

# CURRICULUM VITAE

TANDY WARNOW  
FOUNDER PROFESSOR OF COMPUTER SCIENCE

## 1 Contact Information

*Department of Computer Science*  
*The University of Illinois at Urbana-Champaign*  
Email: [warnow@illinois.edu](mailto:warnow@illinois.edu)  
Homepage: <http://tandy.cs.illinois.edu>

## 2 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.

## 3 Professional Appointments

- Associate Head for the Department of Computer Science, The University of Illinois at Urbana-Champaign, 2017-2018.
- Founder Professor of Computer Science, the University of Illinois at Urbana-Champaign, 2014-present.
- Member, Carl R. Woese Institute for Genomic Biology. Affiliate of the National Center for Supercomputing Applications (NCSA) and the Unit for Criticism and Interpretive Theory. Affiliate faculty member in the Departments of Mathematics, Electrical and Computer Engineering, Statistics, Animal Biology, Entomology, Plant Biology, and Bioengineering, 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

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

## 6 Current and Former Graduate Students

Current:

- Sarah Christensen (PhD student in Computer Science, PhD expected 2022)
- Erin Molloy (PhD student and NSF graduate fellow in Computer Science at UIUC, co-supervised with Bill Gropp, PhD expected 2020)
- Michael Nute (PhD student in Statistics at UIUC, PhD expected 2019)
- Srilakshmi Pattabiraman (PhD student in Electrical and Computer Engineering, co-supervised with Olgica Milenkovic, PhD expected 2022)
- Pranjali Vachaspati (PhD student and NSF graduate fellow in Computer Science at UIUC, PhD expected 2019)

Former:

- Md. Shamsuzzoha Bayzid (PhD Fall 2016). Assistant Professor, Department of Computer Science and Engineering (CSE), Bangladesh University of Engineering and Technology.
- 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 and Chair of Computer Science at Rice University.
- Serita Nelesen (PhD December 2009), Software developer for Neural Planet
- Nam-phuong 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), Lecturer, Department of Mathematics, University of Tennessee at Knoxville
- Li-San Wang (PhD May 2003), Associate Professor of Pathology and Laboratory Medicine at the University of Pennsylvania.
- Shibu Yooseph (PhD received 2000), Professor of Computer Science at Central Florida University

## 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, Tübingen University, Germany)
- Nam-phuong Nguyen (now at UCSD CS, postdoc with Vineet Bafna)
- Ken Rice (now retired)
- Katherine St. John (Professor of Computer Science, Hunter College, CUNY)
- Elizabeth Sweedyk (Associate Professor of Computer Science, Harvey Mudd College)
- Shel Swenson (Lecturer, University of Tennessee at Knoxville, Mathematics Department)

## 8 Current Grant Support

- 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. (This grant ends August 2019.)
- 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. (This grant ends August 2019.)

- 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 August 14, 2019 (no-cost extension). Award Amount: \$861,625. (No Co-PIs).

## 9 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.

## 10 National and International Service

- Co-organizer, IPAM (Institute for Pure and Applied Mathematics) long program, “Science at Extreme Scales: Where Big Data Meets Large-Scale Computing” Fall 2018
- Faculty, Strategies and Techniques for Analyzing Microbial Population Structures (STAMPS) at Marine Biology Laboratory at Woods Hole, 2017, 2018
- Member, Faculty of 1000, 2017-present
- Genome 10K, Council Member, 2015-present
- Paris Kanellakis Award Committee Member, 2015-present (chair 2017-2018)
- 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.

- Conference co-chair, Intelligent Systems for Molecular Biology (ISMB) 2018.
- Program committee member: 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; ICALP 2005; ISMB 2006, 2007, 2008, 2009, 2012, 2013, 2014, and 2016; JOBIM 2000; RECOMB 1997, 2001, 2002, 2004, 2009, 2010, 2011, 2014, 2016, and 2018; RECOMB-CG 2015, 2017, and 2018; SODA 2001; STOC 1998; WABI 2001, 2002 2004, 2005, 2006, 2009, 2010, 2015, and 2018; 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.

## 11 Invited Lectures

### 2019

- January 25, 2019. Indiana University at Bloomington, Distinguished Lecture, Department of Computer Science
- 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” (HTML)
- April 30, European Bioinformatics Institute, Cambridge UK
- May 28-30, The 6th International Conference on Algorithms for Computational Biology (AlCoB 2019), Berkeley

### 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. (PDF) (PPTX) 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 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)
- Bardonecchia, 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.
- 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.

## Publications

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.
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. 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*.
84. 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.
85. 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.
86. Nichols, J. and T. Warnow, 2008. "Tutorial on computational linguistic phylogeny." *Linguistics and Language Compass*, Vol. 2, Issue 5, September 2008, pages 760-820.
87. 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
88. 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.
89. Swenson, M., F. Barbançon, C.R. Linder, and T. Warnow, 2009. "A simulation study comparing supertree and combined analysis methods using SMIDGen." *Proceedings of the Workshop on Algorithms in Bioinformatics (WABI)*, 2009.
90. Bradner, J.E., N. West, M.L. Grachan, E. Greenberg, S.J. Haggarty, T. Warnow and R. Mazitschek, 2010. "Chemical phylogenetics of histone deacetylases", *Nature Chemical Biology*, 6, pp. 238-243; published online 7 February 2010.
91. Swenson, M.S., F. Barbançon, C.R. Linder, and T. Warnow, 2010. "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. (This journal version contains additional results compared to the WABI conference version.)

92. Swenson, M.S., R. Suri, C.R. Linder, and T. Warnow, 2010. "An experimental study of Quartets MaxCut and other supertree methods." Proceedings of WABI (Workshop on Algorithms for Bioinformatics) 2010.
93. Linder, C.R., R. Suri, K. Liu, and T. Warnow, 2010. "Benchmark datasets and software for developing and testing methods for large-scale multiple sequence alignment and phylogenetic inference". PLoS Currents: Tree of Life, 2010 Nov 18;2:RRN1195. doi: 10.1371/currents.RRN1195.
94. Liu, K., C.R. Linder, and T. Warnow, 2010. "Multiple sequence alignment: a major challenge to large-scale phylogenetics," 2010. PLoS Currents: Tree of Life, 2010 November 19; 2: RRN1198. doi: 10.1371/currents.RRN1198.
95. Swenson, M.S., R. Suri, C.R. Linder, and T. Warnow, 2011. "An experimental study of Quartets MaxCut and other supertree methods." Journal of Algorithms for Molecular Biology, 6(7) (19 April 2011), special issue of selected papers from WABI 2010. (This journal version contains additional results compared to the WABI conference version.)
96. Wang, L.-S., J. Leebens-Mack, K. Wall, K. Beckmann, C. de Pamphilis, and T. Warnow., 2011. "The impact of multiple sequence alignment on phylogeny estimation", IEEE Transactions on Computational Biology and Bioinformatics (TCBB), July 2011, pp. 1108-1119.
97. Yu, Y., T. Warnow, and L. Nakhleh, 2011. "Algorithms for MDC-based Multi-locus Phylogeny Inference: beyond rooted binary gene trees on single alleles." Proceedings of RECOMB 2011, and Journal of Computational Biology 2011, 18(11):1543-1559.
98. Yang, J. and T. Warnow, 2011. "Fast and accurate methods for phylogenomic analyses." 2011. RECOMB-CG 2011 and BMC Bioinformatics 12(Suppl 9): S4 (5 October 2011).
99. Mirarab, S. and T. Warnow, 2011. "FastSP: Linear time calculation of alignment accuracy." Bioinformatics 27(23):3250-3258.
100. Liu, K., C. Randal Linder, and T. Warnow, 2012. "RAxML and FastTree: Comparing Two Methods for Large-Scale Maximum Likelihood Phylogeny Estimation." PLoS-ONE 6(11): e27731. doi:10.1371/journal.pone.0027731.
101. Liu, K., T.J. Warnow, M.T. Holder, S. Nelesen, J. Yu, A. Stamatakis, and C.R. Linder, 2012. "SATé-II: Very Fast and Accurate Simultaneous Estimation of Multiple Sequence Alignments and Phylogenetic Trees". Systematic Biology 61(1):90-106.
102. Swenson, M.S., R. Suri, C.R. Linder, and T. Warnow, 2012. "SuperFine: fast and accurate supertree estimation." Systematic Biology, 61(2):214-227.
103. Mirarab, S., N. Nguyen, and T. Warnow, 2012. "SEPP: SATé-Enabled Phylogenetic Placement." Pacific Symposium on Biocomputing.
104. Neves, D.T., J.L. Sobral, K. Pingali, and T. Warnow, 2012. "Parallelizing Superfine." 27th Symposium on Applied Computing (ACM-SAC), Bioinformatics, 2012, pages 1361–1367, doi = 10.1145/2231936.2231992.
105. Bayzid, Md. S., and T. Warnow, 2012. "Estimating optimal species trees from incomplete gene trees under deep coalescence." Journal of Computational Biology, June 2012, Vol. 19, No. 6:591-605, special issue for Simon Tavaré and Mike Waterman.

106. Nguyen, N., S. Mirarab, and T. Warnow, 2012. "MRL and SuperFine+MRL: new supertree methods." 2012. *J. Algorithms for Molecular Biology*, 7:3, special issue for the Programme for Phylogenetics at the Sir Isaac Newton Institute for Mathematical Sciences, Cambridge University.
107. Liu, K. and T. Warnow, 2012. "Treelength Optimization for Phylogeny Estimation." 2012. *PLoS One*, 7(3):e33104.
108. Warnow, T., 2012. "Standard maximum likelihood analyses of alignments with gaps can be statistically inconsistent." *PLoS Currents Tree of Life*, doi:10.1371/currents.RRN1308.
109. Nelesen, S., K. Liu, L.-S. Wang, C.R. Linder, and T. Warnow, 2012. "DACTAL: divide-and-conquer trees (almost) without alignments." *ISMB 2012 and Bioinformatics*, Vol. 28, pages i274-i282.
110. Barbançon, F., S. Evans, L. Nakhleh, Dr. Ringe, and T. Warnow, 2013. "An experimental study comparing linguistic phylogenetic reconstruction methods". *Diachronica* 2013, 30(2): 143-170. (An initial version of this paper was presented at the conference *Languages and Genes*, held at UC Santa Barbara, and organized by Bernard Comrie.)
111. Bayzid, M.S., S. Mirarab, and T. Warnow, 2013. "Inferring optimal species trees under duplication and loss". *Proceedings, Pacific Symposium on Biocomputing*, Volume 18, 250-261.
112. Bayzid, M. S. and T. Warnow, 2013. "Naive binning improves phylogenomic analyses". *Bioinformatics*. 29(18):2277-2284.
113. Warnow, T, 2013. "Large-scale multiple sequence alignment and phylogeny estimation", Chapter 6 (pages 85-146) in *Models and Algorithms for Genome Evolution*, edited by Cedric Chauve, Nadia El-Mabrouk and Eric Tannier, Springer series on Computational Biology, Volume 19.
114. Mirarab, S., N. Nguyen, and T. Warnow, 2014. "PASTA: ultra-large multiple sequence alignment." *Proceedings RECOMB 2014*. An extended version of this paper appears in the *Journal of Computational Biology*.
115. Mirarab, S. R. Reaz, Md. S. Bayzid, T. Zimmermann, M.S. Swenson, and T. Warnow (2014). "ASTRAL: Genome-Scale Coalescent-Based Species Tree Estimation". *Proceedings of the European Conference on Computational Biology (ECCB) 2014 and Bioinformatics (2014)* 30 (17): i541-i548, doi: 10.1093/bioinformatics/btu462.
116. Bayzid, Md. S., T. Hunt, and T. Warnow (2014). "Disk Covering Methods Improve Phylogenomic Analyses". *Proceedings of RECOMB-CG (Comparative Genomics)*, 2014 and *BMC Genomics* 15 (Suppl. 6): S7.
117. Zimmermann, T., S. Mirarab and T. Warnow (2014). "BBCA: Improving the scalability of \*BEAST using random binning". *Proceedings of RECOMB-CG (Comparative Genomics)*, 2014 and *BMC Genomics* 15 (Suppl. 6): S11.
118. Mirarab, S., Md. S. Bayzid, and T. Warnow (2014). "Evaluating summary methods for multi-locus species tree estimation in the presence of incomplete lineage sorting". *Systematic Biology* 65 (3): 366-380, 2016. (First appeared online in 2014, doi = 10.1093/sysbio/syu063)
119. Wickett, N., S. Mirarab, N. Nguyen, T. Warnow, E. Carpenter, N. Matasci, S. Ayyampalayam, M. S. Barker, J. G. Burleigh, M. A. Gitzendanner, B. R. Ruhfel, E. Wafula, J. P. Der, S. W. Graham, S. Mathews, M. Melkonian, D. E. Soltis, P. S. Soltis, N. W. Miles, C. J. Rothfels, L. Pokorny, A. J. Shaw, L. DeGironimo, D. W. Stevenson, B. Surek, J. C. Villarreal, B. Roure,

- H. Philippe, C. W. dePamphilis, T. Chen, M. K. Deyholos, R. S. Baucom, T. M. Kutchan, M. M. Augustin, J. Wang, Y. Zhang, Z. Tian, Z. Yan, X. Wu, X. Sun, G. Ka-Shu Wong, and J. Leebens-Mack. “Phylotranscriptomic analysis of the origin and early diversification of land plants”, *Proceedings of the National Academy of Sciences*, 2014; volume 111 no. 45, E4859-E4868, published ahead of print October 29, 2014, doi:10.1073/pnas.1323926111.
120. Nguyen, N., S. Mirarab, B. Liu, M. Pop, and T. Warnow (2014). “TIPP:Taxonomic Identification and Phylogenetic Profiling.” *Bioinformatics*, 2014, 30 (24): 3548-3555.
  121. Mirarab, S., N. Nguyen, and T. Warnow (2014). “PASTA: ultra-large multiple sequence alignment for nucleotide and amino acid sequences”. *Journal of Computational Biology*, 22(5): 377-386, 2015 (first appeared online in 2014). This is an extended version of the RECOMB paper (#114).
  122. Mirarab, S., Md. S. Bayzid, B. Boussau, and T. Warnow (2014). “Statistical binning enables an accurate coalescent-based estimation of the avian tree”. *Science*, 12 December 2014: 1250463.
  123. Jarvis, E.D., S. Mirarab, A. J. Aberer, B. Li, P. Houde, C. Li, S. Y. W. Ho, B. C. Faircloth, B. Nabholz, J. T. Howard, A. Suh, C. C. Weber, R. R. da Fonseca, J. Li, F. Zhang, H. Li, L. Zhou, N. Narula, L. Liu, G. Ganapathy, B. Boussau, Md. S. Bayzid, V. Zavidovych, S. Subramanian, T. Gabaldon, S. Capella-Gutierrez, J. Huerta-Cepas, B. Rekepalli, K. Munch, M. Schierup, B. Lindow, W. C. Warren, D. Ray, R. E. Green, M. W. Bruford, X. Zhan, A. Dixon, S. Li, N. Li, Y. Huang, E. P. Derryberry, M. F. Bertelsen, F. H. Sheldon, R. T. Brumfield, C. V. Mello, P. V. Lovell, M. Wirthlin, M. P. C. Schneider, F. Prosdocimi, J. A. Samaniego, A. M. V. Velazquez, A. Alfaro-Nunez, P. F. Campos, B. Petersen, T. Sicheritz-Ponten, A. Pas, T. Bailey, P. Scofield, M. Bunce, D. M. Lambert, Q. Zhou, P. Perelman, A. C. Driskell, B. Shapiro, Z. Xiong, Y. Zeng, S. Liu, Z. Li, B. Liu, K. Wu, J. Xiao, X. Yinqi, Q. Zheng, Y. Zhang, H. Yang, J. Wang, L. Smeds, F. E. Rheindt, M. Braun, J. Fjeldsa, L. Orlando, F. K. Barker, K. A. Jansson, W. Johnson, K.-P. Koepfli, S. O’Brien, D. Haussler, O. A. Ryder, C. Rahbek, E. Willerslev, G. R. Graves, T. C. Glenn, J. McCormack, D. Burt, H. Ellegren, P. Alstrom, S. V. Edwards, A. Stamatakis, D. P. Mindell, J. Cracraft, E. L. Braun, T. Warnow, W. Jun, M. T. P. Gilbert, and G. Zhang (2014). “Whole-genome analyses resolve early branches in the tree of life of modern birds.” *Science* 12 December 2014: 1320-1331. (Co-corresponding author)
  124. Matasci, N., L.-H. Hung, Z. Yan, E. Carpenter, N. J. Wickett, S. Mirarab, N. Nguyen, T. Warnow, S. Ayyampalayam, M. Barker, J. G. Burleigh, M. A. Gitzendanner, E. Wafula, J. P. Der, C. dePamphilis, B. Roure, H. Philippe, B. Ruhfel, N. Miles, S. Graham, S. Mathews, B. Surek, M. Melkonian, D. Soltis, P. Soltis, C. Rothfels, L. Pokorny, J. Shaw, L. DeGironimo, D. Stevenson, J. Villarreal, T. Chen, T. Kutchan, M. Rolf, R. Baucom, M. Deyholos, R. Samudrala, Z. Tian, X. Wu, X. Sun, Y. Zhang, J. Wang, J. Leebens-Mack, and G. K-S. Wang (2014). Data access for the 1,000 Plants (1KP) project. *GigaScience* 2014 3:17, DOI: 10.1186/2047-217X-3-17.
  125. Nguyen, N., S. Mirarab, K. Kumar, and T. Warnow (2015). “Ultra-large alignments using phylogeny-aware profiles”, *Proceedings of Research in Computational Biology (RECOMB) 2015 and Genome Biology* 16:124, 2015. **Highly accessed**
  126. Bayzid, Md. S., S. Mirarab, B. Boussau, and T. Warnow (2015). “Weighted Statistical Binning: enabling statistically consistent genome-scale phylogenetic analyses”, *PLOS One* 10(6): e0129183, 2015.
  127. Mirarab, S. and T. Warnow (2015). “ASTRAL-II: coalescent-based species tree estimation with many hundreds of taxa and thousands of genes”, *ISMB 2015*, and *Bioinformatics*, 31(12):i44-i52, 2015.

128. Roch, S., and T. Warnow (2015). “On the robustness to gene tree estimation error (or lack thereof) of coalescent-based species tree methods”, *Points of View, Systematic Biology*, 64(4):663-676, 2015.
129. Warnow, T (2015). “Concatenation analyses in the presence of incomplete lineage sorting”, *PLOS Currents: Tree of Life* 2015 May 22. Edition 1.  
doi: 10.1371/currents.tol.8d41ac0f13d1abedf4c4a59f5d17b1f7.
130. Davidson, R., P. Vachaspati, S. Mirarab, and T. Warnow (2015). “Phylogenomic species tree estimation in the presence of incomplete lineage sorting and horizontal gene transfer”. *RECOMB-Comparative Genomics, and BMC Genomics*, 2015, 16 (Suppl 10): S1.
131. Chou, J., A. Gupta, S. Yaduvanshi, R. Davidson, M. Nute, S. Mirarab and T. Warnow (2015). “A comparative study of SVDquartets and other coalescent-based species tree estimation methods”. *RECOMB-Comparative Genomics, and BMC Genomics*, 2015, 16 (Suppl 10): S2.
132. Vachaspati, P. and T. Warnow (2015). “ASTRID: Accurate Species TREes from Internode Distances”. *RECOMB-Comparative Genomics, and BMC Genomics*, 2015, 16 (Suppl. 10): S3.
133. Cracraft, J., P. Houde, S.Y.W. Ho, D.P. Mindell, J. Fjeldså, B. Lindow, S.V. Edwards, C. Rahbek, S. Mirarab, T. Warnow, M.T.P. Gilbert, G. Zhang, E.L. Braun, and E.D. Jarvis (2015). Response to Comment on “Whole-genome analyses resolve early branches in the tree of life of modern birds”. *Science*, 2015, volume 349, number 6255, doi = 10.1126/science.aab1578.
134. Mirarab, S., Md. S. Bayzid, B. Boussau, and T. Warnow (2015). Response to Comment on “Statistical binning enables an accurate coalescent-based estimation of the avian tree”. *Science*, 2015, volume 350, number 6257, p. 171, DOI: 10.1126/science.aaa7719.
135. Jarvis, E.D., S. Mirarab, A.A. Aberer, B. Li, P. Houde, C. Li, S. Ho, B. Faircloth, B. Nabholz, J. T. Howard, A. Suh, C. C. Weber, R. R. da Fonseca, A. Alfaro-Nunez, N. Narula, L. Liu, D. Burt, H. Ellegren, S. Edwards, A. Stamatakis, D. Mindell, J. Cracraft, E. Braun, T. Warnow, W. Jun, M.T.P. Gilbert, G. Zhang, and The Avian Phylogenomics Consortium (2015). Phylogenomic analyses data of the avian phylogenomics project. *GigaScience* 2015, 4:4, DOI:10.1186/s13742-014-0038-1.
136. Tarver, J.E., M. d. Reis, S. Mirarab, R. J. Moran, S. Parker, J.E. O’Reilly, B.L. King, M.J. O’Connell, R.J. Asher, T. Warnow, K. J. Peterson, P.C.J. Donoghue, and D. Pisani (2016). The interrelationships of placental mammals and the limits of phylogenetic inference. *Genome Biology and Evolution* 2016, 8(2): 330-344.
137. Nguyen, N., T. Warnow, M. Pop, and B. White (2016). A perspective on 16S rRNA operational taxonomic unit clustering using sequence similarity. *Nature Biofilms and Microbiomes* 2, Article number 16004 (2016), doi:10.1038/npjbiofilms.2016.4.
138. Hansen, T., S. Mollerup, N. Nguyen, L. Vinner, N. White, M. Coghlan, D. Alquezar-Planas, T. Joshi, R. Jensen, H. Fridholm, K. Kjaransdottir, T. Mourier, T. Warnow, G. Belsham, T. Gilbert, L. Orlando, M. Bunce, E. Willerslev, L. Nielsen, and A. Hansen (2016). High diversity of picornaviruses in rats from different continents revealed by deep sequencing. (Nature Publishing Group) *Emerging Microbes & Infections* 5(8): e90.
139. Nguyen, N., M. Nute, S. Mirarab, and T. Warnow (2016). HIPPI: Highly Accurate Protein Family Classification with Ensembles of HMMs. *BMC Bioinformatics* 17(10): 89, special issue for RECOMB-CG.



140. Nute, M. and T. Warnow (2016). Scaling statistical multiple sequence alignment to large datasets. *BMC Bioinformatics* 17(1): 135, special issue for RECOMB-CG.
141. Uricchio, L., T. Warnow, and N. Rosenberg (2016). An analytical upper bound on the number of loci required for all splits of a species tree to appear in a set of gene trees. *BMC Bioinformatics* 17(14): 241, special issue for RECOMB-CG.
142. Vachaspati, P. and T. Warnow (2016). FastRFS: Fast and Accurate Robinson-Foulds Supertrees using Constrained Exact Optimization *Bioinformatics* 2016; doi: 10.1093/bioinformatics/btw600. (Special issue for papers from RECOMB-CG)
143. Welch, L., C. Brooksbank, R. Schwartz, S.L. Morgan, B. Gaeta, A.M. Kilpatrick, D. Mietchen, B.L. Moore, N. Mulder, M. Pauley, W. Pearson, P. Radivojac, N. Rosenberg, A. Rosenwald, G. Rustici, and T. Warnow (2016). Applying, Evaluating and Refining Bioinformatics Core Competencies (An Update from the Curriculum Task Force of ISCB's Education Committee). *PLoS Comput Biol* 12(5): e1004943, 2016.
144. Boyd, B.M., J.M. Allen, N. Nguyen, A.D. Sweet, T. Warnow, M.D. Shapiro, S.M. Villa, S.E. Bush, D.H. Clayton, and K.P. Johnson (2017). Phylogenomics using target-restricted assembly resolves intra-generic relationships of parasitic lice (Phthiraptera: *Columbicola*). *Systematic Biology* 2017, doi: 10.1093/sysbio/syx027.
145. Allen, J.M., B. Boyd, N. Nguyen, P. Vachaspati, T. Warnow, D.I. Huang, P.G. Grady, K.C. Bell, Q.C. Cronk, L. Mugisha, B.R. Pittendrigh, L.M. Soledad, D.L. Reed, and K.P. Johnson. Phylogenomics from whole genome sequences using aTRAM. *Systematic Biology* 2017, doi:10.1093/sysbio/syw105.
146. Boyd, B.M., J.M. Allen, N. Nguyen, P. Vachaspati, Z.S. Quicksall, T. Warnow, L. Mugisha, K.P. Johnson, and D.L. Reed. Primates, Lice and Bacteria: Speciation and Genome Evolution in the Symbionts of Hominid Lice. *Molecular Biology and Evolution* 2017; 34 (7): 1743-1757. doi: 10.1093/molbev/msx117
147. Christensen, S., E. Molloy, P. Vachaspati, and T. Warnow. Optimal Completion of Incomplete Gene Trees in Polynomial Time. , 17th International Workshop on Algorithms for Bioinformatics (WABI) 2017. *Lecture Notes in Computer Science (LNCS)*, Springer.
148. Bayzid, M.S. and T. Warnow. Gene Tree Parsimony for Incomplete Gene Trees. 17th International Workshop on Algorithms for Bioinformatics (WABI) 2017. *Lecture Notes in Computer Science (LNCS)*, Springer.
149. Molloy, E. and T. Warnow. To Include or Not to Include: The Impact of Gene Filtering on Species Tree Estimation Methods. *Systematic Biology*, Volume 67, Issue 2, 1 March 2018, pages 285-303. <https://doi.org/10.1093/sysbio/syx077>.
150. Vachaspati, P. and T. Warnow. Enhancing searches for optimal trees using SIESTA. *Proceedings RECOMB-CG (RECOMB International Workshop on Comparative Genomics) 2017*, *Lecture Notes in Computer Science book series (LNCS, volume 10562)*, pages 232-255.
151. Warnow, T. *Computational Phylogenetics: An Introduction to Designing Methods for Phylogeny Estimation*. Cambridge University Press.
152. Bayzid, Md S. and T. Warnow. Gene tree parsimony for incomplete gene trees: addressing true biological loss. *Algorithms for Molecular Biology*, 13:1., 2018. DOI: 10.1186/s13015-017-0120-1.

153. Eiserhardt, W., A. Antonelli, D.J. Bennett, L.R. Botigue, J.G. Burleigh, S. Dodsworth, B.J. Enquist, F. Forest, J.T. Kim, A.M. Kozlov, I.J. Leitch, B.S. Maitner, S. Mirarab, W.H. Piel, O.A. Perez-Escobar, L. Pokorny, C. Rahbek, B. Sandel, S.A. Smith, A. Stamatakis, R.A. Vos, T. Warnow, W.J. Baker. A roadmap for global synthesis of the plant tree of life. *American Journal of Botany*, Vol. 105, Issue 3, 2018. doi:10.1002/ajb2.1041.
154. Christensen, S., E. Molloy, P. Vachaspati, and T. Warnow. OCTAL: Optimal Completion of Gene Trees in Polynomial Time. *Algorithms for Molecular Biology*, volume 13, number 6, 2018. <https://doi.org/10.1186/s13015-018-0124-5>.
155. Vachaspati, P. and T. Warnow. SIESTA: Enhancing searches for optimal supertrees and species trees. *BMC Genomics*, 19(Suppl 5):252, 2018. DOI: 10.1186/s12864-018-4621-1.
156. Nute, M., E. Molloy, J. Chou, and T. Warnow. The Performance of Coalescent-Based Species Tree Estimation Methods under Models of Missing Data. *BMC Genomics*, 19(Suppl 5):286, 2018. DOI: 10.1186/s12864-018-4619-8.
157. Vachaspati, P. and T. Warnow. SVDquest: Improving SVDquartets species tree estimation using exact optimization within a constrained search space. *Molecular Phylogenetics and Evolution*, Vol. 124, pp. 122-136, 2018. DOI:10.1016/j.ympev.2018.03.006.
158. Johnson, K.P., N. Nguyen, A.D. Sweet, B.M. Boyd, T. Warnow, and J.M. Allen (2018). Simultaneous radiation of bird and mammal lice following the K-Pg boundary. *Biology Letters*, Vol. 14, page 20180141, DOI: 10.1098/rsbl.2018.0141
159. Zhang, Q., S. Rao, and T. Warnow. New absolute fast converging phylogeny estimation methods with improved scalability and accuracy. *Proceedings of WABI (Workshop on Algorithms for Bioinformatics) 2018*. DOI: 10.4230/LIPIcs.WABI.2018
160. Pattabiraman, S. and T. Warnow. Are Profile Hidden Markov Models Identifiable? *Proceedings of ACM-BCB 2018*, pages 448-456, doi:10.1145/3233547.3233563.
161. Collins, K. and T. Warnow. PASTA for Proteins. *Bioinformatics, Applications Note*, 2018. <https://doi.org/10.1093/bioinformatics/bty495>
162. Molloy, E. and T. Warnow. NJMerge: A generic technique for scaling phylogeny estimation methods and its application to species trees. *Proceedings of RECOMB-CG (Satellite conference for Comparative Genomics)*, Lecture Notes in Computer Science, vol 11183. Springer.
163. Roch, S., M. Nute, and T. Warnow. Long-branch attraction in species tree estimation: inconsistency of partitioned likelihood and topology-based summary methods. Preliminary version at arXiv:1803.02800. *Systematic Biology*, syy061, <https://doi.org/10.1093/sysbio/syy061>
164. Nute, M.G., E. Saleh, and T. Warnow. Evaluating Statistical Multiple Sequence Alignment in Comparison to Other Alignment Methods on Protein Data Sets. *Systematic Biology* syy068, 2018, doi:10.1093/sysbio/syy068.
165. N. Shah, M. Nute, T. Warnow, and M. Pop. Misunderstood parameter of NCBI BLAST impacts the correctness of bioinformatics workflows. *Bioinformatics*, byt833, 2018.