

# Tools for comparing connectomes: evaluating the bilateral symmetry of a whole insect brain

**Benjamin D. Pedigo**

(he/him) -  [bpedigo@jhu.edu](mailto:bpedigo@jhu.edu)

*NeuroData lab*

*Johns Hopkins University - Biomedical Engineering*

## Team



Michael  
Winding



Mike  
Powell



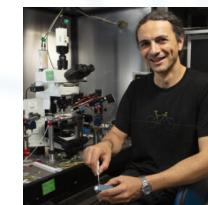
Eric  
Bridgeford



Ali  
Saad-Eldin



Marta  
Zlatic



Albert  
Cardona



Carey  
Priebe



Joshua  
Vogelstein

# Comparative connectomics

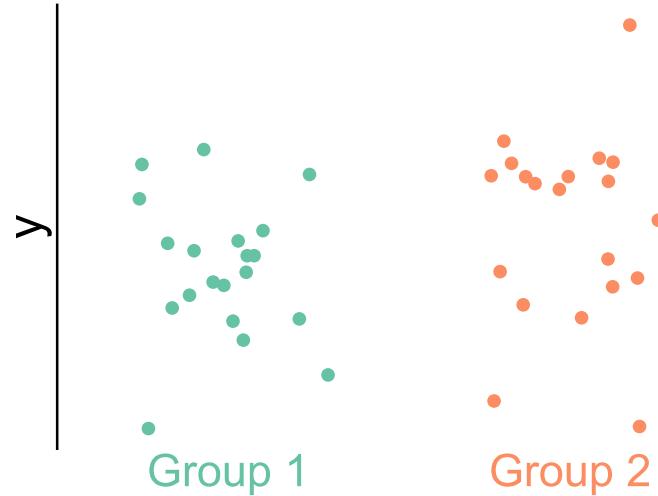
- Connectomes  $\leftrightarrow \{\text{disease, evolution, development, experience, ...}\}$
- As related connectomes are mapped, we'll want evaluate the *significance* and *nature* of differences between them

## Examples for today's talk

1. Are the **left** and **right** sides of the larva brain connectome **different**?
2. How can we *automatically* estimate neuron pairing between brain hemispheres?

# Testing for differences

Are these two populations different?

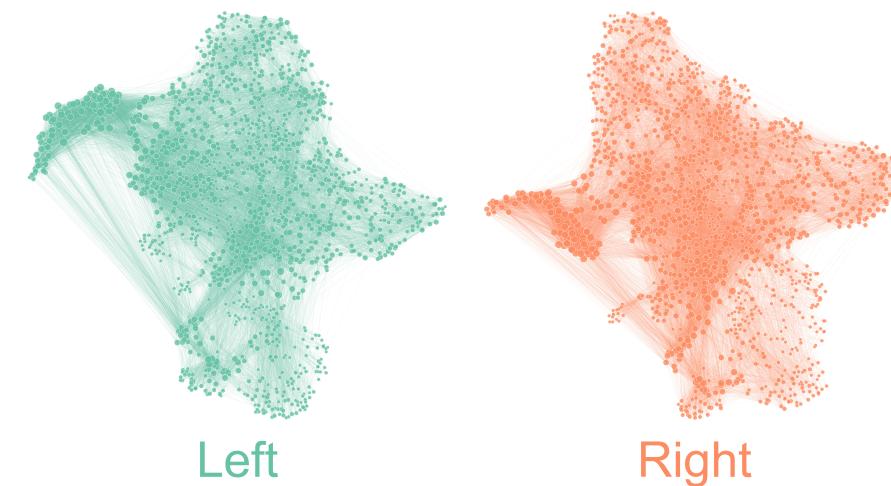


$$Y^{(1)} \sim F^{(1)}$$

$$Y^{(2)} \sim F^{(2)}$$

$$H_0 : F^{(1)} = F^{(2)} \text{ vs. } H_A : F^{(1)} \neq F^{(2)}$$

Are these two *networks* different?



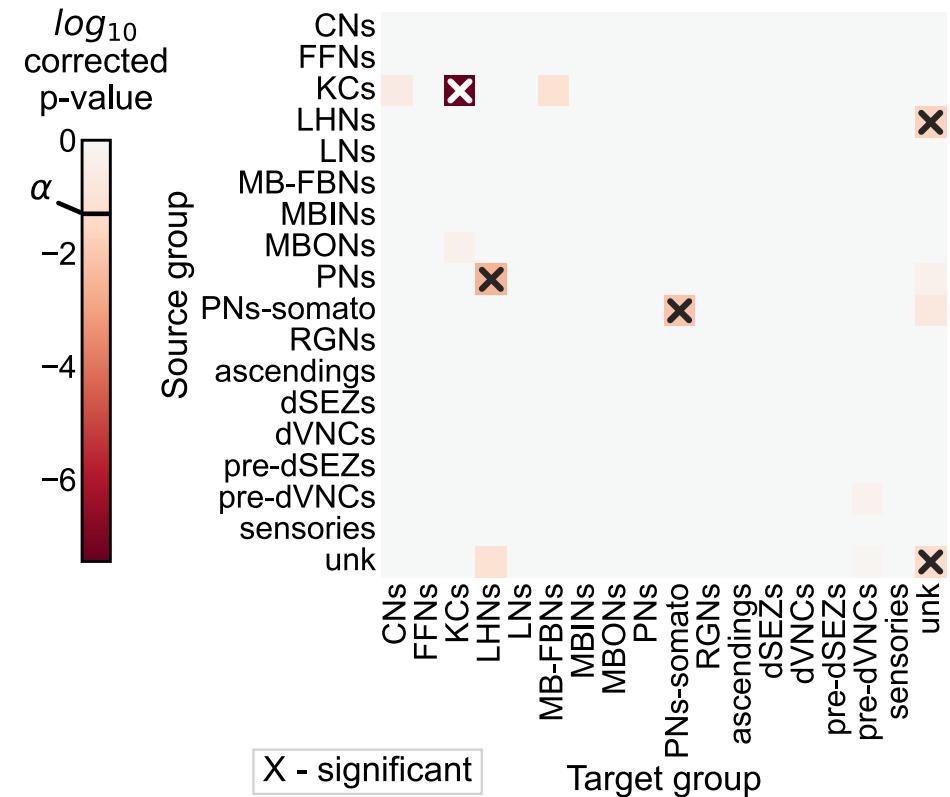
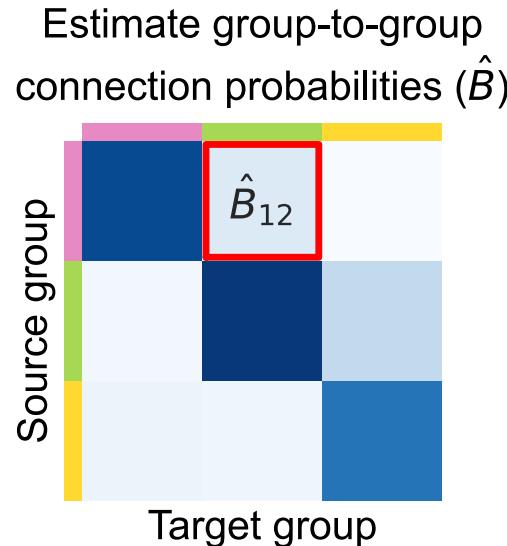
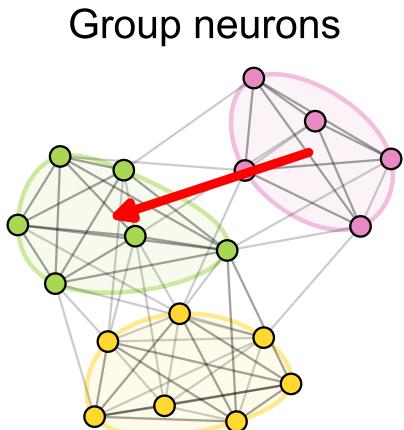
$$A^{(L)} \sim F^{(L)}$$

$$H_0 : F^{(L)} = F^{(R)} \text{ vs. } H_A : F^{(L)} \neq F^{(R)}$$

Many ways to write what "symmetry" means! (different  $F$ , different statistics)

# Example: testing for differences in cell type connections

- Fit block models to both hemispheres



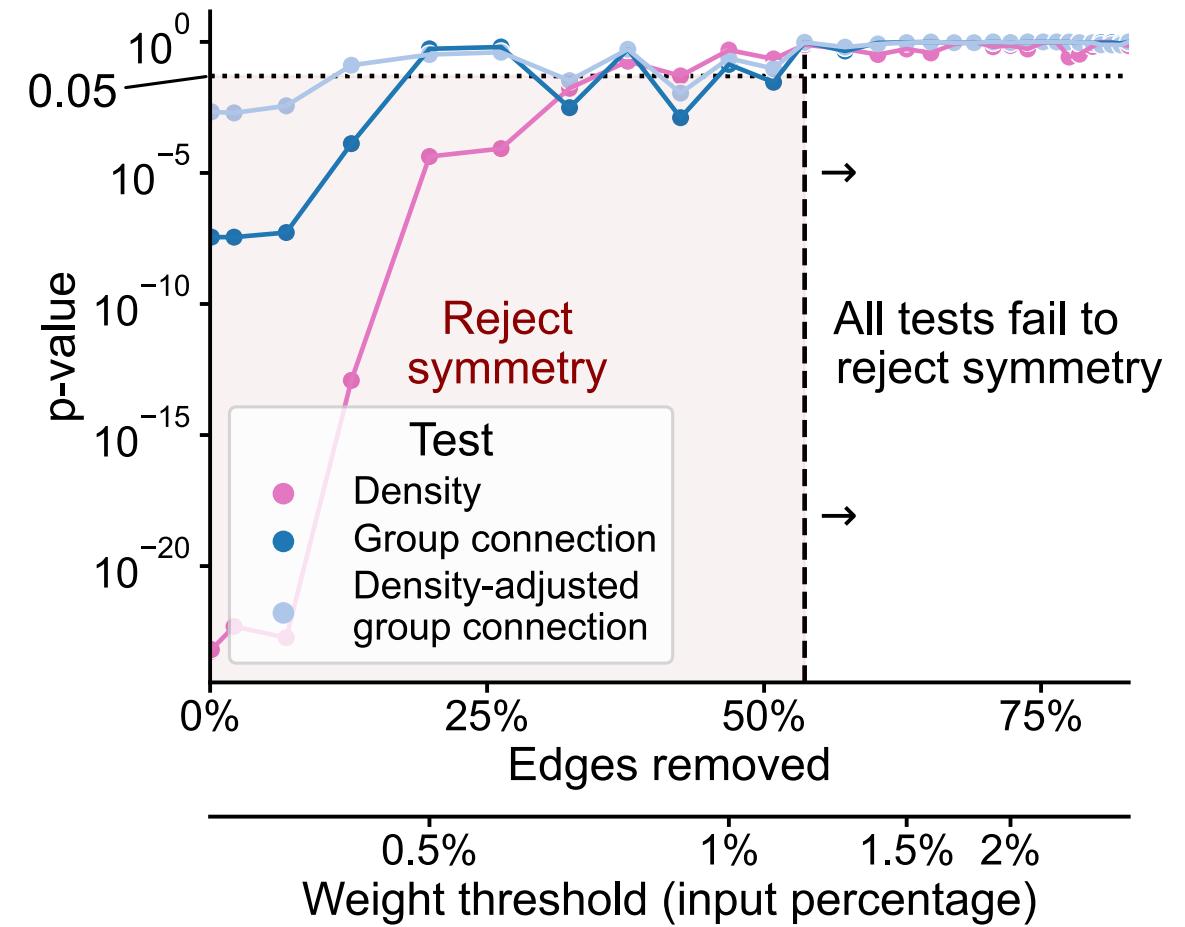
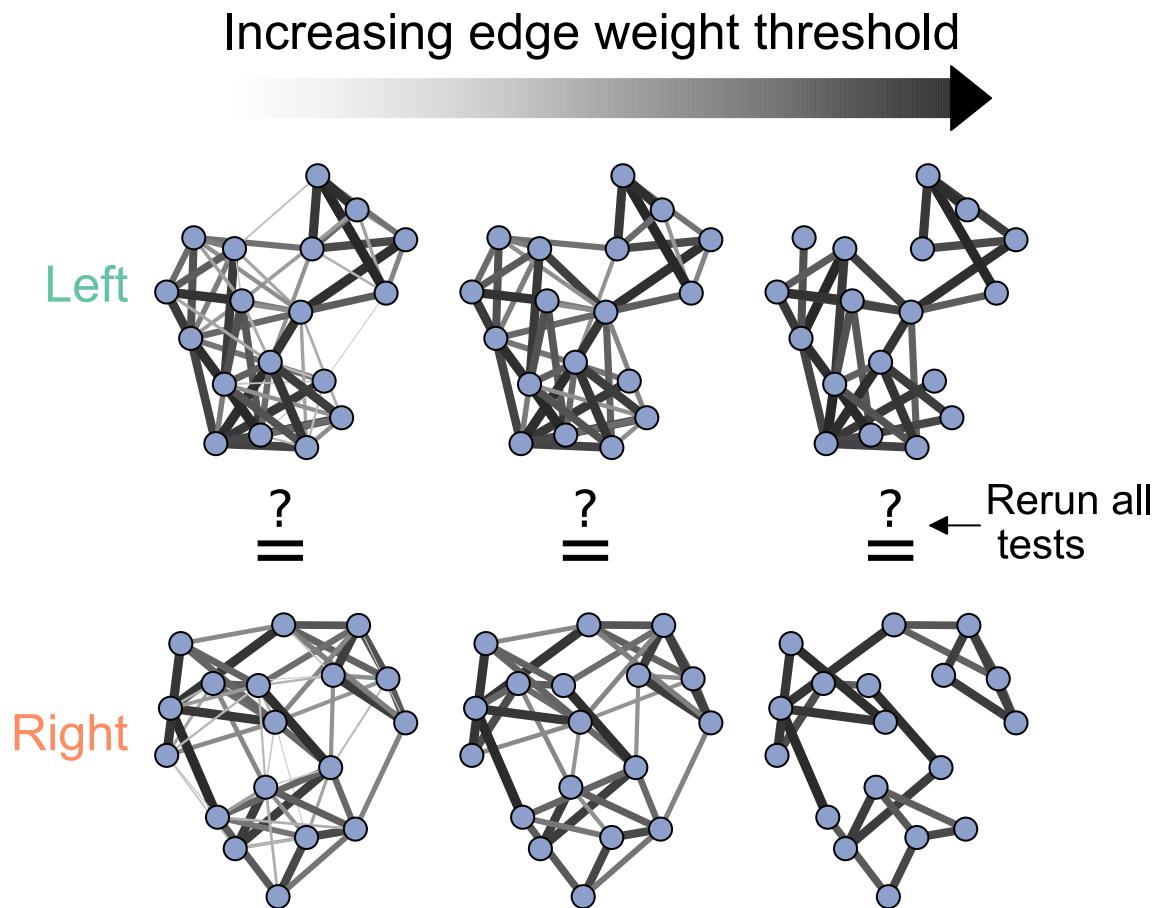
- Compare connection probabilities:

$$H_0 : B^{(L)} = B^{(R)}$$

$$H_A : B^{(L)} \neq B^{(R)}$$

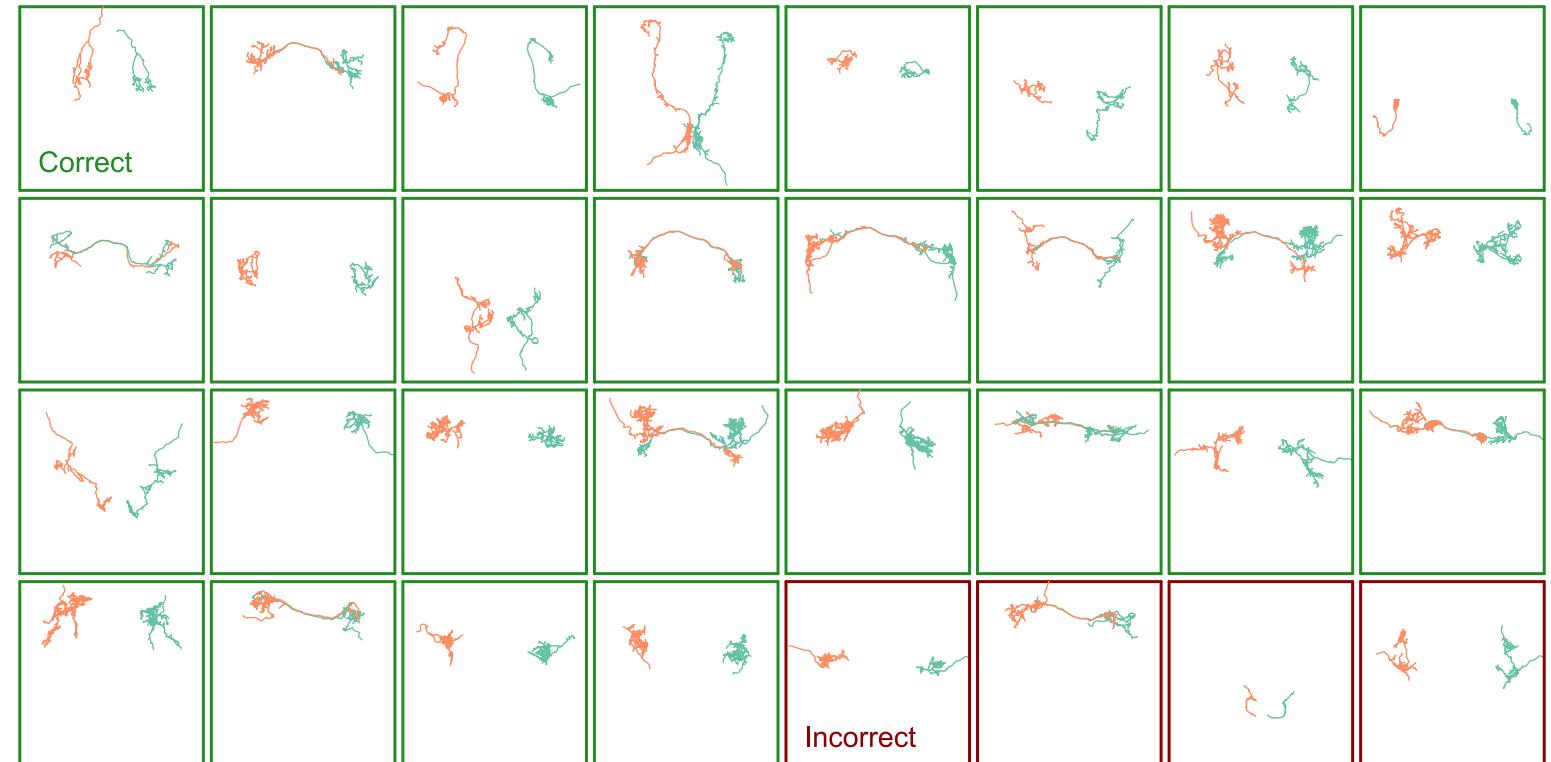
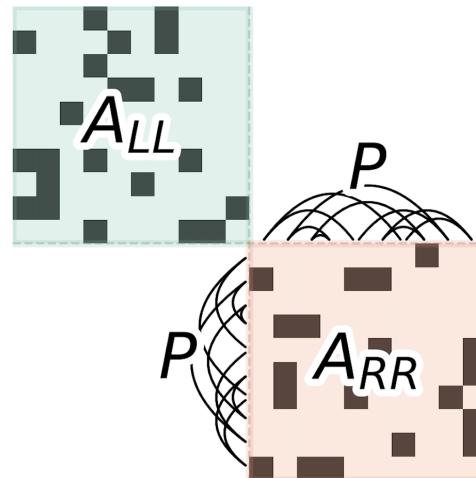
Overall comparison:  $p < 10^{-7}$

# Examining the effect of edge weights



# Estimating neuron pairing using graph matching

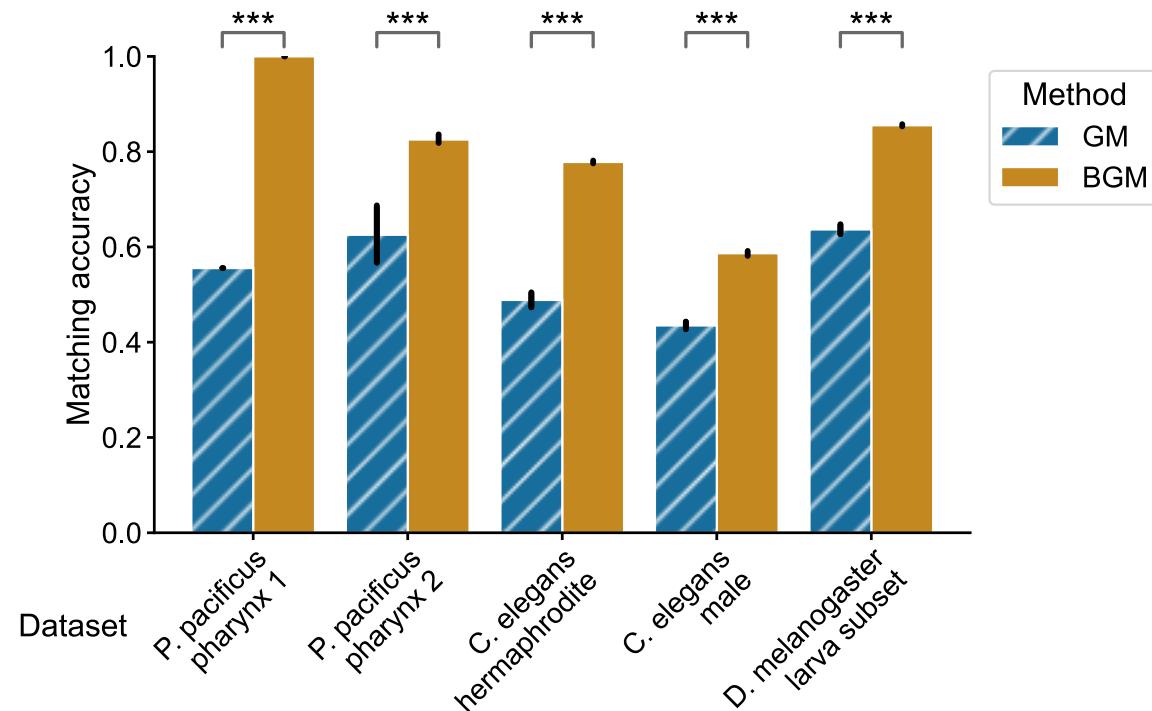
Graph matching (GM)



Morphologies of pairs predicted from connectivity.  
~80-85% agreement with an expert annotator.

# Improving graph matching to suit connectomes

Incorporating contralateral connections improves matching accuracy



Improving accuracy and scalability

## Graph Matching via Optimal Transport

Ali Saad-Eldin<sup>\*1</sup>, Benjamin D. Pedigo<sup>†1</sup>, Carey E. Priebe<sup>2</sup>, and Joshua T. Vogelstein<sup>‡1,3</sup>

Runs in ~1hr for 10k node networks

# Conclusions

- Demonstrated novel tools for comparing connectomes, case study on symmetry in a *Drosophila* larva
  - Model-based network comparison
  - Improved methods for matching neurons via connectivity
- Can be applied more generally to compare connectomes!
- *Ongoing work:* combining testing and matching frameworks to evaluate stereotypy at the edge-level
- **Have other network analysis questions? Let's chat!**

Slides, code, papers, contact



✉ [bpedigo@jhu.edu](mailto:bpedigo@jhu.edu)

🐦 [@bpedigod](https://twitter.com/bpedigod)

🌐 [bdpedigo.github.io](https://bdpedigo.github.io)