

Eleanor Wedell

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EDUCATION

University of Illinois Urbana-Champaign

Doctor of Philosophy in Computer Science, GPA 3.87

Urbana-Champaign, IL

Aug. 2022 – May 2026 (expected)

University of Illinois Urbana-Champaign

Master of Science in Computer Science, GPA 3.89

Urbana-Champaign, IL

Aug. 2020 – May 2022

- Thesis Title: SCAMPP: Scalable Alignment-based Phylogenetic Placement

Drexel University

Bachelor of Science in Mathematics, cum laude, GPA 3.67

Philadelphia, PA

Aug. 2013 – Aug. 2015

RESEARCH SUMMARY

I do applied algorithms research in two different areas: network science and computational biology, aiming to provide the best accuracy of all current methods while enabling scalability to large difficult datasets. Within network science, I have focused on community detection methods, and I have developed new methods (and in particular a new ensemble method) that achieve high accuracy and scalability to very large networks with many millions of nodes. Within computational biology, I have focused on methods for microbiome analysis, especially of metagenomic datasets, and have developed new methods (TIPP3 and TIPP-SD) that provide better accuracy than current state-of-the-art methods when datasets have sequencing error or come from species whose genomes are not available in public repositories. A key contribution of my research are two new methods (SCAMPP and BSCAMPP) that enable scalable phylogenetic placement based on maximum likelihood, allowing for sequences to be placed into phylogenies with hundreds of thousands of sequences more accurately than previously possible. My current work is in three areas: (1) examining deep neural networks for use in large-scale phylogeny estimation, (2) extensions of my methods for microbiome analysis to viral sequences, and (3) new methods for multiple sequence alignment of large datasets with sequence length heterogeneity.

EXPERIENCE

Research Assistant of Professor Tandy Warnow

University of Illinois Urbana-Champaign

Aug. 2020 – Present

Urbana-Champaign, IL

Teaching Assistant

University of Illinois Urbana-Champaign

Aug. 2020 – Present

Urbana-Champaign, IL

- CS 581 Algorithms in Genomic Biology (Sp. 2025, Fa. 2021)
- CS 128 Introduction to Computer Science II (Fa. 2023, Sp. 2024, Fa. 2024)
- CS 125 Introduction to Computer Science (Fa. 2020)
- CS 102 Little Bits to Big Ideas (Sp. 2021)
- Prepared and conduct weekly labs and quiz/midterm preparatory sessions

C3.ai DTI Curriculum Development Intern

University of Illinois Urbana-Champaign

April 2021 – May 2021

Urbana-Champaign, IL

- Tested the cloud computing platform and provided feedback for instructors at C3.ai Digital Transformation Institute for the development of new AI and machine learning courses introduced by C3.ai

Programmer Analyst

Innovative Software Solutions, Inc.

Feb. 2016 – Jan. 2020

Maple Shade, NJ

- Designed, developed, and maintained custom programs for employer auditing modules for new client installs | Programmed under strict deadlines for accurate reporting for >100K 1099s, W2s, and tax files in year-end team | Enhanced, tested, and debugged code for contributions team, providing annuity distributions and loan processing

TECHNICAL SKILLS

Languages: Python, C/C++, Java, COBOL, Matlab, Bash Scripting

Developer Tools: Linux, Git, VS Code, Neovim

Libraries: OpenMP, MPI, Dendropy, Pytorch, Treeswift, Networkit, igraph, GoTree

Relevant Graduate Coursework: Algorithms, Algorithmic Genomic Biology, Generative Models for BioMedicine & Life Science, Artificial Intelligence, ML for Bioinformatics, Deep Learning, Parallel Programming, Computational Cancer Genomics, Computational Scientometrics

1. **Wedell E.**, Cai Y., Warnow T. (2021) Scalable and Accurate Phylogenetic Placement Using pplacer-XR. In: *Martín-Vide C., Vega-Rodríguez M.A., Wheeler T. (eds) Algorithms for Computational Biology* (AlCoB 2021). https://doi.org/10.1007/978-3-030-74432-8_7.
2. **Wedell E.**, Park M., Korobskiy D., Warnow T., Chacko G. (2022) Center-Periphery Structure in Communities. *Quantitative Science Studies*, 3(1), 289-314. <https://doi.org/10.1162/qss.a.00184>.
3. **Wedell E.**, Cai Y., Warnow T. (2022). SCAMPP: Scaling Alignment-based Phylogenetic Placement to Large Trees. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 20(2), 1417-1430. <https://doi.org/10.1109/TCBB.2022.3170386>.
4. **Wedell E.**, Shen C., Warnow T. (2023) BATCH-SCAMPP: Scaling Phylogenetic Placement Methods to Place Many Sequences (Abstract). In *23rd International Workshop on Algorithms in Bioinformatics* (WABI 2023). <https://doi.org/10.4230/LIPIcs.WABI.2023.3> (This paper was peer-reviewed and accepted as a paper and an oral presentation for WABI; we provided a one-page abstract instead of a full paper so we could submit to a journal.)
5. Tabatabaee Y., **Wedell E.**, Park M., Warnow T. (2024) FastEnsemble: A new scalable ensemble clustering method. *13th International Conference on Complex Networks and their Applications* (CNA 2024). https://doi.org/10.1007/978-3-031-82435-7_5
6. Shen, C., **Wedell, E.**, Pop, M., Warnow, T. (2025). TIPP3 and TIPP3-fast: Improved abundance profiling in metagenomics. *PLOS Computational Biology*, 21(4), e1012593. <https://doi.org/10.1371/journal.pcbi.1012593>
7. **Wedell, E.**, Shen, C., Warnow, T. (2025). BSCAMPP: Batch-Scaled Phylogenetic Placement on Large Trees. *IEEE Transactions on Computational Biology and Bioinformatics*. <https://doi.ieeecomputersociety.org/10.1109/TCBBIO.2025.3562281>
8. Shen, C., **Wedell, E.**, Warnow, T. (2025). TIPP-SD: A New Method for Species Detection in Microbiomes. *The 16th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2025)*. <https://doi.org/10.1101/2025.08.27.672749> (This paper was peer-reviewed and accepted as a paper and an oral presentation for ACM-BCB; we provided a one-page abstract instead of a full paper so we could submit to a journal.)
9. Y. Tabatabaee, **E. Wedell**, M. Park, T. Warnow. FastEnsemble: Scalable ensemble clustering on large networks. *PLOS Complex Systems* (2025). <https://doi.org/10.1371/journal.pcsy.0000069>

BOOK CHAPTERS

1. **Wedell E.**, Shen C., Warnow T. (2025) Phylogenetic placement using SCAMPP and Batch-SCAMPP. *Methods in Molecular Biology* [XX: XXX-XXX], ms. in press Springer. The book ‘Evolutionary Genomics, Edited by G. Caetano-Anollés’

JOURNAL SUBMISSIONS

1. Shen, C., **Wedell, E.**, Warnow, T. (2025). TIPP-SD: A New Method for Species Detection in Microbiomes. *Submitted for review*. <https://doi.org/10.1101/2025.08.27.672749>

PROFESSIONAL SERVICE AND LEADERSHIP ROLES

Reviewer – Sub-reviewed for RECOMB conference 2023

Supervisor-Undergraduate Research, *UIUC Fall 2023* – Oversaw and mentored undergraduate researcher

Co-Organizer – the mini-conference for UIUC students and faculty in the bioinformatics and computational biology group to present and discuss current research (scheduled for spring 2026). I am one of three PhD students charged with organizing the event.

AWARDS AND FELLOWSHIPS

Siebel Scholar, Class of 2022 – awarded annually for academic excellence and demonstrated leadership

SURGE Fellowship – August 2022 - January 2025

Wing Kai Cheng Fellowship – August 2022 - May 2023

Honorable Mention NSF-GRFP – 2022

Debra and Ira Cohen Graduate Fellowship in Computer Science – January 2025 - May 2025

University Block Grant Fellowship – January 2025 - May 2025

TALKS

- **TIPP-SD: A New Method for Species Detection in Microbiomes**
 - The 16th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB), October 2025
- **BSCAMPP and SCAMPP Overview and Software Demo** [talk]
 - Institute for Mathematical and Statistical Innovation – Contemporary Challenges in Large Scale Sequence Alignments and Phylogenies (IMSI), August 2025
- **BATCH-SCAMPP: Scaling phylogenetic placement methods to place many sequences**
 - The 23rd International Workshop on Algorithms in Bioinformatics (WABI), September 2023
- **Scalable and Accurate Phylogenetic Placement Using pplacer-XR**
 - 7th-8th International Conference on Algorithms for Computational Biology (AlCoB), November 2021

SOFTWARE

SCAMPP This is software for phylogenetic placement of sequences into large phylogenies based on maximum likelihood, achieving high accuracy and scalability to very large trees (tested up to 200,000 leaves). | *Python, C++, OpenMP, Treeswift* | <https://github.com/chry04/PLUSplacer>

BSCAMPP This is an algorithmic modification of SCAMPP to enable it to achieve runtime that is sublinear in the number of sequences that are added to a large phylogeny. | *Python, C++, OpenMP, Treeswift* | <https://github.com/ewedell/BSCAMPP>

IKC This is code for Iterative k-core clustering, designed for use in finding center-periphery clusters. | *Python, Networkit, Networkx* | <https://github.com/chackoge/ERNIE.Plus/tree/master/Illinois/clustering/eleanor/code>

FastEnsemble This new scalable ensemble method for consensus clustering is the most accurate method on networks with less obvious clusters. | *C++, Python, Networkx, iGraph* | <https://github.com/ytabatabaee/fast-ensemble>

TIPP3 This abundance profiling and taxon identification method is the most accurate method on PacBio reads and reads from genomes not known to the reference database. | *Python, Java, BLAST, Dendropy* | <https://github.com/c5shen/TIPP3/tree/main>

TIPP-SD This species detection method builds on the TIPP3 code, and is the most accurate method tested for species detection, especially where your datasets contain low abundance species. | *Python, Java, BLAST, Dendropy* | <https://github.com/c5shen/TIPP3/tree/main>