Curriculum Vitae
Erin K. Molloy

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University of Maryland, College Park   Verified reviews   [Web of Science]

Experience

Dates are formatted as year/month/day.

Education

2020/08	**Ph.D.**, Computer Science, *University of Illinois at Urbana-Champaign (IL, USA)*
	Dissertation: Supertree-like methods for genome-scale species tree estimation
	Advisors: Tandy Warnow and William Gropp
	Qualifying Exam: Scientific Computing
2011/06	B.A., Physics, *University of Chicago (IL, USA)*

Employment

2021/07– present	**Assistant Professor**, Department of Computer Science
	University of Maryland, College Park (MD, USA)
	University of Maryland Institute for Advanced Computer Studies (UMIACS)
	Center for Bioinformatics and Computational Biology (CBCB)
	Applied Math, Statistics, & Scientific Computation (AMSC) Graduate Program
	The Biological Sciences (BISI) Graduate Program
	Behavior, Ecology, Evolution, & Systematics (BEES) Area
	Computational Biology, Bioinformatics, and Genomics (CBBG) Area
2020/07–2021/07	Post-doctoral Researcher, Department of Computer Science
	University of California, Los Angeles (CA, USA)
	Advisor: Sriram Sankararaman
2013/08–2020/07	Graduate Research Fellow, Department of Computer Science
	University of Illinois at Urbana-Champaign (IL, USA)
	Advisors: Tandy Warnow and William Gropp
2011/08–2013/05	Associate Research Specialist, Department of Psychiatry
	University of Wisconsin-Madison (WI, USA)
	Advisor: Ramus Birn

Fellowships and Awards

2019	Rising Stars in Electrical Engineering and Computer Science (EECS)
2019	Travel fellowship ISMB 2019, *International Society of Computational Biology*

2017, 2019	Ira and Debra Cohen Graduate Fellowship in Computer Science, *University of Illinois at Urbana-Champaign (IL, USA)*
2015	**NSF Graduate Research Fellowship**, *National Science Foundation (USA)*
2014	Thomas M. Siebel Fellowship, *University of Illinois at Urbana-Champaign (IL, USA)*
2013	NSF Neuroengineering IGERT Fellowship, *National Science Foundation (USA)*
2013	State Farm Companies Foundation Doctoral Scholarship, *University of Illinois at Urbana-Champaign (IL, USA)*

Publication summary since joining UMD

Summary of papers published since I joined UMD in July 2021, excluding papers co-authored with my PhD and/or post-doc advisors.

Refereed Journal Articles (9 total)

Algorithms for Molecular Biology ×3 (2 last author)

BMC Genomics ×1

Genome Research ×2 (1 last author)

Heredity ×1

Systematic Biology ×1 (1 first author)

The Bulletin of the Society of Systematic Biologists ×1

Refereed Conference Proceedings (5 total)

RECOMB ×2 (1 last author)

WABI ×3 (2 last author)

Publication List

Underline indicates authors are members of Molloy Lab or student that I supervised / co-supervise
†Indicates equal contributors
*Indicates corresponding author
*Indicates paper is an extended version of conference papers (extended means the paper includes new results – theoretical, empirical, or both – and often a more thorough discussion of related work)

Preprints and Submitted Papers

P2. Keskus, Bryant, Ahmad, Yoo, Aganezov, Goretsky, Donmez, Lansdon, Rodriguez, Park, Liu, Cui, Gardner, McNulty, Sacco, Shetty, Zhao, Tran, Narzisi, Helland, Cook, Chang, Kolesnikov, Carroll, **Molloy**, Pushel, Guest, Pastinen, Shafin, Miga, Malikić, Day, Robine, Sahinalp, Dean, Farooqi, Paten, Kolmogorov* (2024) Severus: accurate detection and characterization of somatic structural variation in tumor genomes using long reads. *Submitted*.

P1. Hirsch, M. G., S. Pal, F. Rashidi Mehrabadi, S. Malikic, E. Pérez-Guijarro, C. Gruen, A. Sassano, E. Péerez- Guijarro, Merlino, C. Sahinalp, **E.K. Molloy**, C. Day*, T. M. Przytycka* (2024) Stochastic modelling of single-cell gene expression adaptation reveals non-genomic contribution to evolution of tumor subclones. *Submitted*.

Refereed Book Chapters

B1. **Molloy, E.K.** & T. Warnow (2023) Large-scale species tree estimation. In L. Kubatko & L. Knowles (Eds.), *Species Tree Inference: A Guide to Methods and Applications*. Princeton University Press. [link]

Refereed Journal Articles

*J31. Kahn[†], J., T. Rubel[†], **E.K. Molloy**, L. Dhulipala, R. Patro* (2024) Fast, Parallel, and Cache-friendly Suffix Array Construction. *Algorithms for Molecular Biology (Special Issue for WABI 2023)*, accepted. [link]

J30. Björner, M., **E.K. Molloy**, C. Dewey, C. Solís-Lemus* (2024) Detectability of varied hybridization scenarios using genome-scale hybrid detection methods. *The Bulletin of the Society of Systematic Biologists*, accepted. [link].

J29. K. Bell*, A. Noreuil, **E.K. Molloy**, M. Fritz (2024) Genetic and behavioral differences between above and below ground *Culex pipiens* bioforms. *Heredity*, accepted. [link]

*J28. Dai, J., T. Rubel, Y. Han, **E.K. Molloy*** (2024) Dollo-CDP: A polynomial time algorithm for the clade-constrained large Dollo parsimony problem. *Algorithms for Molecular Biology (Special issue for **WABI 2023**)* 19:2. [link]

J27. Y. Han & **E.K. Molloy*** (2023) Quartets enable statistically consistent estimation of cell lineage trees under an unbiased error and missingness model. *Algorithms for Molecular Biology (Special issue for invited **WABI 2023** papers)* 18:19. [link]

J26. Han Y. & **E.K. Molloy*** (2023) Improving quartet graph construction for scalable and accurate species tree estimation from gene trees. *Genome Research* 33:1042–1052. [link]
▷ Special issue for invited **RECOMB 2023** papers – acceptance rate 19.6%

J25. Liu, Y., X.C. Li, F. Rashidi Mehrabadi, A.A. Schäffer, D. Pratt, D.R. Crawford, S Malikić, **E.K. Molloy**, V. Gopalan, S.M. Mount, E. Ruppin, K. Aldape, S.C. Sahinalp (2023) Single-cell methylation sequencing data reveals succinct metastatic migration histories and tumor progression models. *Genome Research* 33:1089–1100. [link]
▷ Special issue for invited **RECOMB 2023** papers – acceptance rate 19.6%

J24. Commichaux, S., H. Rand, K. Javkar, **E.K. Molloy**, J.B. Pettengill, A. Pightling, M. Hoffmann, M. Pop, V. Jayeola, S. Foley, Y. Luo (2023) Assessment of plasmids for relating the 2020 Salmonella enterica serovar Newport onion outbreak to farms implicated by the outbreak investigation. *BMC Genomics* 24(1):1–18. [link]

J23. **Molloy***, **E.K.**, J. Gatesy, M.S. Springer* (2022) Theoretical and practical considerations when using retroelement insertions to estimate species trees in the anomaly zone. *Systematic Biology* 71(3):721–740. [link]

J22. Chiu, A.M., **E.K. Molloy**, Z. Tan, A. Talwalkar, S. Sankararaman* (2022) Inferring population structure in biobank-scale genomic data. *American Journal of Human Genetics* 109(4):727–737. [link]

J21. **Molloy***, **E.K.**, A. Durvasula, S. Sankararaman* (2021) Advancing admixture graph estimation via maximum likelihood network orientation. *Bioinformatics* 37(Supplement 1):i142–i150. [link]
▷ Special issue for **ISMB/ECCB 2020** – acceptance rate 18.6%

J20. Yu, X., T. Le, S. Christensen, **E.K. Molloy**, T. Warnow (2021) Using Robinson-Foulds supertrees in divide-and-conquer phylogeny estimation. *Algorithms for Molecular Biology (Special issue for **WABI 2020**)* 16:12. [link]

*J19. Legried, B., **E.K. Molloy**, T. Warnow, S. Roch* (2021) Polynomial-time statistical estimation of species trees under gene duplication and loss. *Journal of Computational Biology* 28(5):452–468. [link]
▷ Special issue for **RECOMB 2020** papers

J18. Shah, N. **E.K. Molloy**, M. Pop*, T. Warnow* (2021) TIPP2: Metagenomic taxonomic profiling using phylogenetic markers. *Bioinformatics* 37(13):1839–1845. [link]

*J17. Le, T., A. Sy, **E.K. Molloy**, Q. Zhang, S. Rao, T. Warnow* (2021) Using Constrained-INC for large-scale gene tree and species tree estimation. *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 18(1):2–15. [link]

J16. Zhang, C., C. Scornavacca, **E.K. Molloy**, S. Mirarab* (2020) ASTRAL-Pro: Quartet-based species tree inference despite paralogy. *Molecular Biology and Evolution* 37(11):3292–3307. [link]

J15. **Molloy*, E.K.** & T. Warnow* (2020) FastMulRFS: Fast and highly accurate species tree estimation under generic gene duplication and loss models. *Bioinformatics* 36(Supplement 1):i57–i65. [link]
▷ Special issue for **ISMB 2020** – acceptance rate 19.4%

J14. Springer*, M.S., **E.K. Molloy**, D.B. Sloan, M.P. Simmons, J. Gatesy* (2020) ILS-Aware analysis of low-homoplasy retroelement insertions: Inference of species trees and introgression using quartets. *Journal of Heredity* 11(2):147–168. [link]
▷ Editor's choice

*J13. Christensen, S., **E.K. Molloy**, P. Vachaspati, A. Yammanuru, T. Warnow* (2020) Non-parametric correction of estimated gene trees using TRACTION. *Algorithms for Molecular Biology (Special issue for WABI 2019)* 15:1. [link]

J12. **Molloy, E.K.** & T. Warnow* (2019) TreeMerge: A new method for improving the scalability of species tree estimation methods. *Bioinformatics* 35(14):i417–i426. [link]
▷ Special issue for **ISMB/ECCB 2019** – acceptance rate 18.9%

*J11. **Molloy*, E.K.** & T. Warnow (2019) Statistically consistent divide-and-conquer pipelines for phylogeny estimation using NJMerge. *Algorithms for Molecular Biology (Special issue for RECOMB-CG 2018)* 14:14. [link]

J10. Kruepke*, M., **E.K. Molloy**, K.W. Bresin, A.K. Barbey, E. Verona (2018) A brief assessment tool for investigating facets of moral judgment from realistic moral vignettes. *Behavior Research Methods* 50(3):922–936. [link]

*J9. Nute, M., J. Chou, **E.K. Molloy**, T. Warnow* (2018) The performance of coalescent-based species tree estimation methods under models of missing data. *BMC Genomics (Special issue for RECOMB-CG 2017)* 19:286. [link]

J8. **Molloy, E.K.** & T. Warnow* (2018) To include or not to include: The impact of gene filtering on species tree estimation methods. *Systematic Biology* 67(2):285–303. [link]

J7. Christensen, S., **E.K. Molloy**, P. Vachaspati, T. Warnow (2018) OCTAL: Optimal completion of gene trees in polynomial time. *Algorithms for Molecular Biology (Special issue for WABI 2017)* 13:6. [link]

J6. Patriat*, R., **E.K. Molloy**, R. M. Birn (2015) Using edge voxel information to improve motion regression for rs-fMRI connectivity studies. *Brain Connectivity* 5(9):582–595. [link]

J5. Birn*, R.M., M.D. Cornejo, **E.K. Molloy**, R. Patriat, T.B. Meier, G.R. Kirk, V.A. Nair, M.E. Meyerand, V. Prabhakran (2014) The influence of physiological noise correction on test-retest reliability of resting-state functional connectivity. *Brain Connectivity* 4(7):511–522. [link]

J4. **Molloy, E.K.**, M.E. Meyerand, R.M. Birn* (2014) The influence of spatial resolution and smoothing on the detectability of resting-state and task fMRI. *Neuroimage* 86:221–230. [link]

J3. Birn*, R. M., **E.K. Molloy**, R. Patriat, T. Parker, T.B. Meier, G.R. Kirk, V.A. Nair, M.E. Meyerand, V. Prabhakran (2013) The effect of scan length on the reliability of resting-state fMRI connectivity estimates. *Neuroimage* 83:550–558. [link]

J2. Patriat, R., **E.K. Molloy**, T. B. Meier, G. R. Kirk, V. A. Nair, M. E. Meyerand, V. Prabhakran, R. M. Birn* (2013) The effect of resting condition on resting-state fMRI reliability and consistency: A comparison between resting with eyes opened, closed, and fixated. *Neuroimage* 78:463–473. [link]

J1. 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, R.M. Birn (2012) Developmental pathways to amygdala-prefrontal function and internalizing symptoms in adolescence. *Nature Neuroscience* 15:1736–1741. [link]

Refereed Conference Proceedings

C11. Dai, J., T. Rubel, Y. Han, **E.K. Molloy*** (2023) Leveraging constraints plus dynamic programming for the large Dollo parsimony problem. *23rd International Workshop on Algorithms and Bioinformatics (WABI 2023)*, LIPIcs 273:5. [link]

C10. Han, Y. & **E.K. Molloy*** (2023) Quartets enable statistically consistent estimation of cell lineage trees under an unbiased error and missingness model (Abstract). *23rd International Workshop on Algorithms and Bioinformatics (WABI 2023)*, LIPIcs 273:8. [link] (Full paper reviewed; see [preprint])

C9. Kahn†, J., T. Rubel†, L. Dhulipala, **E.K. Molloy**, R. Patro (2023) Fast, Parallel, and Cache-friendly Suffix Array Construction. *23rd International Workshop on Algorithms and Bioinformatics (WABI 2023)*, LIPIcs 273:16. [link]

C8. Han, Y. & **E.K. Molloy*** (2023) TREE-QMC: Improving quartet graph construction for scalable and accurate species tree estimation from gene trees (Abstract). *27th International Conference on Research in Computational Molecular Biology (RECOMB 2023)*. [link]

C7. Liu, Y., X.C. Li, F. Rashidi Mehrabadi, A.A. Schäffer, D. Pratt, D.R. Crawford, S. Malikić, **E.K. Molloy**, V. Gopalan, S.M. Mount, E. Ruppin, K. Aldape, S.C. Sahinalp (2023) Single-cell methylation sequencing data reveals succinct metastatic migration histories and tumor progression models (Abstract). *27th International Conference on Research in Computational Molecular Biology (RECOMB 2023)*. [link]

C6. Yu, X., T. Le, S. Christensen, **E.K. Molloy**, T. Warnow (2020) Advancing divide-and-conquer phylogeny estimation using Robinson-Foulds supertrees. *20th International Workshop on Algorithms and Bioinformatics (WABI 2020)*, LIPIcs 172:15. [link]

C5. Legried, B. **E.K. Molloy**, T. Warnow, S. Roch (2020) Polynomial-Time Statistical Estimation of Species Trees Under Gene Duplication and Loss. *24th International Conference on Research in Computational Molecular Biology (RECOMB 2020)*, LNBI 12074:120–135. [link]

C4. Christensen, S., **E.K. Molloy**, P. Vachaspati, T. Warnow (2019) TRACTION: Fast non-parametric improvement of estimated gene trees. *19th International Workshop on Algorithms in Bioinformatics (WABI 2019)*, LIPIcs 143:4. [link]

C3. Le, T., A. Sy, **E.K. Molloy**, Q. Zhang, S. Rao, T. Warnow (2019) Using INC within divide-and-conquer phylogeny estimation. *6th International Conference on Algorithms for Computational Biology (AlCoB 2019)*, LNBI 11488:167–178. [link]

C2. **Molloy, E.K.** & T. Warnow (2018) NJMerge: A generic technique for scaling phylogeny estimation methods and its application to species trees. *16th RECOMB Satellite Conference in Comparative Genomics* *(RECOMB-CG 2018)*, LNBI 11183:260–276. [link]

C1. Christensen, S., **E.K. Molloy**, P. Vachaspati, T. Warnow (2018) Optimal completion of incomplete gene trees in polynomial time using OCTAL. *17th International Workshop on Algorithms in Bioinformatics* *(WABI 2018)*, LIPIcs 88:27. [link]

Open Source Software

- `TREE-QMC` – Species tree estimation from gene trees via quartets

- `Dollo-CDP` – Phylogeny estimation from binary characters via Dollo parsimony

Funding

Grants

2022/06–2025/05	REU Site: Undergraduate Bioinformatics Research in Data Science for Genomics, **Co-PI** (PI: Mihai Pop), *National Science Foundation, Award: $439,615*

Computational Resources

2018/06–2019/06	Optimizing distributed-memory parallel code for constructing ultra-large phylogenetic trees on Blue Waters, **Co-PI** (PI: William Gropp), *Award: 50,000 node hours on Blue Waters supercomputer*
2017/06–2018/06	Designing scalable algorithms for constructing large phylogenetic trees (almost without alignments) on supercomputers, **Co-PI** (PI: William Gropp), *Award: 50,000 node hours on Blue Waters supercomputer*

Advising / Mentoring

PhD Students (6 total; 5 current)

2023/08–present	Rachel Parsons, *Computer Science, University of Maryland, College Park*
2023/08–present	Valerie Wray, *Applied Mathematics, University of Maryland, College Park*
2021/08–present	Yunheng Han, *Computer Science, University of Maryland, College Park* ▷ 1st author on C8/J26 and C10/J27; Co-author on C11/J28
2022/01–present	M.G. Hirsch, *Computer Science, University of Maryland, College Park* Co-advised with Teresa Przytycka (NIH)
▷ Co-author on P1	
2023/06–present	Anton Goretsky, *Computer Science, University of Maryland, College Park* Co-advised with Mikhail Kolmogorov (NIH)
▷ Co-author on P2	
2021/08–2023/08	Tobias Rubel, *Computer Science, University of Maryland, College Park* ▷ 2023 NSF Graduate Research Fellow ▷ Co-author on C9/J31, C11/J28

Undergraduate Students (11 total; 4 current)

*Indicates student was funded by an NSF REU Site Program Grant

2023/01–present	John Bridgers, *Computer Science, University of Maryland, College Park* ▷ 2023 John D. Gannon Scholarship [link]
2023/01–present	Junyan Dai, *Computer Science, University of Maryland, College Park* ▷ 1st author on C11/J28
2022/06–present	Luíz Mata Lopez⋆, *Computer Science, Montgomery College* ▷ 2023 Jack Kent Cooke Foundation Transfer Scholarship [link]
2023/06–2023/08	Madeline Bonanno⋆, *Computer Science and Biology, Tulane University* ▷ Presentation accepted to the 2024 AAAS Emerging Researchers National (ERN) Conference [link]
2023/06–2023/08	Carola Gonzalez Lebron⋆, *Computer Science, University of Dayton*
2022/08–2022/12	Michael Suehle, *Computer Science, University of Maryland, College Park* Degrees: BS completed; Next position CS MS student at University of Maryland, College Park ▷ THESIS: Fast branch length estimation under the multi-species coalescent model using triplets [link]
2022/06–2022/08	Aditya Girish⋆, *Computer Science, Rutgers University*
2019/06–2020/01	Emma Hamel, *Computer Science, University of Illinois at Urbana-Champaign* Degrees: BS completed ▷ Best poster award at undergraduate summer research symposium
2019/06–2020/01	Qikai Yang, *Computer Science, University of Illinois at Urbana-Champaign* Degrees: BS completed; Next position CS MS student at University of Illinois at Urbana-Champaign
2019/06–2019/08	Ananya Yammanuru, *Computer Science, University of Illinois at Urbana-Champaign* Degrees: BS completed; Next position CS PhD student at University of Illinois at Urbana-Champaign ▷ Co-author on J13
2012/06–2012/08	Taurean Parker⋆, *Mathematics-Statistics, University of Rochester* Degrees: BS completed; Next position Data Science MS student at New York University ▷ Co-author on J3

PhD Preliminary and Thesis Exam Committees (8 total)

2023/12–present	Noor Pratap Singh, *Computer Science, University of Maryland, College Park*
2023/11–present	Zexuan Zhao, *Behavior, Ecology, Evolution, and Systematics, University of Maryland, College Park*
2023/07–present	Jamshed Kahn, *Computer Science, University of Maryland, College Park*
2022/11–present	Harihara Subrahmaniam Muralidharan, *Computer Science, University of Maryland, College Park*
2022/09–present	Kristen Behrens, *Behavior, Ecology, Evolution, and Systematics, University of Maryland, College Park*
2021/11–present	Xuan (Cindy) Li, *Computational Biology, Bioinformatics, and Genomics, University of Maryland, College Park*
2021/08–2024/04	Dongze He, *Computational Biology, Bioinformatics, and Genomics, University of Maryland, College Park*
2021/20	Mohsen Zakeri, *Computer Science, University of Maryland, College Park*

Presentations

Invited Talks

2023/11/07	Florida Genetics 2023 Symposium, *University of Florida Genetics Institute (Gainesville, FL, USA)*
2023/08/03	Methodological Innovation, Machine Learning and Big Data Session, *Gordon Research Conference on Ecological and Evolutionary Genomics (Smithfield, RI, USA)*
2023/07/14	Computational Genomics Summer Institute, *University of California, Los Angeles (CA, USA)*
2023/03/18	Combinatorics, Probability and Computation in Molecular Biology Special Session, *American Mathematical Society Southeastern Sectional Meeting (Atlanta, GA, USA)*
2023/03/15	Spring School on Algorithmic Cancer Biology *National Cancer Institute (Bethesda, MD, USA)*
2022/09/07	PANGAIA 2nd Annual Workshop on Computational Pangenomics *(Potsdam, Germany)*
2022/06/28	Towards the network of life: Phylogenetic networks as tools to understand complex evolutionary histories Symposium, *Evolution Conference (Cleveland, OH, USA)*
2021/05/06	Learning Complex Histories From Genetic Data Workshop, *McGill University (Montreal, QC, Canada) – via Zoom* Co-presenter; Main presenter: Sriram Sankararaman
2020/01/05	Panel on Coalescent-based Methods in the Age of Big Data, *Society of Systematic Biologists (SSB) Standalone Meeting (Gainesville, FL, USA)*
2019/04/13	Trees in the Desert: A workshop on ultra-large phylogenetic trees *(Oracle, AZ, USA)* Included hands-on tutorial
2017/08/06	Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) Course, *Marine Biology Laboratory (Woods Hole, MA, USA)* Included hands-on tutorial

Invited Seminars

2023/03/23	Computer Science Colloquium, *Rice University (TX, USA) – via Zoom*
2023/02/02	Ecology, Evolution, & Behavior (EEB) Seminar, *Michigan State University (MI, USA)*
2022/11/10	Algorithms and Complexity in Phylogenetics Online Seminar, *Virtual*
2022/10/12	Physiology and Biophysics Seminar, *Weill Cornell Medical College (NY, USA)*
2022/04/18	Behavior, Ecology, Evolution, & Systematics (BEES) Seminar, *University of Maryland, College Park (MD, USA)*
2022/04/13	Computational Biology, Bioinformatics & Genomics (CBBG) Seminar, *University of Maryland, College Park (MD, USA)*
2021/11/18	Research Frontiers in Biomathematics Seminar, *University of California, Los Angeles (CA, USA) – via Zoom*

2021/09/03	Computer Science Dept. Seminar, *University of Maryland, College Park (MD, USA)*
2020/05/03	Computer Science Dept. Seminar, *University of Maryland, College Park (MD, USA)*
2020/01/30	Evolution Seminar, *University of Wisconsin–Madison (WI, USA)*
2020/01/29	Systems | Information | Learning | Optimization (SILO) Seminar, *University of Wisconsin-Madison (WI, USA)*

Teaching

University at Maryland, College Park

CMSC 829A Algorithmic Evolutionary Biology ▷ Created new course at UMD

    Instructor in Fall 2021/'22/'23

CMSC 498Y Machine Learning and Statistical Inference for Genomics ▷ Created new course at UMD

    Instructor in Spring 2022/'24

CMSC 423 Bioinformatic Algorithms, Databases, and Tools

    Guest Lecturer in Spring 2023

CMSC 250 Discrete Structures

    Guest Lecturer in Fall 2022

CMSC 798E / 801 Department Internal Research Seminar

    Speaker in Fall 2021

CMSC 396H Undergraduate Honors Seminar

    Speaker in Fall 2021/'22

CMSC 800 How to conduct great research

    Panelist in Spring 2022

UNIV 100 UMD Orientation

    Panelist in Fall 2021

University at Illinois at Urbana-Champaign

CS 466 Intro to Bioinformatics

    Recitation leader in Spring 2017
    ▷ On "List of Teachers Ranked as Excellent by their Students"

CS 450 Numerical Analysis

    Recitation leader in Spring 2015
    ▷ On "List of Teachers Ranked as Excellent by their Students"

Outreach Efforts

2022/08/10	CompSciConnect Activity, *Iribe Initiative* (42 middle schoolers across two classes)
2022/08/03	Research Talk, *CARR and BRIDGE REUs* (∼30 undergraduates)

| 2022/04/27 | UMD High School Computing Workshop, *Iribe Initiative* (20 high schoolers) |

Professional Service

Grant Panels

NSF BIO advisory panel in 2021

Conference Program Committees

Research in Computational Molecular Biology (**RECOMB** 2024)

Intelligent Systems for Molecular Biology (**ISMB** 2021/'22/'23/'24)

▷ Proceedings Area Co-Chair for ISMB 2024 (Evolutionary, Comparative and Population Genomics)

International Workshop on Algorithms and Bioinformatics (**WABI** 2021/'22/'23)

IEEE International Workshop on High Performance Computational Biology (**HiCOMB** 2021)

International Symposium on Bioinformatics Research and Applications (**ISBRA** 2022)

Journal Reviewing

Algorithms for Molecular Biology ×2

Bioinformatics ×4

Evolution ×1

Journal of Computational Biology ×5

Journal of Heredity ×1

IEEE Access ×1

IEEE/ACM Transactions in Computational Biology and Bioinformatics ×3

Methods in Ecology and Evolution ×1

Molecular Biology and Evolution ×1

Nature Communication ×1

PLOS Computational Biology ×1

PLOS Genetics ×2

Proceedings of the Royal Society B (Biological Sciences) ×1

Systematic Biology ×9

Organizing

| 2023/04–present | Organizing Committee Member for ICERM Workshop Algorithmic Advances and Implementation Challenges: Developing Practical Tools for Phylogenetic Inference [link] |
| 2021/07–present | EvolCompGen COSI Webinar Organizer, *part of International Society for Computational Biology* |

Department and University Service

University of Maryland, College Park

2023/12–present	Chair Search Committee, *Department of Computer Science*
2023/01–2023/05	Ad Hoc Member of Search Committee (Bioinformatics Representative), *Department of Computer Science*
2023/08–present	Chair of Bioinformatics Field Committee, *Department of Computer Science*
2021/08–present	Graduate Admissions Committee, *Department of Computer Science* ▷ Wrote nomination letter for 2023 Flagship Fellowship (awarded) ▷ Wrote nomination letter for 2022 Flagship Fellowship (awarded but declined) ▷ Wrote nomination letter for 2022 President's Fellowship (awarded but declined)
2022/08–2023/07	Appointment, Promotion and Tenure (APT) Committee, *University of Maryland Institute for Advanced Computer Studies (UMIACS)*
2022/08–2023/07	Seminar Organizer, *Center for Bioinformatics and Computational Biology (CBCB)*

University of Illinois at Urbana-Champaign

2019/05–2019/08	REU Program Committee, *Department of Computer Science*
2016/08–2018/05	Women Empowered in STEM Conference Organizing Committee
2016/08–2018/05	Society of Women Engineers Graduate Student Committee
2014/08–2017/08	Engineering Graduate Student Advisory Committee, *College of Engineering* ▷ Chaired committee from 2015/08–2016/08

Professional Memberships

Association for Computing Machinery (ACM)

International Society for Computational Biology (ISCB)

Society of Systematic Biologists (SSB)

Last updated: April 25, 2024