

Curriculum Vitae

Erin K. Molloy

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University of Maryland, College Park

Webpage [\[ekmolloy.com\]](http://ekmolloy.com)

Citation data [\[Google Scholar\]](#)

Verified reviews [\[Web of Science\]](#)

Experience

Dates are formatted as year/month/day.

Education

- | | |
|---------|--|
| 2020/08 | Ph.D. , Computer Science, <i>University of Illinois at Urbana-Champaign (IL, USA)</i>
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, <i>University of Chicago (IL, USA)</i> |

Employment

- | | |
|------------------|--|
| 2021/07– present | Assistant Professor , Department of Computer Science
<i>University of Maryland, College Park (MD, USA)</i>
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) Concentration |
| 2020/07–2021/07 | Post-doctoral Researcher, Department of Computer Science
<i>University of California, Los Angeles (CA, USA)</i>
PI: Sriram Sankararaman |
| 2013/08–2020/07 | Graduate Research Fellow, Department of Computer Science
<i>University of Illinois at Urbana-Champaign (IL, USA)</i>
PIs: Tandy Warnow and William Gropp |
| 2011/08–2013/05 | Associate Research Specialist, Department of Psychiatry
<i>University of Wisconsin-Madison (WI, USA)</i>
PI: Ramus Birn |

Fellowships and Awards

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|------|--|
| 2019 | Rising Stars in Electrical Engineering and Computer Science (EECS) |
| 2019 | Travel fellowship ISMB 2019, <i>International Society of Computational Biology</i> |

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

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 (4 total)

BMC Genomics ×1

Genome Research ×2 (1 last author)

Systematic Biology ×1 (1 first author)

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

†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

P1. Björner, M., E.K. Molloy, C. Dewey, C. Solís-Lemus* (2022) Detectability of varied hybridization scenarios using genome-scale hybrid detection methods. *arXiv*. [\[link\]](#) **Status:** Under revision at *The Bulletin of the Society of Systematic Biologists*.

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

J26. Han Y. & E.K. Molloy (2023) Improving quartet graph construction for scalable and accurate species tree estimation from gene trees. *Genome Research*, in press. [\[link\]](#)

▷ 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*, in press. [[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* 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 invited **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* 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* 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* 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* 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. *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. Ruppín, K. Aldape, S.C. Sahinalp (2023) Single-cell methylation sequencing data reveals succinct metastatic migration histories and tumor progression models. *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](#)
- [Dollo-CDP](#)

Funding

Grants

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

2021/08–present	Yunheng Han, <i>Computer Science, University of Maryland, College Park</i> ▷ 1st author on C8, J25, C10 and Co-author on C11
2021/08–present	Tobias Rubel, <i>Computer Science, University of Maryland, College Park</i> ▷ 2023 NSF Graduate Research Fellow ▷ Co-author on C9, C11
2022/01–present	M.G. Hirsch, <i>Computer Science, University of Maryland, College Park</i> Co-advised with Teresa Przytycka (NIH)
2023/06–present	Anton Goretsky, <i>Computer Science, University of Maryland, College Park</i> Co-advised with Mikhail Kolmogorov (NIH)

Undergraduate Students (11 total)

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

2023/06–present	Madeline Bonanno*, <i>Computer Science and Biology, Tulane University</i>
2023/01–present	John Bridgers, <i>Computer Science, University of Maryland, College Park</i> ▷ 2023 John D. Gannon Scholarship [link]
2023/01–present	Junyan Dai, <i>Computer Science, University of Maryland, College Park</i> ▷ 1st author on C11
2022/06–present	Luíz Mata Lopez*, <i>Computer Science, Montgomery College</i> ▷ 2023 Jack Kent Cooke Foundation Transfer Scholarship [link]
2023/06–2023/08	Carola Gonzalez Lebron*, <i>Computer Science, University of Dayton</i>
2022/08–2022/12	Michael Suehle, <i>Computer Science, University of Maryland, College Park</i> Degrees: BS completed; Now MS student (Comp Sci) 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*, <i>Computer Science, Rutgers University</i>
2019/06–2020/01	Emma Hamel, <i>Computer Science, University of Illinois at Urbana-Champaign</i> Degrees: BS completed ▷ Best poster award at undergraduate summer research symposium
2019/06–2020/01	Qikai Yang, <i>Computer Science, University of Illinois at Urbana-Champaign</i> Degrees: BS completed; Now MS student (Comp Sci) at University of Illinois at Urbana-Champaign
2019/06–2019/08	Ananya Yammanuru, <i>Computer Science, University of Illinois at Urbana-Champaign</i> Degrees: BS completed; Now PhD student (Comp Sci) at University of Illinois at Urbana-Champaign ▷ Co-author on J13
2012/06–2012/08	Taurean Parker*, <i>Mathematics-Statistics, University of Rochester</i> Degrees: BS completed; MS (Data Science) from New York University ▷ Co-author on J3

PhD Preliminary and Thesis Exam Committees (6 total)

2023/07–present	Jamshed Kahn, <i>Computer Science, University of Maryland, College Park</i>
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2022/11–present	Harihara Subrahmaniam Muralidharan, <i>Computer Science, University of Maryland, College Park</i>
2022/09–present	Kristen Behrens, <i>BISI – BEES (Behavior, Ecology, Evolution, and Systematics), University of Maryland, College Park</i>
2021/11–present	Xuan (Cindy) Li, <i>BISI – CBBG (Computational Biology, Bioinformatics, and Genomics), University of Maryland, College Park</i>
2021/08–present	Dongze He, <i>BISI – CBBG, University of Maryland, College Park</i>
2021/12/20	Mohsen Zakeri, <i>Computer Science, University of Maryland, College Park</i>

Presentations

Invited Seminar Talks

2023/03/23	Computer Science Colloquium, <i>Rice University (TX, USA) – via Zoom</i>
2023/02/02	Ecology, Evolution, & Behavior (EEB) Seminar, <i>Michigan State University (MI, USA)</i>
2022/11/10	Algorithms and Complexity in Phylogenetics Online Seminar, <i>Virtual</i>
2022/10/12	Physiology and Biophysics Seminar, <i>Weill Cornell Medical College (NY, USA)</i>
2022/04/18	Behavior, Ecology, Evolution, & Systematics (BEES) Seminar, <i>University of Maryland, College Park (MD, USA)</i>
2022/04/13	Computational Biology, Bioinformatics & Genomics (CBBG) Seminar, <i>University of Maryland, College Park (MD, USA)</i>
2021/11/18	Research Frontiers in Biomathematics Seminar, <i>University of California, Los Angeles (CA, USA) – via Zoom</i>
2021/09/03	Computer Science Dept. Seminar, <i>University of Maryland, College Park (MD, USA)</i>
2020/05/03	Computer Science Dept. Seminar, <i>University of Maryland, College Park (MD, USA)</i>
2020/01/30	Evolution Seminar, <i>University of Wisconsin–Madison (WI, USA)</i>
2020/01/29	Systems Information Learning Optimization (SILO) Seminar, <i>University of Wisconsin-Madison (WI, USA)</i>

Invited Talks, Panels, or Tutorials at Conferences, Workshops, and Symposia

2023/08/03	Methodological Innovation, Machine Learning and Big Data Session, <i>Gordon Research Conference on Ecological and Evolutionary Genomics (Smithfield, RI, USA)</i>
2023/07/14	Computational Genomics Summer Institute, <i>University of California, Los Angeles (CA, USA)</i>
2023/03/18	Combinatorics, Probability and Computation in Molecular Biology Special Session, <i>American Mathematical Society Southeastern Sectional Meeting (Atlanta, GA, USA)</i>
2023/03/15	Spring School on Algorithmic Cancer Biology <i>National Cancer Institute (Bethesda, MD, USA)</i>
2022/09/07	PANGAIA 2nd Annual Workshop on Computational Pangenomics (<i>Potsdam, Germany</i>)

2022/06/28	Towards the network of life: Phylogenetic networks as tools to understand complex evolutionary histories Symposium, <i>Evolution Conference (Cleveland, OH, USA)</i>
2021/05/06	Learning Complex Histories From Genetic Data Workshop, <i>McGill University (Montreal, QC, Canada) – via Zoom</i> Co-presenter; Main presenter: Sriram Sankararaman
2020/01/05	Panel on Coalescent-based Methods in the Age of Big Data, <i>Society of Systematic Biologists (SSB) Standalone Meeting (Gainesville, FL, USA)</i>
2019/04/13	Trees in the Desert: A workshop on ultra-large phylogenetic trees (<i>Oracle, AZ, USA</i>) Included hands-on tutorial
2018/08/17	Phylogenomics Software Symposium, <i>Evolution Conference (Montpellier, France)</i>
2017/08/06	Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) Course, <i>Marine Biology Laboratory (Woods Hole, MA, USA)</i> Included hands-on tutorial
2015/06/16	Phylogenomics Software Symposium, <i>Evolution Conference (Austin, TX, USA)</i>

Contributed Talks (without proceedings)

2021/01/16	MIC-Phy: Mathematical, Inferential, and Computational Phylogenomics (<i>Virtual</i>) Co-authors: Mark Springer and John Gatesy
2018/11/08	HPC and Data Science for Scientific Discovery Workshop, <i>Institute for Pure and Applied Mathematics (Los Angeles, CA, USA)</i> Co-author: Tandy Warnow
2018/06/05	NCSA Blue Waters Symposium for Petascale Science & Beyond (<i>Sunriver OR, USA</i>) Co-authors: Tandy Warnow and William Gropp
2016/06/18	Evolution Conference (<i>Austin, TX, USA</i>) Co-author: Tandy Warnow
2015/03/26	Copper Mountain Conference on Multigrid Methods (<i>Copper Mountain, CO, USA</i>) Co-authors: Luke Olson and Jacob Schroder

Teaching

University at Maryland, College Park

CMSC 829A Algorithmic Evolutionary Biology ▷ [Created new course](#)

Instructor in Fall 2021/'22/'23

CMSC 498Y Machine Learning and Statistical Inference for Genomics ▷ [Created new course](#)

Instructor in Spring 2022

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, <i>Iribe Initiative</i> (42 middle schoolers across two classes)
2022/08/03	Research Talk, <i>CARR and BRIDGE REUs</i> (~30 undergraduates)
2022/04/27	UMD High School Computing Workshop, <i>Iribe Initiative</i> (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)

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 ×1

Bioinformatics ×4

Evolution ×1

Journal of Computational Biology ×4

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 Workshop III: Developing practical tools for phylogenetic inference, <i>part of ICERM Fall 2024 long program: Theory, Methods, and Applications of Quantitative Phylogenomics</i>
2021/07–present	EvolCompGen COSI Webinar Organizer, <i>part of International Society for Computational Biology</i>

Department and University Service

University of Maryland, College Park

2023/08–present	Bioinformatics Field Committee, <i>Department of Computer Science</i>
2021/08–present	Graduate Admissions Committee, <i>Department of Computer Science</i> ▶ 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, <i>University of Maryland Institute for Advanced Computer Studies (UMIACS)</i>
2022/08–2023/07	Seminar Organizer, <i>Center for Bioinformatics and Computational Biology (CBCB)</i>

University of Illinois at Urbana-Champaign

2019/05–2019/08	REU Program Committee, <i>Department of Computer Science</i>
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, <i>College of Engineering</i> ▶ 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: September 20, 2023