

# Benjamin D. Pedigo

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📄 [bdpedigo.github.io](https://github.com/bdpedigo)

I am a PhD Candidate and NSF Graduate Research Fellow in the Department of Biomedical Engineering at Johns Hopkins University. My research is in the [NeuroData](#) lab where I am advised by [Dr. Joshua T. Vogelstein](#) and co-advised by [Dr. Carey E. Priebe](#). My work focuses on using statistical and computational techniques to help understand [nanoscale connectomes](#). Currently, I am collaborating with [Dr. Marta Zlatic](#) and [Dr. Albert Cardona's](#) groups to analyze the first nanoscale connectome of the *Drosophila* larva brain. I also collaborate with Microsoft Research on the development of [graspologic](#), a Python package for statistical analyses of networks.

## Education & Training

- 08/18 – now **PhD Student**, *Department of Biomedical Engineering*, Johns Hopkins University.  
**Highlighted courses:** Neuro Data Design, Matrix Theory, Sparse Representations in Machine Learning, Neuroscience and Cognition, Probability and Statistics.
- 09/14 – 06/18 **Undergraduate Student**, *Department of Bioengineering*, University of Washington.  
**Highlighted courses:** Neural Coding and Computation, Neural Engineering, Neural Tech Studio, Computational Methods of Data Analysis, Data Structures and Algorithms, High Performance Scientific Computing.

## Positions Held

### Current Position

- 08/18 – now **PhD Candidate**, *Department of Biomedical Engineering*, Supervised by Dr. Joshua T. Vogelstein and co-supervised by Dr. Carey E. Priebe, Johns Hopkins University.  
**Research:** Analysis of nanoscale connectomes, network statistics, Python network data science.

### Previous Positions

- 05/21 – 08-20 **Research Intern**, *Societal Resilience*, Supervised by Jonathan Larson, Microsoft Research.  
**Research:** Organizational communication networks and their relation to reporting structures.
- 06/20 – 08-20 **Research Intern**, *Team Essex*, Supervised by Weiwei Yang and Dr. Chris White, Microsoft Research.  
**Research:** Network embedding and visualization techniques, network traversal embeddings.
- 06/17 – 09/17 **Computational Neuroanatomy Intern**, *Neural Coding Group*, Supervised by Dr. Nuno da Costa, Allen Institute for Brain Science.  
**Research:** Nanoscale connectomes, quality control for image alignment, Python development.
- 07/16 – 06/18 **Undergraduate Researcher**, *Center for Sensorimotor Neural Engineering*, Supervised by Dr. Chet Moritz and Dr. Sarah Mondello, University of Washington.  
**Research:** Optogenetic spinal cord stimulation after spinal cord injury.
- 07/15 – 07/16 **Undergraduate Researcher**, *Department of Biology*, Supervised by Dr. Emily Carrington and Dr. Matthew N. George, University of Washington.  
**Research:** Biomechanical properties of marine mussel attachments.

## Awards & Honors

- 2022 **Trainee Highlight Award**, [BRAIN Initiative Meeting](#).
- 2020 **NSF Graduate Research Fellowship**.
- 2018 **Summa Cum Laude**, University of Washington.  
Top 0.5% of graduating class.
- 2017 **Levinson Emerging Scholars Award**, University of Washington.
- 2017 **UW Institute for Neuroengineering Undergraduate Fellowship**, University of Washington.

- 2016 **Center for Sensorimotor Neural Engineering Undergraduate Fellowship**, University of Washington.
- 2016 **Mary Gates Research Scholarship**, University of Washington.
- 2015 **Mary Gates Research Scholarship**, University of Washington.
- 2014 - 2018 **Dean's List**, University of Washington.

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## Publications and Preprints

† denotes equal contribution

- [1] **B. D. Pedigo**, M. Powell, E. W. Bridgeford, M. Winding, C. E. Priebe, and J. T. Vogelstein. “Generative network modeling reveals quantitative definitions of bilateral symmetry exhibited by a whole insect brain connectome”. In: *bioRxiv* (Dec. 2022). DOI: [10.1101/2022.11.28.518219](https://doi.org/10.1101/2022.11.28.518219). URL: <https://www.biorxiv.org/content/10.1101/2022.11.28.518219>.
- [2] M. Winding†, **B. D. Pedigo**†, C. L. Barnes, H. G. Patsolic, Y. Park, T. Kazimiers, A. Fushiki, I. V. Andrade, F. Li, J. Valdes-Aleman, A. Khandelwal, N. Randel, E. Barsotti, A. Correia, R. D. Fetter, V. Hartenstein, C. E. Priebe, J. T. Vogelstein, A. Cardona, and M. Zlatic. “The connectome of an insect brain”. In: *bioRxiv* (Nov. 2022). DOI: [10.1101/2022.11.28.516756](https://doi.org/10.1101/2022.11.28.516756). URL: <https://www.biorxiv.org/content/10.1101/2022.11.28.516756v1>.
- [3] **B. D. Pedigo**, M. Winding, C. E. Priebe, and J. T. Vogelstein. “Bisected graph matching improves automated pairing of bilaterally homologous neurons from connectomes”. In: *Network Neuroscience* (Oct. 2022), pp. 1–29. ISSN: 2472-1751. URL: [https://doi.org/10.1162/netn\\_a\\_00287](https://doi.org/10.1162/netn_a_00287).
- [4] A. Saad-Eldin, **B. D. Pedigo**, C. E. Priebe, and J. T. Vogelstein. “Graph Matching via Optimal Transport”. In: *arXiv preprint arXiv:2111.05366* (2021). URL: <https://arxiv.org/abs/2111.05366>.
- [5] H. S. Helm, M. Abdin, **B. D. Pedigo**, S. Mahajan, V. Lyzinski, Y. Park, A. Basu, C. M. White, W. Yang, C. E. Priebe, et al. “Leveraging semantically similar queries for ranking via combining representations”. In: *arXiv preprint arXiv:2106.12621* (2021). URL: <https://arxiv.org/abs/2106.12621>.
- [6] J. Chung, E. Bridgeford, J. Arroyo, **B. D. Pedigo**, A. Saad-Eldin, V. Gopalakrishnan, L. Xiang, C. E. Priebe, and J. T. Vogelstein. “Statistical Connectomics”. In: *Annual Review of Statistics and Its Application* 8 (2021), pp. 463–492. URL: <https://www.annualreviews.org/doi/abs/10.1146/annurev-statistics-042720-023234>.
- [7] V. Gopalakrishnan, J. Chung, E. Bridgeford, **B. D. Pedigo**, J. Arroyo, L. Upchurch, G. A. Johnson, N. Wang, Y. Park, C. E. Priebe, and J. T. Vogelstein. “Multiscale Comparative Connectomics”. In: *arXiv preprint arXiv:2011.14990* (2020). URL: <https://arxiv.org/abs/2011.14990>.
- [8] A. S. Charles, B. Falk, N. Turner, T. D. Pereira, D. Tward, **B. D. Pedigo**, J. Chung, R. Burns, S. S. Ghosh, J. M. Kebschull, et al. “Toward Community-Driven Big Open Brain Science: Open Big Data and Tools for Structure, Function, and Genetics”. In: *Annual Review of Neuroscience* 43 (2020). URL: <https://www.annualreviews.org/doi/abs/10.1146/annurev-neuro-100119-110036>.
- [9] T. L. Athey, T. Liu, **B. D. Pedigo**, and J. T. Vogelstein. “AutoGMM: Automatic and Hierarchical Gaussian Mixture Modeling in Python”. In: *arXiv preprint arXiv:1909.02688* (2019). URL: <https://arxiv.org/abs/1909.02688>.
- [10] J. Chung†, **B. D. Pedigo**†, E. W. Bridgeford, B. K. Varjavand, H. S. Helm, and J. T. Vogelstein. “GraSPy: Graph Statistics in Python.” In: *Journal of Machine Learning Research* 20.158 (2019), pp. 1–7. URL: <https://arxiv.org/abs/1904.05329>.
- [11] J. T. Vogelstein, E. W. Bridgeford, **B. D. Pedigo**, J. Chung, K. Levin, B. Mensh, and C. E. Priebe. “Connectal coding: discovering the structures linking cognitive phenotypes to individual histories”. In: *Current opinion in neurobiology* 55 (2019), pp. 199–212. URL: <https://www.sciencedirect.com/science/article/pii/S0959438818301430>.

- [12] M. N. George, **B. D. Pedigo**, and E. Carrington. “Hypoxia weakens mussel attachment by interrupting DOPA cross-linking during adhesive plaque curing”. In: *Journal of The Royal Society Interface* 15.147 (2018), p. 20180489. URL: <https://royalsocietypublishing.org/doi/full/10.1098/rsif.2018.0489>.

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## Talks

- [1] **B. D. Pedigo**. “Bisected graph matching improves automated pairing of bilaterally homologous neurons from connectomes”. In: Neuromatch 5.0, Sept. 2022.
- [2] **B. D. Pedigo**. “Tools for comparing connectomes: case studies from two sides of a larval *Drosophila* brain”. In: Princeton University (Murthy and Seung labs), July 2022.
- [3] **B. D. Pedigo**. “Tools for comparing connectomes: evaluating the bilateral symmetry of a whole insect brain”. In: Berlin Connectomics Meeting, May 2022.
- [4] **B. D. Pedigo**. “Hypothesis testing for connectome comparisons: a statistical analysis of bilateral symmetry in an insect brain connectome”. In: Drexel University Biomedical Engineering and Neuroscience, Invited Seminar, Mar. 2022.
- [5] **B. D. Pedigo**, M. Winding, M. Zlatic, A. Cardona, C. E. Priebe, and J. T. Vogelstein. “Maggot brain, mirror image? A statistical analysis of bilateral symmetry in an insect brain connectome”. In: Neuromatch 4.0, Selected Talk, Dec. 2021.
- [6] **B. D. Pedigo** and J. T. Vogelstein. “graspologic: A python package for rigorous statistical analysis of populations of attributed connectomes”. In: BRAIN Informatics Webinar, Oct. 2021.
- [7] **B. D. Pedigo**. “Network data science for bilateral brains: Applications in the larval *Drosophila* connectome”. In: Brain Connectivity Workshop 5, Invited Talk, Mar. 2021.
- [8] **B. D. Pedigo**, M. Winding, A. Saad-Eldin, T. Liu, A. Cardona, M. Zlatic, C. E. Priebe, and J. T. Vogelstein. “Statistical tools for nanoscale connectomics: clustering neurons in the *Drosophila* larva brain and other applications”. In: Neuromatch 3.0, Oct. 2020.
- [9] A. Saad-Eldin, **B. D. Pedigo**, Y. Park, C. E. Priebe, and J. T. Vogelstein. “NeuroGraph-Match”. In: Neuromatch 3.0, Oct. 2020.
- [10] T. Liu, **B. D. Pedigo**, T. L. Athey, and J. T. Vogelstein. “Hierarchical stochastic block modeling in the *Drosophila* connectome”. In: Neuromatch 3.0, Oct. 2020.
- [11] V. Gopalakrishnan, J. Chung, E. Bridgeford, J. Arroyo, **B. D. Pedigo**, C. E. Priebe, and J. T. Vogelstein. “Statistical Methods for Multiscale Comparative Connectomics”. In: Neuromatch 3.0, Oct. 2020.

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## Poster Presentations

- [1] **B. D. Pedigo**, M. Powell, E. W. Bridgeford, M. Winding, C. E. Priebe, and J. T. Vogelstein. “Generative network modeling reveals a first quantitative definition of bilateral symmetry exhibited by a whole insect brain connectome”. In: From Neuroscience to Artificially Intelligent Systems (NAISys), Cold Spring Harbor Laboratory, NY, USA, Mar. 2022.
- [2] **B. D. Pedigo**, M. Winding, M. Zlatic, A. Cardona, C. E. Priebe, and J. T. Vogelstein. “A quantitative comparison of a complete connectome to artificial intelligence architectures”. In: From Neuroscience to Artificially Intelligent Systems (NAISys), Cold Spring Harbor Laboratory, NY, USA, Nov. 2020.
- [3] **B. D. Pedigo**, J. Chung, E. W. Bridgeford, B. Varjavand, C. E. Priebe, and J. T. Vogelstein. “GrASPy: an Open Source Python Package for Statistical Connectomics”. In: Max Planck/HHMI Connectomics Meeting, Berlin, Germany, Apr. 2019.
- [4] **B. D. Pedigo**, S. E. Mondello, A. E. Fishedick, and C. T. Moritz. “Optimization of optogenetic stimulation for spinal cord injury rehabilitation”. In: UW Undergraduate Research Symposium, Seattle, WA, USA, May 2018.
- [5] **B. D. Pedigo**, S. E. Mondello, A. E. Fishedick, and C. T. Moritz. “Investigation of optogenetic-induced damage to the rat spinal cord”. In: Center for Sensorimotor Neural Engineering Summer Symposium, Seattle, WA, USA, Aug. 2017.
- [6] **B. D. Pedigo**, S. E. Mondello, A. E. Fishedick, and C. T. Moritz. “Optimization of optogenetic spinal cord stimulation”. In: UW Undergraduate Research Symposium, Seattle, WA, USA, May 2017.

- [7] **B. D. Pedigo**, M. N. George, and E. Carrington. “Effects of environmental factors on Mytilus mussel adhesion”. In: UW Undergraduate Research Symposium, Seattle, WA, USA, May 2016.

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## Software

**graspologic**, [github.com/microsoft/graspologic](https://github.com/microsoft/graspologic), Co-lead developer/maintainer.

A Python package for statistical analysis of network data, co-developed by NeuroData lab and Microsoft Research. Used in production at Microsoft and almost 100k downloads. Formerly known as GraSPy.

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## Mentoring

- 08/21 - now **Kareef Ullah**, *Undergraduate Researcher*, BME, JHU.  
Ensured statistical tests were reproducible and implemented network configuration models in graspologic. Currently investigating a *Platynereis* connectome.
- 06/22 - 09/22 **Audrey Herskovits**, *Undergraduate Researcher*, CS, UMD.  
Implemented improved methods for semi-seeded pointcloud alignment in graspologic.
- 06/21 - 06/22 **Diane Lee**, *Undergraduate Researcher*, BME, JHU.  
Led development of new visualization tools into graspologic and investigated methods for quantitative network comparison.
- 01/20 - 12/21 **Ali Saad-Eldin**, *Master’s Researcher*, BME, JHU.  
Led integration of graph matching tools into SciPy. Developed a new graph matching technique and wrote a manuscript on it. Currently at Amazon.
- 06/19 - 08/19 **Kareef Ullah**, *High School Summer Intern*, BME, JHU.
- 06/19 - 07/19 **Kiki Zhang**, *High School Summer Intern*, BME, JHU.

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## Teaching

- Intersession 2022 **Network Data Science**, *EN.580.129(13)*, Instructor and course creator.  
Johns Hopkins University
- Fall/Spring 2020/2021 **NeuroData Design I & II**, *EN.580.237/437/637*, Team Lead.  
Johns Hopkins University
- Fall/Spring 2019/2020 **NeuroData Design I & II**, *EN.580.237/437/637*, TA.  
Johns Hopkins University
- Spring 2018 **Biomedical Signals and Sensors**, *BIOEN 316*, TA.  
University of Washington
- Spring 2017 **Biomedical Signals and Sensors**, *BIOEN 316*, TA.  
University of Washington

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## Service and Organizations

- 2022 - now **Mentorship Chair**, *BME Application Assistance Program*, Johns Hopkins University.
- 2022 - now **Life Sciences Advisor**, *A-Level Capital*.
- 2020 - now **Mentor**, *BME Application Assistance Program*, Johns Hopkins University.  
Reviewed application materials for applicants from underrepresented backgrounds
- 2017 - 2018 **President and Founder**, *Synaptech*, University of Washington.  
Student organization for undergraduates in neural engineering
- 2017 - 2018 **Undergraduate Representative**, *Center for Sensorimotor Neural Engineering*, University of Washington.
- 2017 - 2018 **President**, *Bird Club*, University of Washington.
- 2016 - 2017 **Treasurer**, *Bird Club*, University of Washington.
- 2017 - 2018 **Mentor**, *BioExpo*, Northwest Association for Biomedical Research.

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## Languages and Tools

Proficient **English, Python (NumPy, Pandas, Scikit-learn, SciPy, Seaborn, Matplotlib, NetworkX, Jupyter Notebooks, JupyterBook), Git, MATLAB, L<sup>A</sup>T<sub>E</sub>X.**

Inproficient **R, C++, Java, Blender, HTML.**