

Kevin J. Liu

Phone: 1-512-905-8246
Email: kevin.liu@rice.edu
Homepage: <http://www.cs.rice.edu/~k123>

P.O. Box 1892
MS-132
Houston, TX 77251-1892

Research Interests

Computational biology: computational phylogenetics (especially simultaneous alignment and phylogeny estimation), large-scale phylogenetic and alignment estimation at scales approaching the Tree of Life, multiple sequence alignment, population genetics, and functional implications of evolutionary patterns.

Algorithm design and empirical performance studies.

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

Research

Refereed Journal and Conference Publications

1. K. Liu and T. 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).
2. S. Nelesen, K. Liu, L. S. Wang, C. R. Linder, and T. Warnow, “DACTAL: divide-and-conquer trees (almost) without alignments,” Proceedings of Intelligent Systems for Molecular Biology (ISMB), accepted for publication, 2012. *Acceptance rate of 13%*.
3. S. Nelesen, K. Liu, L. S. Wang, C. R. Linder, and T. Warnow, “DACTAL: divide-and-conquer trees (almost) without alignments,” Bioinformatics, accepted for publication, 2012.
4. K. Liu, T. 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).
5. K. Liu, C. R. Linder, and T. 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).

6. K. Liu, C. R. Linder, and T. 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).
7. C. R. Linder, R. Suri, K. Liu, and T. 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).
8. K. Liu, S. Raghavan, S. Nelesen, C. R. Linder, T. 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*.
9. K. Liu, S. Nelesen, S. Raghavan, C. R. Linder, T. 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).
10. S. Nelesen, K. Liu, D. Zhao, C. R. Linder, T. Warnow, “The Effect of the Guide Tree on Multiple Sequence Alignments and Subsequent Phylogenetic Analyses,” *Pacific Symposium on Biocomputing*, vol. 13, pp. 15-24, 2008, doi: [10.1142/9789812776136_0004](https://doi.org/10.1142/9789812776136_0004).

Working Manuscripts

M. J. Braun, K. Liu, E. L. Braun, C. R. Linder, and T. Warnow, “The Impact of Diverse Sequence Alignment Methods on Estimates of the Avian Tree of Life,” in preparation.

Scientific Software

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. Warnow, 2011.

SATé-II, a method for very fast and accurate simultaneous estimation of alignments and trees, with T. Warnow, M. T. Holder, S. Nelesen, J. Yu, A. Stamatakis, and C. R. Linder, 2011.

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. Warnow, 2009.

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

Presentations

“Fast and Accurate Co-estimation of Large-scale Phylogenetic Alignments and Trees.” Massachusetts Institute of Technology Computer Science and Artificial Intelligence Laboratory, Boston, MA, 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, 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, July 22, 2009.

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

Academic Experience

Rice University

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, Spring 2012–present.

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

Student programmer, Project LISTEN, School of Computer Science, website at <http://www.cs.cmu.edu/~listen/>, 1997–1998.

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

University Service

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.

Refereeing

Molecular Biology and Evolution

RECOMB

SODA

Honors & Awards

Fellowships

National Library of Medicine (NLM) Keck Postdoctoral Fellowship, 2012.

Microelectronics and Computer Development Doctoral Fellowship, 2004–2005.

NSF Graduate Fellowship Honorable Mention, 2005.

Awards

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.

References

Available upon request.