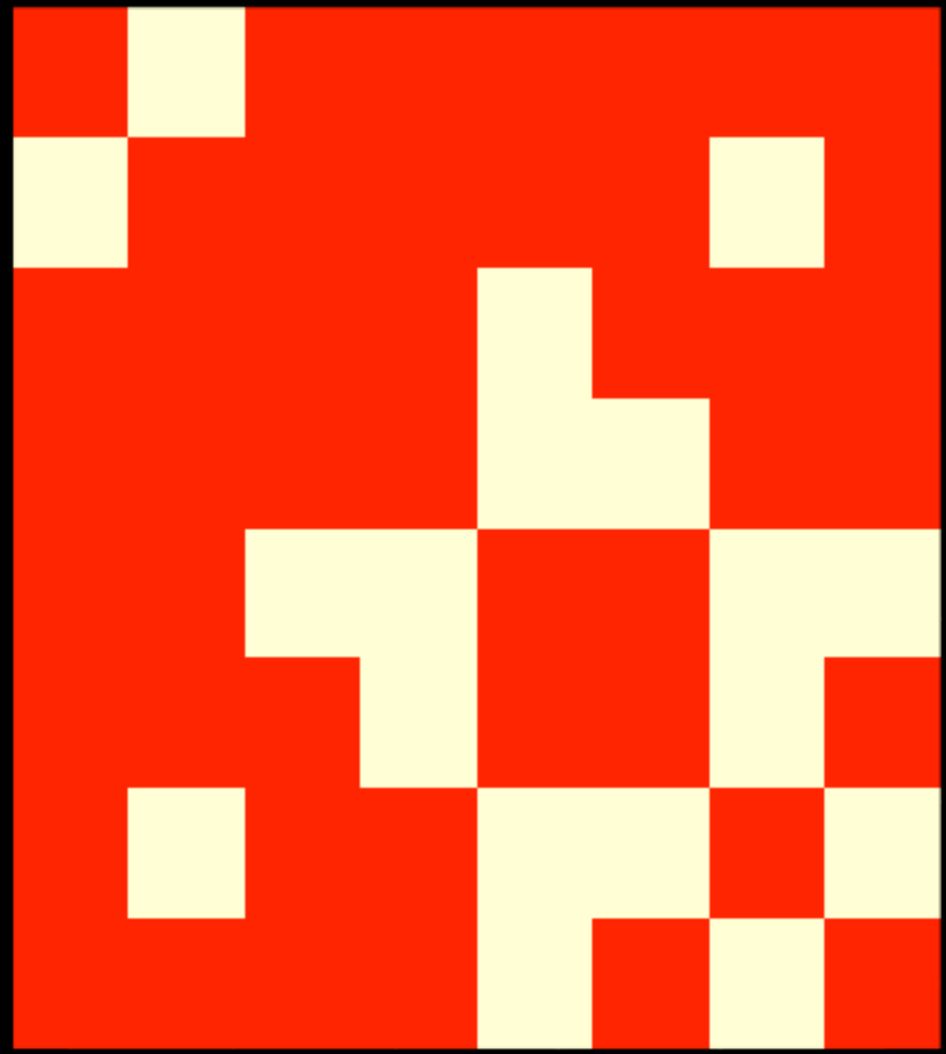
- each edge has a weight
- weights can be positive, negative, integer, zero, etc.



weighted graph
(2D layout)

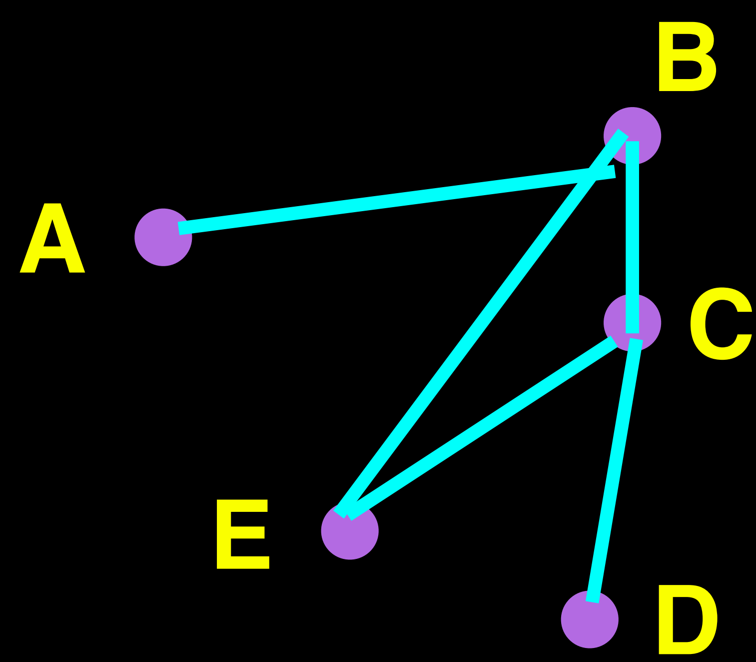


weighted graph
(adjacency matrix)



elements of A can take any value

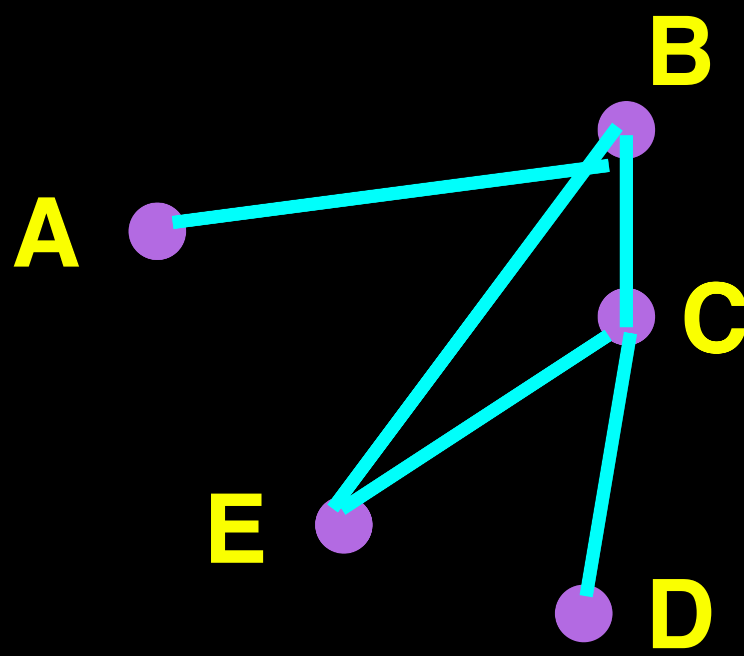
vertex attributed graph



A: L
B: R
C: R
D: L
E: L

categorical
attributes

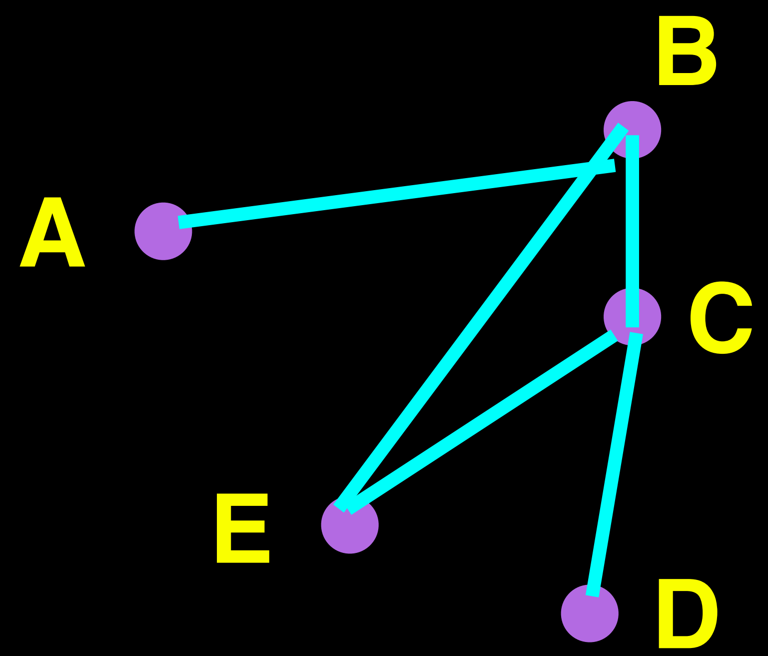
vertex attributed graph



A: 6
B: 4
C: 0.2
D: 8.7
E:-3.14

numerical
attributes

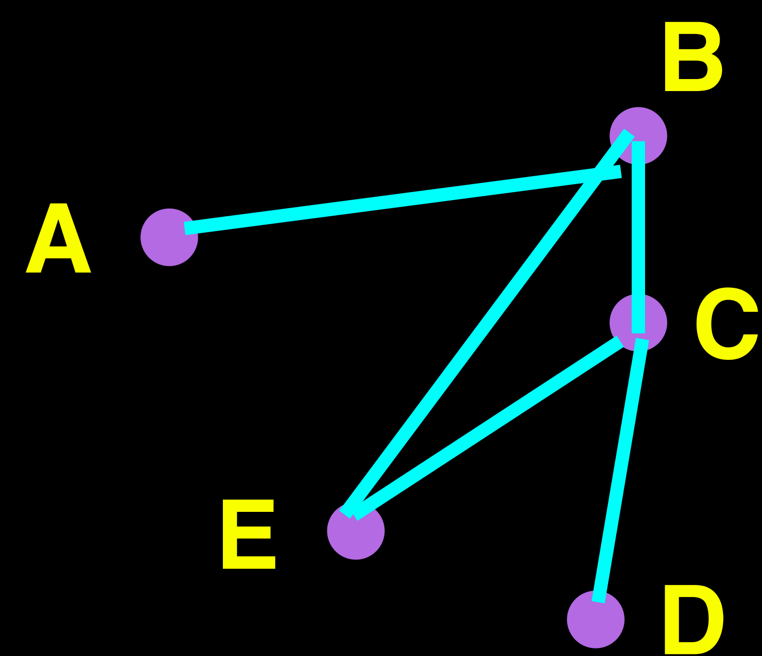
vertex attributed graph



A: (6,5,7)
B: (4,0,9)
C: (1,8,6)
D: (5,5,2)
E: (8,3,9)

multi-dimensional
attributes

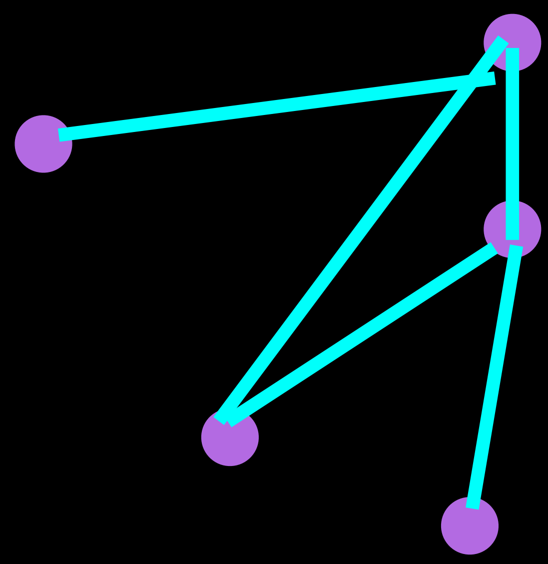
edge attributed graph



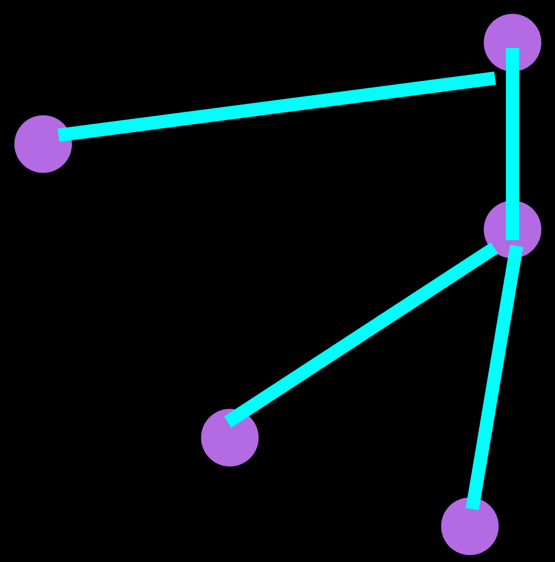
AB: 6
BC: 4
BE: 0.2
CE: 8.7
CD:-3.14

numerical attributes

graph attributed graphs

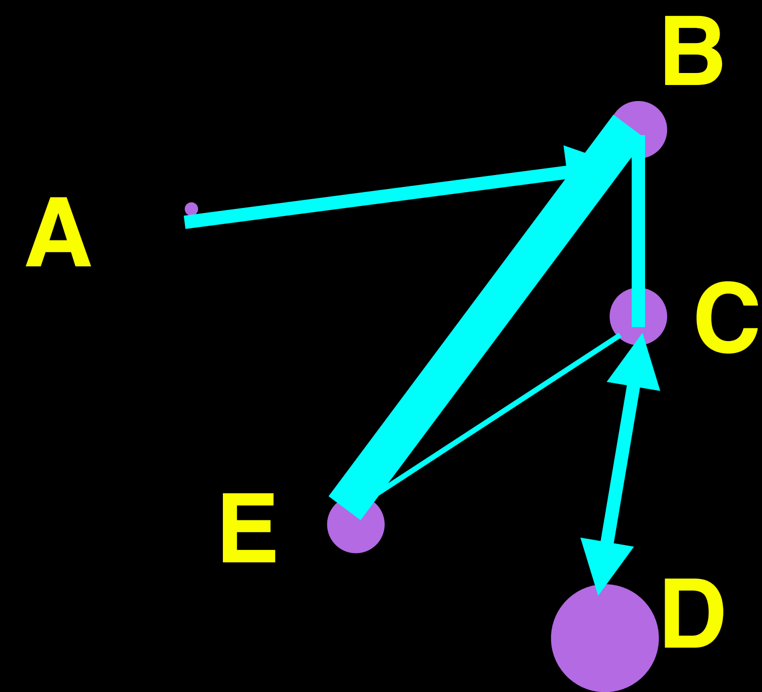


subject 1



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

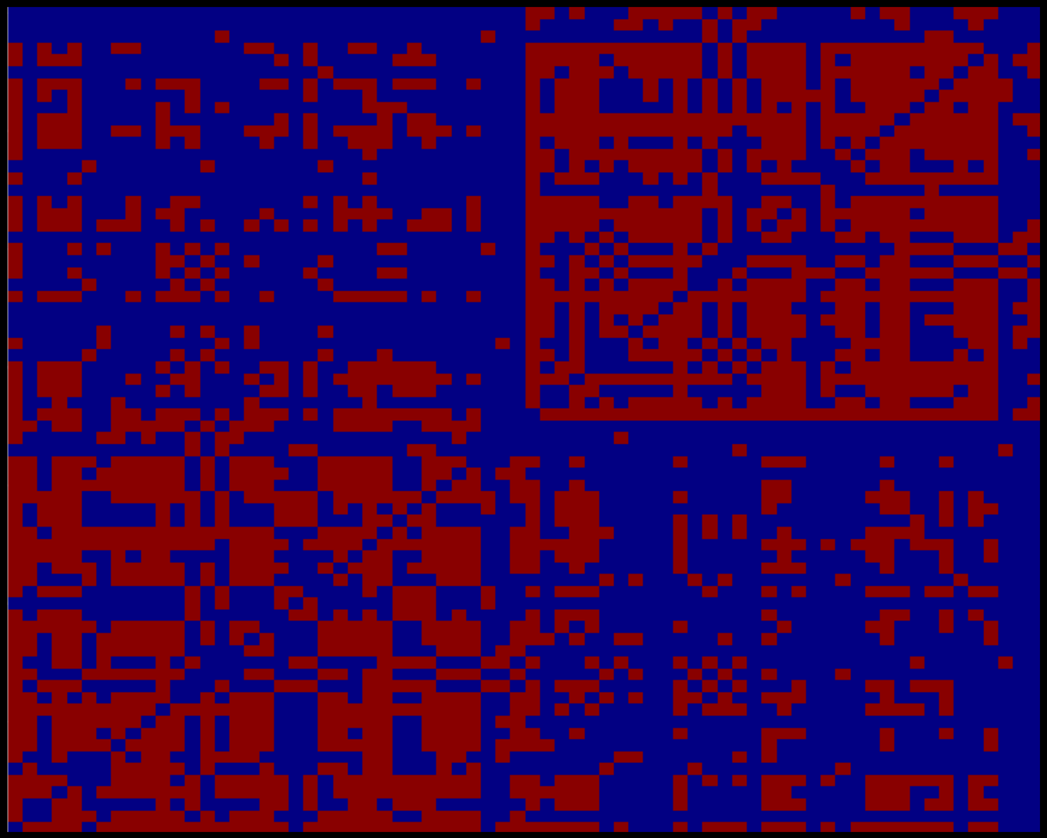
Latent Structure Model

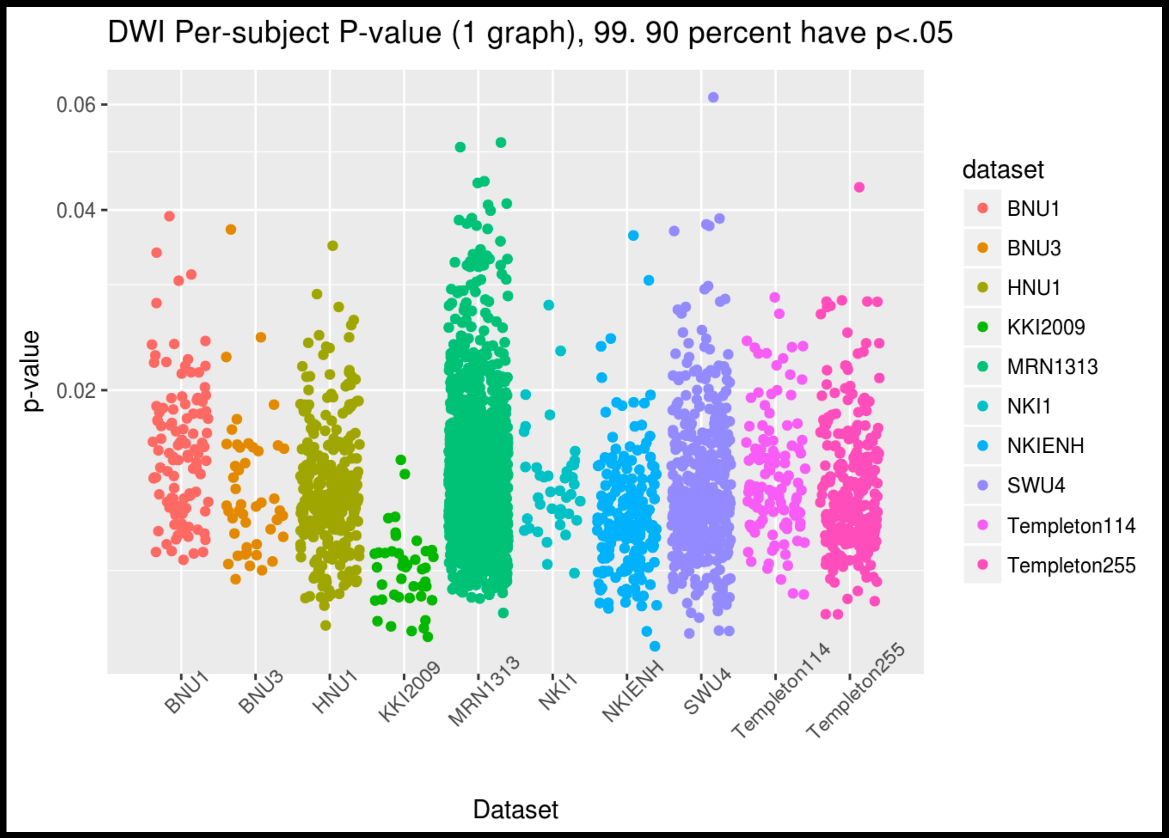
- Each vertex can have latent & observed variable
  - can be categorical, numerical, vectors, etc.
- The latent variables have structure
  - can be cluster, nonlinear relationships, hierarchy, etc.

applications

Human DTI Connectome Code

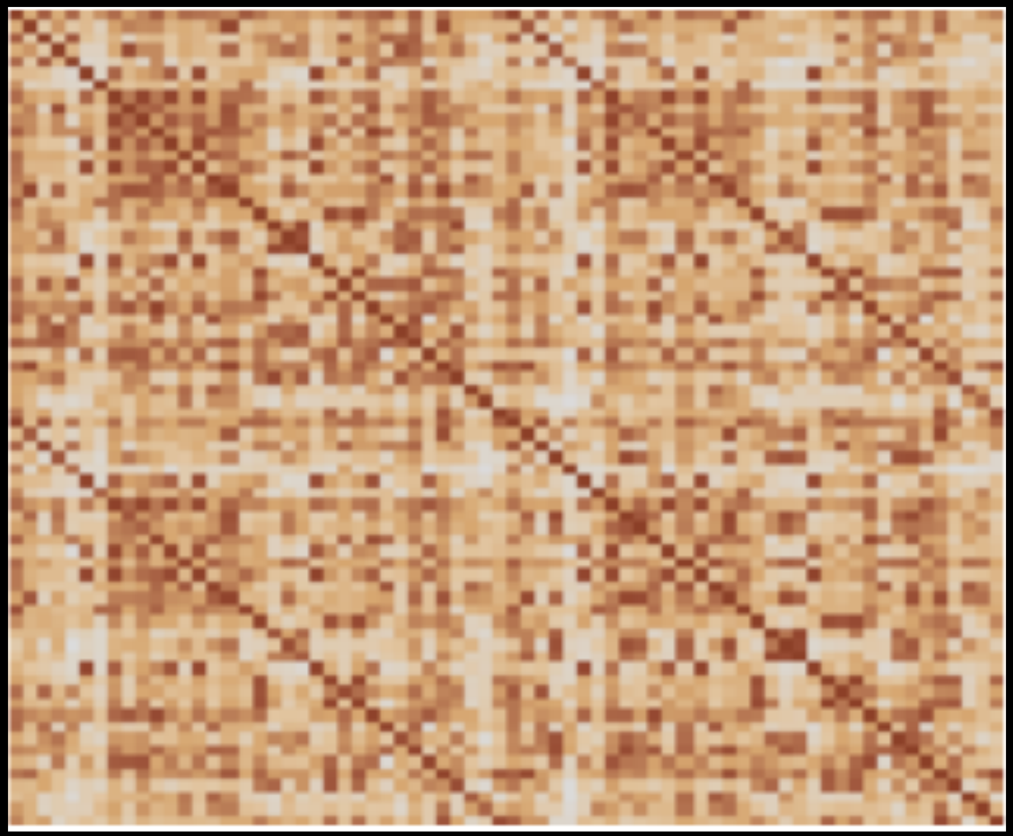
ipsilateral connections are stronger than contralateral

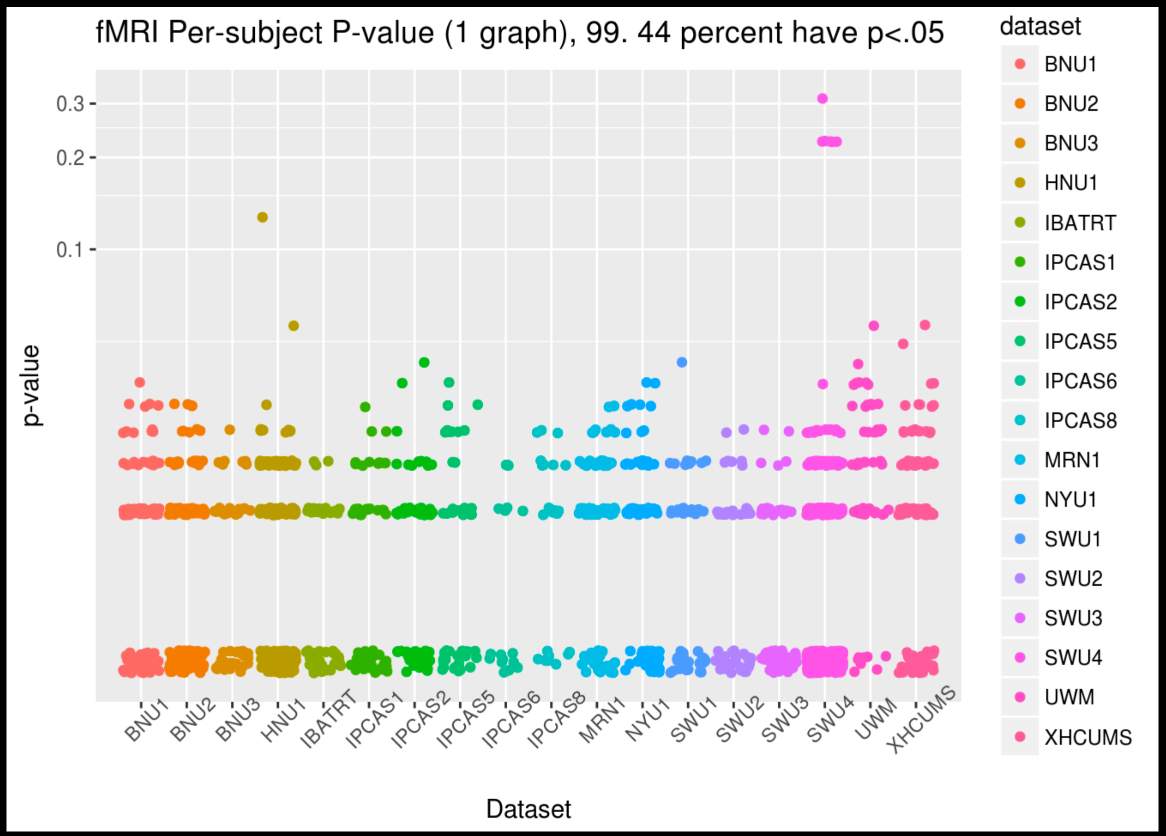




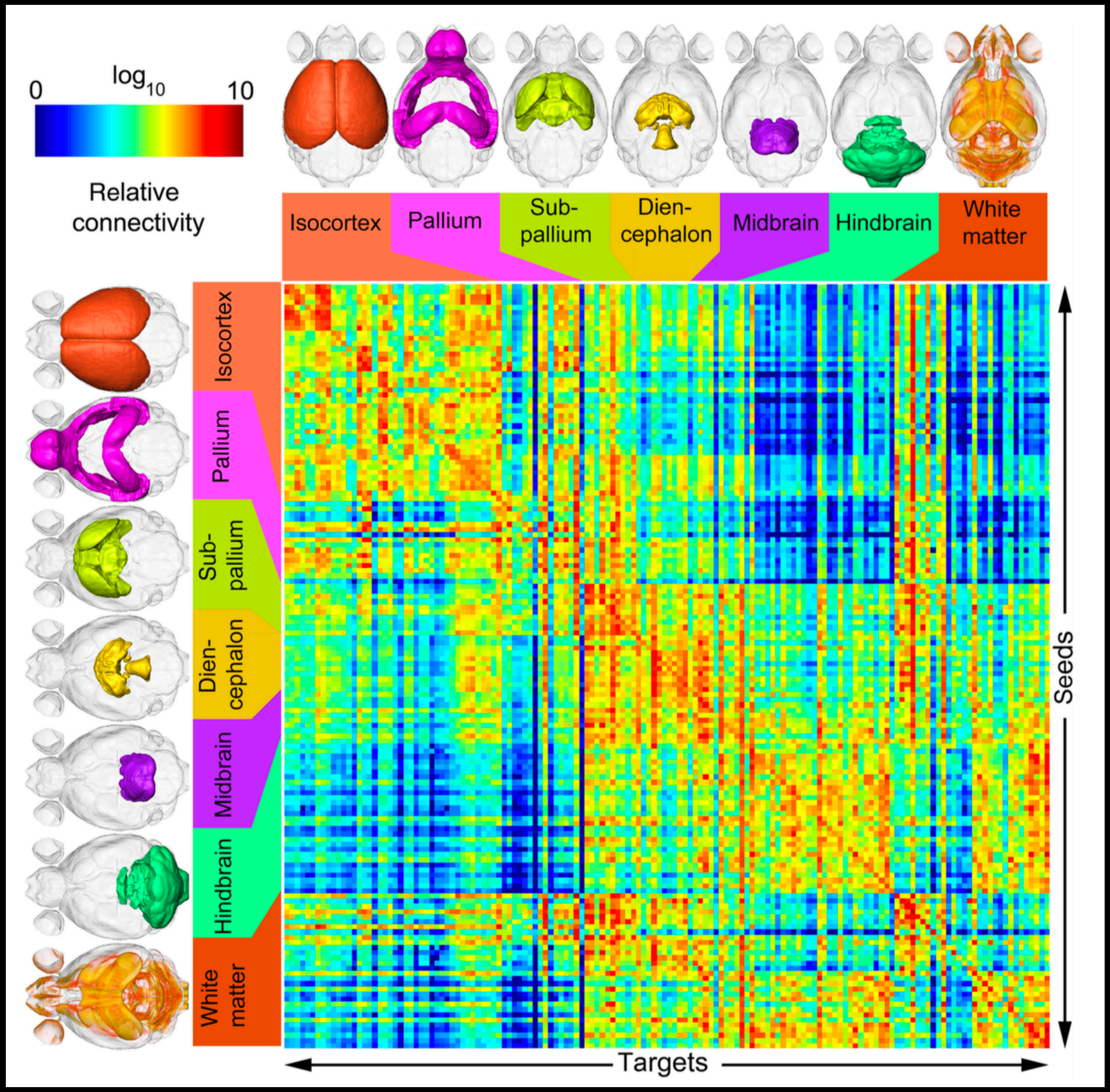
Human fMRI Connectome Code

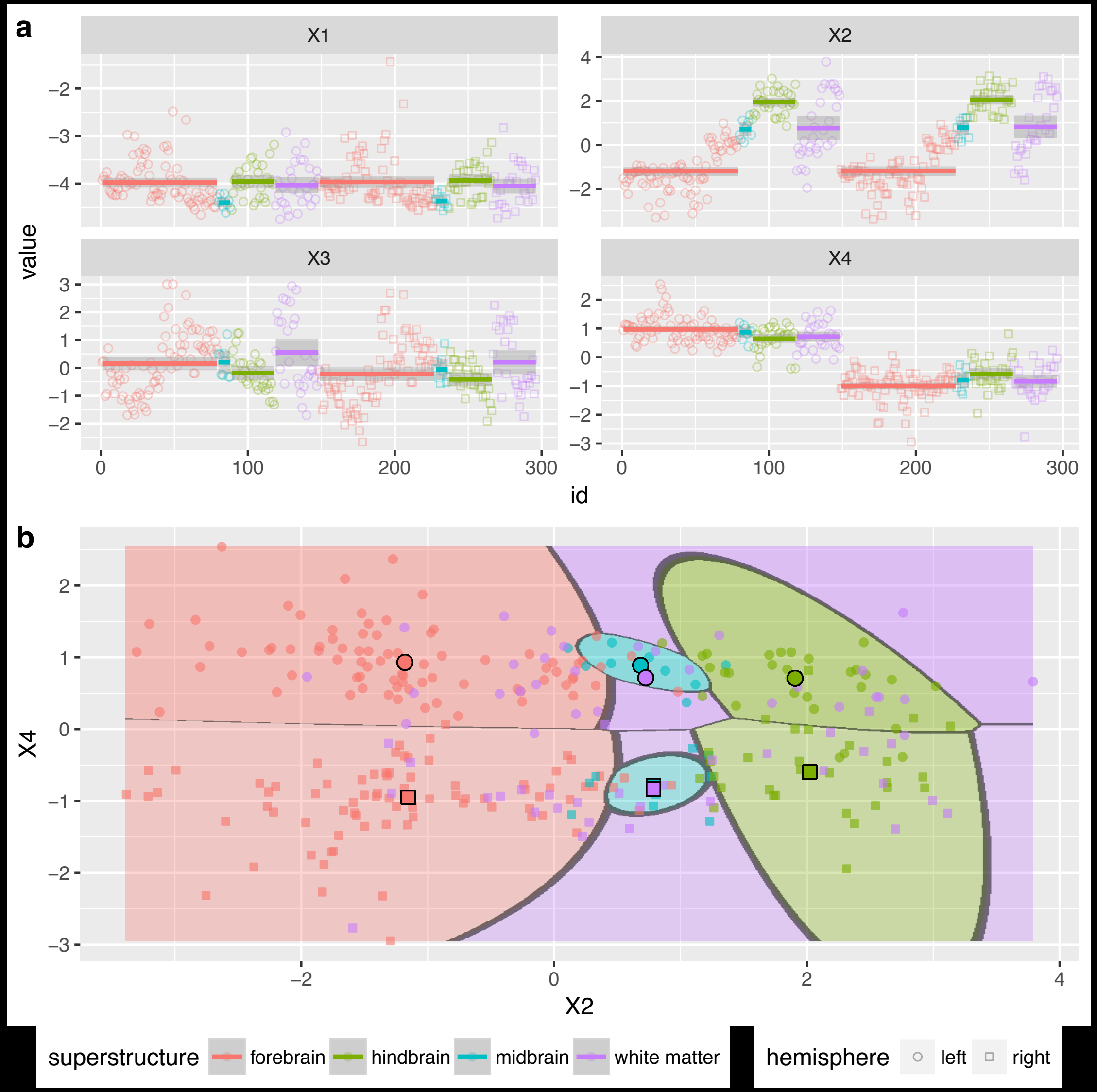
bilateral connections are stronger than non-bilateral



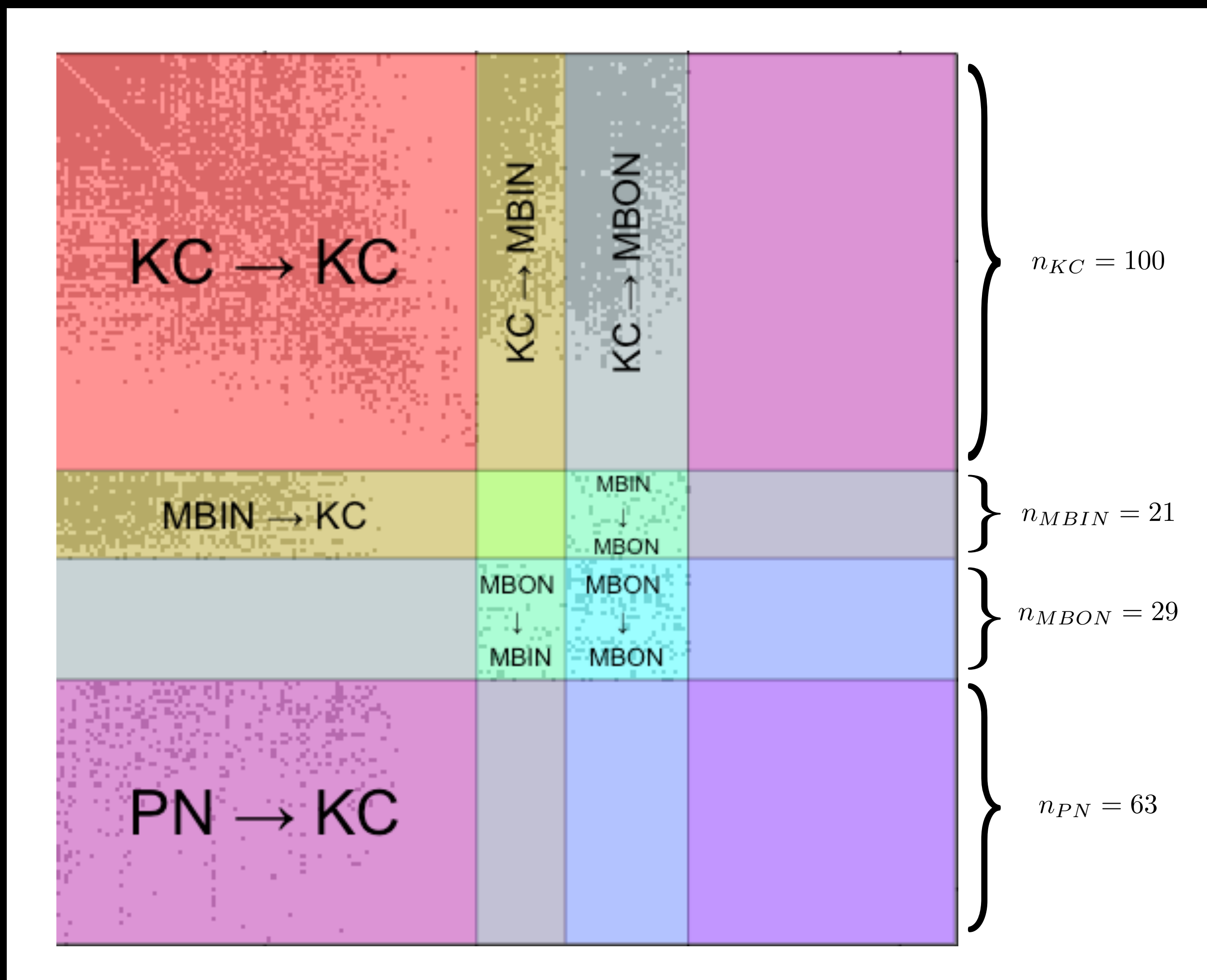


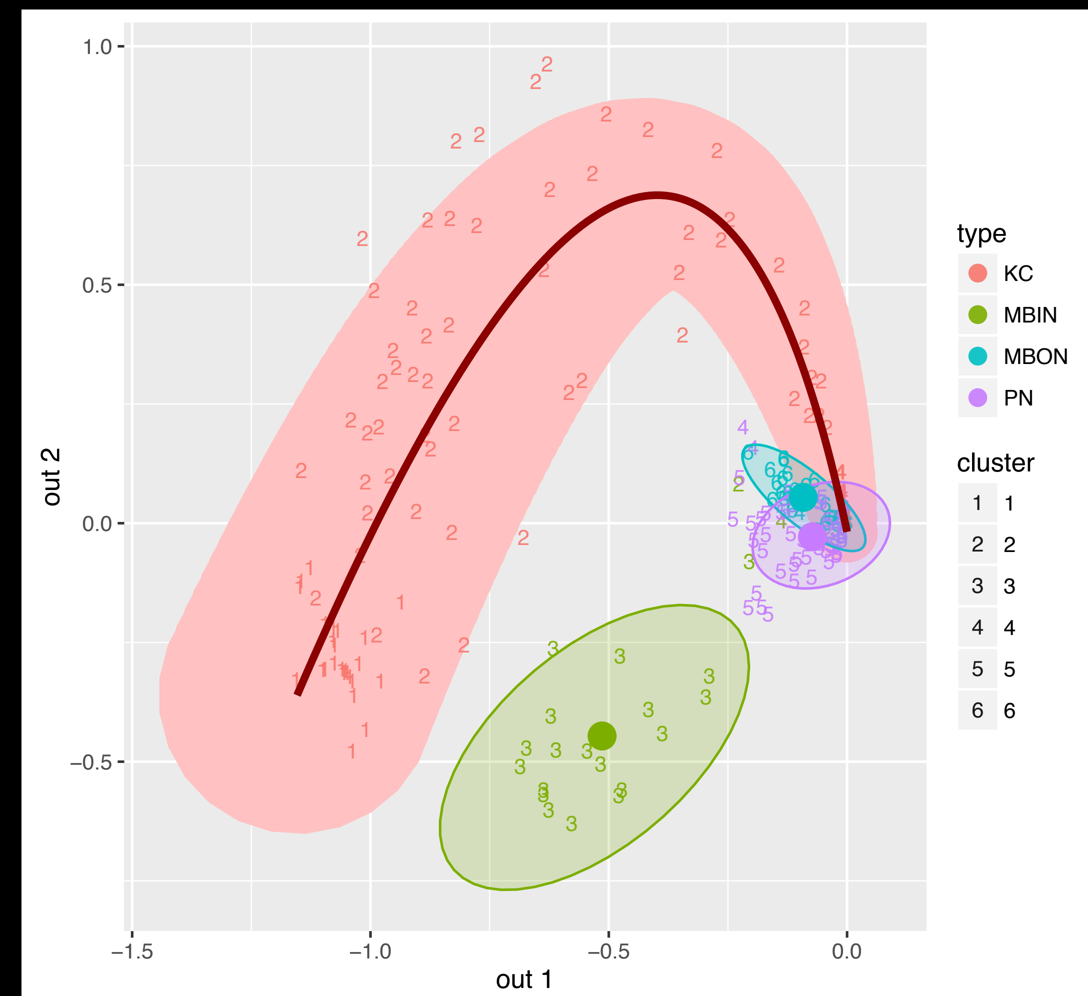
Mouse Connectome Code



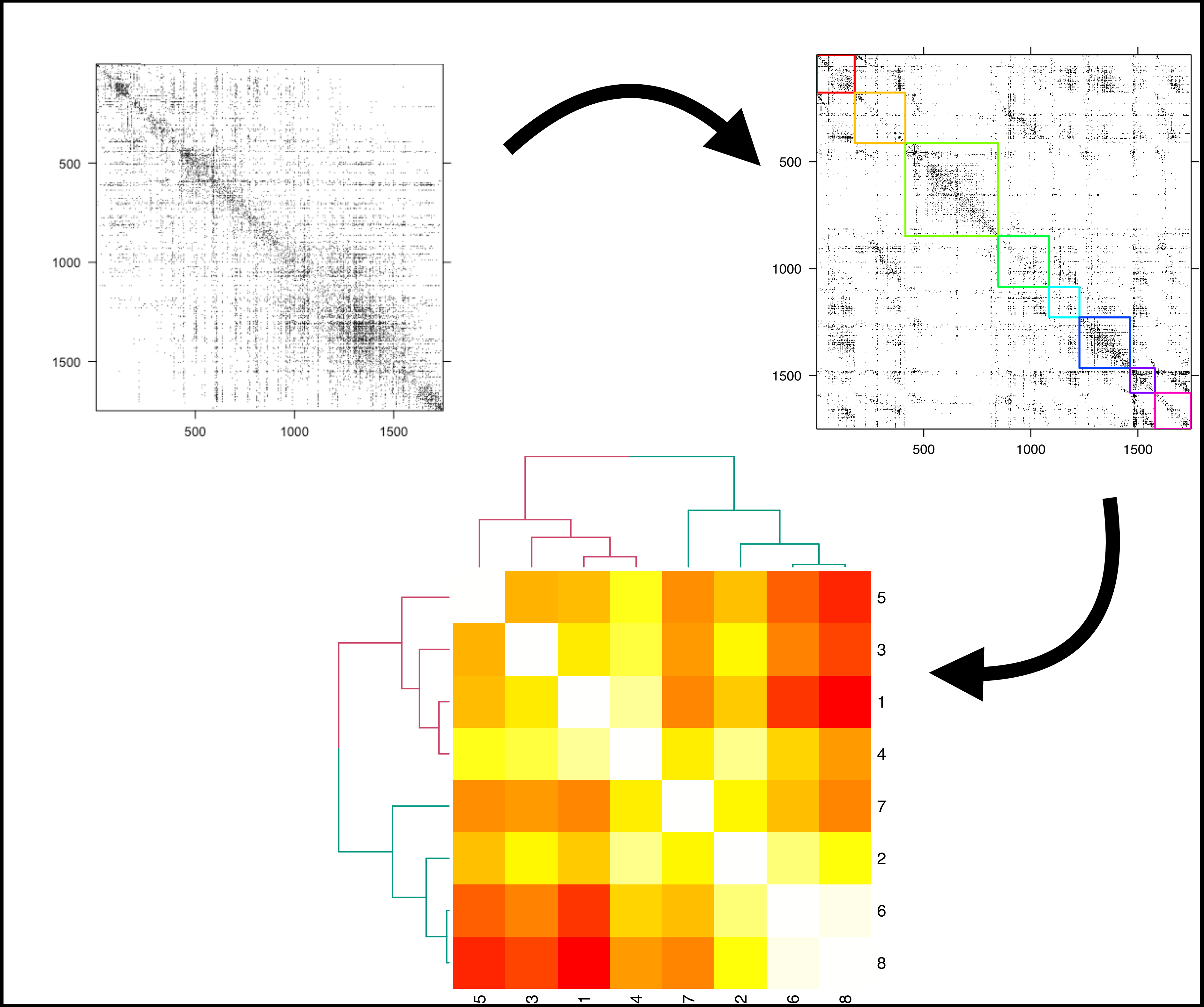


Larval Drosophila Mushroom Body Connectome Code





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?

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