

Maggot brain, mirror image? A statistical analysis of bilateral symmetry in an insect brain connectome

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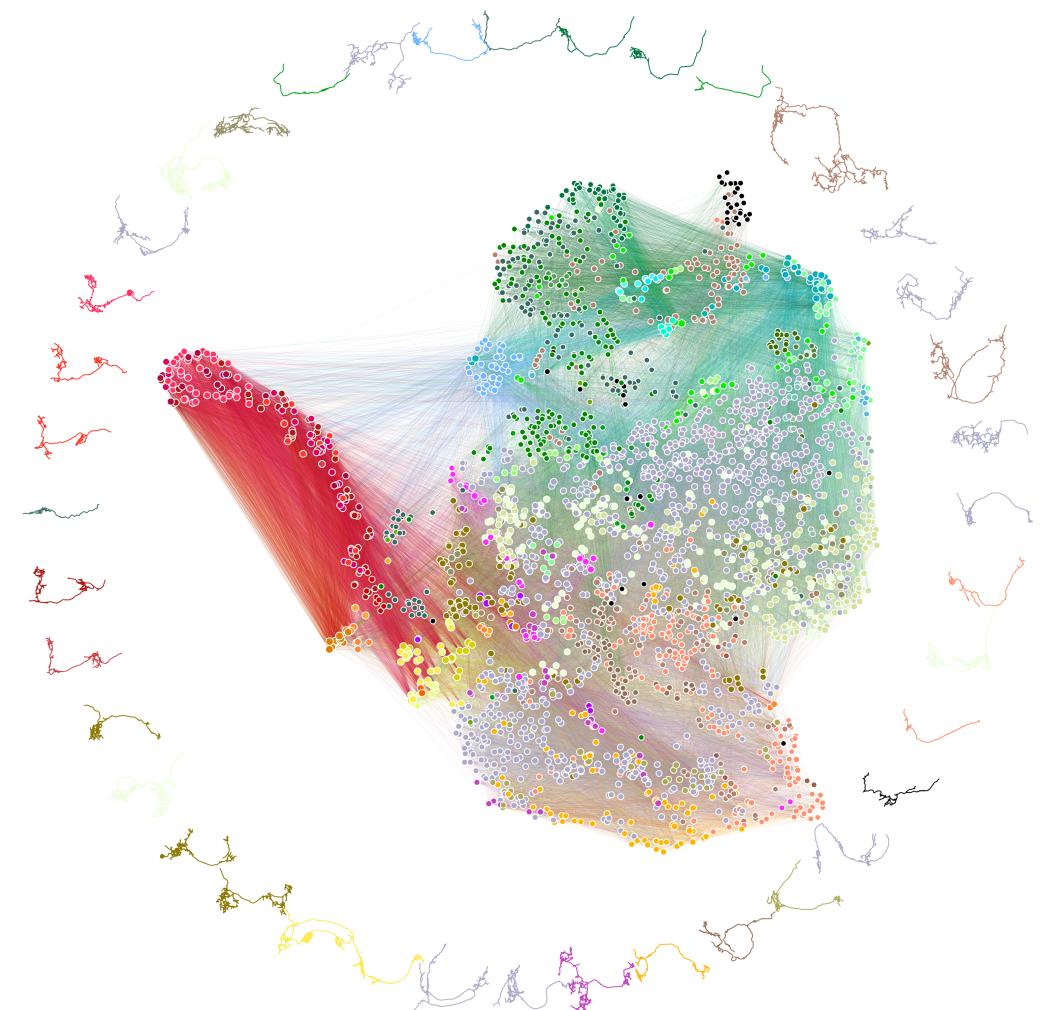
Johns Hopkins University

NeuroData lab

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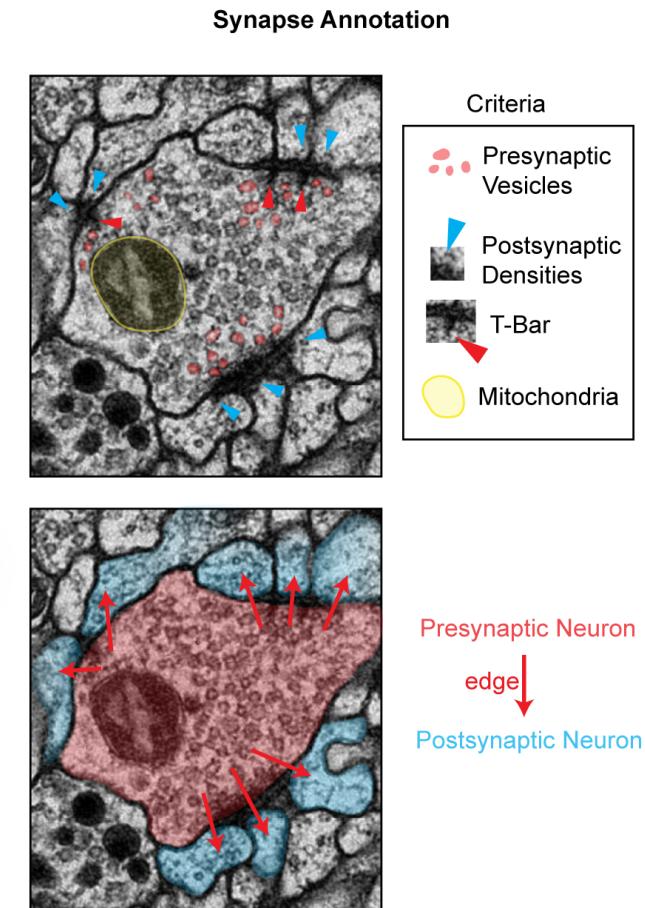
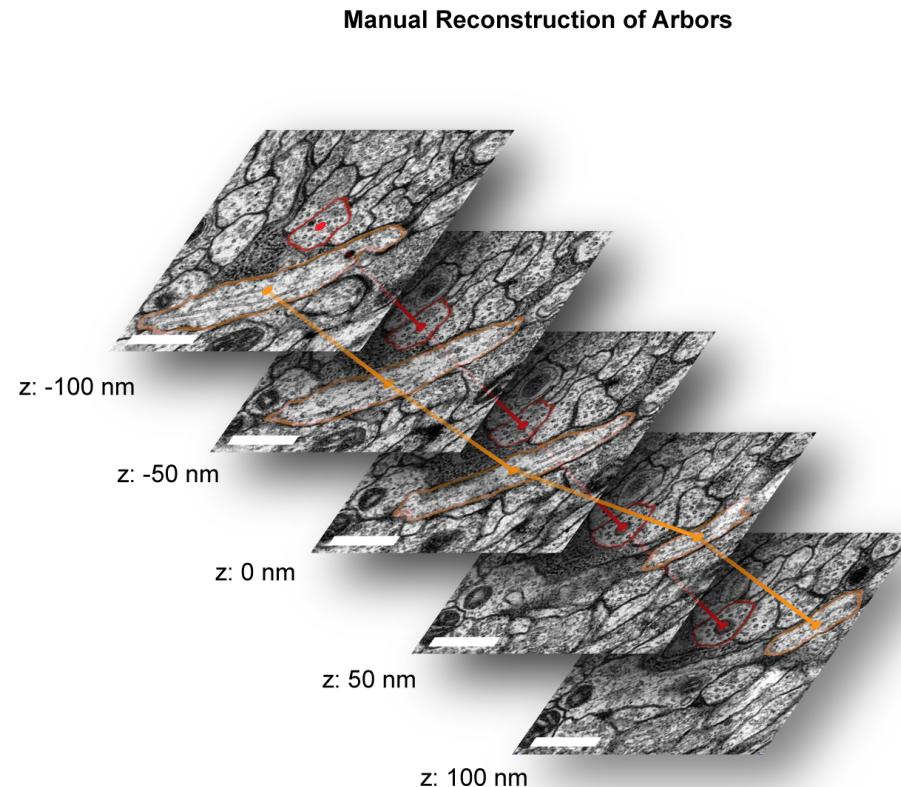
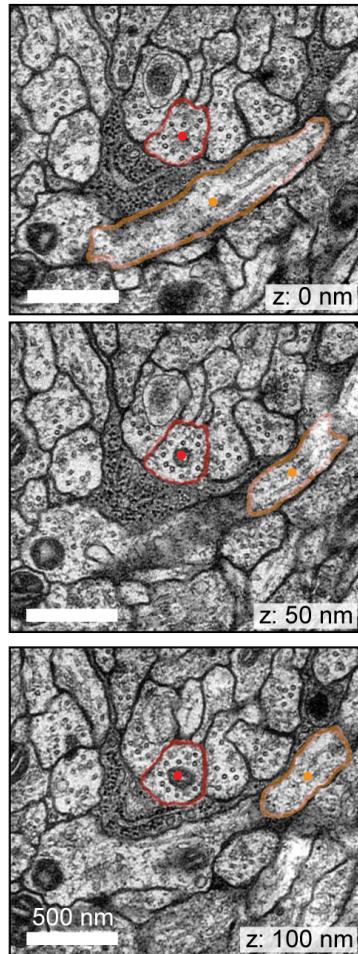
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My requests

- Feedback, feedback, feedback
 - Especially with figures

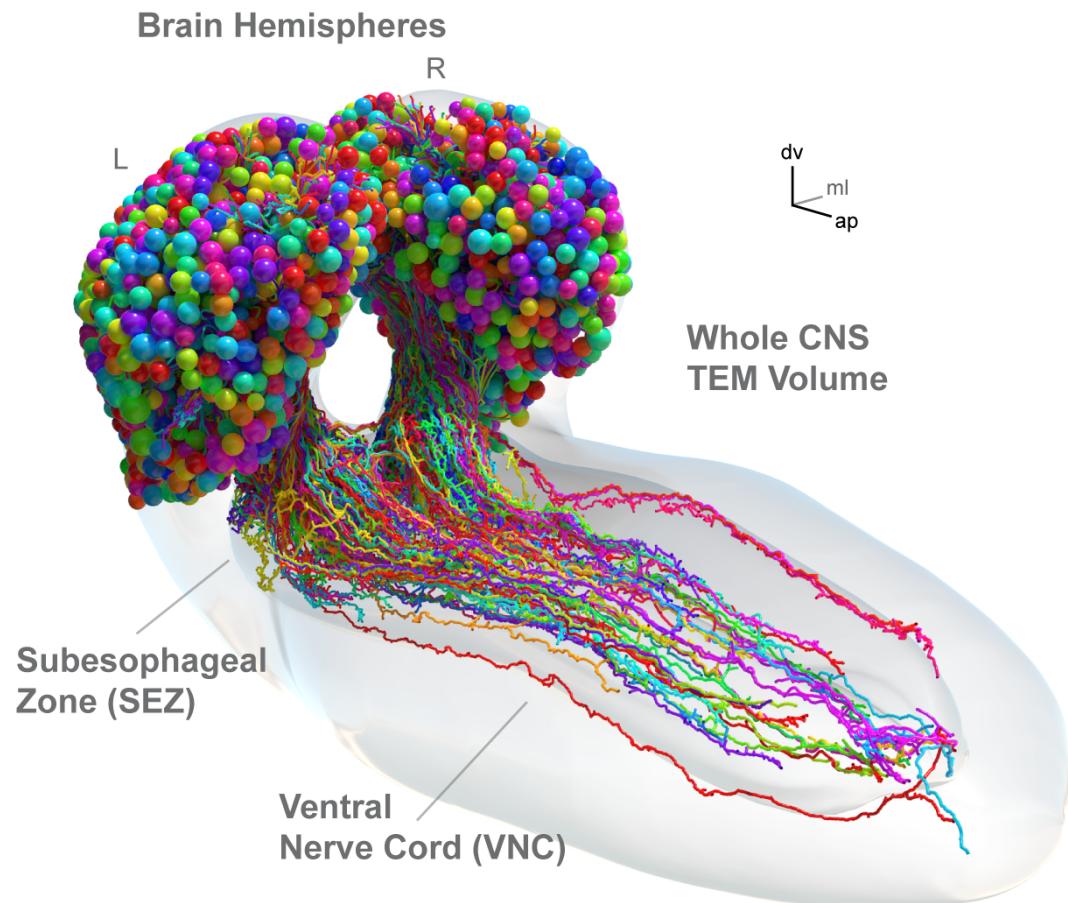
Electron microscopy connectomics



Drosophila larva (AKA a maggot) brain connectome

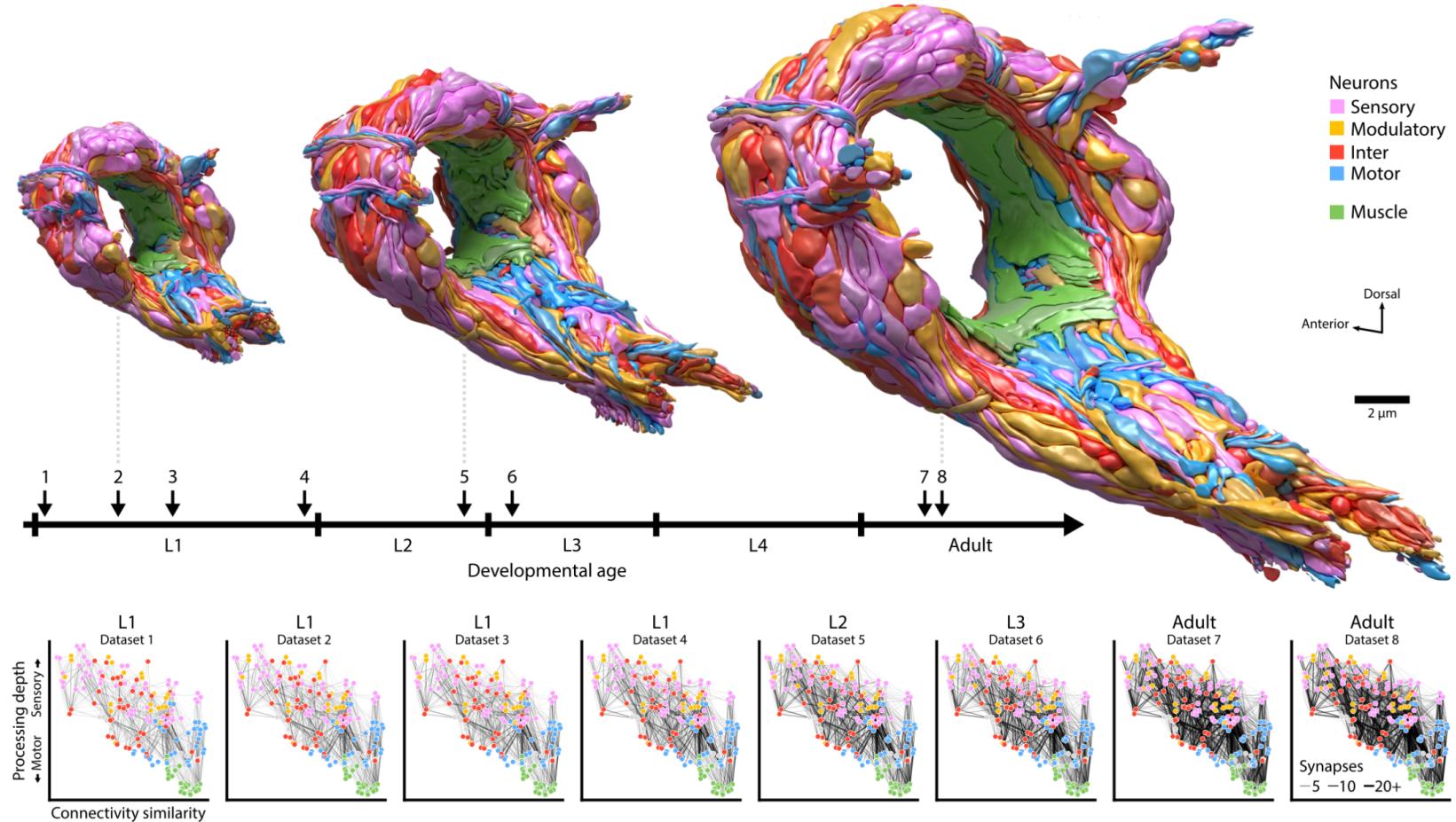
See [Michael Windings's talk](#)

- First whole-brain, single-cell connectome of any insect
- ~3000 neurons, ~544K synapses
- Both hemispheres of the brain reconstructed

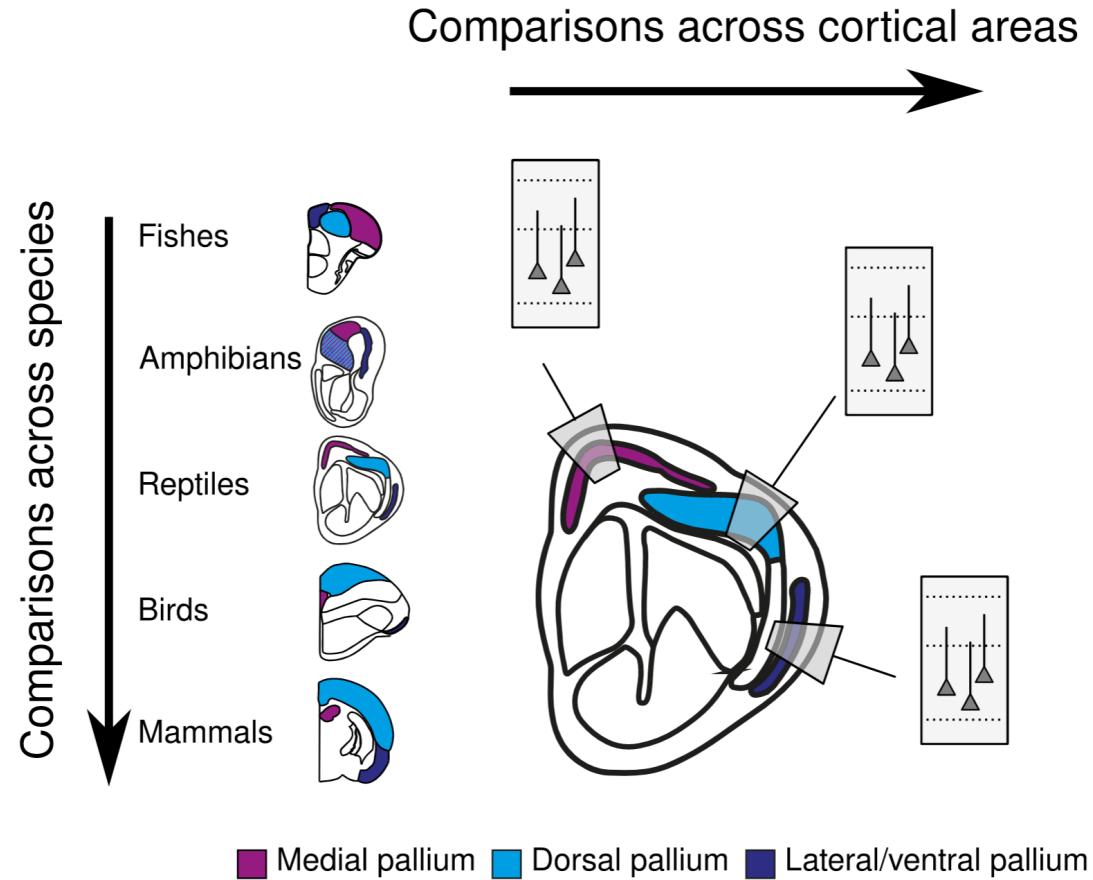


Many connectomics questions require comparison

Connectomes across development



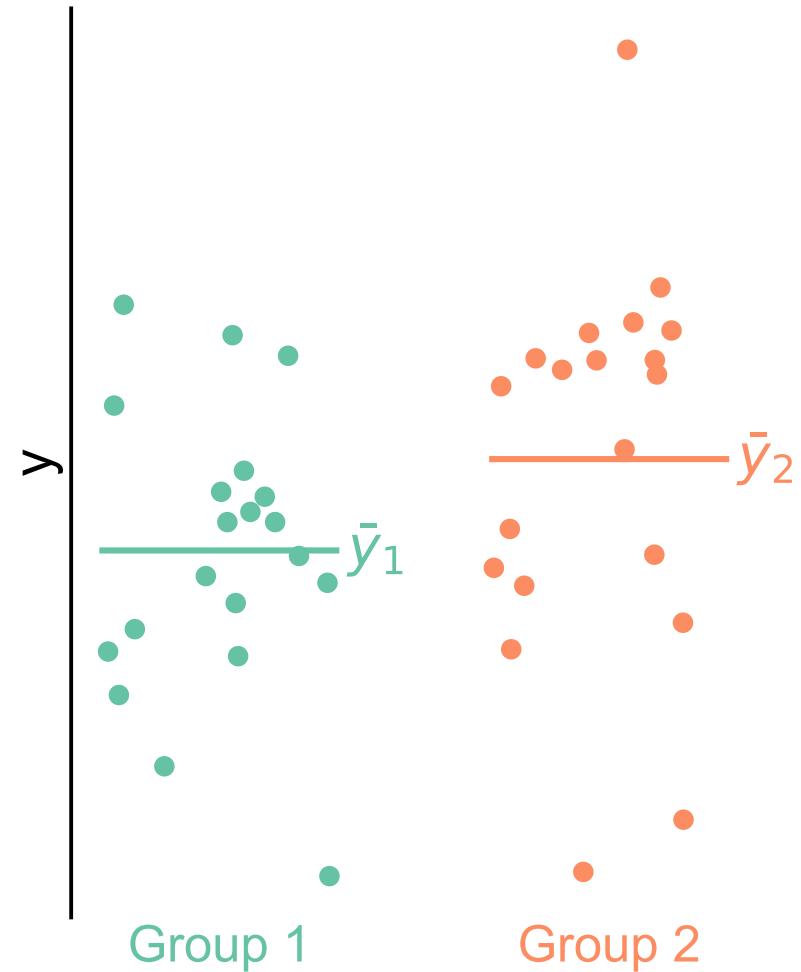
Connectomes across evolution, cortex



Are the **left** and **right** sides of this connectome
the same?

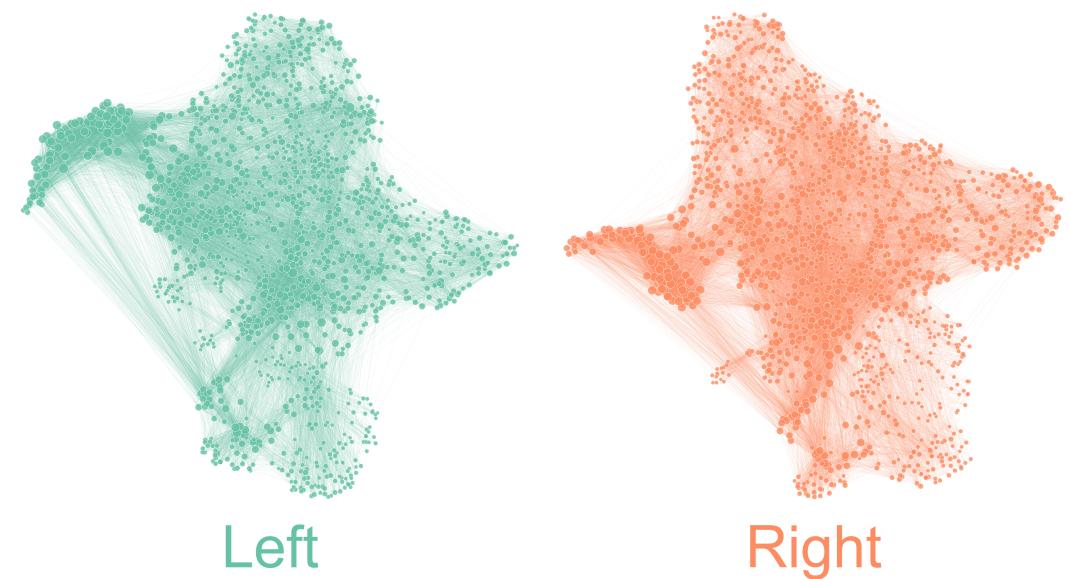
Are these populations the same?

- Known as two-sample testing
- $Y^{(1)} \sim F^{(1)}$, $Y^{(2)} \sim F^{(2)}$
- $H_0 : F^{(1)} = F^{(2)}$
- $H_A : F^{(1)} \neq F^{(2)}$



Are these two *networks* the same?

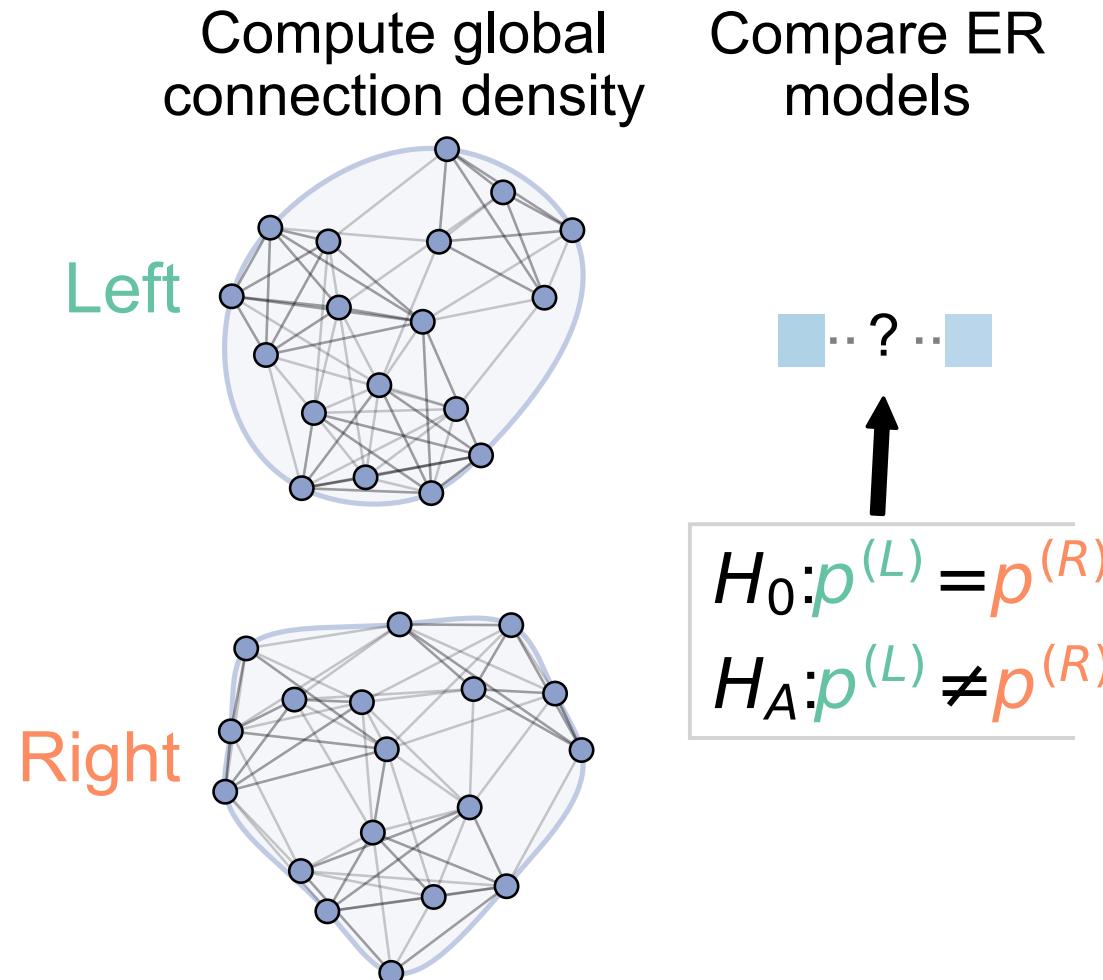
- Want a two-network-sample test!
- $A^{(L)} \sim F^{(L)}$, $A^{(R)} \sim F^{(R)}$
- $H_0 : F^{(L)} = F^{(R)}$
 $H_A : F^{(L)} \neq F^{(R)}$



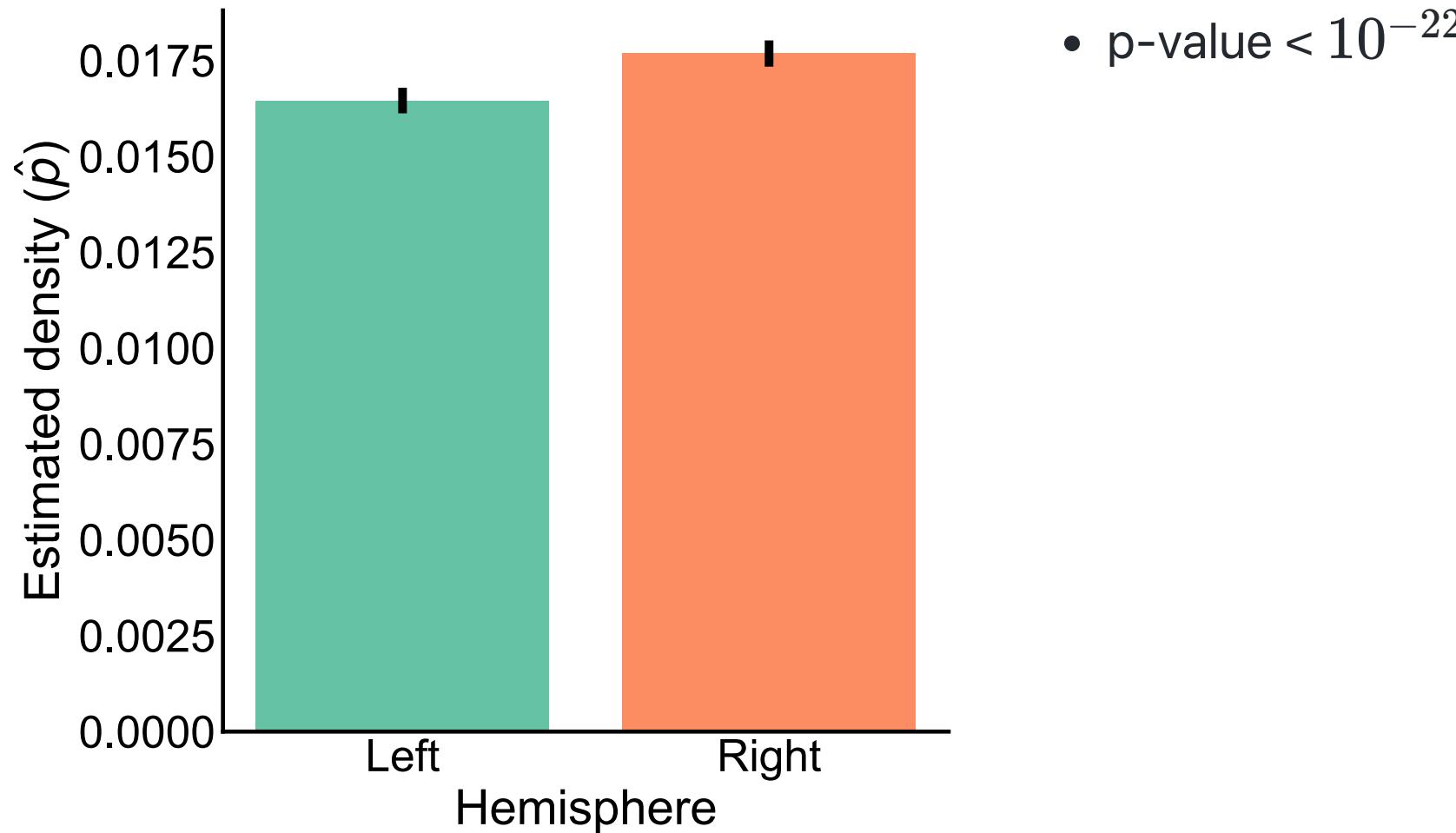
Assumptions

- We know the direction of synapses, so network is *directed*.
- For simplicity (for now), consider networks to be *unweighted*.
- For simplicity (for now), consider the **left** → **left** and **right** → **right** (*ipsilateral*) connections only.

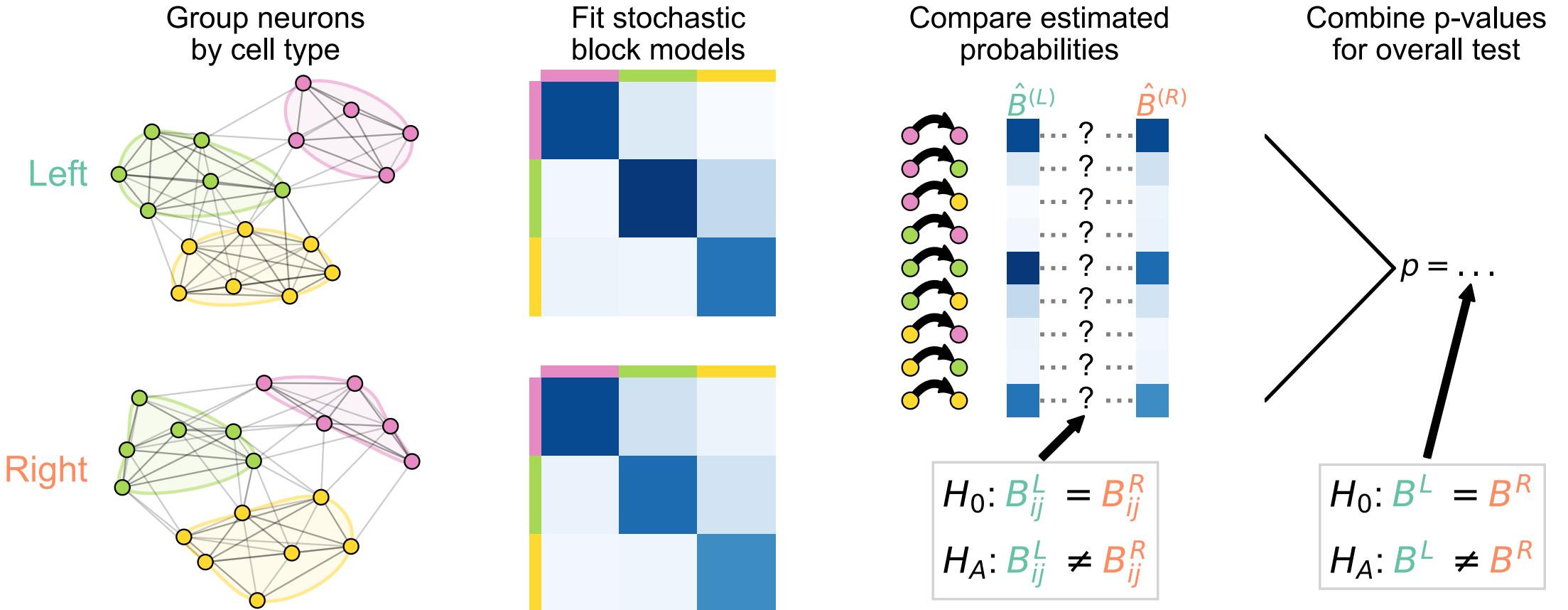
Density-based testing: Erdos-Renyi (ER) model



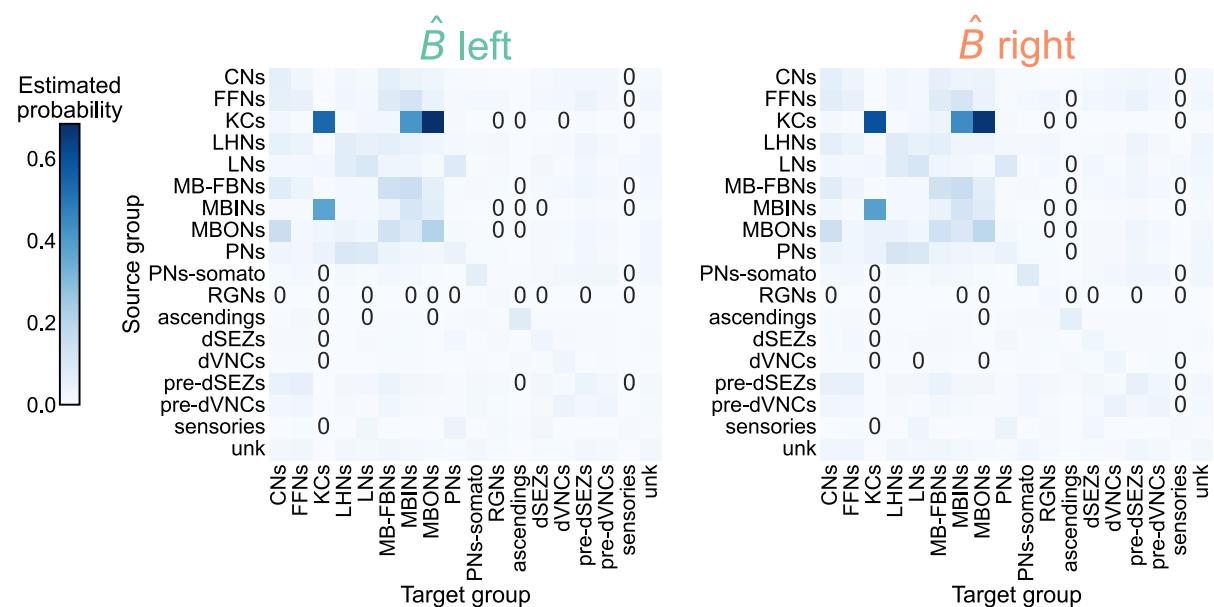
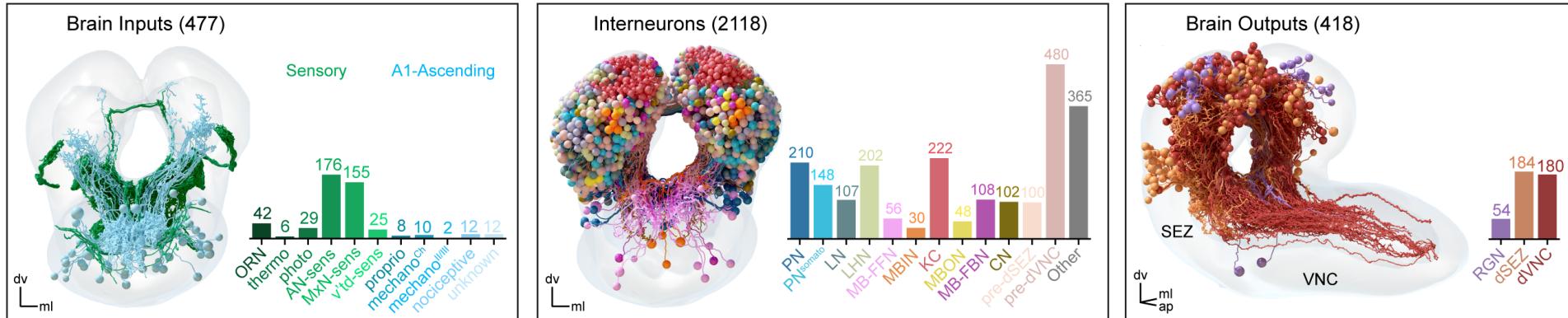
We detect a difference in density



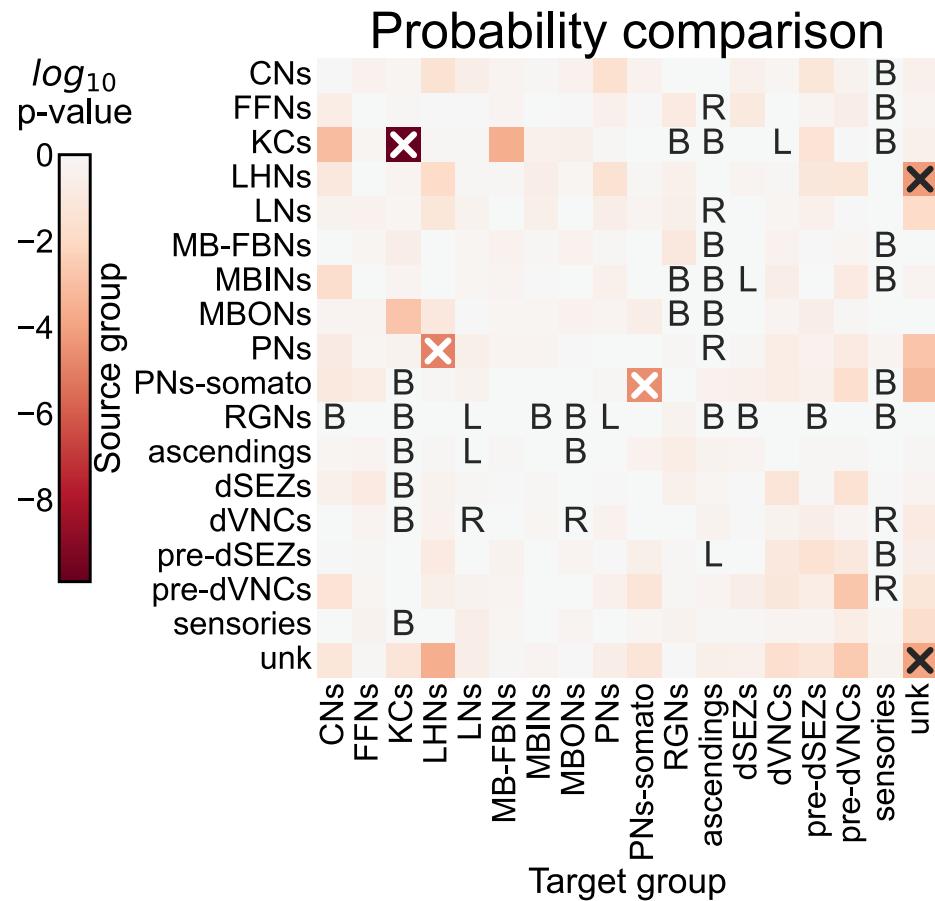
Group-based testing: stochastic block model (SBM)



Connection probabilities between groups



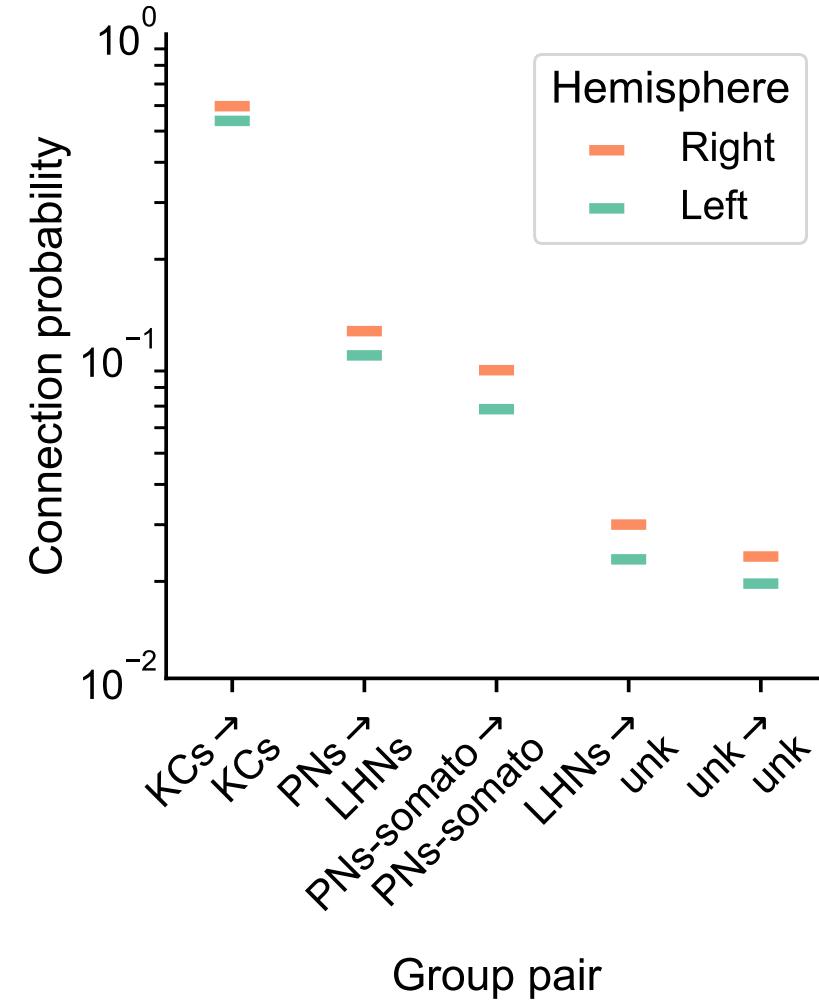
We detect a difference in group-to-group connection probabilities



- After multiple comparison, find 5 group-to-group connections which are significantly different
- Combine (uncorrected) p-values (like a meta-analysis), leads to p-value for overall test of $< 10^{-7}$

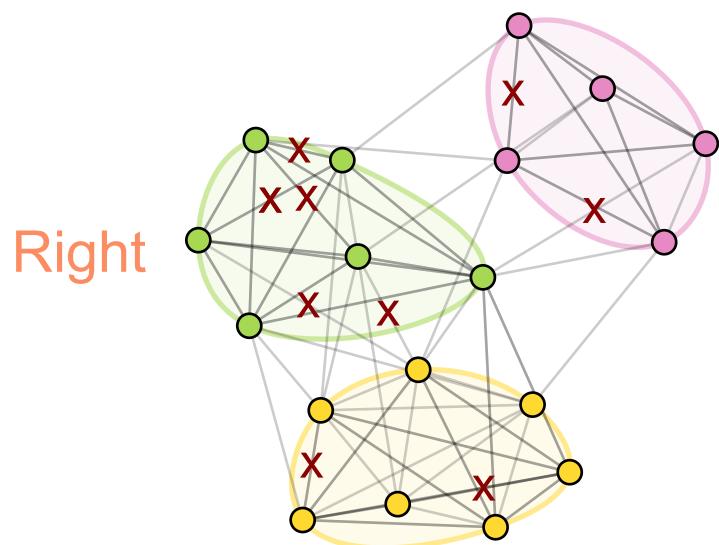
Should we be surprised?

- Already saw that even the overall densities were different
- For all significant comparisons, probabilities on the right hemisphere were higher
- Maybe the right is just a "scaled up" version of the left?
 - $H_0 : B^{(L)} = cB^{(R)}$ where c is a density-adjusting constant, $\frac{p^{(L)}}{p^{(R)}}$

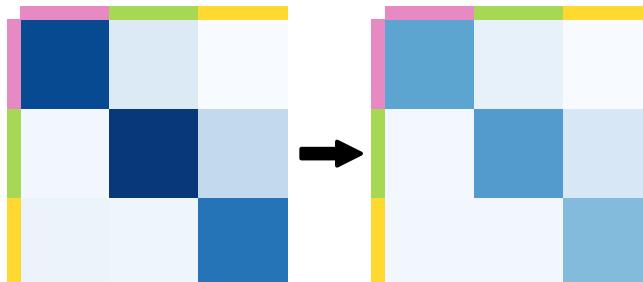


Adjusting for a difference in density

Randomly subsample edges

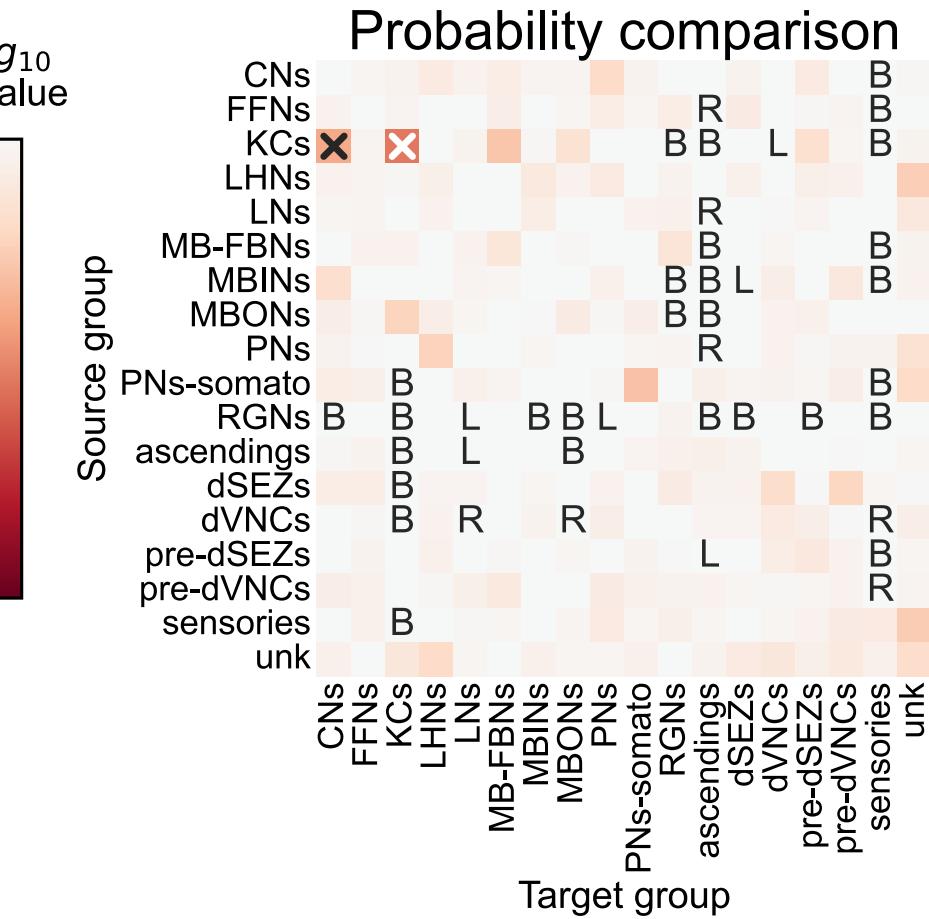
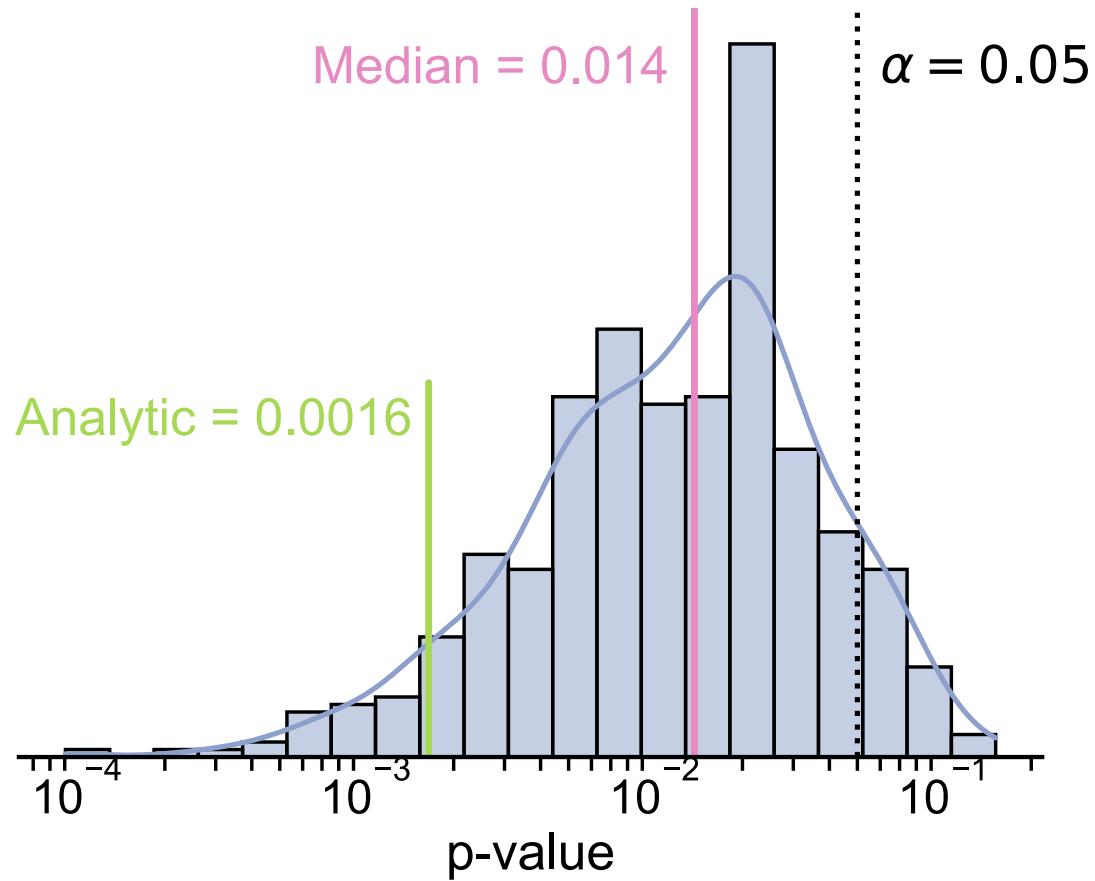


Adjust connection probabilities

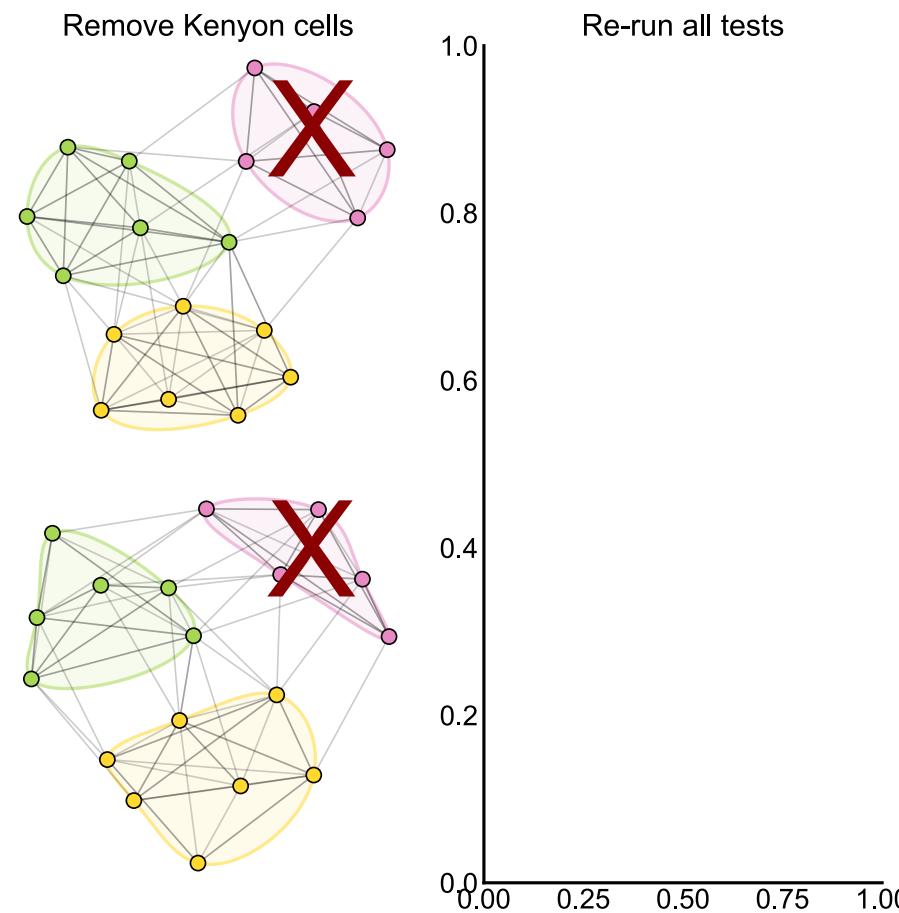


Rerun SBM testing

Even with an adjustment, still detect a difference



So the Kenyon cells are the only group with remaining differences...



- ER test: $p < 10^{-26}$
- SBM test: $p \approx 0.0027$
- Adjusted SBM test: $p \approx 0.43$

But wait, there's more (tests one could run)!

To sum up...

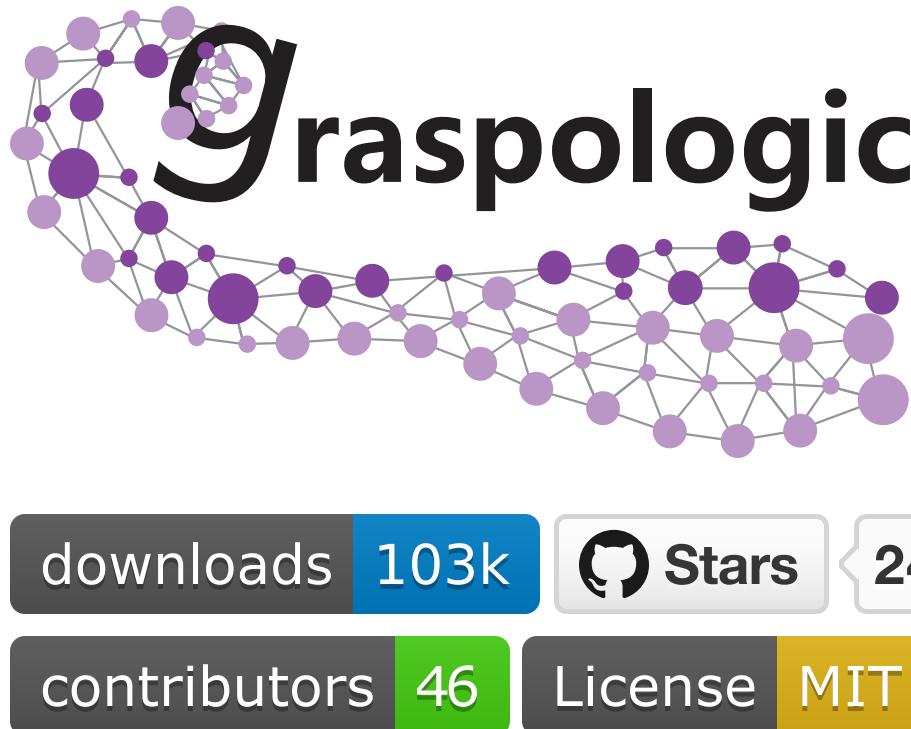
Model	H_0 (vs. $H_A \neq$)	KC	p-value	Interpretation
ER	$p^{(L)} = p^{(R)}$	+	$< 10^{-23}$	Reject densities the same
SBM	$B^{(L)} = B^{(R)}$	+	$< 10^{-7}$	Reject group connection probabilities the same
aSBM	$B^{(L)} = cB^{(R)}$	+	≈ 0.0016	Reject above even after accounting for density
ER	$p^{(L)} = p^{(R)}$	-	$< 10^{-26}$	Reject densities the same (w/o KCs)
SBM	$B^{(L)} = B^{(R)}$	-	≈ 0.0027	Reject group connection probabilities the same (w/o KCs)
aSBM	$B^{(L)} = cB^{(R)}$	-	≈ 0.43	Don't reject above after density adjustment (w/o KCs)

More generally

- We studied simple ways of framing a network two sample test
- We found that it can be important to "mod out" by other simple network statistics if you don't care about them (like density)
- We provide recommendations for what to run for you future connectome comparisons

graspologic:

github.com/microsoft/graspologic



This work:

github.com/neurodata/bilateral-connectome



Bilateral Connectome

Search this book...

Abstract

PRELIMINARIES

Introduction

Outline

Unmatched vs. matched networks

Larval *Drosophila melanogaster* brain connectome



The Erdos-Renyi (ER) model

The **Erdos-Renyi (ER) model** is one of the simplest network models. This model treats the probability of each potential edge in the network occurring to be the same. In other words, all edges between any two nodes are equally likely.

Math

Let n be the number of nodes. We say that for all (i, j) , $i \neq j$, with i and j both running from $1 \dots n$, the probability of the edge (i, j) occurring is:

$$P[A_{ij} = 1] = p_{ij} = p$$

Where p is the global connection probability.

Each element of the adjacency matrix A is then

Acknowledgements

Johns Hopkins University

Mike Powell, Eric Bridgeford, Carey Priebe, Joshua Vogelstein, Kareef Ullah, Diane Lee, Sambit Panda, Jaewon Chung, Ali Saad-Eldin, NeuroData lab

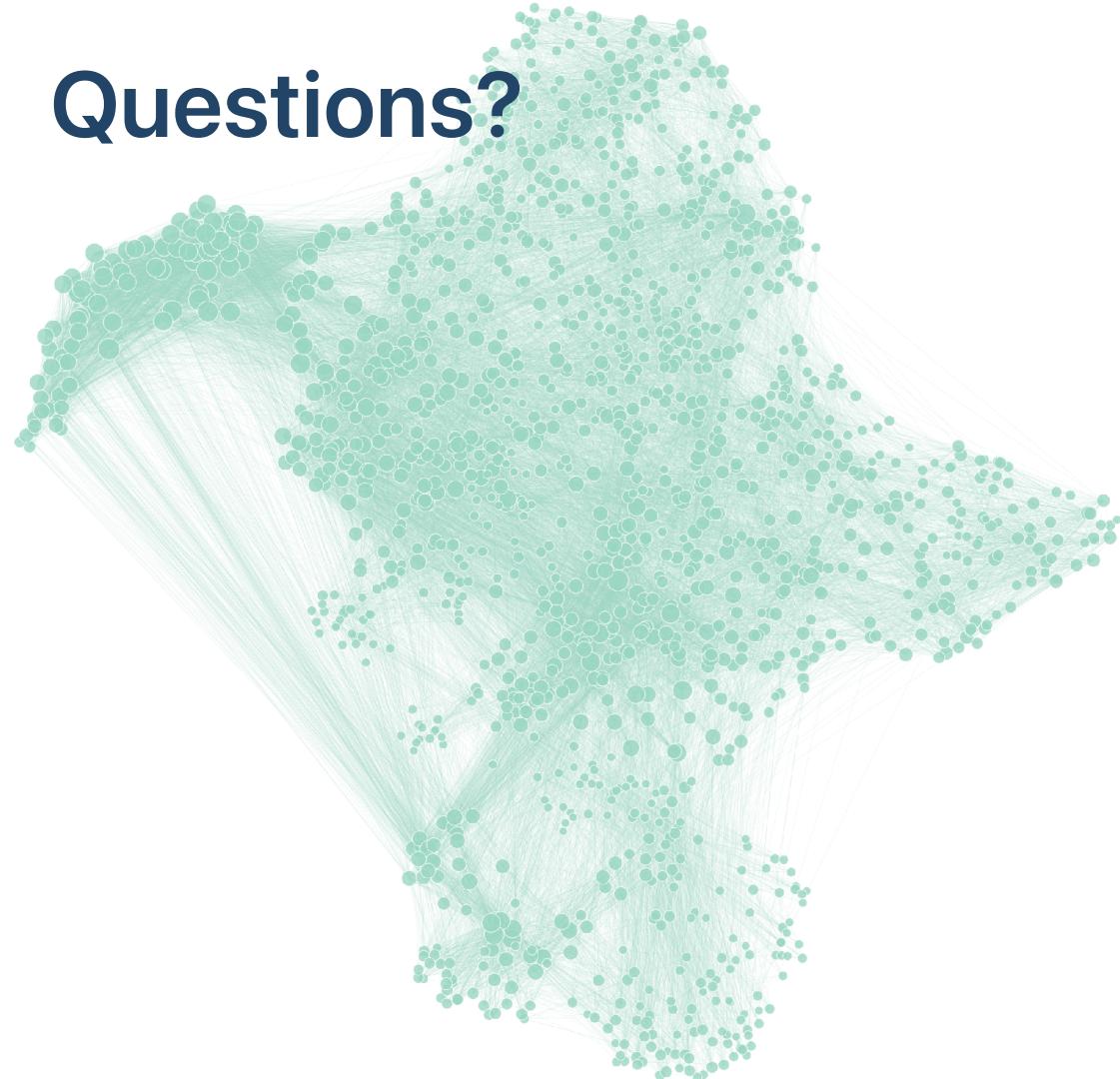
University of Cambridge / MRC Laboratory of Molecular Biology

Michael Winding, Albert Cardona, Marta Zlatic, Chris Barnes

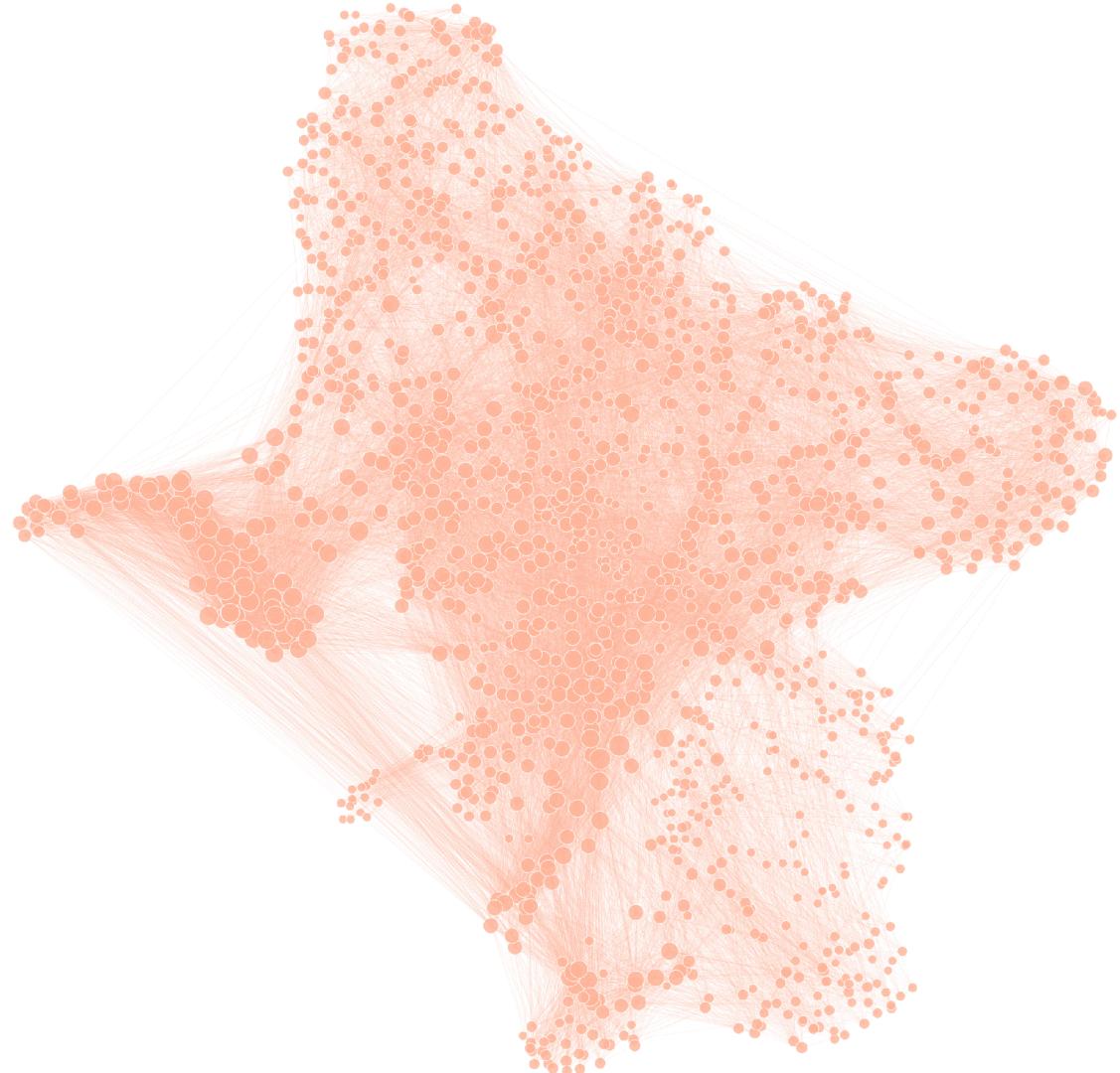
Microsoft Research

Hayden Helm, Dax Pryce, Nick Caurvina, Bryan Tower, Patrick Bourke, Jonathan McLean, Carolyn Buractaon, Amber Hoak

Questions?



Left



Right

