

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

Benjamin D. Pedigo

(he/him) -  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

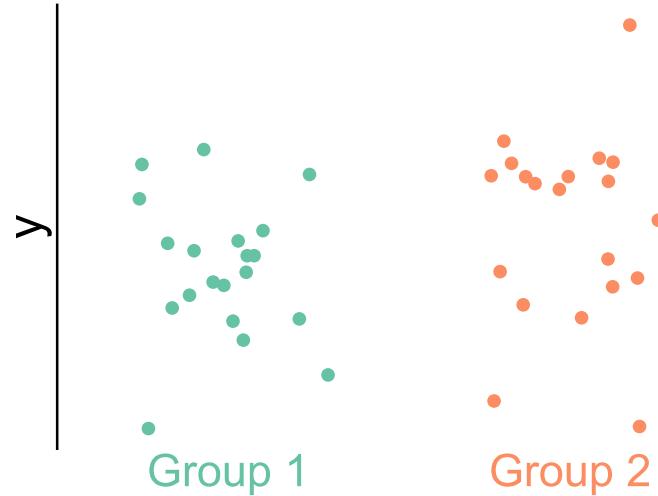
- Connectomes $\leftrightarrow \{\text{disease, evolution, development, experience, ...}\}$
- As related connectomes are mapped, we'll want evaluate the *significance* and *nature* of differences between them

Examples for today's talk

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

Testing for differences

Are these two populations different?

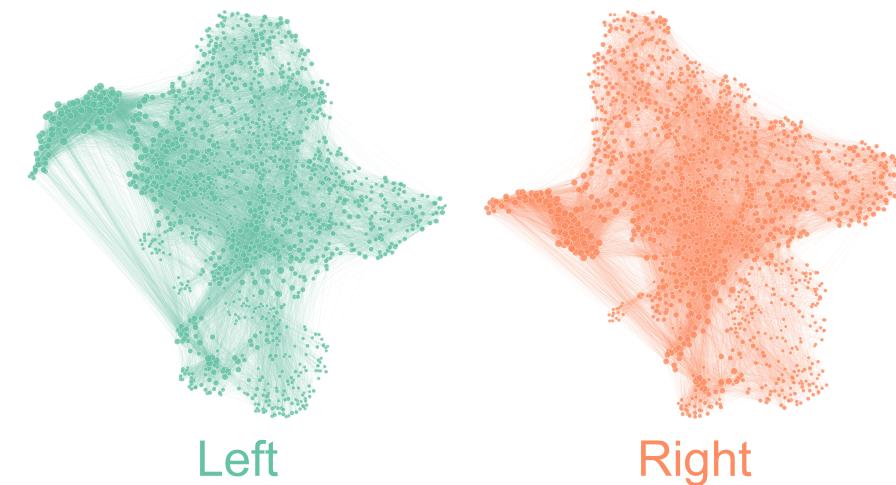


$$Y^{(1)} \sim F^{(1)}$$

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

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

Are these two *networks* different?



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

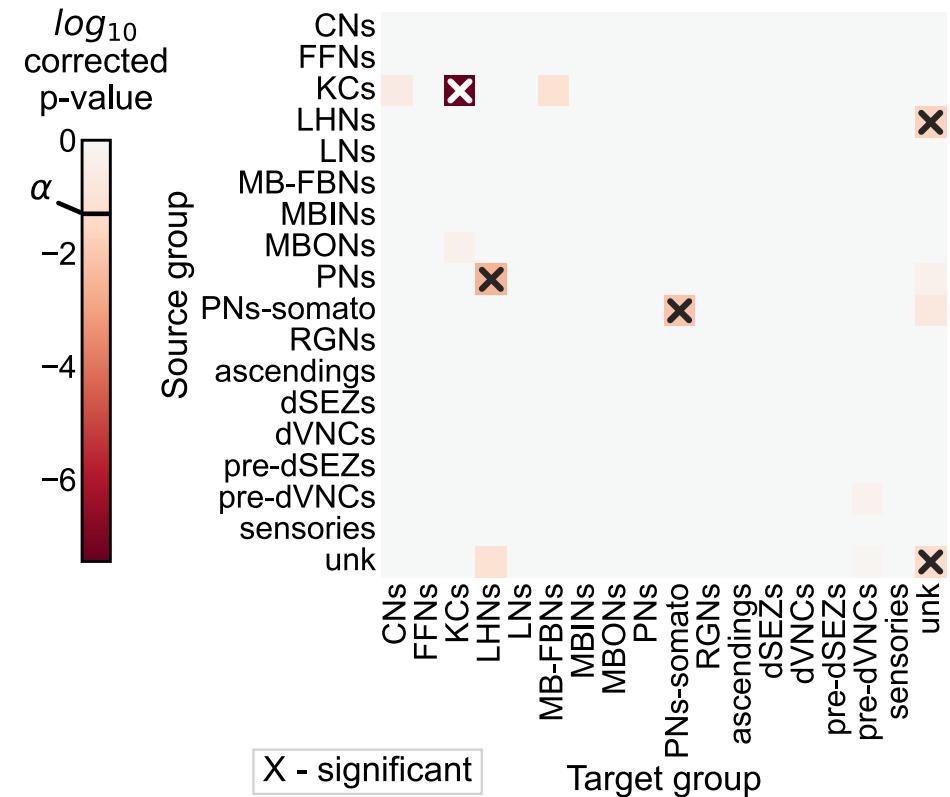
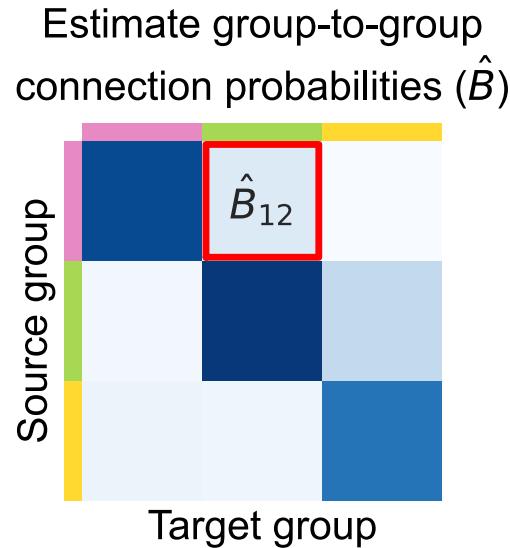
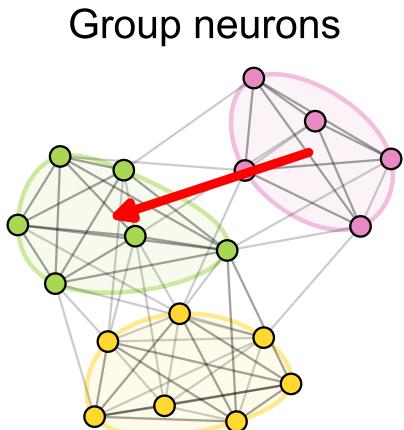
$$A^{(R)} \sim F^{(R)}$$

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

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



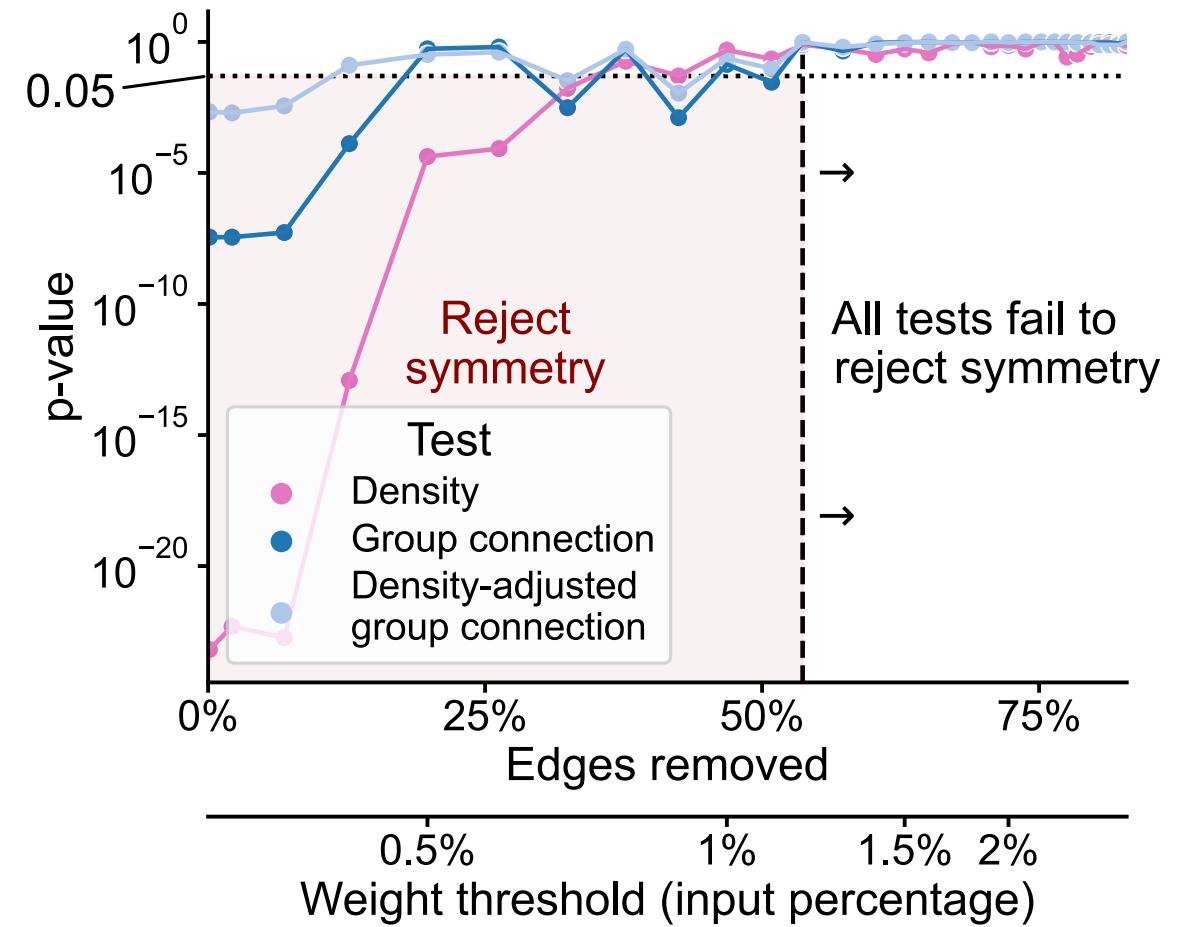
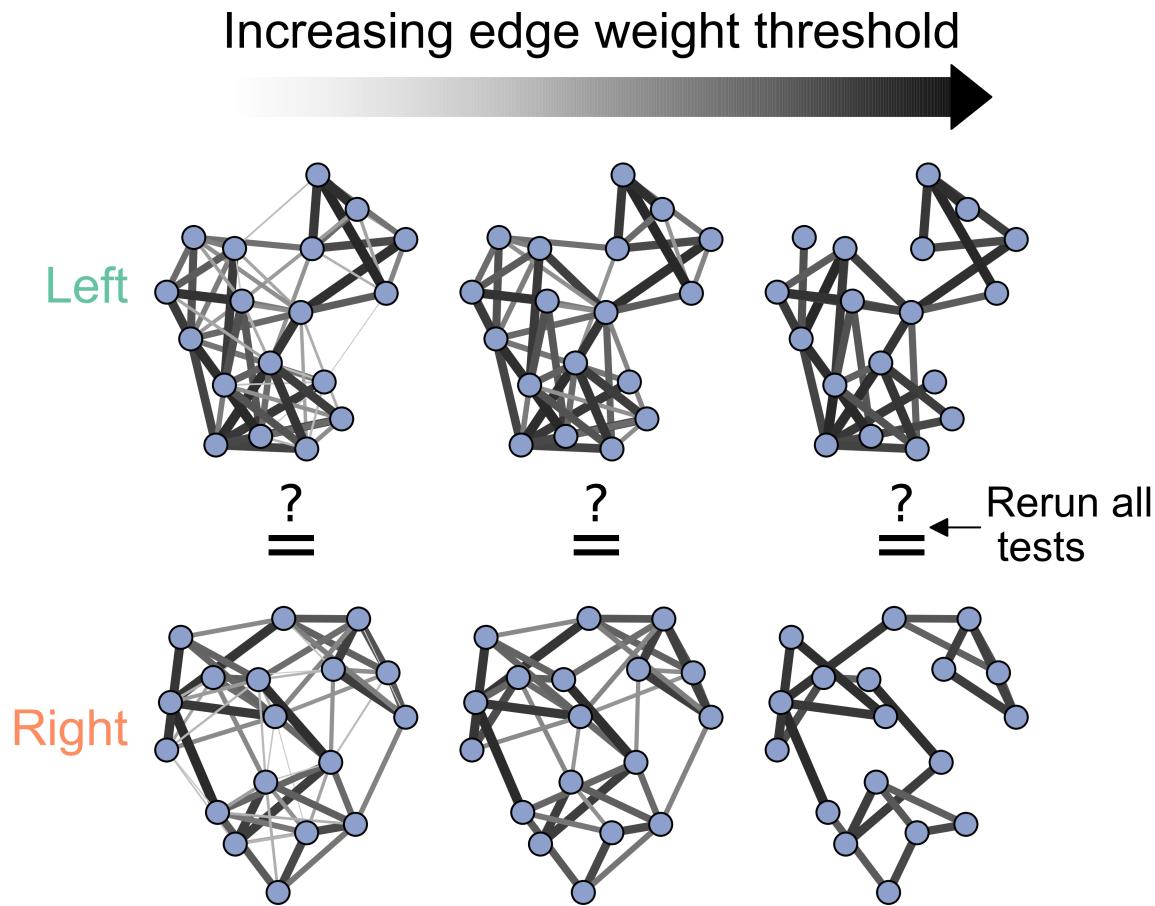
- Compare connection probabilities:

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

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

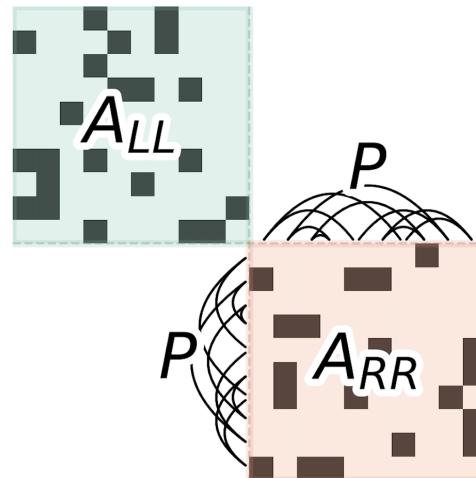
Overall comparison: $p < 10^{-7}$

Examining the effect of edge weights

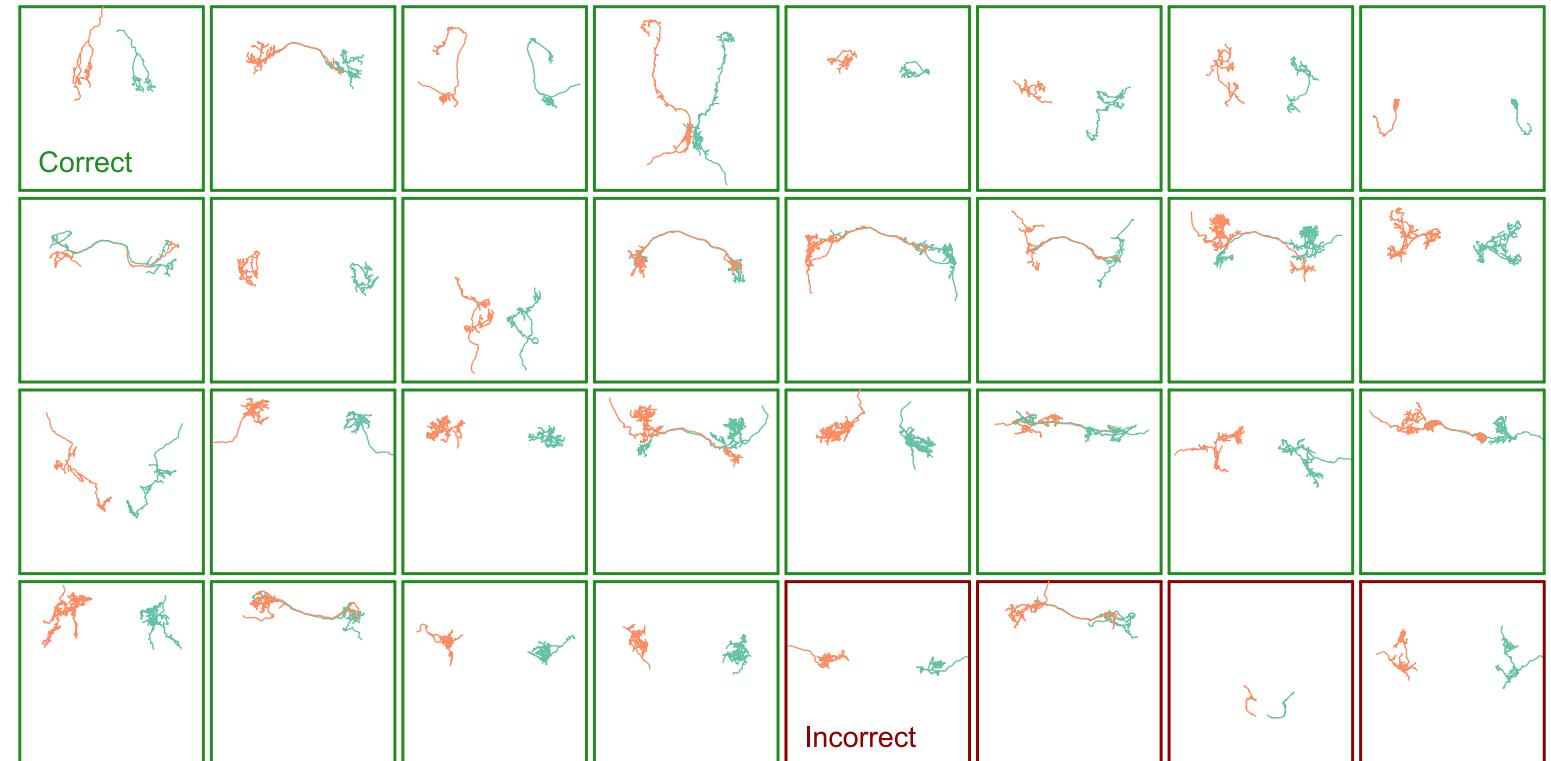


Estimating neuron pairing using graph matching

Graph matching (GM)



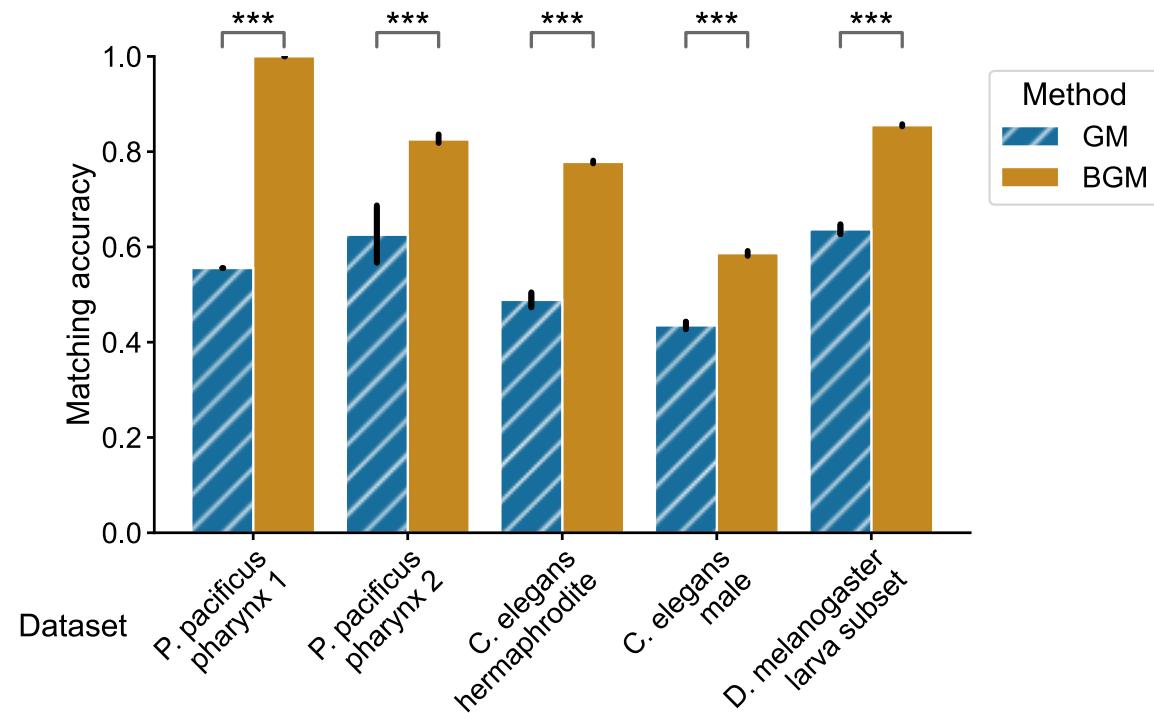
$$\min_P \left\| A_{LL} - P A_{RR} P^T \right\|_F^2$$



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^{*1}, Benjamin D. Pedigo^{†1}, Carey E. Priebe², and Joshua T. Vogelstein^{‡1,3}

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

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

🌐 bdpedigo.github.io