

# Kevin J. Liu

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Department of Computer Science & Engineering  
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## Education

Ph.D. Computer Science, University of Texas at Austin, 2004–2011.

Dissertation: Fast and Accurate Estimation of Large-Scale Phylogenetic Alignments and Trees

Supervised by Professor Tandy Warnow

Co-supervised by Professor C. Randal Linder

B.S. Computer Science, Carnegie Mellon University, 1997–2000.

University Honors

## Academic Experience

### *Michigan State University*

Assistant Professor, Department of Computer Science and Engineering, 2014–present.

### *Rice University*

NIH National Library of Medicine Keck Fellow, supervised by Professor Luay K. Nakhleh, Department of Computer Science, and co-supervised by Professor Michael H. Kohn, Department of Ecology and Evolutionary Biology, 2012–2014.

Postdoctoral Fellow, supervised by Professor Luay K. Nakhleh, Department of Computer Science, Fall 2011.

### *University of Texas at Austin*

Postdoctoral Fellow, supervised by Professor Tandy Warnow, Center for Computational Biology and Bioinformatics and Computer Sciences Department, Summer 2011.

Research Assistant, supervised by Professor Tandy Warnow, Department of Computer Science, and co-supervised by Professor C. Randal Linder, Section of Integrative Biology, Spring 2006–Spring 2011.

Teaching Assistant, CS 394C Algorithms for Computational Biology, Department of Computer Science, Fall 2009.

Teaching Assistant, CS 329E Elements of Ethics in Computer Science, Department of Computer Science, Fall 2005.

*Carnegie Mellon University*

Undergraduate Research Assistant, Project LISTEN, School of Computer Science, 1997–1998.

**Research Interests**

Computational biology and bioinformatics

Phylogenomics and phylogenetics

Comparative genomics

Functional genomics

Population genetics

Algorithm design and empirical performance studies

**Research***Grant Support*

BEACON Grant: “Genomic and Computational Dissection of the Function and Evolution of Life History Transitions.” **Co-Principal Investigator**. Other co-PIs: H. J. Goldsby, J. H. A. Hoffmann, and R. L. Young. 2019–2020. Total amount: \$85,311. BEACON, an NSF Center for the Study of Evolution in Action (NSF Cooperative Agreement DBI-0939454).

IOS 1740874: “PGR: Transcriptional and Translational Regulation of Gene Expression by Gene Structure, Codon Usage and tRNAs in Grasses.” **Co-Principal Investigator**. Other PI/co-PIs: K. Childs, N. Jiang, and Y. Yang. 2018–2022. Total amount to MSU: \$2,561,077. National Science Foundation, USA.

DGE 1828149: “NRT-HDR: Intersecting Computational and Data Science to Address Grand Challenges in Plant Biology.” **Co-Principal Investigator**. Other PI/co-PIs: S.-H. Shiu, J. A. P. Benitez, C. R. Buell, K. Childs, D. Chitwood, K. Cichy, E. Farre, E. Grotewold, Y. Hsu, J. Jiang, T. Long, E. Munch, C. Niederhuth, B. O’Shea, R. VanBuren, J. Wang, Y. Xie, and M. Yan. 2018–2023. Total amount to MSU: \$2,999,967. National Science Foundation, USA.

CCF 1714417: “Fast and Accurate Computational Tools for Large-Scale Evolutionary Inference: a Phylogenetic Network Approach.” **Principal Investigator**. 2017–2021. Total amount to MSU: \$404,748. National Science Foundation, USA.

Research Experiences for Undergraduates (REU) supplement award. 2020–2021. Total amount to MSU: \$24,000. National Science Foundation, USA.

DEB 1737898: “Dimensions: Phylogenetic and Functional Diversity of Tripartite Plant-Fungal-Bacterial Symbioses.” **co-Principal Investigator**. Other PI/co-PIs: G. M. Bonito, P. P. Edger, and B. Hamberger. 2017–2022. Total amount to MSU: \$1,749,984. National Science Foundation, USA.

Dimensions Broadening Participation Research Experiences for Undergraduates (D-BP-REU) supplement award. 2017–2018. Total amount to MSU: \$20,000. National Science Foundation, USA.

CCF 1565719: “CRII: Novel Evolutionary Models and Algorithms to Connect Genomic Sequence and Phenotypic Data.” **Principal Investigator**. 2016–2019. Total amount to MSU: \$174,968. National Science Foundation, USA.

BEACON Grant: “A Novel Phylogenomic Framework for Forensic DNA Localization.” **Co-Principal Investigator**. Other co-PI: G. M. Bonito. 2017–2018. Total amount: \$67,119. BEACON, an NSF Center for the Study of Evolution in Action (NSF Cooperative Agreement DBI-0939454).

BEACON Grant: “A Phylogenomic Study of Adaptive Co-evolution Between Early Diverging Fungi and Obligate Bacterial Endosymbionts in the *Burkholderiaceae*.” **Co-Principal Investigator**. Other co-PI: G. M. Bonito. 2016–2017. Total amount: \$65,414. BEACON, an NSF Center for the Study of Evolution in Action (NSF Cooperative Agreement DBI-0939454).

XSEDE Allocation Grant: “Fast and Accurate Computational Tools for Large-Scale Evolutionary Inference.” **Principal Investigator**. 2016–2017. Total amount: 50,000 service units (SUs). National Science Foundation, USA.

The MSU WaterCube Program Grant: “Microbial Communities in Global Groundwaters: An Evolutionary and Ecological Perspective.” **Co-Principal Investigator**. Other co-PIs: J. B. Rose and M. O. Schrenk. 2015–2017. Total amount: \$60,000. The MSU Water Science Network, Michigan State University.

### *Book Chapters*

1. K. J. Liu and T. J. Warnow, Large-scale multiple sequence alignment and tree estimation using SATé. In *Methods in Molecular Biology: Multiple Sequence Alignment*, D. Russell (editor). New York: Springer; 2014. p. 219-244, DOI: [10.1007/978-1-62703-646-7\\_15](https://doi.org/10.1007/978-1-62703-646-7_15).

### *Refereed Journal and Conference Publications*

1. W. Wang, J. Smith, H. A. Hejase, and K. J. Liu, “Non-parametric and semi-parametric support estimation using SEquential RESampling random walks on biomolecular sequences”, *Algorithms for Molecular Biology*, vol. 15, no. 1, p. 7, 2020, DOI: [10.1186/s13015-020-00167-0](https://doi.org/10.1186/s13015-020-00167-0).
2. S. P. Mullen, N. W. VanKuren, W. Zhang, S. Nallu, E. B. Kristiansen, Q. Wuyun, K. J. Liu, R. I. Hill, A. Briscoe, and M. R. Kronforst, “Disentangling population history and character evolution among hybridizing lineages,” *Molecular Biology and Evolution*, vol. 37, issue 5, 2020, DOI: [10.1093/molbev/msaa004](https://doi.org/10.1093/molbev/msaa004).
3. W. Wang, Q. Wuyun, and K. J. Liu, “An application of random walk resampling to phylogenetic HMM inference and learning,” *IEEE Transactions on NanoBioscience*, vol. 19, no. 3, pp. 506-517, 2020, DOI: [10.1109/TNB.2020.2991302](https://doi.org/10.1109/TNB.2020.2991302).
4. W. Wang, Q. Wuyun, and K. J. Liu, “An application of random walk resampling to phylogenetic HMM inference and learning,” *Proceedings of the 2019 IEEE International Conference on Bioinformatics and Biomedicine (BIBM)*, pp. 44-51, 2019, DOI: [10.1109/BIBM47256.2019.8983223](https://doi.org/10.1109/BIBM47256.2019.8983223).
5. Q. Wuyun, N. W. VanKuren, M. Kronforst, S. P. Mullen, and K. J. Liu, “Scalable statistical introgression mapping using approximate coalescent-based inference,” *Proceedings of the 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB '19)*, ACM, New York, NY, USA, pp. 535, 2019, DOI: [10.1145/3307339.3342165](https://doi.org/10.1145/3307339.3342165).

6. H. A. Hejase, N. VandePol, G. M. Bonito, and K. J. Liu, "FastNet: fast and accurate statistical inference of phylogenetic networks using large-scale genomic sequence data", Proceedings of the Sixteenth RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Magog-Orford, Québec, Canada, 2018. Conference paper published in Springer LNCS, vol. 11183, pp. 242-259, 2018, DOI: [10.1007/978-3-030-00834-5\\_14](https://doi.org/10.1007/978-3-030-00834-5_14).
7. W. Wang, J. Smith, H. A. Hejase, and K. J. Liu, "Non-parametric and semi-parametric support estimation using SEquential RESampling random walks on biomolecular sequences", Proceedings of the Sixteenth RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Magog-Orford, Québec, Canada, 2018. Conference paper published in Springer LNCS, vol. 11183, pp. 294-308, 2018, DOI: [10.1007/978-3-030-00834-5\\_17](https://doi.org/10.1007/978-3-030-00834-5_17).
8. H. A. Hejase, N. VandePol, G. M. Bonito, P. P. Edger, and K. J. Liu, "Coal-Miner: a statistical method for GWA studies of quantitative traits with complex evolutionary origins," Proceedings of the 8th ACM International Conference on Bioinformatics, Computational Biology, and Health Informatics, pp. 107-114, 2017, DOI: [10.1145/3107411.3107490](https://doi.org/10.1145/3107411.3107490).
9. H. A. Hejase and K. J. Liu, "A scalability study of phylogenetic network inference methods using empirical datasets and simulations involving a single reticulation," BMC Bioinformatics, vol. 17, no. 1, p. 422, 2016, DOI: [10.1186/s12859-016-1277-1](https://doi.org/10.1186/s12859-016-1277-1).
10. Z. Wang and K. J. Liu, "A performance study of the impact of recombination on species tree analysis," Proceedings of the Fourteenth RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Montréal, Quebec, Canada, 2016. Journal version published in BMC Genomics, vol. 17, no. 10, pp. 165-174, 2016, DOI: [10.1186/s12864-016-3104-5](https://doi.org/10.1186/s12864-016-3104-5).
11. H. A. Hejase and K. J. Liu, "Mapping the genomic architecture of adaptive traits with interspecific introgressive origin: a coalescent-based approach," Proceedings of the Fourteenth Asia Pacific Bioinformatics Conference (APBC), San Francisco, CA, USA, 2016. Journal version published in BMC Genomics, vol. 17(Suppl 1), no. 8, pp. 41-57, 2016, DOI: [10.1186/s12864-015-2298-2](https://doi.org/10.1186/s12864-015-2298-2).
12. K. J. Liu, E. Steinberg, A. Yozzo, Y. Song, M. H. Kohn, and L. K. Nakhleh, "Interspecific introgressive origin of genomic diversity in the house mouse," Proceedings of the National Academy of Sciences of the United States of America, vol. 112, no. 1, pp. 196-201, 2015, DOI: [10.1073/pnas.1406298111](https://doi.org/10.1073/pnas.1406298111).
13. K. J. Liu, J. Dai, K. Truong, Y. Song, M. H. Kohn, and L. K. Nakhleh, "An HMM-based comparative genomic framework for detecting introgression in eukaryotes," PLoS Computational Biology, vol. 10, no. 6, p. e1003649, 2014, DOI: [10.1371/journal.pcbi.1003649](https://doi.org/10.1371/journal.pcbi.1003649).
14. Y. Yu, J. Dong, K. J. Liu, and L. K. Nakhleh, "Maximum likelihood inference of reticulate evolutionary histories," Proceedings of the National Academy of Sciences of the United States of America, vol. 111, no. 46, pp. 16448-16453, 2014, DOI: [10.1073/pnas.1407950111](https://doi.org/10.1073/pnas.1407950111).
15. K. J. Liu, T. J. Warnow, M. T. Holder, S. Nelesen, J. Yu, A. Stamatakis, C. R. Linder, "SATé-II: very fast and accurate simultaneous estimation of multiple sequence alignments and phylogenetic trees," Systematic Biology, vol. 61, no. 1, pp. 90-106, 2012, DOI: [10.1093/sysbio/syr095](https://doi.org/10.1093/sysbio/syr095).
16. K. J. Liu and T. J. Warnow, "Treelength optimization for phylogeny estimation," PLoS ONE, vol. 7, no. 3:e33104, 2012, DOI: [10.1371/journal.pone.0033104](https://doi.org/10.1371/journal.pone.0033104).
17. S. Nelesen, K. J. Liu, L. S. Wang, C. R. Linder, and T. J. Warnow, "DACTAL: divide-and-conquer trees (almost) without alignments," Proceedings of Intelligent Systems for Molecular Biology (ISMB), Long Beach, CA, USA, 2012. *Acceptance rate of 13%*. Journal version

- published in *Bioinformatics*, vol. 28, no. 12, pp. i274-i282, 2012, DOI: [10.1093/bioinformatics/bts218](https://doi.org/10.1093/bioinformatics/bts218).
18. K. J. Liu, C. R. Linder, and T. J. Warnow, "RAxML and FastTree: comparing two methods for large-scale maximum likelihood phylogeny estimation," *PLoS ONE*, vol. 6, no. 11:e27731, 2011, DOI: [10.1371/journal.pone.0027731](https://doi.org/10.1371/journal.pone.0027731).
  19. K. J. Liu, C. R. Linder, and T. J. Warnow. "Multiple sequence alignment: a major challenge to large-scale phylogenetics," *PLoS Currents: Tree of Life*, 2010, DOI: [10.1371/currents.RRN1198](https://doi.org/10.1371/currents.RRN1198).
  20. C. R. Linder, R. Suri, K. J. Liu, and T. J. Warnow. "Benchmark datasets and software for developing and testing methods for large-scale multiple sequence alignment and phylogenetic inference," *PLoS Currents: Tree of Life*, 2010, DOI: [10.1371/currents.RRN1195](https://doi.org/10.1371/currents.RRN1195).
  21. K. J. Liu, S. Raghavan, S. Nelesen, C. R. Linder, T. J. Warnow, "Rapid and accurate large-scale coestimation of sequence alignments and phylogenetic trees," *Science*, vol. 324, no. 5934, pp. 1561-1564, 19 June 2009, DOI: [10.1126/science.1171243](https://doi.org/10.1126/science.1171243). *Selected by Faculty of 1000 Ecology*.
  22. K. J. Liu, S. Nelesen, S. Raghavan, C. R. Linder, T. J. Warnow, "Barking up the wrong tree-length: the impact of gap penalty on alignment and tree accuracy," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, vol. 6, no. 1, pp. 7-21, Jan.-Mar. 2009, DOI: [10.1109/TCBB.2008.63](https://doi.org/10.1109/TCBB.2008.63).
  23. S. Nelesen, K. J. Liu, D. Zhao, C. R. Linder, T. J. Warnow, "The effect of the guide tree on multiple sequence alignments and subsequent phylogenetic analyses," *Proceedings of the Pacific Symposium on Biocomputing*, Kohala Coast, Hawaii, USA, 2008. Journal version published in *Biocomputing*, vol. 13, pp. 15-24, 2008, DOI: [10.1142/9789812776136\\_0004](https://doi.org/10.1142/9789812776136_0004).

### *Working Manuscripts*

- "New techniques for phylogenetic multiple sequence alignment," in preparation.
- "New non-parametric techniques for phylogenetic support estimation," in preparation.
- "A performance study of co-phylogenetic inference methods," in preparation.
- "New statistical methods for detecting local evolutionary rate heterogeneity," in preparation.
- "Scalable statistical inference of species phylogenies from large-scale resequenced genomic datasets," in preparation.
- "A phylogenomic study of adaptive co-evolution between early diverging fungi and obligate bacterial endosymbionts in the *Burkholderiaceae*," in preparation.

### *Scientific Software*

[Coal-Miner](#), a coalescent-based method for detecting significant statistical associations between genomic loci and a quantitative trait – where both sets of characters have complex evolutionary origins, with H. A. Hejase, 2017.

[Coal-Map](#), a coalescent-based method for detecting significant statistical associations between genomic loci and a quantitative trait with interspecific introgressive origin, with H. A. Hejase, 2016.

**PhyloNet-HMM**, an HMM-based comparative genomic method for the analysis of complex evolutionary histories, with J. Dai, K. Truong, Y. Song, M. H. Kohn, and L. K. Nakhleh, 2014.

**DACTAL**, a method for estimation of phylogenies from datasets with tens of thousands of nucleotide sequences and kilobases of sequence length, with S. Nelesen, L. S. Wang, C. R. Linder, and T. J. Warnow, 2012.

**SATé-II**, a method for very fast and accurate simultaneous estimation of alignments and trees, with T. J. Warnow, M. T. Holder, S. Nelesen, J. Yu, A. Stamatakis, and C. R. Linder, 2012.

**SATé-I**, a method for fast and accurate maximum likelihood simultaneous estimation of alignments and trees, with S. Raghavan, S. Nelesen, C. R. Linder, and T. J. Warnow, 2009.

**BeeTLe**, a method for estimation of alignments and trees by optimizing treelength, with T. J. Warnow, 2012.

**POY\***, a method for estimation of alignments and trees by optimizing treelength, with S. Nelesen, S. Raghavan, C. R. Linder, T. J. Warnow, 2009.

### *Invited Presentations*

“Genome-wide Association Mapping in the Context of Complex Evolutionary Histories: New Phylogenomic Approaches.” Society of Systematic Biologists Symposium on Phylogenetic Approaches to Connecting Genotypes to Phenotypes. Held at the 2017 Evolution Scientific Meeting, Portland, OR, USA, June 25, 2017.

### *Contributed/Conference Presentations*

“Estimating Statistical Support Using Random Walk Resampling of Biomolecular Sequences.” BEACON 2020 Congress, Michigan State University, East Lansing, MI, USA, August 12, 2020.

“Estimating Statistical Support Using Random Walk Resampling of Biomolecular Sequences.” 4th Annual Research Symposium of the Michigan State University Ecology, Evolutionary Biology, and Behavior Program, East Lansing, MI, USA, May 7, 2020.

“Scalable Statistical Introgression Mapping Using Approximate Coalescent-Based Inference.” 10th ACM International Conference on Bioinformatics, Computational Biology and Health Informatics (BCB '19), Niagara Falls, NY, USA, September 10, 2019.

“Uncovering the Interspecific Introgressive Origins of the House Mouse Genome.” 3rd Annual Research Symposium of the Michigan State University Ecology, Evolutionary Biology, and Behavior Program, East Lansing, MI, USA, April 29, 2019.

“FastNet: Fast and Accurate Statistical Inference of Phylogenetic Networks using Large-scale Genomic Sequence Data.” 16th Annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Magog-Orford, Québec, Canada, October 9-12, 2018.

“Non-parametric and Semi-parametric Support Estimation using SEquential RESampling Random Walks on Biomolecular Sequences”, 16th Annual RECOMB Comparative Genomics Satellite Conference (RECOMB-CG), Magog-Orford, Québec, Canada, October 9-12, 2018.

“Fast and Accurate Inference of Phylogenetic Networks Using Large-scale Genomic Sequence Data.” MSU Interfacing Computational & Plant Science (IMPACTS) Symposium, Michigan State University, East Lansing, MI, USA, August 22, 2018.

“Fast and Accurate Inference of Phylogenetic Networks Using Large-scale Genomic Sequence Data.” BEACON 2018 Congress, Michigan State University, East Lansing, MI, USA, August 10, 2018.

“Fast and Accurate Inference of Phylogenetic Networks Using Large-scale Genomic Sequence Data.” 2nd Annual Research Symposium of the Michigan State University Ecology, Evolutionary Biology, and Behavior Program, East Lansing, MI, USA, April 30, 2018.

“Coal-Miner: a Coalescent-based Method for GWA Studies of Quantitative Traits with Complex Evolutionary Origins.” ACM-BCB 2017, Boston, MA, August 21, 2017.

“Coal-Miner: a Coalescent-based Method for GWA Studies of Quantitative Traits with Complex Evolutionary Origins.” BEACON 2017 Congress, Michigan State University, East Lansing, MI, USA, August 2, 2017.

“What Can Computational Thinking and Evolutionary Thinking Do For Human Health and the Life Sciences?” MSU iCER ACRES seminar, East Lansing, MI, USA, June 8, 2017.

“Fast and Accurate Inference of Phylogenetic Networks Using Large-scale Genomic Sequence Data.” 1st Annual Research Symposium of the Michigan State University Ecology, Evolutionary Biology, and Behavior Program, East Lansing, MI, USA, May 1, 2017.

“A Performance Study of the Impact of Recombination on Species Tree Analysis.” 14th RECOMB Comparative Genomics Satellite Conference, Montréal, Québec, Canada, October 12, 2016.

“Fast and Accurate Inference of Phylogenetic Networks using Large-scale Genomic Sequence Data.” BEACON 2016 Congress, Michigan State University, East Lansing, MI, USA, August 11, 2016.

“PhyloNet-HMM: A Comparative Genomic Framework for Detecting Introgression in Eukaryotes.” 2016 iEvoBio Meeting, Austin, TX, USA, June 21, 2016.

“Fast and Accurate Inference of Phylogenetic Networks using Large-scale Genomic Sequence Data.” 2016 Evolution Scientific Meeting, Austin, TX, USA, June 18, 2016.

“Microbial Communities in Global Groundwaters: An Evolutionary and Ecological Perspective.” WaterCube meeting, Michigan State University, East Lansing, MI, USA, December 2, 2015.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” BEACON 2015 Congress, Michigan State University, East Lansing, MI, USA, August 16, 2015.

“Mapping the Genomic Architecture of Adaptive Introgressed Traits: A Coalescent-Based Approach.” Society for Systematic Biologists Standalone Meeting, Ann Arbor, MI, May 21, 2015.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” Division of Engineering Research seminar series, Michigan State University, East Lansing, MI, USA, April 7, 2015.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” CompPLB group, Michigan State University, East Lansing, MI, USA, February 11, 2015.

“Interspecific Introgressive Origin of Genomic Diversity in the House Mouse.” The BEACON Center for the Study of Evolution in Action seminar series, Michigan State University, East Lansing, MI, USA, September 19, 2014.

“An HMM-based Comparative Genomics Framework for Analyzing Complex Evolutionary Scenarios.” The University of Texas at Austin, Austin, TX, USA, May 31, 2014.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” The Jackson Laboratory, Bar Harbor, ME, USA, April 8, 2014.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” Saarland University Multimodal Computing and Informatics Cluster of Excellence, Saarbrücken, Germany, March 25, 2014.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” University of Houston Department of Computer Science, Houston, TX, USA, March 21, 2014.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” Michigan State University Department of Computer Science and Engineering, East Lansing, MI, USA, March 17, 2014.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” Colorado State University Department of Computer Science, Ft. Collins, CO, USA, March 5, 2014.

“Stochastic Models and Algorithms for Large-scale Comparative Genomics under Complex Evolutionary Scenarios.” Texas Tech University Department of Computer Science, Lubbock, TX, USA, February 24, 2014.

“Interspecific Introgressive Origin of Genomic Diversity in the House Mouse.” Guest lecture for Rice University EBIO 561, Houston, TX, USA, September 4, 2013.

“Pleiotropy and Polygenes in Adaptive Hybridized Gene Clusters in Mice.” NIH National Library of Medicine Informatics Training Conference, Salt Lake City, UT, USA, June 18, 2013.

“Mosaic Signatures of Natural Hybridization in the House Mouse Genome.” Progress meeting for NSF 1062463 “ABI Innovation: Novel Methodologies for Genome-scale Evolutionary Analysis of Multi-locus Data”, University of Texas at Austin, Austin, TX, USA, February 18, 2013.

“Population Genomics of the Mouse and its Functional Implications.” NIH National Library of Medicine Informatics Training Conference, Madison, WI, USA, June 26, 2012.

“Fast and Accurate Co-estimation of Large-scale Phylogenetic Alignments and Trees.” Massachusetts Institute of Technology Computer Science and Artificial Intelligence Laboratory, Boston, MA, USA, April 13, 2011.

“Fast and Accurate Co-estimation of Large-scale Phylogenetic Alignments and Trees.” Graduate Representative Association of Computer Sciences Speaker Series, University of Texas at Austin, Austin, TX, USA, May 4, 2010.

“Simultaneous Alignment and Tree Estimation (SATé): a Fast and Accurate Method for Difficult Datasets with Many Taxa.” Cyberinfrastructure for Phylogenetic Research (CIPRES) Project All-Hands Meeting, University of California at Berkeley, Berkeley, CA, USA, July 22, 2009.

“Gap-attentive Phylogenetic Methods.” Cyberinfrastructure for Phylogenetic Research (CIPRES) Project All-Hands Meeting, University of Texas at Austin, Austin, TX, USA, February 4, 2006.



## Teaching

### *Courses at Michigan State University*

CSE 331 Algorithms and Data Structures: spring 2016, spring 2017.

CSE 431 Algorithm Engineering: spring 2020, spring 2021.

CSE 491 Introduction to Computational Biology and Bioinformatics: spring 2019.

CSE 836 Computational Comparative Genomics: fall 2014, fall 2016.

CSE 841 Artificial Intelligence: fall 2015, fall 2017, fall 2018, fall 2019, fall 2020.

## Industry Experience

Software developer I, Oracle Corporation, 2001–2004.

Software engineer I, Smartpipes Corporation, 2001.

Intern, Oracle Corporation, summer 2000.

Intern, Fujitsu Network Communications, summer 1999.

Intern, UHD Inc., contractor at National Institutes of Health. summer 1998.

## Professional Activities

### *Conference Committee Membership*

PC member, The 11th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2020. Virtual conference.

PC member, The 17th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) 2019. Montpellier, France.

PC member, The 10th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2019. Niagara Falls, NY, USA.

PC member, The 16th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) 2018. Magog-Orford, Québec, Canada.

PC member, The 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2018. Washington, DC, USA.

PC member, The 15th RECOMB Comparative Genomics Satellite Conference (RECOMB-CG) 2017. Barcelona, Spain.

Track chair and PC member, The 8th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB) 2017. Boston, MA, USA.

*National/International Service*

NSF panelist: 2016, 2017, 2018, 2019, 2020.

NSF ad hoc reviewer: 2016 and 2017.

NIH GVE study section member: 2018.

L'Agence Nationale de Recherche (ANR)/The French National Research Agency: 2018.

Thrust Group leader for BEACON, an NSF Science and Technology Center (STC) for the Study of Evolution in Action: 2017 Thrust Group 1 "Genomes, Genetic Architectures & Evolvability".

*University Service*

Member, Graduate Studies and Research Committee, Department of Computer Science and Engineering, Michigan State University, 2014 – present.

Member, Recruitment Committee, NSF NRT-IMPACTS Training Program, Michigan State University, 2020 – 2021.

Co-chair, Student Faculty Recruiting Committee, Department of Computer Science, University of Texas at Austin, 2008.

Student member, Faculty Recruiting Committee, Department of Computer Science, University of Texas at Austin, 2008.

*Reviewer*

Molecular Biology and Evolution

Systematic Biology

BMC Evolutionary Biology

Algorithmica

PLOS ONE

RECOMB

RECOMB-CG

ACM BCB

SODA

**Honors & Awards***Fellowships*

NIH National Library of Medicine Keck Postdoctoral Fellowship, 2012–2014.

Microelectronics and Computer Development Doctoral Fellowship, 2004–2005.

NSF Graduate Fellowship Honorable Mention, 2005.

*Awards*

2014 Postdoctoral Preparation Institute Travel Award from the Federation of American Societies for Experimental Biology, Summer 2014.

AAAS/Science Program for Excellence in Science, 2013.

University of Texas Office of Graduate Studies Professional Development Award, Fall 2007.

Shell Merit Scholarship, 1997–2000.

Andrew Carnegie Merit Scholarship, 1997-2000.

Junior Achievement Merit Scholarship, 1998.

Chinese Professionals Club Merit Scholarship, 1997.

Society of Automotive Engineers Merit Scholarship, 1997.

National Merit Competition Finalist, 1997.

**Current Ph.D. and M.S. Students Supervised/Co-supervised**

Wei Wang, Department of Computer Science and Engineering, Michigan State University.  
Joined group as a Ph.D. student in fall 2016.  
Website: <https://wangwe90.github.io/>.

Qiqige Wuyun, Department of Computer Science and Engineering, Michigan State University.  
Joined group as a Ph.D. student in fall 2017.

Meijun Gao, Department of Computer Science and Engineering, Michigan State University.  
Joined group as a Ph.D. student in fall 2019.

Julia Zheng, Department of Computer Science and Engineering and Ecology, Evolutionary Biology, and Behavior (EEBB) Program, Michigan State University.  
Joined group as a Ph.D. student in fall 2019.

Ahmad Hejase Bazzi, Department of Computer Science and Engineering, Michigan State University.  
Joined group as a Ph.D. student in spring 2020.

Md. Alamin, Department of Computer Science and Engineering, Michigan State University.  
Joined group as a Ph.D. student in fall 2020.

Rei Doko, Department of Computer Science and Engineering, Michigan State University.  
Joined group as a Ph.D. student in fall 2020.

## Past Ph.D. and M.S. Students Supervised/Co-supervised

Hussein Hejase, Department of Computer Science and Engineering, Michigan State University. Joined group as a Ph.D. student in fall 2014.  
Ph.D. awarded in December 2017.  
Ph.D. dissertation title: “Scalable Phylogenetic Analysis and Functional Interpretation of Genomes with Complex Evolutionary Histories.”  
Archived MSU website: <https://www.cse.msu.edu/~hijazihu/>.  
First position after graduation: Post-doctoral researcher in Dr. Adam Siepel’s research group at Cold Spring Harbor Laboratory.  
Current position: Scientist in Computational Sciences/Discovery Sciences R&D Team at Janssen Pharmaceutica (part of Johnson & Johnson).

Daria Tarasova, Department of Computer Science and Engineering, Michigan State University. Joined group as an M.S. student in fall 2018.  
M.S. awarded in May 2020.

## Undergraduate and High School Students Supervised/Co-supervised

Heather Noonan, Department of Computer Science and Engineering and Honors College, Michigan State University. Supported by MSU Professorial Assistantship (PA) program.

Andrew Haas, Department of Computer Science and Engineering, Michigan State University. Summer research internship through MSU EnSURE program.

Jason Nitkiewicz, Department of Computer Science and Engineering and Honors College, Michigan State University. Supported by MSU Professorial Assistantship (PA) program.

Anushka Murthy, Department of Biomedical Engineering, Columbia University. Summer research internship through MSU EnSURE program.

Ahmad Hejasebazzi, Department of Computer Science and Engineering, Michigan State University. Internship through MSU EnSURE program.

Rei Doko, Department of Computer Science and Engineering, Michigan State University. Summer research internship through MSU EnSURE program. Academic year research internship.

Cyprian Blunt, Department of Computer Science and Engineering, Michigan State University. Internship through MSU EnSURE program.

Jack Smith, Department of Computer Science and Engineering, Michigan State University. Internship through MSU EnSURE program.

Shulammit Lim, Olathe North High School (Olathe, KS, USA). Internship through MSU High School Honors Science Program.

David York, Department of Computer Science and Engineering, Michigan State University.

Keerthana Kolisetty, Department of Computer Science and Engineering and Honors College, Michigan State University. Supported by MSU Professorial Assistantship (PA) program.

Anushka Murthy, Okemos High School (Okemos, MI, USA) Honors Science Research Program. Currently pursuing a B.S. in Biomedical Engineering at Columbia University.

Yayu Zhou, Department of Mathematics/Department of Statistics, University of Illinois Urbana-Champaign. Internship through MSU EnSURE program.

Giang Nguyen, Department of Computer Science, Grinnell College. Internship through MSU EnSURE program.

Nicholas Hanson-Holtry, Department of Computer Science, Rice University.

Ethan Steinberg, Department of Computer Science, Rice University.

Alexander Yozzo, Department of Computer Science, Rice University.

Eileen Jingxuan Dai, Department of Computer Science, Rice University.

Kathy Truong, Department of Computer Science, Rice University.

Ugochukwu C. Anokwuru, Department of Natural Sciences, Chemistry Program, Huston-Tillotson University.

Mussie K. Araya, Department of Biomedical Engineering, The University of Texas at Austin.

Ian Wilbanks, Department of Computer Science, The University of Texas at Austin.

Cemre Mengü, Department of Computer Science, The University of Texas at Austin.