

CURRICULUM VITAE

ERIN MOLLOY

Post-doctoral Scholar
University of California, Los Angeles

CONTACT INFORMATION

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EDUCATION

- Ph.D., Computer Science, University of Illinois at Urbana-Champaign, 8/2020.
Dissertation: Supertree-like methods for genome-scale species tree estimation
Committee: Drs. Tandy Warnow (advisor), William Gropp (co-advisor), Marc Snir, Luay Nakhleh (Rice University)
- B.A., Physics, University of Chicago, 6/2011.

AWARDS

Fellowships and Awards

- Rising Stars in Electrical Engineering and Computer Science (EECS), 2019.
- Travel fellowship, Intelligent Systems for Molecular Biology (ISMB), 2019.
- Ira and Debra Cohen Graduate Fellowship in Computer Science, 8/2017–5/2018 and 8/2019–5/2020.
- NSF Graduate Research Fellowship, 8/2015–8/2017 and 6/2018–6/2019.
- Thomas M. Siebel Fellowship, 8/2014–12/2014.
- NSF Neuroengineering Integrated Graduate Education and Research Training (IGERT) Fellowship, 8/2013–8/2014.
- State Farm Companies Foundation Doctoral Scholarship, 8/2013–5/2014.

Research Support

- Exploratory Allocation, Blue Waters supercomputer, 2018. [Awarded 50,000 node hours for proposal, Optimizing distributed-memory parallel code for constructing ultra-large phylogenetic trees on Blue Waters.]
- Exploratory Allocation, Blue Waters supercomputer, 2017. [Awarded 50,000 node hours for proposal, Designing scalable algorithms for constructing large phylogenetic trees (almost without alignments) on supercomputers.]

Program Awards

- Science at Extreme Scales: Big Data Meets Large-Scale Computing, Institute for Pure and Applied Mathematics, Fall 2019. [12-week program]
- NSF Research Experience for Undergraduates (REU) in Computational Biology and Biostatistics, University of Wisconsin-Madison, Summer 2010. [12-week program]
- NIH Summer Institute for Training in Biostatistics, University of Wisconsin-Madison, Summer 2009. [6-week program]

Teaching Awards

- List of Teachers Ranked as Excellent by their Students, University of Illinois at Urbana-Champaign, Spring 2017. [Awarded for my recitation section: CS 466 Intro to Bioinformatics.]
- List of Teachers Ranked as Excellent by their Students, University of Illinois at Urbana-Champaign, Spring 2015. [Awarded for my recitation section: CS 450 Numerical Analysis.]

RESEARCH EXPERIENCE

- Graduate Research Fellow, Department of Computer Science, University of Illinois at Urbana-Champaign, 8/2015–present. [with Dr. Tandy Warnow; see journal articles #7–9, #11–13, and #15–16]
- Graduate Research Fellow, Department of Computer Science, University of Illinois at Urbana-Champaign, 8/2014–5/2015. [with Dr. Luke Olson; see talk #1.]
- Graduate Research Fellow, Beckman Institute, University of Illinois at Urbana-Champaign, 8/2013–8/2014. [with Dr. Aron Barbey; see journal article #10]
- Associate Research Specialist, Health Emotions Research Institute, University of Wisconsin-Madison, 8/2011–5/2013. [with Dr. Rasmus Birn; see journal articles #1–3 and #5–6]
- Undergraduate Research Assistant, Department of Medical Physics, University of Wisconsin-Madison, Summer 2010. [with Dr. Rasmus Birn; see journal article #4]
- Undergraduate Research Assistant, Department of Cardiology, University of Chicago

Hospitals, Spring 2010. [with Drs. John Faranbach and Elizabeth McNally; hourly position running PCR, gel electrophoresis, and TOPO PCR cloning experiments]

- High School Research Assistant, Department of Pediatrics, Medical College of Wisconsin, 9/2006–5/2007. [with Drs. Jill Gershan and Rimas Orentas; see poster #1]

BOOK CHAPTERS

- **Molloy, E. K.** and T. Warnow, “Large-scale Species Tree Estimation,” Under revision. [Edited by Drs. Laura Kubatko and Lacey Knowles]

RESEARCH PUBLICATIONS

Peer-reviewed Journal Articles

Extended versions of conference papers include new results (theoretical, empirical, or both) as well as more thorough discussions of related work.

17. Zhang, C., C. Scornavacca, **E. K. Molloy**, and S. Mirarab, “ASTRAL-Pro: quartet-based species tree inference despite paralogy,” *Molecular Biology and Evolution*, In press.
16. **Molloy, E. K.** and T. Warnow, “FastMulRFS: Fast and highly accurate species tree estimation under generic gene duplication and loss models,” *Bioinformatics* vol. 36, no. Supplement_1, pp. i57–i65. [Special issue for **ISMB 2020** – acceptance rate 19.4%].
15. Le, T., A. Sy, **E. K. Molloy**, Q. Zhang, S. Rao, and T. Warnow, “Using Constrained-INC for Large-scale Gene Tree and Species Tree Estimation,” *IEEE/ACM Transactions on Computational Biology and Bioinformatics*. [Extended version of **AICoB 2019** paper]
14. Springer, M. S., **E. K. Molloy**, D. B. Sloan, M. P. Simmons, and J. Gatesy, “ILS-Aware Analysis of Low-Homoplasy Retroelement Insertions: Inference of Species Trees and Introgression Using Quartets,” *Journal of Heredity*, vol. 11, no. 2, pp. 147–168. [Editor’s Choice]
13. Christensen, S., **E. K. Molloy**, P. Vachaspati, A. Yammanuru, and T. Warnow, “Non-parametric correction of estimated gene trees using TRACTION,” *Algorithms for Molecular Biology*, vol. 15, pp. 1:1–1:18, January 2020. [Extended version of **WABI 2019** paper]
12. **Molloy, E. K.** and T. Warnow, “TreeMerge: A new method for improving the scalability of species tree estimation methods,” *Bioinformatics*, vol. 35, pp. i417–i426, July 2019. [Special issue for **ISMB 2019** – acceptance rate 18.9%]

11. **Molloy, E. K.** and T. Warnow, “Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge,” *Algorithms for Molecular Biology*, vol. 14, pp. 14:1–14:17, July 2019. [Extended version of **RECOMB-CG 2018** paper]
10. Kruepke, M., **E. K. Molloy**, K. W. Bresin, A. K. Barbey, and E. Verona, “A Brief Assessment Tool for Investigating Facets of Moral Judgment from Realistic Moral Vignettes,” *Behavior Research Methods*, vol. 50, no. 3, pp. 922–936, June 2018.
9. Nute, M., J. Chou, **E. K. Molloy**, and T. Warnow, “The Performance of Coalescent-Based Species Tree Estimation Methods under Models of Missing Data,” *BMC Genomics*, vol. 19, pp. 286:1–286:22, May 2018. [Extended version of **RECOMB-CG 2017** paper]
8. **Molloy, E. K.** and T. Warnow, “To include or not to include: The Impact of Gene Filtering on Species Tree Estimation Methods,” *Systematic Biology*, vol. 67, no. 2, pp. 285–303, March 2018.
7. Christensen, S., **E. K. Molloy**, P. Vachaspati, and T. Warnow, “OCTAL: Optimal completion of gene trees in polynomial time,” *Algorithms for Molecular Biology*, vol. 13, pp. 6:1–6:18, March 2018. [Extended version of **WABI 2017** paper]
6. Patriat, R., **E. K. Molloy**, and R. M. Birn, “Using Edge Voxel Information to Improve Motion Regression for rs-fMRI Connectivity Studies,” *Brain connectivity*, vol. 5, no. 9, pp. 582–595, November 2015.
5. Birn, R. M., M. D. Cornejo, **E. K. Molloy**, R. Patriat, T. B. Meier, G. R. Kirk, V. A. Nair, M. E. Meyerand, and V. Prabhakran, “The Influence of Physiological Noise Correction on Test-Retest Reliability of Resting-State Functional Connectivity,” *Brain connectivity*, vol. 4, no. 7, pp. 511–522, August 2014.
4. **Molloy, E. K.**, M. E. Meyerand, and R. M. Birn, “The influence of spatial resolution and smoothing on the detectability of resting-state and task fMRI,” *Neuroimage*, vol. 86, pp. 221–230, February 2014.
3. Birn, R. M., **E. K. Molloy**, R. Patriat, T. Parker, T. B. Meier, G. R. Kirk, V. A. Nair, M. E. Meyerand, and V. Prabhakran, “The effect of scan length on the reliability of resting-state fMRI connectivity estimates,” *Neuroimage*, vol. 83, pp. 550–558, December 2013.
2. Patriat, R., **E. K. Molloy**, T. B. Meier, G. R. Kirk, V. A. Nair, M. E. Meyerand, V. Prabhakran, and R. M. Birn, “The effect of resting condition on resting-state fMRI reliability and consistency: A comparison between resting with eyes opened, closed, and fixated,” *Neuroimage*, vol. 78, pp. 463–473, September 2013.
1. Burghy, C. A., D. E. Stodola, P. L. Ruttle, **E. K. Molloy**, J. M. Armstrong, J. A. Oler, M. E. Fox, A. S. Hayes, N. H. Kalin, M. J. Essex, R. J. Davidson, and R. M. Birn, “Developmental pathways to amygdala-prefrontal function and internalizing symptoms in adolescence,” *Nature Neuroscience*, vol. 15, pp. 1736–1741, November 2012.

Peer-reviewed Conference Proceedings

5. Legried, B., **E. K. Molloy**, T. Warnow, and S. Roch, “Polynomial-Time Statistical Estimation of Species Trees under Gene Duplication and Loss,” Accepted to the *24th International Conference on Research in Computational Molecular Biology*. [**RECOMB 2020**]
4. Christensen, S., **E. K. Molloy**, P. Vachaspati, and T. Warnow, “TRACTION: Fast non-parametric improvement of estimated gene trees,” in *19th International Workshop on Algorithms in Bioinformatics*, ser. Leibniz International Proceedings in Informatics, vol. 143, pp. 4:1–4:16, 2019. [**WABI 2019**]
3. Le, T., A. Sy, **E. K. Molloy**, Q. Zhang, S. Rao, and T. Warnow, “Using INC within Divide-and-Conquer Phylogeny Estimation,” in *6th International Conference on Algorithms for Computational Biology*, ser. Springer Lecture Notes in Computer Science, vol. 11488, pp. 167–178, 2019. [**AICoB 2019**]
2. **Molloy, E. K.** and T. Warnow, “NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees,” in *16th RECOMB International Conference on Comparative Genomics*, ser. Springer Lecture Notes in Computer Science, vol. 11183, pp. 260–276, 2018. [**RECOMB-CG 2018**]
1. Christensen, S., **E. K. Molloy**, P. Vachaspati, and T. Warnow, “Optimal completion of incomplete gene trees in polynomial time using OCTAL,” in *17th International Workshop on Algorithms in Bioinformatics*, ser. Leibniz International Proceedings in Informatics, vol. 88, pp. 27:1–27:14, 2017. [**WABI 2018**]

PRESENTATIONS

Seminar Talks

3. “Supertree-like Methods for Advancing Evolutionary Genomic Biology,” Computer Science Department Seminar, University of Maryland, College Park (MD, USA), March 2020. [Invited by Dr. Mihai Pop]
2. “Species tree estimation in the presence of incomplete lineage sorting or gene duplication/loss,” Evolution Seminar Series, University of Wisconsin, Madison (WI, USA), January 2020. [Invited by Dr. Sébastien Roch and Dr. Chris Hittinger]
1. “Advancing genome-scale phylogenomics through Disjoint Tree Merger methods,” Systems | Information | Learning | Optimization (SILO) Seminar, University of Wisconsin, Madison (WI, USA), January 2020. [Invited by Dr. Claudia Solís-Lemus]

Conference/Workshop Talks and Panels

10. “Panel: Coalescent-based Methods in the Age of Big Data,” Society of Systematic Biologists (SSB) Standalone Meeting, Gainesville (FL, USA), January 2020. [Invited by Dr. Claudia Solís-Lemus]

9. “TreeMerge: A new method for improving the scalability of species tree estimation methods,” *27th Conference on Intelligent Systems for Molecular Biology (ISMB)*, Basel (Switzerland), July 2019.
8. “New divide-and-conquer approaches for constructing species trees from large genomic datasets,” *Trees in the Desert: A workshop on ultra-large phylogenetic trees*, Oracle (AZ, USA), April 2019. [Invited by Dr. Michael Sanderson]
7. “Scaling species tree estimation methods to large datasets using NJMerge,” *HPC and Data Science for Scientific Discovery Workshop*, Institute for Pure and Applied Mathematics, Los Angeles (CA, USA), November 2018.
6. “NJMerge: A Generic Technique for Scaling Phylogeny Estimation Methods and Its Application to Species Trees,” *16th RECOMB International conference on Comparative Genomics (RECOMB-CG)*, Magog-Orford (QC, Canada), October 2018.
5. “Scaling species tree estimation methods to large datasets using NJMerge,” *Phylogenomics Software Symposium*, Montpellier (France), August 2018. [Invited by Dr. Tandy Warnow]
4. “Designing parallel algorithms for constructing large phylogenetic trees on Blue Waters,” *NCSA Blue Waters Symposium for Petascale Science and Beyond*, Sunriver (OR, USA), June 2018.
3. “To include or not to include: The impact of missing data on summary methods for species tree estimation,” *Evolution*, Austin (TX, USA), June 2016.
2. “To include or not to include: The impact of missing data on summary methods for species tree estimation,” *Phylogenomics Symposium and Software School*, Austin (TX, USA), June 2016. [Invited by Dr. Tandy Warnow]
1. “Is the ideal prolongation operator always “ideal” for a particular coarse/fine splitting?,” *17th Copper Mountain Conference on Multigrid Methods*, Copper Mountain (CO, USA), March 2015.

Posters

3. “A nearly alignment-free approach to large-scale gene tree estimation using TreeMerge,” *6th International Conference on Algorithms for Computational Biology (AlCoB)*, Berkeley (CA, USA), May 2019.
2. “To include or not to include: The impact of missing data on summary methods for species tree estimation,” *Molecules as documents of evolutionary history*, CNRS, Roscoff (France), May 2016.
1. “Bypassing Replicative Senescence in Primary Mouse Mammary Tumor Cells with Viral Oncogenes,” *Intel International Science and Engineering Fair*, Albuquerque (NM, USA), May 2007.

Hands-on Tutorials

2. “Species tree estimation using new divide-and-conquer pipelines,” *Trees in the Desert: A workshop on ultra-large phylogenetic trees*, Oracle (AZ, USA), April 2019.
1. “Metagenomic Analysis using Phylogeny-Aware Profiles,” *Strategies and Techniques for Analyzing Microbial Population Structures*, Woods Hole (MA, USA), August 2017.

TEACHING EXPERIENCE

- Instructor for Graduate Academy for College Teaching, Center for Innovation in Teaching and Learning, University of Illinois at Urbana-Champaign, 2016–present.
- Organizer and Research Mentor, Summer Research Experience for Undergraduates (REU) Program in Computational Phylogenomics, Department of Computer Science, University of Illinois at Urbana-Champaign, Summer 2019. [Organized summer REU program including tutorials, journal clubs, and weekly lab meetings; mentored four undergraduate students (rising sophomores and juniors) on research projects. Learn more at <http://erinkmolloy.web.illinois.edu/reu2019.html>]
- Teaching Assistant for CS 466 Introduction to Bioinformatics, Department of Computer Science, University of Illinois at Urbana-Champaign, Spring 2017. [Included leading a weekly recitation section.]
- Teaching Assistant for CS 450 Numerical Analysis, Department of Computer Science, University of Illinois at Urbana-Champaign, Spring 2015. [Included leading a weekly recitation section.]
- Ad Hoc Teaching Assistant for MED PHYS/NTP 651 Methods for Neuroimaging Research, Department of Medical Physics, University of Wisconsin-Madison, Fall 2012.

UNDERGRADUATE STUDENT SUPERVISION

4. Emma Hamel, Department of Computer Science, University of Illinois at Urbana-Champaign, Summer 2019–present. [Won best poster award at department’s undergraduate summer research symposium 2019.]
3. Qikai Yang, Department of Computer Science, University of Illinois at Urbana-Champaign, Summer 2019–present.
2. Ananya Yamanuru, Department of Computer Science, University of Illinois at Urbana-Champaign, Summer 2019. [Contributed to journal article #14.]
1. Taurean Parker, Department of Medical Physics, University of Wisconsin-Madison, Summer 2012. [Contributed to journal article #3.]

SERVICE

Departmental Service

- Summer Research Experience for Undergraduates (REU) Program Committee Member, Department of Computer Science, University of Illinois at Urbana-Champaign, Summer 2019.
- Seminar Organizer, Institute for Pure and Applied Mathematics, Fall 2018.
- Prospective Graduate Student Ambassador, Department of Computer Science, University of Illinois at Urbana-Champaign, Winters 2013–18.
- Graduate Student Applications Reviewer, Department of Computer Science, University of Illinois at Urbana-Champaign, Winter 2016.

University Service

- Engineering Graduate Student Advisory Committee Member, College of Engineering, University of Illinois at Urbana-Champaign, 8/2014–8/2017. [Chaired committee from 8/2015–8/2016.]

Climate, Diversity, and Inclusion

- Women Empowered in STEM Conference Organizing Committee Member, College of Engineering, University of Illinois at Urbana-Champaign, 8/2016–5/2018.
- Society of Women Engineers Graduate Student Committee Member, College of Engineering, University of Illinois at Urbana-Champaign, 8/2016–5/2018.

Conference and Journal Submission Reviewer

- Systematic Biology [Ad hoc]
- PLOS Computational Biology [Ad hoc]
- Workshop on Algorithms in Bioinformatics [Subreviewer for WABI 2019]
- Research in Computational Molecular Biology [Subreviewer for RECOMB 2019]

PROFESSIONAL MEMBERSHIPS

- Association for Computing Machinery (ACM)
- International Society for Computational Biology (ISCB)
- Society for Industrial and Applied Mathematics (SIAM)
- Society of Systematic Biologists (SSB)