

CURRICULUM VITAE

TANDY WARNOW
FOUNDER PROFESSOR OF ENGINEERING

CONTACT INFORMATION

Departments of Bioengineering and Computer Science
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RESEARCH INTERESTS

Phylogenetic tree inference in biology and historical linguistics, multiple sequence alignment, metagenomic analysis, big data, statistical inference, probabilistic analysis of algorithms, machine learning, combinatorial and graph-theoretic algorithms, and experimental performance studies of algorithms.

PROFESSIONAL APPOINTMENTS

- Founder Professor of Engineering, the University of Illinois at Urbana-Champaign, 2014-present.
- Professor of Bioengineering and Computer Science, The University of Illinois at Urbana-Champaign. Member, Biocomplexity theme, Carl R. Woese Institute for Genomic Biology. Affiliate of the National Center for Supercomputing Applications (NCSA). Affiliate faculty in the Departments of Mathematics, Electrical and Computer Engineering, Statistics, Animal Biology, Entomology, and Plant Biology. 2014-present.
- National Science Foundation, Program Director for Big Data, July 2012-July 2013.
- Member, Big Data Senior Steering Group of NITRD (The Networking and Information Technology Research and Development Program), subcommittee of the National Technology Council (coordinating federal agencies), 2012-2013
- Departmental Scholar, Institute for Pure and Applied Mathematics, UCLA, Fall 2011
- Visiting Researcher, University of Maryland, 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 - 2014
 - 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

- Fellow of the Association for Computing Machinery (ACM), 2016. Citation: *For contributions to mathematical theory, algorithms, and software for large-scale molecular phylogenetics and historical linguistics.*
- Founder Professor of Engineering, the University of Illinois at Urbana-Champaign, 2014-present
- David Bruton, Jr. Centennial Professorship in Computer Science, 2010 - 2014
- John Simon Guggenheim Foundation Fellowship, 2011, *New problems in evolutionary estimation.*
- 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 GRADUATE STUDENTS

Current:

- Md. Shamsuzzoha Bayzid (5th year PhD student in Computer Science at the University of Texas at Austin, PhD expected Fall 2016)
- Sarah Christensen (first year CS PhD student at UIUC)
- Ally Kaminsky (first year CS PhD student at UIUC)
- Erin Molloy (3rd year PhD student in Computer Science at UIUC, co-supervised with Bill Gropp, NSF graduate fellow)
- Michael Nute (5th year PhD student in Statistics at UIUC, CompGen fellowship)
- Ehsan Saleh (first year CS PhD student at UIUC)
- Pranjal Vachaspati (3rd year PhD student in Computer Science at UIUC, NSF graduate fellow)

Former:

- Ganesh Ganapathy (PhD August 2006), Apple Computers
- Ashu Gupta (MS May 2016, Computer Science at the University of Illinois at Urbana-Champaign), now at Apple
- Kevin Liu (PhD May 2011), Assistant Professor of Computer Science, Michigan State University
- Siavash Mirarab (PhD August 2015), Assistant Professor of Electrical and Computer Engineering, UCSD

- Luay Nakhleh (PhD May 2004), Professor of Computer Science at Rice University.
- Serita Nelesen (PhD December 2009), Assistant Professor of Computer Science at Calvin College.
- Nam Nguyen (PhD August 2014), postdoctoral researcher at UCSD with Vineet Bafna
- Usman Roshan (PhD May 2004), Associate Professor of Computer Science at NJIT.
- Michelle Swenson (PhD May 2009), visiting instructor Emory University Department of Mathematics
- Li-San Wang (PhD May 2003), Associate Professor of Medicine at the University of Pennsylvania.
- Shibu Yooseph (PhD received 2000), Professor at Central Florida University

CURRENT POSTDOCTORAL ADVISEES

- Ruth Davidson (NSF Postdoctoral Fellow in Mathematics)

FORMER POSTDOCTORAL ADVISEES

- Kevin Atteson (Chief Quant at Summer Road)
- François Barbançon (now at Palantir Technologies, Palo Alto, CA)
- Dannie Durand (Associate Professor of Biology and of Computer Science, Carnegie Mellon University)
- Daniel Huson (C4 Professor of Bioinformatics, Tübingen University, Germany)
- Nam-phuong Nguyen (now at UCSD CS, postdoc with Vineet Bafna)
- Ken Rice (now retired)
- Katherine St. John (Professor of Mathematics and Computer Science, Lehman College, CUNY)
- Elizabeth Sweedyk (Associate Professor of Computer Science, Harvey Mudd College)
- Shel Swenson (visiting faculty, Emory University, Mathematics & Computer Science)

CURRENT GRANT SUPPORT

- NSF grant III:AF:1513629. This is a collaborative grant with the University of Maryland, for new methods for metagenomic dataset analysis, building on our TIPP method for taxon identification of reads in a metagenomic sample. (This grant ends August 2019.)
- NSF CCF 15-35977, AitF: Full: Collaborative Research: Graph-Theoretic Algorithms to Improve Phylogenomic Analyses. I am the overall PI, and this project is collaborative with Satish Rao (UC Berkeley PI) and Chandra Chekuri (UIUC). We are developing new theoretical computer science and discrete algorithms for improving the estimation of large species and gene

trees, and specifically enabling statistical methods to scale to ultra-large datasets. (This grant ends August 2019.)

- NSF DBI:1458652. ABI Innovation: New methods for multiple sequence alignment with improved accuracy and scalability. PI Warnow. August 15, 2015 to August 14, 2018. Award Amount: \$861,625. (No Co-PIs).

RECENT GRANT SUPPORT

- NSF DBI-1062335/1461364. Collaborative Research: Novel Methodologies for Genome-scale Evolutionary Analysis of Multi-locus data. PI, 2010-2013. \$349,999. Collaborative grant with Rice University and Stanford University. 2010-2013 (extended to 2016).
- NSF DEB 0733029 (ATOL): Collaborative Research: Large-Scale Simultaneous Multiple Alignment and Phylogeny Estimation. Overall PI: Warnow. 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. 2007-2011 (extended to 2014).
- 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

- Genome 10K Executive Committee Member, 2015-present
- Paris Kanellakis Award Committee Member, 2015-present
- WABI (Workshop on Algorithms for Bioinformatics) Steering Committee 2013-present
- Co-organizer, IPAM (Institute for Pure and Applied Mathematics) workshop on Multiple Sequence Alignment, 2015
- Co-organizer, programme on Mathematical, Statistical and Computational Aspects of the new science of Metagenomics, Sir Isaac Newton Institute of Mathematical Sciences, Cambridge University, 2012-2014
- Program Director for Big Data, National Science Foundation, July 2012 - July 2013
- Chair, NIH BDMA (Biodata Management and Analysis) Study Section, 2010-2012
- 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, 2006-2012.
- 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: Great Lakes Bioinformatics (GLBIO) 2017; Combinatorics and Computing (COCOON) 2003; European Conference on Computational Biology (ECCB) 2008; Track for Evolution and Phylogeny, Intelligent Systems for Molecular Biology (ISMB) 2006, 2007, 2008, 2011, 2013, and 2014; ACM-SIAM Symposium on Discrete Algorithms (SODA) 1999; Workshop on Algorithms for Bioinformatics (WABI) 2009; Great Lakes Bioinformatics (GLBIO) 2016.

- Program committee member: AAAI 2015; ALLENEX 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; GLBIO 2016; ICALP 2005; ISMB 2006, 2007, 2008, 2009, 2012, 2013, 2014, and 2016; JOBIM 2000; RECOMB 1997, 2001, 2002, 2004, 2009, 2010, 2011, 2014, and 2016; RECOMB-CG 2015; SODA 2001; STOC 1998; FOCS 1996; WABI 2001, 2002 2004, 2005, 2006, 2009, 2010, and 2015; and WADS 2001.
- NSF Panelist, 1995, 1996, 2000, 2001, 2002, 2003, 2007, and 2016.
- Proposal reviewer for NSERC, 1999-2006.
- Reviewer for faculty candidates at the Royal Institute of Technology in Stockholm, Sweden, 1999.

INVITED LECTURES

2016

- NYU CS department, November 2016.
- CLIMB conference, Lausanne, Switzerland, November 2016.
- Statistics Department seminar, University of Chicago. October 2016.
- Georgia Tech, Math Department. October, 2016.
- Princeton CS Department. October, 2016.
- U Penn Math Department. October, 2016.
- CMU Computational Biology. September, 2016.
- Using Ensembles of HMMs for Grand Challenges in Bioinformatics, as part of the Schloss Dagstuhl seminar Next generation sequencing - Algorithms and Software for Biomedical Applications August, 2016.
- New methods for coalescent-based species tree estimation: ASTRAL, ASTRID, and statistical binning, University of Oxford, Statistics. August 2016.
- New methods for coalescent-based species tree estimation: ASTRAL, ASTRID, and statistical binning and How to construct large trees, University of Trento, Italy. August, 2016.
- SIAM Conference Discrete Math, Georgia State University, Atlanta, Georgia, USA. June, 2016.
- Blue Waters Symposium, Oregon. (PDF) (PPTX) June, 2016.
- Austin, Texas Phylogenomics Symposium, Advances in Multiple Sequence Alignment June, 2016.
- Austin, Texas. Evolution 2016 meeting. New methods for coalescent-based species tree estimation: ASTRAL, ASTRID, and statistical binning. June, 2016.
- UCSD Bioinformatics seminar, May 2016
- MIT Computer Science, May 2016
- Molecules as documents of evolutionary history: 50 years after Roscoff (Brittany), France, May 2016

- Co-evolution in proteins and RNA, theory and experiments, Cargese, Corsica, April 2016
- PhyloPizza, Smithsonian Institute, March 2016
- CEHG Symposium at Stanford University, March 2016
- Toyota Technology Institute of Chicago, February 2016
- ITA (Information Theory and Applications), Plenary Talk, February 2016
- University of Washington, Combi seminar, February 2016
- UC Davis, Genomics Institute, January 2016.
- UC San Francisco, January 2016
- UC Berkeley, Museum of Comparative Zoology, January 2016
- Pacific Symposium on Biocomputing, January 2016

2015

- HHMI (Howard Hughes Medical Institute), November 2015
- University of California at San Diego, Distinguished Lecture, November 2015
- American Mathematical Society, Chicago, October 2015
- Program for Evolutionary Dynamics, Harvard University, October 2015
- University of Maryland, September 2015
- Duke University, September 2015
- Annual meeting of the Society for Molecular Biology and Evolution, July 2015
- Great Lakes Bioinformatics Conference; Keynote speaker, May 2015
- Genome 10K, March 2015
- National Center for Supercomputing Applications, February 2015
- IPAM (Institute for Pure and Applied Mathematics at UCLA), January 2015

2014

- Department of Computer Science, Swarthmore College, December 2014
- Institute for Genomic Biology, University of Illinois at Urbana-Champaign, November 2014
- Institute for Biomedical Informatics, The University of Pennsylvania, October 2014
- Mathematics Colloquium, University of Illinois at Urbana-Champaign, October 2014
- Gotham Seminar on Genomics & Statistics, Columbia University, October 2014
- Department of Computer Science, Case Western University, September 2014 (Distinguished Lecture)
- Pacific Northwestern National Laboratories, September 2014

- Simons Institute for the Theory of Computing (Berkeley), April 2014
- Copenhagen University, March 2014
- Newton Institute for Mathematical Sciences at Cambridge University, March 2014
- Janelia Farm (HHMI), February 2014

2013

- MAGE (Models and Algorithms for Genome Evolution), *plenary speaker* August 2013; invited by Nadia El-Mabrouk (Univ Montreal, Computer Science)
- Evolution 2014 annual meeting, Symposium on Practical Phylogenomics, invited by David Posada (Biology, University of Vigo)
- IPAM (Institute for Pure and Applied Mathematics) *plenary speaker*, June 2013; invited by Eleazar Eskin (UCLA CS)
- 10K Genome, Hollywood; invited by David Haussler (UCSC, Computer Science)
- Janelia Farm (Howard Hughes Medical Institute), March 2013; invited by Sean Eddy
- Smithsonian Institution, Frontiers in Phylogenomics, invited by Charles Mitter (University of Maryland, Entomology)

2012

- Computational and Statistical Phylogenomics, Vigo, Spain, Sept 2012; invited by David Posada (University of Vigo Biology)
- M.I.T. Bioinformatics, May 2012; invited by Bonnie Berger (MIT CS)
- Smithsonian Institution, May 2012; invited by Mike Braun
- J Craig Venter Institute, May 2012; invited by Karen Nelson
- UCLA Computational Biosciences, April 2012; invited by Matteo Pelligrini (UCLA Biology)
- University of Southern California, Symposium for Mike Waterman and Simon Tavaré, March 2012; invited by Fengzhu Sun (USC Computational Biology)
- University of Pennsylvania, Bio-Mathematics Seminar, March 2012; invited by Robin Pemantle (Penn Mathematics) and Junhyong Kim (Penn Biology)

2011

- Janelia Farm, Dec 2011; invited by Sean Eddy
- Science Faculty Colloquium, Bristol University, *distinguished lecture*, Dec 2011
- Univ Wisconsin Biostatistics, Nov 2011; invited by Cecile Ané (Biostatistics)
- UCLA Institute for Pure and Applied Mathematics (IPAM), Nov 2011; invited by Eleazar Eskin (UCLA CS)
- Heilbronn Annual Conference, University of Bristol, England, September 2011; *plenary speaker*, invited by Trevor Wooley (Bristol Mathematics)

- J Craig Venter Institute, Oct 2011; invited by Shibu Yooseph
- Newton Institute, University of Cambridge, June 2011; invited by Vincent Moulton (University of East Anglia, UK)
- UC Berkeley, Lens on the Sciences, May 2011; invited by Mike Jordan and Dick Karp (Berkeley CS)
- Princeton University, Ecology and Evolutionary Biology, May 2011; invited by Laura Landweber (Princeton EEB)
- University of Maryland, April 2011
- Harvard University, invited by Stuart Shieber (Harvard CS) and Naomi Pierce (Harvard OEB)
- Bardonnechia, Italy; invited by Riccardo Zecchina (Physics, University of Turin), February 2011

2010

- Brown University, December 2010; *distinguished lecture*, invited by Ben Raphael (Brown CS)
- North Carolina State University, Department of Mathematics, December 2010; invited by Loek Helminck
- Microsoft Research, Computational Aspects of Biological Information, December 2010; invited by Jennifer Chayes (MSRE) and Riccardo Zecchina (Turin Physics)
- Washington Area Phylogenetics Consortium PHYLO-PIZZA, December 2010; invited by Mike Braun (Smithsonian Institute)
- Microsoft Research New England, November 2010; invited by Jennifer Chayes
- Johns Hopkins University, Department of Computer Science, November 2010; invited by Rao Kosaraju (JHU CS)
- Dartmouth College, Department of Computer Science, November 2010; invited by Peter Winkler (Dartmouth Math and CS)
- iEvolBio conference, Evolution Meeting, June 2010.
- RECOMB Bioinformatics Education Conference, May 2010; invited by Pavel Pevzner (UCSD CS)
- Illinois Language and Linguistics Society conference (ILLS 2), May 2010.
- University of Illinois at Chicago, April 2010; invited by Jerry Bona (UIC Mathematics)
- University of Chicago, April 2010; invited by Wen-Hsiung Li (Univ Chicago Biology)
- Princeton University, Computer Science Colloquium, Feb 2010; invited by Olga Troyanskaya (Princeton CS)
- NESCENT (National Evolutionary Synthesis Center), Feb 2010; invited by Allen Rodrigo (NESCENT)
- CMU-UPitt, Computational Biology Seminar, Feb 2010;
- Yale University Computer Science Colloquium, Jan 2010; invited by Joan Feigenbaum (Yale CS)

2009

- Workshop on Molecular Evolution and Phylogenetics, SAMSI, April 2009.
- Swadesh Centenary Conference, Leipzig, Germany, *plenary speaker*, January, 2009.

2008

- Harvard Symposium on The Science of The Human Past, Dec 5, 2008; invited by Stuart Shieber (Harvard, CS)
- European Conference on Complex Systems Science (ECCS08), Sept 11-17, 2008; *plenary speaker*, invited by Riccardo Zecchina (Turin, Physics)
- School of Computer and Communication Sciences at EPFL, June 12, 2008; *distinguished lecture*, invited by Bernard Moret (EPFL Computer Science)
- MIEP (Mathematics and Informatics in Evolution and Phylogeny), June 2008; invited by Olivier Gascuel (Montpellier Computer Science)
- Department of Computer Sciences, Northwestern University, May 2, 2008
- School of Informatics, Indiana University, April 11, 2008
- Department of EECS, UC Berkeley, Distinguished Lecture, Feb. 6, 2008; invited by Dick Karp (Berkeley CS)
- EECS Colloquium, UC Berkeley, Feb. 2008; invited by Satish Rao (Berkeley CS)

Distinguished lectures and keynote talks before 2008

- 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; invited by David Bader (GaTech CS)
- Department of Computer Science, UC Davis, Distinguished Lecture, Nov. 15, 2007; invited by Dan Gusfield (UCD CS)
- Plenary talk, Workshop on Graph Algorithms (WG'06), Bergen, Norway, June 2006.
- Mathematics Department, Distinguished Lecture, The University of South Carolina, March 28, 2006; invited by Laszlo Székely (USC Math)
- Symposium on Languages and Genes, The University of California at Santa Barbara, Sept. 2006.
- Symposium on Stochastic Processes and Applications, Plenary talk, June 27, 2005).
- 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

- University of Illinois at Chicago, Department of Computer Sciences, distinguished lecture, 2003.
- Annual meeting, Mathematics Association of America (2003), Invited Lecture.
- SMOBE (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.
- University of Toronto, Department of Computer Science. Distinguished Lecture. April 2002; invited by Toni Pitassi (Toronto CS)
- Distinguished Lecture. Department of Computer Science, University of British Columbia, January 2001; invited by Anne Condon (UBC CS)
- SCOPH (Showcase on Competing Technologies for Phylogenetics: A RECOMB Phylogenetics Conference, April 2001, Montreal Canada; invited by David Sankoff
- 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.
- Plenary talk, Deep Green. June 2, 2000, University of Maryland, College Park, MD.

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, 1992. "Two Strikes Against Perfect Phylogeny", Proc. 19th Int'l Colloq. on Automata, Languages, and Programming (ICALP92), Springer Verlag, pages 273-283, 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. Yoosheph, 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.
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