Curriculum Vitae

Tandy Warnow
Grainger Distinguished Chair in Engineering

1 Contact Information

Department of Computer Science
The University of Illinois at Urbana-Champaign
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2 Research Interests

Algorithms and statistical estimation problems in biology, historical linguistics, and network analysis. Specific interests include: phylogenetic tree inference in biology and historical linguistics, multiple sequence alignment, metagenomic analysis, and community detection in large-scale networks. Techniques used include statistical inference, probabilistic analysis of algorithms, machine learning, combinatorial and graph-theoretic algorithms, and experimental performance studies of algorithms.

3 Professional Appointments

- Member, Computational Genomics Research Board of Recents Working Group, NCBI, NIH, 2022-present

- Co-Chief Scientist, C3.ai Digital Transformation Institute, 2017-2018, 2020-present

- Grainger Distinguished Chair in Engineering, 2020-present

- Associate Head for Computer Science, 2019-present

- Special advisor to the Head of the Department of Computer Science, 2016-2021

- Founder Professor of Computer Science, the University of Illinois at Urbana-Champaign, 2014-2019

- Member, Carl R. Woese Institute for Genomic Biology. Affiliate of the National Center for Supercomputing Applications (NCSA), Coordinated Sciences Laboratory, and the Unit for Criticism and Interpretive Theory. Affiliate faculty member in the Departments of Mathematics, Electrical and Computer Engineering, Bioengineering, Statistics, Entomology, Plant Biology, and Evolution, Ecology, and Behavior, 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.

4 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.

5 Honors

Teaching Honors   List of Teachers Rated Excellent by their students

- Spring 2017 for CS 466 and CS 581

- Spring 2018 for CS 581

- Fall 2020 for CS 581 (Outstanding)

- Fall 2021 for CS 581

Elected Fellow

- Elected fellow, American Association for the Advancement of Science (AAAS), 2021

- Fellow of the International Society for Computational Biology (ISCB), 2017.

- Fellow of the Association for Computing Machinery (ACM), 2015. Citation: *For contributions to mathematical theory, algorithms, and software for large-scale molecular phylogenetics and historical linguistics.*

Research Honors

- ISCB Award for Contributions by a Senior Scientist, 2024

- Grainger Distinguished Chair in Engineering, UIUC, 2020-present

- *Language* (Journal of the Linguistic Society of America), included one of my papers (Nakhleh, Ringe, and Warnow, '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) in their selection of top 20 papers from 1986-2016 (see https://www.linguisticsociety.org/content/best-language-volume-iii)

- Elected member, Electorate Nominating Committee (ENC) of the Section on Information, Computing, & Communication, American Association for the Advancement of Science (AAAS), 2019

- Founder Professor of Engineering, the University of Illinois at Urbana-Champaign, 2014-2020

- 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.*

Other Honors

- 2023 Campus Award for Excellence in Faculty Mentoring. University of Illinois Urbana-Champaign.

- 2022 College Award for Excellence in Faculty Mentoring, Grainger College of Engineering, University of Illinois Urbana-Champaign

6 Current and Former Graduate Students

Current:

- Baqiao Liu (PhD student, started 2020)

- Minhyuk Park (PhD student, started 2021)

- Chengze Shen (PhD student, started 2020)

- Yasamin Tabatabaee (PhD student, started 2021)

- Eleanor Wedell (PhD student, started 2022)

- James Willson (PhD student, started 2020)

- The-Anh Le (PhD student, started 2022)

Former:

- Md. Shamsuzzoha Bayzid (PhD Univ Texas at Austin, 2016). Associate Professor, Department of Computer Science and Engineering (CSE), Bangladesh University of Engineering and Technology.

- Sarah Christensen (PhD student, UIUC Computer Science, co-advised with Mohammed El-Kebir), PhD 2020. Now working at D.E. Shaw

- Gillian Chu (MS student PEEC program UIUC, degree 2022), now PhD student in Computer Science at Princeton University.

- Ganesh Ganapathy (PhD Univ Texas Austin, August 2006), Data Scientist at Apple Computers in Austin, Texas

- Ashu Gupta (MS May 2016, Computer Science at the University of Illinois at Urbana-Champaign), now Software Engineer at Apple Computers in Cupertino, California

- Kevin Liu (PhD Univ Texas at Austin, May 2011), Associate Professor of Computer Science, Michigan State University

- Siavash Mirarab (PhD Univ Texas at Austin, August 2015), Associate Professor of Electrical and Computer Engineering, UCSD

- Erin Molloy (PhD UIUC, August 2020, co-advised with Bill Gropp), Assistant Professor of Computer Science, Univ Maryland.

- Luay Nakhleh (PhD Univ Texas at Austin, May 2004), Dean of Engineering and Professor of Computer Science at Rice University.

- Serita Nelesen (PhD Univ Texas at Austin, December 2009), Software developer for Neural Planet

- Nam-phuong Nguyen (PhD Univ Texas at Austin, August 2014), Principal Scientist in Computational Biology at Zentalis Pharmaceuticals

- Michael Nute (PhD student UIUC Statistics, 2019), became postdoctoral researcher at Rice University, now working for a start-up

- Usman Roshan (PhD Univ Texas at Austin, May 2004), Associate Professor of Computer Science at NJIT.

- Vladimir Smirnov (PhD UIUC, August 2021), postdoctoral researcher at Cambridge University with Richard Durbin

- Michelle (Shel) Swenson (PhD Univ Texas at Austin Mathematics, May 2009), Senior Lecturer, Department of Mathematics, University of Tennessee at Knoxville

- Pranjal Vachaspati (PhD UIUC, December 2019), Senior Software Engineer at Toast

- Li-San Wang (PhD Univ Texas Austin, May 2003), Professor of Pathology and Laboratory Medicine at the University of Pennsylvania.

- Shibu Yooseph (PhD Univ Pennsylvania, received 2000), Professor of Computer Science at Central Florida University

- Xilin Yu (MS UIUC, 2019), software engineer at Google (Seattle).

7   Former Postdoctoral Advisees

- Kevin Atteson (Chief Quant at Summer Road)

- François Barbançon (now self-employed)

- Ruth Davidson (NSF Postdoctoral Fellow in Mathematics, now J.L. Doob Research Assistant Professor in the Department of Mathematics at UIUC)

- Dannie Durand (Associate Professor of Biology and of Computer Science, Carnegie Mellon University)

- Daniel Huson (C4 Professor of Bioinformatics, Tubingen University, Germany)

- Nam-phuong Nguyen, now Principal Scientist in Computational Biology at Zentalis Pharmaceuticals

- Ken Rice (now retired)

- Katherine St. John (Professor of Computer Science, Hunter College, CUNY)

- Elizabeth Sweedyk (retired, Associate Professor of Computer Science, Harvey Mudd College)

- Shel Swenson (Senior Lecturer, University of Tennessee at Knoxville, Mathematics Department)

- Paul Zaharias (now Researcher, Institute of Systematics, Evolution, Biodiversity at the National Museum of Natural History, France)

8   Current Grant Support

- National Science Foundation (NSF) 2006069, IIBR Informatics: Advancing Bioinformatics Methods using Ensembles of Profile Hidden Markov Models. PI Warnow (Co-PI: Jian Peng), August 15, 2020 to August 14, 2024. This project will extend the theory foundations of ensembles of profile HMMs, and use them for protein structure and function prediction.

- National Science Foundation (NSF) 2316233, Collaborative Research: PPoSS: LARGE: General-Purpose Scalable Technologies for Fundamental Graph Problems, PI: Joseph Torellas (my role; Co-PI), 2023-2028. This is a collaborative grant led by UIUC (PI: Torellas, Co-PIs: Charith Mendis, Hanghang Tong, Karrie Karahalios, and Tandy Warnow). Total funding: $3,900,000.

9   Recent Grant Support

- National Science Foundation (NSF) DBI:1458652. ABI Innovation: New methods for multiple sequence alignment with improved accuracy and scalability. PI Warnow. August 15, 2015 to July 31, 2021 (no-cost extension). Award Amount: $861,625. (No Co-PIs).

- National Science Foundation (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.

- National Science Foundation (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.

- 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.

10   National and International Service

- Member, NLM BOR Comparative Genomics Resource (CGR) Working Group, 2022-present
- Member, Fellow Selection Committee, International Society for Computational Biology (ISCB), 2023, 2024.
- Member, AAAS Election Nomination Committee (Section T), 2019-2020
- Faculty, Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) at Marine Biology Laboratory at Woods Hole, 2017-2019
- Member, Faculty of 1000, 2017-present
- Genome 10K, Council Member, 2015-2019
- Paris Kanellakis Award Committee Member, 2015-2019 (chair 2017-2018)
- WABI (Workshop on Algorithms for Bioinformatics) Steering Committee 2013-2022
- Co-organizer, IPAM (Institute for Pure and Applied Mathematics) long program, "Science at Extreme Scales: Where Big Data Meets Large-Scale Computing" Fall 2018
- 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 Commmittee 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 Cyberinfranstructure (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.
- Conference co-chair, Intelligent Systems for Molecular Biology (ISMB) 2018.
- Program committee co-chair: 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, 2014; Great Lakes Bioinformatics (GLBIO) 2016, 2017; ACM-SIAM Symposium on Discrete Algorithms (SODA) 1999; Workshop on Algorithms for Bioinformatics (WABI) 2009;
- Program committee member: ACM-BCB 2017; AAAI 2015; ALENEX 2005; COCOON 1998 and 2003; EACL 2012 Joint Workshop of LINGVIS (Visualization of Linguistic Patterns) and UNCLH (Uncovering Language History from Multilingual Resources); FOCS 1996; FUN 2001; GLBIO 2016 and 2017; ICALP 2005; ISMB 2006-2009, 2011-2014, 2016, 2019, and 2023; JOBIM 2000; RECOMB 1997, 2001, 2002, 2004, 2009-2011, 2014, 2016, 2018, 2019, and 2021. RECOMB-CG 2015-2019, 2023, and 2024; SODA 2001; STOC 1998; Scandinvavian Symposium on Algorithms and theory (SWAT) 2024; WABI 2001, 2002, 2004-2006, 2009, 2010, 2015, 2018-2023; and WADS 2001.
- NSF Panelist, 1995, 1996, 2000, 2001, 2002, 2003, 2007, 2016, and 2019.
- Proposal reviewer for NSERC, 1999-2006.
- Reviewer for faculty candidates at the Royal Institute of Technology in Stockholm, Sweden, 1999.

11   University Service

University service at UIUC

- Member, Illini Hall and Altgeld Hall Renovation Committee, 2023-present

- Faculty Senate, 2018-2020

- NCSA Allocations: PC member 2014-present

Grainger College of Engineering at UIUC

- Chair, Anti-Racism Task Force, 2020

- Chair, Grainger Engineering Breakthroughs Initiative (GEBI) Professorship committee, 2020-2024

- Member, Climate Diversity and Inclusiveness committee (COE), 2019

- Member, Search committee for the Dean of Engineering, 2018

- Member, Grainger Chairs and Professorship search committee (BigData), 2015-2016, 2018-present

- Member, COE Promotion and Tenure Committee, 2017-2019

- Member, Awards committee for College of Engineering, 2016-2017, 2023-2024

Department of Computer Science at UIUC

- Area Chair, Bioionformatics and Computational Biology research area, 2015-present

- Co-Director (with N. Amato and M. Vishwanathan), Future Faculty Fellows Postdoc program, Department of Computer Science, 2022-2024;

- Associate Head of the Department of Computer Science, 2017-2018, 2019-present

- Special Advisor to the Head of the CS Department, 2016-2021

- Chair (elected), Promotion and Tenure Committee, CS Department, 2018-2019

- Chair (elected), Faculty Advisory Committee, Department of Computer Science, 2016-2017

- Chair, Tenure Track Faculty Mentoring Committee, 2018-2019

- Chair, CS Department P&T committee, 2018-2019

- Area Chair, Bioinformatics and Computational Biology group, CS department, 2015-2019, 2022-present

- Member, P&T committee, CS department, 2015-2017, 2018-2019, 2021-2022

- Member, Graduate Admissions Committee, Department of Computer Science, 2014-2016, 2022-present

- Member, Internal Advisory Committee, CS department, 2015-2017

- Member, Named Professorship committee, CS department, 2015-present

- Chair, Big Research Initiatives Committee, 2017-2018, 2019-2021

- Member, GEBI committee for Department of Computer Science, 2017-2019

- Member, Governance committee, CS department, 2015-2017

Department of Mathematics at UIUC

- Canary Professorship search, 2022-2023

Department of Bioengineering at UIUC

- Chair (elected), Internal Advisory Committee, Department of Bioengineering (2017)

- Chair, Awards Committee, Bioengineering Department, 2016-2017

- Member, Internal Advisory Committee for Bioengineering, 2015-2017

- Member, PhD preliminary exam committee, Bioengineering, 2015-2016

- Member, P&T committee for Bioengineering, 2014-2017

- Member, Named Professorship committee for Bioengineering, 2014-2017

- PhD preliminary exam committee, Bioengineering, 2014-2015

12 Invited Lectures

2024

- April 25, University of Georgia

- July 11, Keynote talk at ISMB, Montreal

- July 16 (approx), CGSI at UCLA

2023

- May 3. Kew Royal Botanical Gardens, London UK.

- June 12. Sandia National Laboratories, Livermore CA

- July 18, Society of Mathematical Biology Annual Meeting, Columbus OH

2022

- Feb 21-25. IMSI. "Challenges in Microbial Phylogenetics"

- May 16. "Building and Growing Large Phylogenies". UCLA Biology

- May 19-21. Symposium for Mike Waterman's 80th birthday, at USC (Los Angeles)

- July 6-15 UCLA Computational Genomics Summer Institute

- July 18-23, Simons Institute for the Theory of Computing

- Sept 16. American Museum of Natural History and Rockfeller University.

- Sept 16. Rockefeller University

- Sept 19. Princeton University, Dept of Computer Science

- Sept 22. BSC Life Session/Bioinfo4Women seminar

- Nov 10. EMBO

- Nov 18, Plant Biology seminar at UIUC

2021

- February 1, IHP, Paris, France, conference on Phylogeny and Inference.

- June 16, Keynote talk (10:30 AM) at MCEB

- June 22, SBE (Systematics, Biogeography, and Evolution).

- July 8 SMBE (Society for Molecular Biology and Evolution) 2021. Invited talk in Symposium 32, "Large-scale phylogeny using novel computational and statistical tools".

- Aug 30-Sept 3, 2021. IMSI (University of Chicago), Symposium on Eliciting Structure in Genomics Data.

- September 28-30, 2021. Genomic population structures of microbial pathogens. Royal Society, London, UK.

- Dec 12-17, IPAM reunion, Big Data Meets Large Scale Computing, Lake Arrowhead, CA

2020

- February 24-26, 2020, Copenhagen, Denmark, Bird 10K Workshop

- February 27, 2020. Natural History Museum, London, UK

- All invitations from March onward were cancelled due to COVID-19

2019

- February 13, 2019. University of Pennsylvania, Penn Bioinformatics Forum. March 22, 2019. University of Pennsylvania, Penn Linguistics Conference, Panel on "Interplay between Linguistics and Biology"

- March 22, 2019. University of Pennsylvania, Penn Linguistics Conference, Panel on "Interplay between Linguistics and Biology"

- April 5, 2019. Harvey Mudd College, Computer Science Department seminar

- April 12-14, 2019. "Trees in the Desert 2019", a workshop on ultra-large phylogenetic trees, Tucson AZ

- April 30, 2019. European Bioinformatics Institute, Cambridge UK

- May 13-15, NIMBIOS, Knoxville TN Scientific Collaboration Enabled by High Performance Computing

- May 24, University of Chicago, Department of Computer Science

- May 27, Symposium at UC Berkeley on Phylogenomics

- May 28-30, The 6th International Conference on Algorithms for Computational Biology (AlCoB 2019), Berkeley

- June 17-19, Systematics Association Biennial, Bristol UK

- August 28, Genome 10K Conference, New York

- September 13, UCLA, Department of Statistics, Los Angeles CA

- October 18, Statistics Graduate Student Seminar, UIUC

- November 7, Mathematical Biology Seminar, UIUC

- November 15, UC Irvine, Department of Computer Science

- November 22, Plant Biology, UIUC

2018

- January 5, 2018. Hunter College, Department of Mathematics

- March 16, 2018. UCLA, Bioinformatics program

- April 4, 2018. UIUC, Pathobiology Seminar

- April 19, 2018. Imperial College, London. Colloquium, Department of Mathematics.

- April 21-24, 2018, Plenary talk, RECOMB (Paris, France)

- May 8, 2018. CRA-W Distinguished Lecture, UCLA Computer Science.

- June 1-3, 2018. Society for Systematic Biologists, standalone meeting, Ohio State University.

- June 4-8, 2018. SIAM Discrete Mathematics Annual Meeting, Foundations of Data Science. Denver, Colorado.

- August 13, 2018. Statistics Department seminar, Oxford University.

- September 14, 2018. Advances in Phylogenomics, Genome 10K conference

- October 29, 2018. Northwestern University, Department of Applied Mathematics

- November 7, 2018, IPAM (at UCLA)

- November 16, 2018. Kew Royal Botanical Gardens, London UK

2017

- NIPS Workshop on Advances in Modeling and Learning Interactions from Complex Data, Long Beach CA, December 8, 2017.

- Kew Royal Botanical Gardens, October 5, 2017.

- Keynote speaker, ACM-BCB and WABI, Cambridge, MA. August 20-23, 2017.

- STAMPS, Marine Biology Laboratory at Woods Hole, August 6, 2017.

- Keynote speaker. IPDPS (IEEE International Parallel and Distributed Processing) Symposium, Orlando FL. May 30, 2017.

- NeLLi: From New Lineages of Life to New Functions at the DOE Joint Genome Institute (JGI). April 5, 2017.

- Second Workshop on Statistical and Algorithmic Challenges in Microbiome Data Analysis at The Broad Institute of MIT and Harvard, in Cambridge, MA. February 16-17, 2017.

- Plant Biology, UIUC. January 27, 2017.

2016

- Simons Center, New York City. December 2016.

- National Institutes of Health, NLM. December 2016.

- NYU CS department, November 2016.

- CLIMB conference, Lausanne, Switzerland, November 2016.

- Statistics Department Colloquium, University of Chicago. October 2016.

- Georgia Tech, Math Department IMPACT Distinguished Lecture. October, 2016.

- Georgia Tech, CSE Department. Distinguished Lecture. October, 2016.

- Princeton CS Department. October, 2016.

- University of Pennsylvania, 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.

- Oxford University Statistics Department. August 2016.

- University of Trento, Italy. August, 2016.

- SIAM Conference Discrete Math, Georgia State University, Atlanta, Georgia, USA. June, 2016.

- Blue Waters Symposium, Oregon. June, 2016.

- Austin, Texas Phylogenomics Symposium, Advances in Multiple Sequence Alignment June, 2016.

- Austin, Texas. Evolution 2016 meeting. June, 2016.

- UCSD Bioinformatics seminar, May 2016

- MIT Computer Science conference on historical linguistics, 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 Illinios 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 (Darthouth 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 Székély (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.

- 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.

- 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.

13   Diversity Activities

My diversity statement is on my webpage at http://tandy.cs.illinois.edu/warnow-diversity.html.

- Chair, Anti-Racism Task Force, Grainger College of Engineering, 2020

- Member, Climate Diversity and Inclusiveness committee (College of Engineering), 2019

- Visit to Monticello Middle School to talk with 6th, 7th, and 8th grade students about computer science, 2019

- Visits to student groups focusing on women (e.g., CRA-W at UCLA) in computer science, bioinformatics, etc., 2017-present

- Mentoring (informal) of women assistant professors and postdocs in CS and mathematics about how to succeed in academia (e.g., at NIMBIOS, 2019).

- Regular participation in programs within the CS department for undergraduate women students.

14 Publications

Books

1. Warnow, T. *Computational Phylogenetics: An Introduction to Designing Methods for Phylogeny Estimation.* Cambridge University Press, 2017.

Edited volumes

1. Bioinformatics and Phylogenetics: Seminal Contributions of Bernard Moret, Edited by Tandy Warnow, Springer 2019, DOI: 10.1007/978-3-030-10837-3

Edited Conference Proceedings

1. Proceedings of the Tenth Annual ACM-SIAM Symposium on Discrete Algorithms, 17-19 January 1999, Baltimore, Maryland, USA. Robert Endre Tarjan and Tandy J. Warnow, eds. ACM/SIAM 1999, ISBN 0-89871-434-6.

2. Computing and Combinatorics: Proceedings of the 9th Annual International Conference, CO-COON 2003, Big Sky, MT, USA, July 25-28, 2003. Binhui Zhu and Tandy Warnow, eds. Lecture Notes in Computer Science DOI: 10.1007/3-540-45071-8.

3. Algorithms in Bioinformatics, Proceedings of the 9th International Workshop, WABI 2009, Philadelphia, PA, USA, September 12-13, 2009. Steven Salzberg and Tandy Warnow, eds. Lecture Notes in Computer Science 5724, Springer 2009, ISBN 978-3-642-04240-9

Journal and Refereed Conference Publications

1. S. Kannan, E. Lawler, and T. Warnow, 1990. Determining the Evolutionary Tree. Proceedings of the First ACM-SIAM Symposium on Discrete Algorithms (SODA) 1990, pp. 475-484.

2. S. Kannan and T. Warnow, 1990. Inferring Evolutionary History from DNA Sequences. Proceedings of the Foundations of Computer Science (FOCS) 1990, pp. 362-371.

3. 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.)

4. 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*.

5. Steel, M. and T. Warnow, 1993. "Kaikoura Tree Theorems: The Maximum Agreement Subtree Problem." *Information Processing Letters,* 48, pp. 77-82.

6. M. Farach, S. Kannan, and T. Warnow, 1993. A robust model for finding optimal evolutionary trees. Proceedings of the Symposium on the Theory of Computing (STOC) 1993.

7. T. Warnow, 1993. Tree Compatibility and Inferring Evolutionary History. Proceedings, ACM-SIAM Symposium on Discrete Algorithms (SODA) 1993.

8. Warnow, T., 1993. "Constructing phylogenetic trees efficiently using compatibility criteria." *New Zealand Journal of Botany*, Vol. 31, pp. 239-248.

9. 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.)

10. 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.)

11. 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.)

12. 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.)

13. 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.)

14. A. Taylor, D. Ringe, and T. Warnow. "Character-based reconstruction of a linguistic cladogram." Proceedings of the 12th International Conference on Historical Linguistics (Manchester, August 1995).

15. Kannan, S. and T. Warnow, 1995. "A fast algorithm for the computation and enumeration of perfect phylogenies" SIAM J. Computing, Vol. 26, No. 6, pp. 1749-1763. (A preliminary version appeared in SODA 1995).

16. Kannan, S., T. Warnow, and S. Yooseph, 1995. "Computing the local consensus of trees." Proceedings SODA 1995, pp. 68-77.

17. 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.

18. M. Bonet, C.A. Phillips, T. Warnow, and S. Yooseph, 1999. Constructing evolutionary trees in the presence of polymorphic characters. Proceedings, ACM Symposium on the Theory of Computing (STOC), 1996.

19. 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.

20. 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)

21. 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.)

22. M. Henzinger, V. King, and T. Warnow, 1996. Constructing a tree from homeomorphic subtrees, with applications to computational molecular biology, SODA 1996, pp. 333-340.

23. 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.)

24. 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.

25. Erdős, P. L., M. Steel, L. Székély, 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.

26. Warnow, T. 1997. "Mathematical approaches to comparative linguistics." *Proceedings of the National Academy of Sciences*, Vol. 94, pp. 6585-6590, 1997.

27. Kannan, S. and T. Warnow, 1997. "A fast algorithm for the computation and enumeration of perfect phylogenies." SIAM J. Computing, Vol. 26, No. 6, pp. 1749-1763. (A preliminary version appeared in SODA 1995).

28. 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.

29. Erdös, 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.

30. Kannan, S., T. Warnow, and S. Yooseph, 1998. "Computing the local consensus of trees." *SIAM J. Computing*, Vol. 27, No. 6, pp. 1695-1724. (This is an extended version of a paper that appeared in SODA 1995).

31. 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.

32. 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.

33. 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.

34. 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.

35. Erdős, P. L., M. Steel, L. Székély, 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.)

36. Erdős, P. L., M. Steel, L. Székély, 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.)

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41. 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.

42. 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`.

43. 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.

44. 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.

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46. 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.

47. 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.

48. 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.

49. 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.

50. 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.

51. 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.

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57. 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.

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