

Yufeng Wu

Professor

Computer Science and Engineering Department
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EDUCATION

Ph.D. in Computer Science, University of California, Davis, June 2007

Advisor: Professor Dan Gusfield

Master of Computer Science, University of Illinois at Urbana-Champaign, May 1998

M.S. in Mechanical Engineering, Southern Illinois University at Carbondale, June 1996

B.E. in Mechanical Engineering, and B.E. (minor) in Computer Science and Technology, Tsinghua University (P.R. China), July 1994

RESEARCH EXPERIENCE

Professor, Computer Science and Engineering Dept., University of Connecticut, 2021-now

Associate Professor (with tenure), Computer Science and Engineering Dept., University of Connecticut, 2013-2021

Assistant Professor, Computer Science and Engineering Dept., University of Connecticut, 2007-2013

Graduate Student Researcher, Dept. of Computer Science, UC Davis, 2004-2007

Research Assistant, Imaging System Lab, U. of Illinois at Urbana-Champaign, 1997-1998

Graduate Research Assistant, Southern Illinois Univ. at Carbondale, 1995-1996

INDUSTRY EXPERIENCE

Software Engineer, PrairieComm, Inc. (now part of Freescale Semiconductor, Inc.), Rolling Meadows, IL, 1998-2003

RESEARCH INTERESTS

I am broadly interested in computational biology and bioinformatics. I am especially interested in solving biologically motivated problems using algorithmic and computational approaches. My current work is focused on algorithmic problems in population genomics, phylogenetics and next-generation sequencing.

PUBLICATIONS

Journal Publications

1. Louxin Zhang, Niloufar Abhari, Caroline Colijn and *Yufeng Wu*, A fast and scalable method for inferring phylogenetic networks from trees by aligning lineage taxon strings, *Genome Research*, in press, 2023.

2. Yiming Zhang and *Yufeng Wu*, Joint Inference of Ancestry and Genotypes of Parents from a Small Number of Children, *iScience*, 25: 104768, 2022.
3. Xin Li and *Yufeng Wu*, Detecting genomic deletions from high-throughput sequence data with unsupervised learning, *BMC Bioinformatics*, 23: 568, 2022.
4. Jingwen Pei, Yiming Zhang, Rasmus Nielsen and *Yufeng Wu*, Inferring the ancestry of parents and grandparents from genetic data, *PLoS Computational Biology*, 16(8): e1008065, 2020.
5. MJ Inkman, K Jayachandran, TM Ellis, F Ruiz, MD McLellan, CA Miller, *Yufeng Wu*, Akinyemi I Ojesina, Julie K Schwarz and Jin Zhang, HPV-EM: an accurate HPV detection and genotyping EM algorithm. *Scientific reports*, 10 (1), 1-12, 2020.
6. *Yufeng Wu*, Inference of Population Admixture Network from Local Gene Genealogies: a Coalescent-based Maximum Likelihood Approach, *Bioinformatics* (supplement for ISMB 2020 conference), 36:i326-i334, 2020.
7. *Yufeng Wu*, Accurate and Efficient Cell Lineage Tree Inference from Noisy Single Cell Data: the Maximum Likelihood Perfect Phylogeny Approach, *Bioinformatics*, 36:742-750, 2020.
8. Xin Li and *Yufeng Wu*, Detecting circular RNA from high-throughput sequence data with de Bruijn graph, *BMC Genomics*, 21:193, 2020.
9. Zhongjia Wu, *Yufeng Wu* and Jingyang Gao, InvBFM: finding genomic inversions from high-throughput sequence data based on feature mining, *BMC Genomics*, 21:173, 2020.
10. Rute R da Fonseca, Alvarina Couto, Andre M Machado, Brona Brejova, Carolin B Albertin, Filipe Silva, Paul Gardner, Tobias Baril, Alex Hayward, Alexandre Campos, ngela M Ribeiro, Inigo Barrio-Hernandez, Henk-Jan Hoving, Ricardo Tafur-Jimenez, Chong Chu, Barbara Frazo, Bent Petersen, Fernando Pealoza, Francesco Musacchia, Graham C Alexander, Hugo Osrio, Inger Winkelmann, Oleg Simakov, Simon Rasmussen, M Ziaur Rahman, Davide Pisani, Jakob Vinther, Erich Jarvis, Guojie Zhang, Jan M Strugnell, L Filipe C Castro, Olivier Fedrigo, Mateus Patricio, Qiye Li, Sara Rocha, Agostinho Antunes, *Yufeng Wu*, Bin Ma, Remo Sanges, Tomas Vinar, Blagoy Blagoev, Thomas Sicheritz-Ponten, Rasmus Nielsen, M Thomas P Gilbert. A draft genome sequence of the elusive giant squid, *Architeuthis dux*, *GigaScience*, Volume 9, Issue 1, January 2020, giz152.
11. Lei Cai, *Yufeng Wu* and Jingyang Gao, DeepSV: Accurate calling of genomic deletions from high throughput sequencing data using deep convolutional neural network, *BMC Bioinformatics*, 20:665, 2019.
12. Chong Chu, Xin Li, and *Yufeng Wu*, GAPPadder: A Sensitive Approach for Closing Gaps on Draft Genomes with Short Sequence Reads, *BMC Genomics*, 20:426, 2019.
13. Rebekah L Rogers, Long Zhou, Chong Chu, Roberto Mrquez, Ammon Corl, Tyler Linderoth, Layla Freeborn, Matthew D MacManes, Zijun Xiong, Jiao Zheng, Chunxue Guo, Xu Xun, Marcus R Kronforst, Kyle Summers, *Yufeng Wu*, Huanming Yang,

- Corinne L Richards-Zawacki, Guojie Zhang and Rasmus Nielsen, Genomic takeover by transposable elements in the strawberry poison frog, *Molecular Biology and Evolution*, 35:2913-2927, 2018.
14. Xin Li, Chong Chu, Jingwen Pei, Ion Mandoiu and Yufeng Wu, CircMarker: a fast and accurate algorithm for circular RNA detection, *BMC Genomics*, 19:572, 2018.
 15. Jingwen Pei, Chong Chu, Xin Li, Bin Lu and Yufeng Wu, CLADES: A Classification-based Machine Learning Method for Species Delimitation from Population Genetic Data, *Molecular Ecology Resources*, 18 (5), 1144-1156, 2018.
 16. Jingwen Pei and Yufeng Wu, "STELLS2: Fast and Accurate Coalescent-based Maximum Likelihood Inference of Species Trees from Gene Tree Topologies", *Bioinformatics*, pages 1789–1797, 2017.
 17. Sajad Mirzaei and Yufeng Wu, RENT+: An Improved Method for Inferring Local Genealogical Trees from Haplotypes with Recombination, *Bioinformatics*, pages 1021–1030, 2017.
 18. Yufeng Wu, "An Algorithm for Computing the Gene Tree Probability under the Multispecies Coalescent and its Application in the Inference of Population Tree", *Bioinformatics* (supplement for ISMB 2016 conference), v. 32, p. i225-i233, 2016.
 19. Sajad Mirzaei and Yufeng Wu, "Fast Construction of Parsimonious Hybridization Networks for Multiple Phylogenetic Trees", v. 13 (3), *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 565-570, 2016.
 20. Chong Chu, Rasmus Nielsen and Yufeng Wu, "REPdenovo: Inferring De Novo Repeat Motifs from Short Sequence Reads", *PLoS One*, 11(3): e0150719, 2016.
 21. Chong Chu and Yufeng Wu, "SpliceJumper: a classification-based approach for calling splicing junctions from RNA-seq data", *BMC Bioinformatics*, 16 Suppl 17:S10, 2015.
 22. Yufeng Wu, "A Coalescent-based Method for Population Tree Inference with Haplotypes", *Bioinformatics*, v.31, p.691-698, 2015.
 23. Chong Chu, Jin Zhang and Yufeng Wu, "GINDEL: accurate genotype calling of insertions and deletions from low coverage population sequence reads", *PLoS One*, 9(11): e113324, 2014.
 24. Yufeng Wu, "An Algorithm for Constructing Parsimonious Hybridization Networks with Multiple Phylogenetic Trees", *Journal of Computational Biology*, 20(10): 792-804, 2013.
 25. Jin Zhang, Jiayin Wang and Yufeng Wu, "An Improved Approach for Accurate and Efficient Calling of Structural Variations with Low-coverage Sequence Data", *BMC Bioinformatics*, v.13 (supplement for RECONB-seq 2012), S6, 2012.
 26. Yufeng Wu, "Coalescent-based Species Tree Inference from Gene Tree Topologies Under Incomplete Lineage Sorting by Maximum Likelihood", *Evolution*, v. 66 (3), p. 763-775, 2012.

27. Jin Zhang and Yufeng Wu, "SVseq: an approach for detecting exact breakpoints of deletions with low-coverage sequence data", *Bioinformatics*, v.27 (23): p. 3228-3234, 2011.
28. Jorge Duitama, Justin Kennedy, Sanjiv Dinakar, Yozen Hernandez, Yufeng Wu and Ion I. Mandoiu, Linkage Disequilibrium Based Genotype Calling from Low-Coverage Shotgun Sequencing Reads, *BMC Bioinformatics*, v.12 (suppl. 1), S53, 2011.
29. Yufeng Wu, "New Methods for Inference of Local Tree Topologies with Recombinant SNP Sequences in Populations", *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, 8(1):182-193, 2011.
30. Yufeng Wu, "Exact Computation of Coalescent Likelihood for Panmictic and Subdivided Populations Under the Infinite Sites Model", *IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)*, special issue of ISBRA 2009, 7(4):611-618, 2010.
31. Yufeng Wu, "Close Lower and Upper Bounds for the Minimum Reticulate Network of Multiple Phylogenetic Trees", *Bioinformatics* (supplement for ISMB 2010), Vol. 26, No. 12, pp. 140-148, 2010.
32. Dan Gusfield and Yufeng Wu, "The Three-State Perfect Phylogeny Problem Reduces to 2-SAT", *Communications in Information and Systems*, Vol. 9, No. 4, pp. 295-302, 2009.
33. Yufeng Wu, "An Analytical Upper Bound on the Minimum Number of Recombinations in the History of SNP Sequences in Populations", *Information Processing Letters (IPL)*, Vol. 109, No. 9, pp. 427-431, 2009.
34. Yufeng Wu, "A practical method for exact computation of subtree prune and regraft distance", *Bioinformatics*, 25(2):190-196, 2009.
35. Yufeng Wu and Dan Gusfield, "A New Recombination Lower Bound and The Minimum Perfect Phylogenetic Forest Problem", *Journal of Combinatorial Optimization*, 16(3), pages 229-247, 2008.
36. Yufeng Wu, "Association Mapping of Complex Diseases with Ancestral Recombination Graphs: Models and Efficient Algorithms", *Journal of Computational Biology (JCB)*, pages 667-684, 2008.
37. Yufeng Wu and Dan Gusfield, "Efficient Computation of Minimum Recombination over Genotypes (not Haplotypes)", *Journal of Bioinformatics and Computational Biology*, 5(2a): pp. 181-200, 2007.
38. Yun S. Song, Zhihong Ding, Dan Gusfield, Charles Langley, and Yufeng Wu, "Algorithms to distinguish the role of gene-conversion from single-crossover recombination in the derivations of SNP sequences in populations", *Journal of Computational Biology (JCB)*, pages 231-245, 2007.
39. Yun S. Song, Yufeng Wu, and Dan Gusfield, "Efficient computation of close lower and upper bounds on the minimum number of needed recombinations in the evolution of

biological sequences”, *Bioinformatics*, 21:i413-i422, *Bioinformatics* Suppl. 1, Proceedings of the thirteenth International Conference on Intelligent Systems for Molecular Biology (*ISMB* 2005).

40. *Yufeng Wu*, Yiming Rong, Weidong Ma and S. R. LeClair, “Automated modular fixture planning: geometric analysis”, *Robotics and Computer-Integrated Manufacturing*, 14:1-15, 1998.
41. *Yufeng Wu*, Yiming Rong, Weidong Ma and S. R. LeClair, “Automated modular fixture planning: Accuracy, clamping, and accessibility analyses”, *Robotics and Computer-Integrated Manufacturing*, 14:17-26, 1998.
42. *Yufeng Wu*, Yiming Rong, and T. C. Chu, “Automated generation of dedicated fixture design”, *International Journal of Computer Applications in Technology*, 10:213-235, 1997.

Conference Publications

1. *Yufeng Wu* and Louxin Zhang, Bounding the Number of Reticulations in a Tree-Child Network That Displays a Set of Trees, in proceedings of RECOMB-CG 2023, to appear, 2023.
2. Lei Cai, *Yufeng Wu* and Gao Jingyang, scSNVIndel. accurate and efficient calling of SNVs and indels from single cell sequencing using integrated Bi-LSTM, in proceedings of IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2020), pages 173-179, 2020.
3. Xiaodong Zhang, Chong Chu, Yao Zhang, *Yufeng Wu*, and Gao Jingyang, Concod: Accurate Consensus-based Approach of Calling Deletions from High-throughput Sequencing Data, in proceedings of IEEE International Conference on Bioinformatics and Biomedicine (BIBM 2016), pages 72-77, 2016.
4. *Yufeng Wu*, “An Algorithm for Constructing Parsimonious Hybridization Networks with Multiple Phylogenetic Trees”, in proceedings of RECOMB 2013: 291-303, 2013.
5. Jiayin Wang, Jin Zhang and *Yufeng Wu*, “Identifying Interacting SNPs with Parallel Fish-Agent based Logic Regression”, in Proceedings of the First IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS 2011), Orlando, Florida, 2011.
6. Jin Zhang and *Yufeng Wu*, “Haplotype Inference from Short Sequence Reads Using a Population Genealogical History Model”, in Proceedings of Pacific Symposium on Biocomputing (*PSB* 2011), pages 288-299, 2011.
7. *Yufeng Wu*, “Bounds on the Minimum Mosaic of Population Sequences Under Recombination”, in Proceedings of CPM 2010, Lecture Notes in Computer Science, No. 6129, pp. 152-163, 2010.
8. *Yufeng Wu* and Jiayin Wang, “Fast Computation of the Exact Hybridization Number of Two Phylogenetic Trees”, in Proceedings of ISBRA 2010, Lecture Notes in Bioinformatics, no. 6053, pp. 203-214, 2010.

9. *Yufeng Wu*, “Exact Computation of Coalescent Likelihood Under the Infinite Sites Model”, in Proceedings of International Symposium on Bioinformatics Research and Applications (*ISBRA* 2009), pp. 209-220, May 13-16, 2009.
10. *Yufeng Wu* and Dan Gusfield, “Improved Algorithms for Inferring the Minimum Mosaic of a Set of Recombinants”, in Proceedings of Eighteenth Annual Symposium on Combinatorial Pattern Matching (*CPM* 2007), pages 150-161, 2007.
11. *Yufeng Wu* and Dan Gusfield, “A New Recombination Lower Bound and The Minimum Perfect Phylogenetic Forest Problem”, in Proceedings of the Thirteenth Annual International Computing and Combinatorics Conference (*COCOON* 2007), pages 16-26, 2007.
12. *Yufeng Wu*, “Association Mapping of Complex Diseases with Ancestral Recombination Graphs: Models and Efficient Algorithms”, in Proceedings of Eleventh Annual International Conference on Research in Computational Molecular Biology (*RECOMB* 2007), LNCS 4453, pages 488-502, 2007.
This paper wins the **best student paper award**.
13. *Yufeng Wu* and Dan Gusfield, “Efficient Computation of Minimum Recombination over Genotypes (not Haplotypes)”, in Proceedings of Life Sciences Society Computational Systems Biology (*CSB*) 2006, pages 145-156.
14. Yun S. Song, Zhihong Ding, Dan Gusfield, Charles Langley, and *Yufeng Wu*, “Algorithms to distinguish the role of gene-conversion from single-crossover recombination in the derivations of SNP sequences in populations”, in Proceedings of the Tenth Annual International Conference on Research in Computational Molecular Biology (*RECOMB* 2006), LNBI Vol. 3909, pages 231-245. Springer, 2006.
15. Yun S. Song, *Yufeng Wu*, and D. Gusfield, “Algorithms for imperfect phylogeny haplotyping (IPPH) with a single homoplasy or recombination event”, in Proceedings of Workshop on Algorithm of Bioinformatics (*WABI* 2005), LNCS 3692, pages 152-164.

RESEARCH FUNDING

Federal Grants

1. III: Small: Computational Methods for Ancestry Inference In Genetics, *PI*, National Science Foundation (IIS, Information Integration and Informatics), \$411,141, September 2019-August 2022.
2. AF: Small: Computational Methods for Large-scale Inference of Population History, *PI*, National Science Foundation (CCF, Algorithmic Foundation), \$405,000, September 2017-August 2022.
3. III: Small: Computational Methods for Analyzing Complex Genomes with Sequence Data, *PI*, National Science Foundation (IIS, Information Integration and Informatics), \$426,342, September 2015-August 2020.

4. AF: Small: Algorithms for Reconstructing Complex Evolutionary History with Discordant Phylogenetic Trees, *PI*, National Science Foundation (CCF, Algorithmic Foundation), \$256,796, July 2011-June 2015.
5. CAREER: Efficient and Accurate Computation for High Throughput Sequencing Related Problems in Population Genomics, *PI*, National Science Foundation (IIS, Information Integration and Informatics), \$512,406, July 2010-June 2017.
6. III: Small: Collaborative Research: Reconstruction of Haplotype Spectra from High-Throughput Sequencing Data, *co-PI* (PI: Ion Mandoiu), National Science Foundation (IIS, Information Integration and Informatics), \$275,257, September 2009-August 2013.
7. III-CXT-Medium: Collaborative Research: Inference of Complex Genealogical Histories in Populations: Algorithms and Applications, *PI*, National Science Foundation (IIS, Information Integration and Informatics), \$321,209, September 2008-August 2012.

Internal Grants from UCONN

1. The Mechanism of Phenotypic Drift in hES Cells, *co-PI*, UCHC/Storrs and Regional Campus Incentive Grants, \$7,500, January 2009-December 2009.
2. Algorithms and Applications of Inferring the Mosaic Patterns in Populations, *PI*, University of Connecticut Research Foundation Large Grant, \$15,000, January 2008-December 2009.

SELECTED TALKS

Computational Approaches for the Inference of Phylogenetic Network, American Mathematical Society Sectional Meeting (invited talk), October 24, 2021.

Accurate and Efficient Cell Lineage Tree Inference from Noisy Single Cell Data: the Maximum Likelihood Perfect Phylogeny Approach, ISMB 2019 (short talk), July 26, 2019.

Accurate and Efficient Cell Tree Inference and Genotype Calling from Noisy Single Cell Data: the Maximum Likelihood Perfect Phylogeny Approach, 8th International Conference on Computational Advances in Bio and Medical Sciences, Las Vegas, October 18, 2018.

Algorithms for Genetics: Population, Genealogy and Recombination, Colloquium at Dept. of Computer Science, Michigan State University, October 6, 2017.

Algorithms and Software tools for Two Problems in Computational Genomics: Inferring Gene Genealogy and Analyzing Genomic Repeats, Xi'an Jiaotong University, December 23, 2016.

Algorithms for Likelihood Computation on Coalescent Theory in Population Genetics, Colloquium at Dept. of Computer Science, Worcester Polytechnic Institute, September 8, 2016.

Algorithms and Applications for Computational Genomics, IBM T.J. Watson Lab, October 10, 2015.

Algorithms for constructing hybridization networks from multiple gene trees, (invited talk), Workshop on Phylogenetic Networks, National University of Singapore, July 2015.

Algorithms and Applications for Likelihood Computation Under Multispecies Coalescent, (invited talk). Coalescent Theory: New Development and Application, University of Montreal, October 6 to 12, 2013.

Efficient Computation of Gene Tree Probability based on Coalescent Theory under Incomplete Lineage Sorting, Highlight talk, ISMB 2013, July 21 to 24, 2013.

An improved approach for accurate and efficient calling of structural variations with low-coverage sequence data, Second Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq 2012). Talk given by Jin Zhang. Barcelona, Spain, April 19-20 2012.

Coalescent-based Species Tree Inference from Gene Tree Topologies Under Incomplete Lineage Sorting by Maximum Likelihood, Phylogenetics: New data, new Phylogenetic challenges, Isaac Newton Institute for Mathematical Sciences, Cambridge, UK, June 2011.

Bioinformatics of Complex Diseases: Models, Methods and New Technologies, Xi'an Jiaotong University, Xi'an, China, May 2011.

Finding Deletions with Exact Break Points from Noisy Low Coverage Paired-end Short Sequence Reads, First Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-seq 2011). Talk given by Jin Zhang. Vancouver, BC, Canada, March 2011.

Inferring Evolutionary History with Network Models in Population Genomics: Challenges and Progress, Structure Discovery in Biology: Motifs, Networks and Phylogenies, Dagstuhl Seminar, Dagstuhl, Germany, June 2010.

Exact Computation of Coalescent Likelihood under the Infinite Sites Model, DIMACS Workshop on Algorithmics in Human Population-Genomics, Rutgers University, Piscataway, NJ. April 2009.

Inference of Complex Genealogical Histories In Populations and Its Application in Mapping Complex Traits, DIMACS Workshop on Computational Issues in Genetic Epidemiology, Rutgers University, Piscataway, NJ. August 2008.

New Methods for Genealogical Network Inference based on Local Tree Topologies with a Set of SNP Sequences in Populations, Mathematics and Informatics in Evolution and Phylogeny conference, Hameau de l'Etoile, France. June 2008.

Algorithms for Association Mapping of Complex Diseases with Ancestral Recombination

Graphs, invited talk at the Third RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes (January 2007), University of Southern California, Los Angeles, CA, USA.

TEACHING

Capable of teaching various undergraduate or graduate courses in computer science, favoring but not limited to the following areas: algorithms in computational biology, seminar in population genomics, graduate algorithms, introduction to bioinformatics, introduction to algorithms and theory of computation, discrete mathematics, data structures, software engineering, C/C++/Java programming, and object-oriented programming.

Courses at University of Connecticut.

- Honor's core: BME/CSE/MCB 1401, Computational Molecular Biology (with Craig Nelson, Molecular and Cell Biology, UCONN). Fall 2009.
- CSE 2102, Introduction to Software Engineering. Spring 2008, fall 2008, spring 2009, fall 2010, spring 2012, spring 2013 and spring 2014.
- CSE 2500, Introduction to Discrete Systems (Honors sections). Fall 2021.
- CSE 3150, Essentials of C++. Spring 2020 and spring 2021.
- CSE 3500, Algorithm and Complexity. Spring 2010, spring 2011, fall 2011, fall 2012, fall 2013, fall and spring from 2016 to 2019.
- CSE 3502, Theory of Computation, fall 2019.
- BME/CSE 3800 and CSE 5800, Bioinformatics. Fall 2009 and fall 2017.
- CSE 4939W, CSE Design Projects. Spring 2010, spring 2011, spring 2019.
- CSE 5095, Research Topics in Bioinformatics, spring 2012.
- CSE 5095, Special Topics on "Introduction to Optimization", spring 2020.
- CSE 5095, Special Topics on "Randomization and Computation", fall 2021.
- CSE 5097, Bioinformatics and Algorithms Seminar, fall 2010 and fall 2011.
- CSE 5500, Algorithms, fall 2020.
- Algorithms for Bioinformatics, graduate special topics in computer science, fall 2007.

HONORS AND AWARDS

UTC Professor for Engineering Innovation, School of Engineering, University of Connecticut. 2020 to 2022.

National Science Foundation Faculty Early Career Development (CAREER) Award: 2010-2017.

Best student paper award, RECOMB 2007.

PROFESSIONAL ACTIVITIES

Member, Scientific Advisory Committee, Institute of System Genomics (ISG), University of Connecticut, 2019 to 2025.

Associate Editor, IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB), 2013 to now.

Finance co-Chair, IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS) 2012 to 2014.

Program Vice Chair (co-chairing the Evolution and Genomics Track), ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM BCB) 2011.

Poster co-Chair, International Symposium on Bioinformatics Research and Applications (2009-2010)

Member of program committee for the following conferences:

Annual International Conference on Research in Computational Molecular Biology (RECOMB): 2012.

International Conference on Intelligent Systems for Molecular Biology (ISMB): 2009-2012.

International Conference on Bioinformatics Models, Methods and Algorithms (BIOINFORMATICS): 2011

Annual Symposium on Combinatorial Pattern Matching (CPM): 2010

International Conference on Bioinformatics and Computational Biology (BICoB): 2009-now

International Symposium on Bioinformatics Research and Applications (ISBRA): 2008-now

IEEE International Conference on Bioinformatics and Biomedicine (BIBM): 2007-now

Workshop on Algorithms in Bioinformatics (WABI): 2018-2019

Asian Pacific Bioinformatics Conference (APBC): 2019.

Reviewers for the following journals:

IEEE/ACM Transaction on Computational Biology and Bioinformatics, SIAM Journal on Computing, Algorithmica, Journal of Discrete Algorithms, Information Processing Letters, Bioinformatics, PLoS Computational Biology, Algorithms for Molecular Biology, BMC Bioinformatics, Journal of Bioinformatics and Computation Biology. Journal of Mathematical Biology, Mathematical Bioscience, Systematic Biology, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, Genome Biology and Evolution, Methods in Ecology and Evolution, Evolution

Ad hoc reviewer, National Science Foundation, 2017, 2018, 2019.

Panelist, National Science Foundation, 2010, 2012, 2013, 2016, 2020.

Referee, Marsden Fund, Royal Society of New Zealand, 2016, 2020.

External PhD dissertation examiner, Dept of Computing, Hong Kong Polytechnic University, 2015.

Member of International Society for Computational Biology.

Member of Society for the Study of Evolution.

STUDENTS

All the following students are from U. of Connecticut (unless otherwise stated).

- Current PhD students as major advisor: Qingqi Lin, Haotian Zhang, and Yiming Zhang.
- Graduated PhD students as major advisor:
 - Jin Zhang (2012). First job: post doc at Washington University at St. Louis. Now: Assistant Professor, Medical School of Washington University at St. Louis.
 - Jiayin Wang (2013). First job: post doc at Washington University at St. Louis. Now: full Professor, Xi'an Jiaotong University, China.
 - Chong Chu (2017). First job: post doc at Harvard Medical School.
 - Sajad Mirzaei (2018). First job: Senior Software Engineer, Box Inc.
 - Jingwen Pei (2018). First job: Computational Biologist, Ancestry. **Distinction:** received the Taylor L. Booth Fellowship (highest honor for UCONN Computer Science and Engineering doctoral students) in 2018.
 - Xin Li (2020). First job: Senior Bioinformatics Analyst, Frederick National Laboratory for Cancer Research, National Cancer Institute.
- Graduated MS students as major advisor: Neil Malik (2022), Ruhua Jiang (2014), Bo Hou (2013), Hang He (2011), Xinyu Que (2009).
- Past undergraduate students: Brittany Nkounkou (received NSF Graduate Research Fellowship and pursued her PhD degree at Cornell U. starting in fall 2012), Nikulaj Volgushev, Greg Frank, Sean Curly, Dibash Chhetri, Yözen Hernández (Hunter College, New York City), Stephen Tetreault (Rhode Island College), Nicolas Woodfield, Chris Oldham (Honor's thesis, 2019), Joseph Warmus (Honor's thesis, 2020).