

# CURRICULUM VITAE

TANDY WARNOW  
DAVID BRUTON, JR. CENTENNIAL PROFESSOR IN COMPUTER  
SCIENCE

---

## CONTACT INFORMATION

*Taylor Hall 2.124, Department of Computer Sciences  
The University of Texas at Austin  
Austin, TX 78712-1188 USA*  
Phone: (Office) 512-471-9724 (Fax) 512-471-8885  
Email: [tandy@cs.utexas.edu](mailto:tandy@cs.utexas.edu)  
Homepage: <http://www.cs.utexas.edu/users/tandy/>

---

## RESEARCH INTERESTS

Phylogenetic tree inference in biology and historical linguistics, combinatorial and graph-theoretic algorithms, statistical inference, and experimental performance studies of algorithms.

---

## PROFESSIONAL APPOINTMENTS

- Departmental Scholar, Institute for Pure and Applied Mathematics, UCLA, Fall 2011
- Visiting Researcher, University of Maryland, Spring and Summer 2011.
- Special Volunteer, NIH, Spring and Summer 2011.
- Visiting Researcher, Smithsonian Institute, Spring and Summer 2011.
- Professeur Invité, Ecole Polytechnique Fédérale de Lausanne (EPFL), Summer 2010.
- Visiting Researcher, Microsoft New England, Fall 2010.
- Visiting Scholar, UC Berkeley, Summer 2009; co-taught (with Johanna Nichols and Donald Ringe) the course *Computational Methods in Linguistic Reconstruction* at the 2009 Linguistic Institute held at Berkeley.
- Visiting Scholar, Program for Evolutionary Dynamics at Harvard University, 2004-2005.
- Radcliffe Institute for Advanced Studies, Emeline Bigelow Conland Fellow, 2003-2004.
- Visiting Scholar, University of California at Berkeley, 2002-2004.
- University of Texas at Austin, 9/1999 - present.
  - Co-Director, Center for Computational Biology and Bioinformatics, 2001-2003

- Professor, Department of Computer Science, University of Texas at Austin (effective 9/1/2003). Assoc. Professor 9/1999-9/2003.
- Member, Texas Institute for Computational and Applied Mathematics, and the Institute for Cellular and Molecular Biology.
- Member, Graduate Programs in Computer Sciences, Molecular Biology, Computational and Applied Mathematics, and the Program in Ecology, Evolution, and Behavior.
- University of Pennsylvania, 9/1993-8/1999.
  - Associate Professor (tenured January 1998), Department of Computer and Information Sciences.
  - Member, Institute for Research in Cognitive Sciences.
  - Co-PI, Graduate and Postdoctoral Research Training Program (RTG) in Computational Biology. (PI: Warren Ewens).
- University of Arizona, 9/1998-8/1999, Visiting Professor, Departments of Computer Science and Ecology and Evolutionary Biology.
- Yale University, 1997-1998, Visiting Researcher, Department of Computer Science.
- Princeton University, 1997-1998, Visiting Professor, Departments of Mathematics and Computer Sciences.
- DIMACS, 1996, visitor.

---

## EDUCATION

- Postdoctoral Fellowship (1991-1992), University of Southern California, with Michael Waterman and Simon Tavaré.
- Ph.D. Mathematics (1991), University of California, Berkeley.  
 Dissertation: *Combinatorial Algorithms for Constructing Phylogenetic Trees*.  
 Committee: Eugene Lawler (advisor), Manuel Blum, David Gale, Dan Gusfield, and Richard Karp.
- B.A. Mathematics (1984), *magna cum lauda*, University of California, Berkeley.

---

## HONORS

- John Simon Guggenheim Foundation Fellowship, 2011, *New problems in evolutionary estimation*.
- David Bruton, Jr. Centennial Professorship in Computer Science, 2010 - present
- Radcliffe Institute for Advanced Study, Emeline Bigelow Conland Fellow, 2003-2004.
- David and Lucile Packard Foundation Fellowship, 1996-2001, *Algorithms for reconstructing evolutionary trees in biology and linguistics*.
- NSF National Young Investigator Award, 1994-99. *Combinatorial Problems in Evolutionary Tree Construction*.

---

## CURRENT AND FORMER DOCTORAL STUDENTS

Current:

- Nam Nguyen (4th year PhD)
- Siavash Mirarab (2nd year PhD)
- Andrei Margea (2nd year PhD)
- Shamsuzzoha Bayzid (2nd year PhD)

Former:

- Ganesh Ganapathy (PhD August 2006), now postdoctoral researcher for Erich Jarvis, Duke University.
- Kevin Liu (PhD May 2011), now postdoctoral fellow in the Department of Computer Science at Rice University.
- Luay Nakhleh (PhD May 2004), now Associate Professor of Computer Science at Rice University.
- Serita Nelesen (PhD December 2009), now Assistant Professor of Computer Science at Calvin College.
- Usman Roshan (PhD May 2004), now Associate Professor of Computer Science at NJIT.
- Michelle Swenson (PhD May 2009), now postdoctoral researcher in the Mathematics Department of the Georgia Institute of Technology).
- Li-San Wang (PhD May 2003), now Assistant Professor of Medicine at the University of Pennsylvania.
- Shibu Yooseph (PhD received 2000), now Director of Informatics at the J. Craig Venter Institute.

---

## POSTDOCTORAL ADVISEES

- Kevin Atteson (now freelance software),
- François Barbançon (now at Palantir Technologies, Palo Alto, CA)
- Dannie Durand (now Assoc. Professor of Biology and of Computer Science, Carnegie Mellon University),
- Daniel Huson (now C4 Professor of Bioinformatics, Tübingen University, Germany),
- Ken Rice (now retired),
- Katherine St. John (now Professor of Mathematics and Computer Science, Lehman College, CUNY),
- Elizabeth Sweedyk (now Assoc. Professor of Computer Science, Harvey Mudd College).
- Shel Swenson (now postdoctoral researcher in Mathematics at Georgia Institute of Technology, starting January 2011).

---

## GRANT SUPPORT

- NSF DEB 0733029 (ATOL): Collaborative Research: Large-Scale Simultaneous Multiple Alignment and Phylogeny Estimation. Overall PI: Warnow, 2007-2012. Collaborative grant with the University of Georgia, The University of Nebraska, and the University of Kansas. Total amount: \$1.7 Million for the entire project. (Current)
- NSF DBI-1062335. Collaborative Research: Novel Methodologies for Genome-scale Evolutionary Analysis of Multi-locus data. PI. \$349,999. Collaborative grant with Rice University and Stanford University. (Current)
- NSF ITR 0331453 (Large): Building the Tree of Life – A National Resource for Phyloinformatics and Computational Phylogenetics. Overall PI: Warnow, 2003-2008 (extended to 2010). Collaborative with four other institutions (UCSD, UNM, Florida State University, and UC Berkeley). Total amount: \$11.6 Million for the entire project. Final report in abridged form available at <http://www.cs.utexas.edu/users/tandy/CIPRES-FINAL.pdf>.
- NSF ITR BCS 0312830 (small): Collaborative Research, Algorithms for Inferring Reticulate Evolution in Historical Linguistics. Overall PI: Warnow, (with Donald Ringe, at the University of Pennsylvania), 2003-2006 (extended to 2009). Total amount: \$344,517.
- NSF ITR/AP 0121680 (medium): Collaborative Research, Reconstructing Complex Evolutionary Histories. Overall PI: Warnow, 2001-2006 (extended to 2009); collaborative with the University of New Mexico. Total amount: \$1,707,458.
- NSF IGERT DGE 0114387: IGERT: Computational Phylogenetics and Applications to Biology. PI: David Hillis, Co-PIs Warnow, Jansen, and Gutell, 2001-2006 (extended to 2008). Total amount: \$2,741,575.
- NSF DEB 0120709: Comparative Chloroplast Genomics: Integrating Computational Methods, Molecular Evolution, and Phylogeny. PI: Robert Jansen, Co-PIs Warnow and Raubeson, 2001-2006. Total amount: \$1,350,000.
- NSF ITR/AP 0121682 (medium): Exploring the Tree of Life, PI: Tandy Warnow, 2001-2004 (extended to 2005). Total amount: \$785,780.
- NSF ITR/AP DEB 011354: Collaborative Research, Computing Optimal Phylogenetic Trees Under Genome Rearrangement Metrics. PI: Robert Jansen, 2001-2004. Participant: Warnow. Total amount: \$288,030.
- NSF 9985991: CISE Research Instrumentation. PI: Doug Burger. Co-PIs: Tandy Warnow, Harrick Vin, Steve Keckler, and Inderjit Dhillon, 2000-2003. Total amount: \$139,481.
- NSF 9512092 (Linguistics): Character-based Methods for Reconstructing the Evolutionary History of Natural Languages. PI: Tandy Warnow. Co-PI's: Donald Ringe and Ann Taylor. 1995-1998. Total amount: \$161,000.
- NSF 9413215 (Research Training, Computational Biology): Statistical and Computational Methods for Data Management and Analysis in Molecular Genetics. PI: Warren Ewens. Co-PI: Tandy Warnow, David Roos, and David Searls. 1994-1999. Total amount: \$1,592,579.
- NSF 9457800 (Theory of Computing): NSF Young Investigator: Computational Problems in Evolutionary Tree Reconstruction, 1994-2000. Total amount: \$275,000.

---

## NATIONAL AND INTERNATIONAL SERVICE

- Chair, NIH BDMA Study Section, 2010-present.
- PLoS Currents: Tree of Life, Board of Reviewers, 2010-present.
- Faculty Recruiting Committee, ETH-Zurich, 2010-2011.
- Advisory Board, IEEE/ACM Transactions on Computational Biology and Bioinformatics, 2006-2009.
- Advisory Board, Springer, Computational Biology Book Series, 2005 - present.
- Participant, Institutes of Medicine Workshop on Interdisciplinary Programs and Academic Health Centers on Tuesday, September 26th, 2006.
- Member, Board of Directors, the International Society for Computational Biology (ISCB), 2001-2004.
- Committee member, National Academy of Sciences Committee on Interdisciplinarity (2003-2004).
- Program committee co-chair, National Academy of Sciences (USA), Japanese-American Frontiers of Science (2003).
- Committee member, National Academy of Sciences, Committee for Biological Cyberinfrastructure (BIOACCI). (2003).
- Committee member, National Research Council Committee on Interdisciplinarity. (2003).
- Program committee, National Academy of Sciences (USA), Japanese-American Frontiers of Science (2002).
- Panelist, Howard Hughes Medical Institute, Postdoctoral Fellowships in Biological Sciences, 2003.
- Program committee co-chair: Workshop on Algorithms for Bioinformatics (WABI) 2009; Evolution and Phylogeny, Intelligent Systems for Molecular Biology (ISMB) 2006, 2007, and 2008; COCOON 2003; and ACM-SIAM Symposium on Discrete Algorithms (SODA), 1999.
- Program committee member: ALENEX 2005; COCOON 1998 and 2003; EACL 2012 Joint Workshop of LINGVIS (Visualization of Linguistic Patterns) and UNCLH (Uncovering Language History from Multilingual Resources); FUN 2001; ICALP 2005; ISMB 2006, 2007, 2008, 2009, and 2012; JOBIM 2000; SODA 2001; STOC 1998; FOCS 1996; RECOMB 1997, 2001, 2002, 2004, 2009, 2010, and 2011; WABI 2001, 2002 2004, 2005, 2006, 2009, and 2010; and WADS 2001.
- Editorial board member: The Journal of Graph Algorithms and Applications (Also, The ACM Journal of Experimental Algorithms, to 2004.)
- NSF Panelist, 1995, 1996, 2000, 2001, 2002, 2003, and 2007.
- Proposal reviewer for NSERC, 1999-2006.
- Reviewer for faculty candidates at the Royal Institute of Technology in Stockholm, Sweden, 1999.
- Reviewer for faculty candidates at ETH, Zurich, Switzerland, 2010.

---

## LECTURES

### Distinguished Lectures and Plenary Talks

- Plenary talk, Deep Green. June 2, 2000, University of Maryland, College Park, MD.
- Distinguished Lecture. Department of Computer Science, University of British Columbia, January 2001.
- SCOPH (Showcase on Competing Technologies for Phylogenetics: A RECOMB Phylogenetics Conference, April 2001, Montreal Canada.
- Plenary talk at the Annual Meeting of the Canadian Applied and Industrial Mathematics Society (CAIMS), June, 2001, Victoria, British Columbia Canada.
- CRA Distinguished lecture, EECS Joint Colloquium, University of California at Berkeley, October, 2001, Berkeley, CA.
- University of Toronto, Department of Computer Science. Distinguished Lecture. April 2002.
- University of Illinois at Chicago, Department of Computer Sciences, distinguished lecture, 2003.
- Annual meeting, Mathematics Association of America (2003), Invited Lecture.
- SMBE (Society for Molecular Biology and Evolution) invited lecture, 2003.
- Radcliffe Institute of Advanced Studies, Conference on Computational Biology: Function, Pathways, Phylogenies and Populations. May 19, 2003
- Invited talk, Mathfest 2003 (annual meeting of the Mathematics Association of America), Boulder, Colorado, July 31, 2003.
- Grace Hopper 2004, invited speaker.
- The McDonald Institute for Archaeological Research at Cambridge University, Summer 2004.
- Virginia Tech (East Coast Indo-European Conference), May 26, 2004
- Symposium on Stochastic Processes and Applications, Plenary talk, June 27, 2005).
- Plenary talk, Workshop on Graph Algorithms (WG'06), Bergen, Norway, June 2006.
- Mathematics Department, Distinguished Lecture, The University of South Carolina, March 28, 2006.
- Symposium on Languages and Genes, The University of California at Santa Barbara, Sept. 2006.
- The Sir Isaac Newton Institute for Mathematical Sciences, September 4, 2007.
- Department of Computer Sciences, University of Nebraska, Distinguished Lecture, Oct. 30, 2007.
- College of Computing, Georgia Inst. of Technology, Distinguished Lecture, Nov. 1, 2007.
- Department of Computer Science, UC Davis, Distinguished Lecture, Nov. 15, 2007.
- Department of EECS, UC Berkeley, Distinguished Lecture, Feb. 6, 2008.
- School of Informatics, Indiana University, April 11, 2008.
- Department of Computer Sciences, Northwestern University, May 2, 2008.

- School of Computer and Communication Sciences at EPFL, June 12, 2008.
- European Conference on Complex Systems Science (ECCS08), Sept 11-17, 2008.
- Harvard Symposium on The Science of The Human Past, Dec 5, 2008.
- European Conference on Complex Systems Science (ECCS08), Sept 11-17, 2008.
- Swadesh Centenary Conference, Leipzig, Germany. January, 2009.
- Brown University, December 2010.
- Heilbronn Annual Conference, University of Bristol, England, September 2011.

### **Other Invited Talks**

- Berkeley Statistics, September 2001.
- Department of Biology, Stanford University, March 2002.
- The California Academy of Sciences, March 2002.
- National Research Council, May 2003.
- Society for Molecular Biology and Evolution (SMBE) 2003.
- Harvard Computer Science, October 2003.
- Cornell Biology, 2003.
- Annual Meeting, Evolution 2003.
- Harvard Organismic and Evolutionary Biology, April 2004.
- Tutorial on computational aspects of phylogenetics, Computational and Systems Biology (CSB) 2004, Stanford University.
- Northeastern University Computer Science, March 7, 2005.
- Harvard University, Linguistics Department, March 21, 2005.
- MIT Computer Science, April 8, 2005.
- Applied Mathematics Colloquium, MIT, April 11, 2005.
- Probability/Statistics Seminar, Heriot-Watt University, Edinburgh, April 18, 2005.
- Linguistics Circle, Edinburgh University, Edinburgh, April 19, 2005.
- Glasgow University, Biology Department, Glasgow, Scotland, April 20, 2005.
- UCLA, Biomathematics, August 2005.
- UCSB, Computer Sciences, August 2005.
- Symposium on compatibility methods, Fifth Biennial Conference of the Systematics Association, Cardiff, Wales, August 2005.
- Mathematical Biosciences Institute (MBI), Phylogeography and Phylogenetics, September 27, 2005.

- 52nd Annual Systematics Symposium at the Missouri Botanical Gardens, October 9, 2005.
- Cornell University, Computer Science Department, February 2006.
- Indiana University, Biology Department, March 2006.
- Indiana University, Department of Mathematics, March 2006.
- Statistical Genetics, North Carolina State University, April 2006.
- Keck Foundation, May 2006.
- National Academy of Sciences, October 2006.
- Edinburgh University, September 2007.
- Manchester University, December 2007.
- Paris X, December 2007.
- EECS Colloquium, UC Berkeley, Feb. 2008.
- MIEP (Mathematics and Informatics in Evolution and Phylogeny), June 2008.
- University of Southern California, November 2008.
- Workshop on Molecular Evolution and Phylogenetics, SAMSI, April 2009.
- Yale University Computer Science Colloquium, Jan 2010.
- Princeton University, Computer Science Colloquium, Feb 2010.
- NESCENT (National Evolutionary Synthesis Center), Feb 2010.
- CMU-UPitt, Computational Biology Seminar, Feb 2010.
- University of Illinois at Chicago, April 2010.
- University of Chicago, April 2010.
- RECOMB Bioinformatics Education Conference, May 2010.
- Illinois Language and Linguistics Society conference (ILLS 2), May 2010.
- iEvolBio conference, Evolution Meeting, June 2010.
- Microsoft Research, November 2010.
- Johns Hopkins University, Department of Computer Science, November 2010.
- Dartmouth College, Department of Computer Science, November 2010.
- North Carolina State University, Department of Mathematics, December 2010.
- Microsoft Research, Computational Aspects of Biological Information, December 2010.
- Washington Area Phylogenetics Consortium PHYLO-PIZZA, December 2010.
- University of Maryland, April 2011
- UC Berkeley, Lens on the Sciences, May 2011
- Princeton University, Ecology and Evolutionary Biology, May 2011
- Newton Institute, University of Cambridge, June 2011

**Publications** (see <http://www.cs.utexas.edu/users/tandy/papers.html>)

1. Kannan, S. and T. Warnow, 1992. "Triangulating Three-Colored Graphs," *SIAM J. on Discrete Mathematics*, Vol. 5 No. 2, pp. 249-258. (A preliminary version appeared in the Proceedings of the ACM/SIAM Symposium on Discrete Algorithms, 1991.)
2. Bodlaender, H., M. R. Fellows, and T. J. Warnow, "Two Strikes Against Perfect Phylogeny", Proc. 19th Int'l Colloq. on Automata, Languages, and Programming ICALP92", Springer Verlag", "273-283", 1992, in *LNCS 623*.
3. Steel, M. and T. Warnow, 1993. "Kaikoura Tree Theorems: The Maximum Agreement Subtree Problem." *Information Processing Letters*, 48, pp. 77-82.
4. Warnow, T. 1993. "Constructing phylogenetic trees efficiently using compatibility criteria." *New Zealand Journal of Botany*, Vol. 31, pp. 239-248.
5. Kannan, S. and T. Warnow, 1994. "Inferring Evolutionary History from DNA Sequences." *SIAM J. on Computing*, Vol. 23, No. 4, pp. 713-737. (A preliminary version of this paper appeared at FOCS 1990.)
6. Warnow, T. 1994. "Tree Compatibility and Inferring Evolutionary History." *Journal of Algorithms*, 16, pp. 388-407. (A preliminary version of this paper appeared at SODA 1993.)
7. McMorris, F. R., T. Warnow, and T. Wimer, 1994. "Triangulating Vertex Colored Graphs." *SIAM J. on Discrete Mathematics*, Vol. 7, No. 2, pp. 296-306. (A preliminary version of this paper appeared at SODA 1993.)
8. Farach, M., S. Kannan, and T. Warnow, 1995. "A Robust Model for Finding Optimal Evolutionary Trees." *Algorithmica*, special issue on Computational Biology, Vol. 13, No. 1, pp. 155-179. (A preliminary version of this paper appeared at STOC 1993.)
9. Kannan, S., and T. Warnow, 1995. "Tree Reconstruction from Partial Orders." *SIAM J. on Computing*, Vol. 24 No. 3, pp. 511-520. (A preliminary version of this paper appeared at WADS.)
10. Kannan, S., T. Warnow, and S. Yooseph, 1995. "Computing the local consensus of trees." *SIAM J. Computing*, Vol. 27, No. 6, pp. 1695-1724. (A preliminary version appeared in the Association for Computing Machinery and the Society of Industrial Applied Mathematics, Proceedings, ACM/SIAM Symposium on Discrete Algorithms, 1995, pp. 68-77.)
11. Taylor, A., D. Ringe, and T. Warnow. 1995. "Character-based reconstruction of a linguistic cladogram." Proceedings of the 12th International Conference on Historical Linguistics (Manchester, August 1995).
12. Warnow, T., D. Ringe, and A. Taylor. 1996. "Reconstructing the evolutionary history of natural languages." Proceedings of ACM-SIAM Symposium on Discrete Algorithms (SODA), 1996, pp. 314-322.
13. Phillips, C. A., and T. Warnow, 1996. "The Asymmetric Median Tree: a new model for building consensus trees." *Discrete Applied Mathematics*, Special Issue on Computational Molecular Biology, 71, pp. 311-335.
14. Goldberg, L. A., P.W. Goldberg, C.A. Phillips, E. Sweedyk, and T. Warnow, 1996. "Minimizing phylogenetic number to find good evolutionary trees." *Discrete Applied Mathematics*, Volume 71, Numbers 1-3, pp. 111-136. (A preliminary version of this paper appeared in *Combinatorial Pattern Matching* 1995)

15. Benham, C., S. Kannan, M. Paterson, and T. Warnow, 1996. "Hen's Teeth and Whale's Feet: Generalized Character Compatibility." *Journal of Computational Biology*. Vol 2. No 4. pp 527-536. (A preliminary version of this appeared in *Combinatorial Pattern Matching*, 1995.)
16. Kannan, S., E. Lawler, and T. Warnow, 1996. "Determining the Evolutionary Tree." *Journal of Algorithms*, 21(1): 26-50. (A preliminary version of this paper appeared at SODA 1990.)
17. Ringe, D., T. Warnow, A. Taylor, A. Michailov, and L. Levison, 1997. "Computational cladistics and the position of Tocharian." In V. Mair (Ed.), *The Bronze Age and Early Iron Age Peoples of Eastern Central Asia*, a special volume of the *Journal of Indoeuropean Studies*.
18. Erdős, P. L., M. Steel, L. Székely, and T. Warnow, 1997. "Local quartet splits of a binary tree infer all quartet splits via one dyadic inference rule." *Computers and Artificial Intelligence*, Number 2, Vol 16, pp. 217-227.
19. Warnow, T. 1997. "Mathematical approaches to comparative linguistics." *Proceedings of the National Academy of Sciences*, Vol. 94, pp. 6585-6590, 1997.
20. Kannan, S. and T. Warnow, 1997. "A fast algorithm for the computation and enumeration of perfect phylogenies when the number of character states is fixed." *SIAM J. Computing*, Vol. 26, No. 6, pp. 1749-1763. (A preliminary version appeared in the proceedings of the ACM/SIAM Symposium on Discrete Algorithms, 1995.)
21. Rice, K. and T. Warnow. 1997. "Parsimony is Hard to Beat!" *Proceedings, Third Annual International Conference of Computing and Combinatorics (COCOON)*, Shanghai, China, 1997, pp. 124-133. T. Jiang and D.T. Lee, Eds.
22. Erdős, P. L., M. Steel, L. Szekeley, and T. Warnow, 1997. Inferring big trees from short sequences. Springer-Verlag Lecture Notes in Computer Science, 1256, P. Degano, R. Gorrieri, A. Marchetti-Spaccamela (Eds.), *Proceedings of the 24th International Congress on Automata, Languages, and Programming (ICALP)*, Bologna, Italy, pp. 827-837.
23. Huson, D., S. Nettles, L. Parida, T. Warnow, and S. Yooseph. 1998. "A Divide-and-Conquer Approach to Tree Reconstruction." *Algorithms and Experiments (ALEX) 1998*. Trento, Italy.
24. Bonet, M., M. Steel, T. Warnow, and S. Yooseph. 1998. "Faster algorithms for solving parsimony and compatibility." *The Journal of Computational Biology*, Vol. 5, No. 3, pp. 409-422. By invitation, for the special issue on selected papers from RECOMB 1998.
25. Huson, D., K. A. Smith and T. Warnow. 1999. "Correcting Large Distances for Phylogenetic Reconstruction." *Proceedings, 3rd Workshop on Algorithms Engineering (WAE)*, London, England, 1999, pp. 273-286.
26. Warnow, T.. 1999. "Some combinatorial problems in phylogenetics." Invited paper, *Proceedings of the International Colloquium on Combinatorics and Graph Theory*, Balatonlelle, Hungary, July 15-20, 1996, eds. A. Gyárfás, L. Lovász, L.A. Székely, Volume 7 of *Bolyai Society Mathematical Studies*, Budapest, pp. 363-413.
27. Erdős, P. L., M. Steel, L. Székely, and T. Warnow. 1999. "A few logs suffice to build almost all trees - I." *Random Structures and Algorithms*, 14, 153-184. (Also appears as DIMACS Technical Report 97-71.)
28. Erdős, P. L., M. Steel, L. Székely, and T. Warnow. 1999. "A few logs suffice to build almost all trees - II." *Theoretical Computer Science*, 221 (1-2) (1999) pp. 77-118, by invitation, in the issue of selected papers from ICALP 1997. (Also appears as DIMACS Technical Report 97-72.)

29. Bonet, M., C.A. Phillips, T. Warnow, and S. Yooseph, 1999. "Constructing evolutionary trees in the presence of polymorphic characters." *SIAM J. Computing*, Vol. 29. No. 1, pp. 103-131. (A preliminary version appeared in the ACM Symposium on the Theory of Computing, 1996.)
30. Henzinger, M., V. King, and T. Warnow. 1999. "Constructing a tree from homeomorphic subtrees, with applications to computational molecular biology." *Algorithmica*, 24(1): 1-13 (1999). (A preliminary version appeared in the Association for Computing Machinery and the Society of Industrial and Applied Mathematics, Proceedings, ACM/SIAM Symposium on Discrete Algorithms, 1996, pp. 333-340.)
31. Huson, D., S. Nettles, and T. Warnow. 1999. "Disk-Covering, a fast converging method for phylogenetic tree reconstruction." Special issue of the *Journal of Computational Biology* for selected papers from RECOMB 1999, Vol. 6, No. 3, 1999, pp. 369-386. (This appeared in a preliminary form in the Proceedings of RECOMB 1999, as "Obtaining highly accurate topology estimates of evolutionary trees from very short sequences." Lyon, France.)
32. Huson, D., S. Nettles, K. Rice, T. Warnow, and S. Yooseph. 1999. "The Hybrid tree reconstruction method." *The Journal of Experimental Algorithmics*, Volume 4, Article 5, 1999. Special issue for selected papers from The Workshop on Algorithms Engineering, Saarbrücken, Germany, 1998. <http://www.jea.acm.org/1999/HusonHybrid/>.
33. Huson, D., L. Vawter, and T. Warnow. 1999. "Solving large scale phylogenetic problems using DCM-2." Proceedings of ISMB (Intelligent Systems for Molecular Biology), (ISMB), Heidelberg 1999, pp. 118-129.
34. Kim, J. and T. Warnow, 1999. "Tutorial on Phylogenetic Tree Estimation." *Intelligent Systems for Molecular Biology, Heidelberg 1999*. See: <http://ismb99.gmd.de/TUTORIALS/Kim/4KimTutorial.ps>.
35. Cosner, M.E., R.K. Jansen, B.M.E. Moret, L.A. Raubeson, L.-S. Wang, T. Warnow, and S. Wyman, 2000. "A new fast heuristic for computing the breakpoint phylogeny and experimental phylogenetic analyses of real and synthetic data," Proc. 8th Int'l Conf. on Intelligent Systems for Molecular Biology (ISMB 2000), San Diego (2000), pp. 104-115.
36. Cosner, M.E., R.K. Jansen, B.M.E. Moret, L.A. Raubeson, L.-S. Wang, T. Warnow, T., and S. Wyman, 2000. "An empirical comparison of phylogenetic methods on chloroplast gene order data in Campanulaceae," in *Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment, and the Evolution of Gene Families*, D. Sankoff and J. Nadeau, eds., Kluwer Academic Publishers, Dordrecht, 2000, pp. 99-121.
37. Bodlaender, H. L., M.R. Fellows, M. T. Hallett, H. T. Wareham, and T. Warnow, 2000. "The hardness of perfect phylogeny, feasible register assignment and other problems on thin colored graphs", *Theoretical Computer Science* 244 (2000), pp. 167-188.
38. St. John, K., T. Warnow, B.M.E. Moret, and L. Vawter, 2001. "Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining," Proc. 12th Ann. Symp. Discrete Algs. (SODA 01), Washington DC, SIAM Press (2001), pp. 196-205.
39. Ganapathy, G. and T. Warnow, 2001. "Finding the Maximum Compatible Tree for a Bounded Number of Trees with Bounded Degree is Solvable in Polynomial Time." In Proceedings of the First International Workshop on Algorithms and Bioinformatics (WABI), 2001, pp. 156-163, Springer Verlag, Olivier Gascuel and Bernard M.E. Moret, eds.

40. Warnow, T., B.M.E. Moret, and K. St. John, 2001. "Absolute convergence: true trees from short sequences," Proc. 12th Ann. Symp. Discrete Algs. (SODA 01), Washington DC, SIAM Press (2001), pp. 186-195.
41. Wang, L.-S. and T. Warnow, 2001. "Estimating true evolutionary distances between genomes." Proceedings, Symposium on the Theory of Computing (STOC), 2001, pp. 637-646.
42. Moret, B.M.E., S. Wyman, D.A. Bader, T. Warnow, and M. Yan, 2001. "A new implementation and detailed study of breakpoint analysis," Proc. 6th Pacific Symp. on Biocomputing (PSB 2001), Hawaii, World Scientific Pub. (2001), pp. 583-594.
43. Moret, B.M.E., L.-S. Wang, T. Warnow, and S. Wyman, 2001. "New approaches for reconstructing phylogenies based on gene order," 9th Int'l Conf. on Intelligent Systems for Molecular Biology (ISMB 2001), Copenhagen, in Bioinformatics 17, Suppl. 1, (2001), pp. S165-S173; chosen as one of the 5 best papers at the conference.
44. Nakhleh, L., K. St. John, U. Roshan, J. Sun, and T. Warnow, 2001. "Designing fast converging phylogenetic methods." 9th Int'l Conf. on Intelligent Systems for Molecular Biology (ISMB 2001), Copenhagen, in Bioinformatics 17, Suppl. 1, (2001), pp. S190-S198.
45. Nakhleh, L., U. Roshan, K. St. John, J. Sun, and T. Warnow, 2001. "The performance of phylogenetic methods on trees of bounded diameter." Proceedings, The First International Workshop on Algorithms in Bioinformatics (WABI), 2001, Lecture Notes in Computer Science (LNCS #2149) pp. 214-226, Springer Verlag, Olivier Gascuel and Bernard M.E. Moret, eds.
46. Moret, B.M.E., D.A. Bader, and T. Warnow, 2001. "High-performance algorithmic engineering for computational phylogenetics," Proc. 2001 Int'l Conf. Computational Science (ICCS 2001), San Francisco, Lecture Notes in Computer Science 2074, pp. 1012-1021, Springer-Verlag.
47. Ringe, D., T. Warnow, and A. Taylor, 2002. "Indo-European and Computational Cladistics", Transactions of the Philological Society, Volume 100: Issue 1, March 2002, pp. 59-129.
48. Nakhleh, L., B.M.E. Moret, U. Roshan, K. St. John, J. Sun, and T. Warnow, 2002. "The Accuracy of Fast Phylogenetic Methods for Large Datasets", Proc. 7th Pacific Symp. on Biocomputing (PSB 2002), Hawaii, World Scientific Pub. (2002), pp. 211-222.
49. Ganapathy, G. and T. Warnow, 2002. Approximating the Complement of the Maximum Compatible Subset of Leaves of  $k$  Trees. In Proceedings of the Fifth International Workshop on Approximation Algorithms for Combinatorial Optimization, pp. 122-134, 2002.
50. Wang, L., R.K. Jansen, B.M.E. Moret, L.A. Raubeson, and T. Warnow, 2002. "Fast Phylogenetic Methods For Genome Rearrangement Evolution: An Empirical Study," Proc. 7th Pacific Symp. on Biocomputing (PSB 2002), Hawaii, World Scientific Pub. (2002), pp. 524-535.
51. Moret, B.M.E., D.A. Bader, and T. Warnow, 2002. "High-performance algorithm engineering for computational phylogenetics," *J. Supercomputing* **22** (2002), pp. 99-111 (special issue on best papers from ICCS'01).
52. Moret, B.M.E., U. Roshan, and T. Warnow, 2002. "Sequence length requirements for phylogenetic methods," Proc. 2nd International Workshop on Algorithms in Bioinformatics (WABI'02), Rome (2002), Lecture Notes in Computer Science (LNCS #2452), pp. 343-356, Springer Verlag, Roderic Guigó and Dan Gusfield, eds.

53. Nakhleh, L., U. Roshan, L. Vawter, and T. Warnow, 2002. "Estimating the deviation from a molecular clock", Proc. 2nd International Workshop on Algorithms in Bioinformatics (WABI02), Rome, Italy (2002), Lecture Notes in Computer Science 2452, pp. 287-299, Springer-Verlag, R. Guido and D. Gusfield, eds.
54. Moret, B.M.E., J. Tang, L.-S. Wang, and T. Warnow, 2002. "Steps toward accurate reconstruction of phylogenies from gene-order data," J. Comput. Syst. Sci. (invited, special issue on computational biology), **65**, 3 (2002), pp. 508-525.
55. Stockham, C., L.-S. Wang, and T. Warnow, 2002. "Statistically-Based Postprocessing of Phylogenetic Analysis Using Clustering," *Bioinformatics*, Vol. 18, Suppl. 1, special issue for the Proceedings of 10th Int'l Conf. on Intelligent Systems for Molecular Biology (ISMB'02). Edmonton, Canada, pp. S285-S293.
56. Moret, B.M.E., L.-S. Wang, and T. Warnow, 2002. "Towards New Software for Computational Phylogenetics," *IEEE Computer* **35**, 7 (July 2002), special issue on Bioinformatics, pp. 55-64.
57. Moret, B.M.E., and T. Warnow, 2002. "Reconstructing optimal phylogenetic trees: A challenge in experimental algorithmics," Lecture Notes in Computer Science 2547, Springer Verlag, 2002, pp. 163-180 (2002).
58. Nakhleh, L., J. Sun, T. Warnow, C.R. Linder, B.M.E. Moret, and A. Tholse, 2003. "Towards the development of computational tools for evaluating phylogenetic network reconstruction methods," Proc. 8th Pacific Symp. on Biocomputing (PSB 2003), pp. 315-326.
59. Spencer, M., B. Bordalejo, L.-S. Wang, A.C. Barbrook, L.R. Mooney, P. Robinson, T. Warnow and C.J. Howe. 2003. "Gene Order Analysis Reveals the History of The Canterbury Tales Manuscripts." *Computers and the Humanities*, 37 (1): pp. 97-109. Feb. 2003. Kluwer Academic Pub.
60. Ganapathy, G., V. Ramachandran, and T. Warnow, 2003. "Better Hill-Climbing Seaches for Parsimony." In Proceedings of the Third International Workshop on Algorithms in Bioinformatics (WABI), pp. 245-258, 2003.
61. St. John, K., T. Warnow, B.M.E. Moret, and L. Vawter, 2003. "Performance study of phylogenetic methods: (unweighted) quartet methods and neighbor-joining". *J. Algorithms* 48, 1 (2003), pp. 173-193 (special issue on the best papers from SODA 2001).
62. Roshan, U., B.M.E. Moret, T.L. Williams, and T. Warnow. 2004. "Performance of supertree methods on various dataset decompositions". In O. R. P. Bininda-Emonds, editor, *Phylogenetic Supertrees: Combining Information to Reveal the Tree of Life*, Volume 3 of *Computational Biology*, pp. 301-328, Kluwer Academics, 2004 (Andreas Dress, series editor).
63. Ganapathy, G., V. Ramachandran, and T. Warnow. 2004. "On Contract-and-Refine-Transformations Between Phylogenetic Trees." In Proceedings of the Fifteenth ACM-SIAM Symposium on Discrete Algorithms (SODA 2004), pp. 893-902.
64. Nakhleh, L., T. Warnow, C.R. Linder 2004. "Reconstructing reticulate evolution in species - theory and practice." In Proceedings of the Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2004), pp. 337-346.
65. Roshan, U., B.M.E. Moret, T.L. Williams, and T. Warnow, 2004. "Rec-I-DCM3: A fast algorithmic technique for reconstructing large phylogenetic trees," Proc. IEEE Computer Society Bioinformatics Conference (CSB) 2004, Stanford University, pp. 98-109 (2004).

66. Moret, B.M.E., L. Nakhleh, T. Warnow, C.R. Linder, A. Tholse, A. Padolina, J. Sun, and R. Timme, 2004. "Phylogenetic networks: modeling, reconstructibility, and accuracy," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Jan. 2004, **1**:(1), pp. 13-23.
67. Evans, S.N. and T. Warnow, 2004, "Unidentifiable divergence times in rates-across-sites models." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, **1**, July 2004, pp. 130-134.
68. Wang, L.-S. and T. Warnow. "Distance-based genome rearrangement phylogeny," 2005. In *Mathematics of Evolution and Phylogeny*, O. Gascuel, ed., Oxford Univ. Press, pp. 353-380.
69. Moret, B.M.E., J. Tang, and T. Warnow, 2005. "Reconstructing phylogenies from gene-content and gene-order data." In *Mathematics of Evolution and Phylogeny*, pp. 321-352, O. Gascuel, ed., Oxford Univ. Press (2005).
70. Moret, B.M.E. and T. Warnow, 2005. "Advances in phylogeny reconstruction from gene order and content data," in *Molecular Evolution: Producing the Biochemical Data, Part B*, E.A. Zimmer and E.H. Roalson, eds., Vol. 395 of *Methods in Enzymology*, Elsevier (May 2005), pp. 673-700.
71. Nakhleh, L., D. Ringe, and T. Warnow, 2005. "Perfect Phylogenetic Networks: A new methodology for reconstructing the evolutionary history of natural languages." *Language (Journal of the Linguistic Society of America)*, **81**(2), pp. 382-420, June 2005.
72. Nakhleh, L., T. Warnow, C.R. Linder, and K. St. John. 2005. "Reconstructing reticulate evolution in species - theory and practice." *The Journal of Computational Biology (special issue for selected papers from RECOMB 2004)*, **12**(6), July 2005, pp. 796-811.
73. Nakhleh, L., T. Warnow, D. Ringe, and S.N. Evans, 2005. "A comparison of phylogenetic reconstruction methods on an IE dataset." *The Transactions of the Philological Society*, Vol. 103, Issue 2, pp. 171-192, August 2005.
74. Ganapathy, G., B. Goodson, R. Jansen, V. Ramachandran, and T. Warnow, 2005. "Pattern identification in biogeography: metrics and algorithms for comparing area cladograms." *Proceedings of the Fifth International Workshop on Algorithms for Bioinformatics (WABI)*, October 2005.
75. Warnow, T. 2005. "Large-scale phylogenetic reconstruction." Book chapter, in S. Aluru (editor), *Handbook of Computational Biology*, Chapman & Hall, CRC Computer and Information Science Series, December 2005.
76. Linder, C.R. and T. Warnow, 2005. "Overview of phylogeny reconstruction." Book chapter, in S. Aluru (editor), *Handbook of Computational Biology*, Chapman & Hall, CRC Computer and Information Science Series, December 2005.
77. Evans, S.N., D. Ringe, and T. Warnow, 2006. "Inference of divergence times as a statistical inverse problem." Book chapter in "Phylogenetic Methods and the Prehistory of Languages," pp. 119-129. Edited by Peter Forster and Colin Renfrew. Edited for the Institute by Chris Scarre (Series Editor) and Dora A. Kemp (Production Editor). Publisher: McDonald Institute for Archaeological Research/University of Cambridge, 2006.
78. Warnow, T., S. N. Evans, D. Ringe, and L. Nakhleh, 2006. "A Stochastic Model of Language Evolution that Incorporates Homoplasy and Borrowing." Book chapter in "Phylogenetic methods and the prehistory of languages", pp.75-87. Edited by Peter Forster and Colin Renfrew. Edited for the Institute by Chris Scarre (Series Editor) and Dora A. Kemp (Production Editor). Publisher: McDonald Institute for Archaeological Research/University of Cambridge.

79. Wang, L.-S. and T. Warnow, 2006. "Reconstructing Chromosomal Evolution." *SIAM J. Computing*, Vol. 36, Issue 2, 99-131.
80. Wang, L.-S., T. Warnow, B.M.E. Moret, R.K. Jansen, and L.A. Raubeson, 2006. "Distance-based Genome Rearrangement Phylogeny." *Journal of Molecular Evolution*. 63(4):473-83.
81. Ganapathy, G., B. Goodson, R. Jansen, H. Le, V. Ramachandran, and T. Warnow, 2006. "Pattern identification in biogeography", *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 3(4):334-346.
82. Leebens-Mack, J.H., T. Vision, E. Brenner, J.E. Bowers, S. Cannon, M.J. Clement, C.W. Cunningham, C. dePamphilis, R. Desalle, J.J. Doyle, J.A. Eisen, X. Gu, J. Harshman, R.K. Jansen, E.A. Kellogg, E.V. Koonin, B.D. Mishler, H. Philippe, J.C. Pires, Y-L. Qiu, S.Y. Rhee, K. Sjolander, D.E. Soltis, P.S. Soltis, D.W. Stevenson, K. Wall, T. Warnow, C. Zmasek, 2006. "Taking the First Steps towards a Standard for Reporting on Phylogenies: Minimum Information about a Phylogenetic Analysis (MIAPA)." *OMICS* 10(2):231-237.
83. Barbançon, F., T. Warnow, D. Ringe, S. Evans, and L. Nakhleh, 2007. "An experimental study comparing linguistic phylogenetic reconstruction methods." To appear, *Diachronica*.
84. Nelesen, S., K. Liu, D. Zhao, R. Linder, and T. Warnow, 2008. "The effect of the guide tree on multiple sequence alignment and subsequent phylogenetic analyses", *Proceedings of the 2008 Pacific Symposium on Biocomputing*.
85. Snir, S., T. Warnow and S. Rao, 2008. "Short Quartet Puzzling: A New Quartet-based Phylogeny Reconstruction Algorithm". *Journal of Computational Biology*, Vol. 15, No. 1, pp. 91-103.
86. Ringe, D. and T. Warnow, 2008. "Linguistic History and Computational Cladistics", book chapter (pages 257-271) in *Origin and Evolution of Languages: Approaches, Models, Paradigms*. Edited by Bernard Laks. Equinox Publishing.
87. Nichols, J. and T. Warnow, 2008. "Tutorial on computational linguistic phylogeny." *Linguistics and Language Compass*, Vol. 2, Issue 5, September 2008, pages 760-820.
88. Liu, K., S. Nelesen, S. Raghavan, C. R. Linder, and T. Warnow, 2009. "Barking up the wrong treelength: 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
89. Liu, K., S. Raghavan, S. Nelesen, C. R. Linder, T. Warnow, 2009. "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.
90. Swenson, M., F. Barbançon, C.R. Linder, and T. Warnow. A simulation study comparing supertree and combined analysis methods using SMIDGen. 2009. *Proceedings of the Workshop on Algorithms in Bioinformatics (WABI)*, 2009.
91. Wang, L.-S., J. Leebens-Mack, K. Wall, K. Beckmann, C. de Pamphilis, and T. Warnow. The impact of multiple sequence alignment on phylogeny estimation, 2009. *Transactions on Computational Biology and Bioinformatics*, 2009.
92. Bradner, J.E., N. West, M.L. Grachan, E. Greenberg, S.J. Haggarty, T. Warnow and R. Mazitschek. Chemical phylogenetics of histone deacetylases, 2010. *Nature Chemical Biology*, 6, pp. 238-243; published online 7 February 2010.

93. Swenson, M.S., F. Barbançon, C.R. Linder, and T. Warnow. A simulation study comparing supertree and combined analysis methods using SMIDGen. 2010. *Journal of Algorithms for Molecular Biology* **5**:8 (4 January 2010), special issue of selected papers from WABI 2009.
94. Swenson, M.S., R. Suri, C.R. Linder, and T. Warnow. An experimental study of Quartets MaxCut and other supertree methods. *Proceedings of WABI (Workshop on Algorithms for Bioinformatics)* 2010.
95. Swenson, M.S., R. Suri, C.R. Linder, and T. Warnow. An experimental study of Quartets MaxCut and other supertree methods. *Journal of Algorithms for Molecular Biology* 2010, special issue of selected papers from WABI 2010.
96. Linder, C.R., 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, 2010. *PLoS Currents: Tree of Life*, first issue.
97. Liu, K., C.R. Linder, and T. Warnow. Multiple sequence alignment: a major challenge to large-scale phylogenetics, 2010. *PLoS Currents: Tree of Life*, first issue.
98. Yu, Y., T. Warnow, and L. Nakhleh. Algorithms for MDC-based Multi-locus Phylogeny Inference. *Proceedings of RECOMB 2011*, and *Journal of Computational Biology*, 2011.
99. Liu, K., T.J. Warnow, M.T. Holder, S. Nelesen, J. Yu, A. Stamatakis, and C.R. Linder. SATé-II: Very Fast and Accurate Simultaneous Estimation of Multiple Sequence Alignments and Phylogenetic Trees. 2011. *Systematic Biology*, in press.
100. Swenson, M.S., R. Suri, C.R. Linder, and T. Warnow. SuperFine: fast and accurate supertree estimation, 2011. *Systematic Biology*, in press.
101. Yang, J. and T. Warnow. Fast and accurate methods for phylogenomic analyses. *RECOMB-CG 2011 and BMC Bioinformatics* **12**(Suppl 9): S4 (5 October 2011).
102. Mirarab, S. and T. Warnow. FastSP: Linear time calculation of alignment accuracy. *Bioinformatics* (2011) **27**(23):3250-3258.
103. Liu, K., C. Randal Linder, and T. Warnow. RAxML and FastTree: Comparing Two Methods for Large-Scale Maximum Likelihood Phylogeny Estimation. *PLoS-ONE* **6**(11): e27731. doi:10.1371/journal.pone.0027731.
104. Mirarab, S., N. Nguyen, and T. Warnow, SEPP: SATé-Enabled Phylogenetic Placement. 2012. *Pacific Symposium on Biocomputing*.
105. Neves, D.T., J.L. Sobral, K. Pingali, and T. Warnow, Parallelizing Superfine. 2012. To appear, 27th Symposium on Applied Computing (ACM-SAC), Bioinformatics, 2012.
106. Bayzid, Md. S., and T. Warnow. Estimating optimal species trees from incomplete gene trees under deep coalescence. 2012. To appear, *Journal of Computational Biology*, special issue for Simon Tavaré and Mike Waterman.
107. Nguyen, N., S. Mirarab, and T. Warnow. MRL and SuperFine+MRL: new supertree methods. 2012. *J. Algorithms for Molecular Biology* 2012, **7**:3, special issue for the Programme for Phylogenetics at the Sir Isaac Newton Institute for Mathematical Sciences, Cambridge University.
108. Liu, K. and T. Warnow. Treelength Optimization for Phylogeny Estimation. 2012. To appear, *PLoS One*.

109. T. Warnow. Standard maximum likelihood analyses of alignments with gaps can be statistically inconsistent. PLoS Currents Tree of Life.
110. Nelesen, S., K. Liu, L.-S. Wang, C.R. Linder, and T. Warnow. DACTAL: divide-and-conquer trees (almost) without alignments. To appear, ISMB 2012.

#### **Papers in preparation**

- Mirarab, S. and T. Warnow. SATé+FastTree. In preparation.
- Nguyen, N., C. Randal Linder, and T. Warnow. Comparison of Different Methods for Masking Alignments. In preparation.
- Braun, M., K. Liu, C.R. Linder, and T. Warnow. SATé and the Avian Tree of Life. In preparation.
- Mirarab, S. and T. Warnow. SATé for amino-acid phylogeny. In preparation.
- Bayzid, Md. S., S. Mirarab, and T. Warnow. Optimizing species trees under gene duplications from gene trees. In preparation.