

# CURRICULUM VITAE

LI-SAN WANG

July 30, 2009

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## PERSONAL INFORMATION

Citizenship: Taiwan  
Visa status: United States Permanent Resident (Greencard)  
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## RESEARCH INTERESTS

My research interests include *disease-related bioinformatic research* (aging, neurodegenerative diseases, and cancer), *computational methods for microarray analysis and systems biology* (semi-parametric and non-parametric analysis, transcription factor prediction and regulatory networks, and genome-wide association study), and *computational phylogenetics* (genome rearrangement phylogeny, phylogenetic multiple sequence alignment, nontree evolution).

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## EDUCATION

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| 05/2003 | Ph.D. in Computer Sciences, University of Texas at Austin<br><i>Thesis title:</i> Large-Scale Phylogenetic Analysis<br><i>Advisor:</i> Tandy Warnow   |
| 06/2000 | M.S., Computer Sciences, University of Texas at Austin.   |
| 06/1996 | M.S., Electrical Engineering, National Taiwan University.<br><i>Thesis title:</i> Design and Implementation of an Adaptive Modeling Unit for Multialphabet Arithmetic Compression<br><i>Advisor:</i> Tzi-Dar Chiueh |
| 06/1994 | B.S., Electrical Engineering, National Taiwan University.   |
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## WORKING EXPERIENCE

DEPARTMENT OF PATHOLOGY AND LABORATORY MEDICINE/INSTITUTE ON AGING/PENN CENTER FOR BIOINFORMATICS (PCBI), UNIVERSITY OF PENNSYLVANIA

01/2007–Present Assistant Professor.

DEPARTMENT OF BIOLOGY/ABRAMSON CANCER INSTITUTE, UNIVERSITY OF PENNSYLVANIA

07/2003–12/2006 Postdoctoral Fellow.

DEPARTMENT OF COMPUTER SCIENCES, UNIVERSITY OF TEXAS AT AUSTIN

07/2000–05/2003 Research assistant.

09/1998–05/2000 Teaching assistant, *Systems Modeling and Computer Systems Architecture*.

ARMY, REPUBLIC OF CHINA (TAIWAN)

09/1996–06/1998 Second lieutenant, infantry.

DEPARTMENT OF ELECTRICAL ENGINEERING, NATIONAL TAIWAN UNIVERSITY

09/1995–06/1996 Research assistant.

09/1994–06/1995 Teaching assistant, *Electronics* (undergraduate).

## AWARDS, HONORS, AND GRANTS

01/2009–12/2010 Co-Principal Investigator, *Genome-wide Analysis of the Double-Stranded RNA Component of Eukaryotic Transcriptomes*, Penn Genome Frontiers Institute (PGFI) Pilot Grant, total amount: \$120,000 (PI: Brian Gregory).

01/2008–12/2008 Principal Investigator, *Novel Bioinformatic Approaches for Modeling Age-Related Gene Expression Progression*, University of Pennsylvania Research Foundation Pilot Grant, total amount: \$24,378.

07/2007–06/2008 Principal Investigator, *The role of G-quadruplexes in senescence through RecQ-dependent pathways*, University of Pennsylvania Institute on Aging Pilot Grant, total amount: \$50,000.

09/2004–12/2006 NIH Postdoctoral Training Grant, Bioinformatics, Program Director: Lyle Unger.

09/2003–08/2004 NIH Postdoctoral Training Grant, Cancer and Immunopathobiology, Program Director: Mark Greene.

08/2002 Student travel fellowship, 10th International Conference on Intelligent Systems for Molecular Biology (ISMB'02).

11/2001 Student travel fellowship, Graduate School, University of Texas.

04/2001 Student travel fellowship, 33rd Symposium on Theory of Computing (STOC'01).

09/1998–06/2000 University of Texas at Austin Departmental Scholarship (2 years).

06/1998 Award for excellence in mandatory military service, Republic of China (Taiwan) Army.

09/1994–06/1996 National Taiwan University Departmental Scholarship.

## PROFESSIONAL SERVICES AND AFFILIATION

- Member, Association for Computing Machinery (ACM), Institute of Electrical and Electronic Engineers (IEEE), Society for Neuroscience (SfN), and International Society for Computational Biology (ISCB).
- Organization team for the Emerging Information Technology Conference (EITC): Publications/Proceedings (2002), Coordinator (2003), Program Committee/Co-chair of Bioinformatics (2004), Coordinator (2006), Co-chair of Organizational Committee and Co-chair Bioinformatics/Systems Biology Track, (2007), Vice-Chair of Advisory and Management Committee, Co-chair, Workshop on Bioinformatics, Biotechnology, Medicine, and Public Health (August 6-7, 2009 at MIT).
- Co-Chair, EITC-Bio 2008 Workshop (June 7, 2008 at Princeton University).

- Program Committee for RECOMB Satellite Workshop on Comparative Genomics (2004), Workshop on Algorithms in Bioinformatics (WABI 2007 and 2009), IEEE International Conference on Bioinformatics and BioEngineering (BIBE 2007) International Symposium on Bioinformatics Research and Applications (ISBRA 2007, 2008, 2009) IEEE International conference on Bioinformatics and Biomedicine (BIBM 2007 and 2008), and International Conference on Bioinformatics and Computational Biology (BICOB 2008 and 2009).
- Grant Proposal Reviewer for *American Mathematical Association, Hong Kong Research Grants Council, US-Israel Binational Science Foundation, Leukemia and Lymphoma Society, and National Security Agency.*
- Referee for journals including *Computational Statistics and Data Analysis, Discrete Applied Mathematics, Gene, IEEE Transaction for Computational Biology and Bioinformatics, BMC Bioinformatics, International Journal of Computer Mathematics, American Journal of Human Genetics, In Silico Biology, Journal of Computational Biology, Journal for Computational Optimization, Mathematical Biology, Molecular Phylogenetics and Evolution, Pattern Recognition, Systematic Biology, Computational Statistics and Data Analysis,* and conferences including *COCOON, EMBC, RECOMB, WABI, BIBE, BIBM, and APBC.*

## PUBLICATIONS

*(Many of my publications are in computer science journals and conference proceedings. Computer science proceedings are peer-reviewed and often considered equally or more prestigious than journals due to their timely and competitive nature. It is also conventional the authors are listed by the alphabetical order of their last names in computer science.)*

### Papers in Peer-Reviewed Journals:

1. Li-San Wang, Jim Leebens-Mack, P. Kerr Wall, Kevin Beckmann, Claude W. dePamphilis, and Tandy Warnow, "The impact of multiple protein sequence alignment on phylogenetic estimation," *IEEE Transactions on Computational Biology and Bioinformatics (TCBB)*, in press.
2. Shane T. Jensen, Sameer Soi, and Li-San Wang, "A Bayesian approach to efficient differential allocation for resampling-based significance testing," *BMC Bioinformatics*, 2009,10:198.
3. Erika L. Pearce, Matthew C. Walsh, Pedro J. Cejas, Gretchen M. Harms, Hao Shen, Li-San Wang, Russell G. Jones, and Yongwon Choi, "Enhancing CD8 T-cell memory by modulating fatty acid metabolism," *Nature*, 2009; DOI: 10.1038/nature08097.
4. Shuzhang Yang, Kai Wang, Brittany Gregory, Wade Berrettini, Li-San Wang, Hakon Hakonarson, and Maja Bucan, "Genomic Landscape of a Three-generation Pedigree Segregating Affective Disorder," *PLoS One*, 2009; 4(2): e4474.
5. Sheng Guo, Li-San Wang, and Junhyong Kim, "Large-Scale Simulation of RNA Macroevolution by an Energy-Dependent Fitness Model," *Systematic Biology*, accepted for publication.
6. Steve G. Hershman, Qijun Chen, Julia Y. Lee, Marina L. Kozak, Peng Yue, Li-San Wang, and F. Brad Johnson, "Genomic distribution and functional analyses of potential G-quadruplex-forming sequences in *Saccharomyces cerevisiae*," *Nucleic Acids Research*, 36(1):144-156, 2008.
7. Larry Singh, Li-San Wang, and Sridhar Hannenhalli, "TREMOR – a tool for retrieving transcriptional modules by incorporating motif covariance," *Nucleic Acids Research*, 35(21):7360-7371, 2007.
8. Logan Everett, Li-San Wang, and Sridhar Hannenhalli, "Dense subgraph computation via stochastic search: application to detect transcriptional modules," *Bioinformatics: Proceedings of The Twelfth International Conference on Intelligent Systems and Molecular Biology (ISMB'06)*, 22(14):e117-e123, 2006.

9. Liying Cui, Jim Leebens-Mack, Li-San Wang, Jijun Tang, Linda Rymarquis, David B. Stern, and Claude W. dePamphilis, “Adaptive Evolution of Chloroplast Genome Structure Inferred Using a Parametric Bootstrap Approach,” *BMC Evolutionary Biology*, 6:13, 2006.
10. Li-San Wang and Tandy Warnow, “Reconstructing Chromosomal Evolution,” *SIAM Journal on Computing*, 36: 99-131, 2006.
11. Li-San Wang, Tandy Warnow, Bernard M.E. Moret, Robert K. Jansen, and Linda A. Raubeson, “Distance-based Genome Rearrangement Phylogeny,” *Journal of Molecular Evolution*, 63(4):473-83, 2006.
12. Fan Ge, Li-San Wang, and Junhyong Kim, “Genome-scale estimates of horizontal gene transfer rates using the COG database,” *Public Library of Science (PLOS) Biology*, 3(10):e316, 2005
13. Sridhar Hannenhalli and Li-San Wang, “Enhanced position weight matrices using mixture models,” *Bioinformatics: Proceedings of The Eleventh International Conference on Intelligent Systems and Molecular Biology (ISMB’05)*, 21(Supp.1):i204-i212, 2005.
14. Matthew Spencer, Barbara Bordalejo, Li-San Wang, Adrian C. Barbrook, Linne R. Mooney, Peter Robinson, Tandy Warnow, and Christopher J. Howe, “Gene Order Analysis Reveals the History of *The Canterbury Tales* Manuscripts,” 37(1):97-109, *Computers and the Humanities*, Feb. 2003.
15. Cara Stockham, Li-San Wang, and Tandy Warnow, “Postprocessing of Phylogenetic Analysis Using Clustering,” *Bioinformatics: Proceedings of the Tenth International Conference on Intelligent Systems for Molecular Biology (ISMB’02)*, 18(Supp.1):285–293, 2002.
16. Bernard M.E. Moret, Jijun Tang, Li-San Wang, and Tandy Warnow, “Steps Toward Accurate Reconstructions of Phylogenies from Gene-Order Data,” *Journal of Computer and System Sciences: Special Issue of Computational Biology*, 65(3):508-525, 2002 (invited article).
17. Bernard M.E. Moret, Li-San Wang, and Tandy Warnow, “New Software for Computational Phylogenetics,” *IEEE Computer: Special Issue on Bioinformatics*, 35(7):55-64, July 2002.
18. Bernard M.E. Moret, Li-San Wang, Tandy Warnow, and Stacia Wyman, “New Approaches for Reconstructing Phylogenies Based on Gene Order,” in *Bioinformatics: Proceedings of the Ninth International Conference on Intelligent Systems for Molecular Biology (ISMB’01)*, 17(Supp.1):165–173, 2001 (this paper was voted as one of the best five papers of the conference).

#### **Book Chapters:**

1. Lauren M.F. Merlo, Li-San Wang, John W. Pepper, Peter S. Rabinovitch and Carlo C. Maley. “Polyploidy, Aneuploidy and the Evolution of Cancer,” In Poon RYC, ed., *Polyploidization and Cancer*, Austin/New York: Landes Bioscience, Inc. and Springer Science+Business Media, in press.
2. Luay Nakhleh and Li-San Wang, “Phylogenetic Networks: Properties and Relationship to Trees and Clusters,” *LNCS Transactions on Computational Systems Biology* 3680, pp. 82-99, 2005 (special invitation).
3. Li-San Wang and Tandy Warnow, “Distance-Based Genome Rearrangement Phylogeny,” in O. Gascuel ed., *Mathematics of Evolution and Phylogeny*, pp. 353–380, Oxford Univ. Press, 2005.
4. Mary E. Cosner, Robert K. Jansen, Bernard M.E. Moret, Linda A. Raubeson, Li-San Wang, Tandy Warnow, and Stacia Wyman, “An Empirical Comparison of Phylogenetic Methods on Chloroplast Gene Order Data in *Campanulaceae*,” in D. Sankoff and J. Nadeau, ed., *Comparative Genomics: Empirical and Analytical Approaches to Gene Order Dynamics, Map Alignment, and the Evolution of Gene Families*, pages 99–121, Kluwer Academic, 2000.

#### **Papers in Peer-Reviewed Conference Proceedings:**

\* *Note: Papers in ISMB'01, ISMB'02, ISMB'05, and ISMB'06 are published in the journal Bioinformatics as special issues, and are listed in the Journal section above*

1. Li-San Wang, Shane T. Jensen, and Sridhar Hannenhalli, “An Interaction-dependent model for transcription factor binding,” *LNCS: Second Annual RECOMB Satellite Workshop on Regulatory Genomics*, Volume 4023, pp. 225-234, 2006.
2. Li-San Wang, Doris Wagner, Chang Seob Kwon, Yanhui Su, and Junhyong Kim, “Transcriptional Target Prediction Using Qualitative Reasoning,” in *Proceedings of the 28th Annual International Conference of the IEEE Engineering in Medicine and Biology Society (EMBC'06)*, pp. 3138-3141, 2006.
3. Angelov Stanislav, Boulos Harb, Sampath Kannan, and Li-San Wang, “Weighted Isotonic Regression under  $L_1$  Norm,” in *Proceedings of the Seventeenth Annual ACM-SIAM Symposium on Discrete Algorithms (SODA'06)*, pp. 783-791, 2006.
4. Jijun Tang and Li-San Wang, “Improving Genome Rearrangement Phylogeny Using Sequence-Style Parsimony,” in *Proceedings of the IEEE Fifth Symposium on Bioinformatics and Bioengineering (BIBE'05)*, pages 137–144.
5. Luay Nakhleh, Derek Ruths, and Li-San Wang, “RIATA-HGT: A Fast and Accurate Heuristic for Reconstructing Horizontal Gene Transfer,” in *Lecture Notes of Computer Science No. 3595: The Eleventh International Computing and Combinatorics Conference (COCOON'05)*, pages 84–93.
6. Luay Nakhleh and Li-San Wang, “Phylogenetic Networks, Trees, and Clusters,” in *Lecture Notes in Computer Science No. 3515: 2005 International Workshop on Bioinformatics Research and Applications (IWBRA'05)*, pages 919–926.
7. Stanislav Angelov, Boulos Harb, Sampath Kannan, Sanjeev Khanna, Junhyong Kim, and Li-San Wang, “Genome Identification and Classification by Short Oligo Arrays,” in *Lecture Notes for Computer Sciences No. 3240: Proceedings for the Fourth Workshop on Algorithms in Bioinformatics (WABI'04)*, pages 400–411, 2004.
8. Li-San Wang, “Genome Rearrangement Phylogeny Using Weighbor,” in *Lecture Notes for Computer Sciences No. 2452: Proceedings for the Second Workshop on Algorithms in Bioinformatics (WABI'02)*, pages 112–125, Springer-Verlag, 2002.
9. Li-San Wang, Robert K. Jansen, Bernard M.E. Moret, Linda A. Raubeson, and Tandy Warnow, “Fast Phylogenetic Methods for Genome Rearrangement Evolution: An Empirical Study,” in *Proceedings of the Fifth Pacific Symposium of Biocomputing (PSB'02)*, pages 524–535, 2002.
10. Li-San Wang, “Exact-IEBP: A New Technique for Estimating Evolutionary Distances Between Whole Genomes,” in *Lecture Notes for Computer Sciences No. 2149: Proceedings for the First Workshop on Algorithms in Bioinformatics (WABI'01)*, pages 175–188, Springer-Verlag, 2001.
11. Li-San Wang and Tandy Warnow. “Estimating True Evolutionary Distances Between Genomes.” in *Proceedings of the Thirty-Third Annual ACM Symposium on the Theory of Computing (STOC'01)*, pages 637–646, ACM Press, 2001.
12. Mary E. Cosner, Robert K. Jansen, Bernard M.E. Moret, Linda A. Raubeson, Li-San Wang, Tandy Warnow, and Stacia Wyman, “A New Fast Heuristic for Computing the Breakpoint Phylogeny and Experimental Phylogenetic Analyses of Real and Synthetic Data,” In *Proceedings of the Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB'00)*, pages 104–115, 2000.

#### **Papers Under Review and Manuscripts:**

1. Shane T. Jensen, Sameer Soi, Li-San Wang, “A Bayesian Approach to Efficient Differential Allocation for Resampling-Based Significance Testing,” submitted to *BMC Bioinformatics*.

2. Li-San Wang, Jim Leebens-Mack, Kerr Wall, Kevin Beckmann, Claude dePamphilis, and Tandy Warnow, "The Impact of Protein Multiple Sequence Alignment on Phylogenetic Estimation," submitted to *IEEE Transaction on Computational Biology and Bioinformatics*.
3. Mingyao Li and Li-San Wang, "A Phylogenetic Approach for Population Stratification Correction in Genetic Association Studies," manuscript for *Bioinformatics*.
4. Kajia Cao, Alice Chen-Plotkin, Josh Plotkin, and Li-San Wang, "Age-correlated gene expression in normal and neurodegenerative human brain tissues," manuscript for *Genome Research*.
5. Jay E. Johnson, Kajia Cao, Paul Ryvkin, Marina Kozak, F. Brad Johnson and Li-San Wang, "Evidence for transcriptional regulation by the Werner and Bloom syndrome proteins via G-quadruplex targets," manuscript for *Genome Research*.
6. Li-San Wang, Alex Chavez, Jay E. Johnson, and F. Brad Johnson, "Evidence of a G4-DNA-related Senescence Signature in Yeast and Human," in preparation for *Genome Research*.
7. Paul Ryvkin, Steve Hershman, Otto Valladares, F. Brad Johnson, and Li-San Wang "G4Pred: Software for G-Quadruplex Sequence Prediction," in preparation for *Bioinformatics*.
8. Li-San Wang, Kai Wang, Andrew Singleton, Maja Bucan, "Search for copy number variation in children with Autism Spectrum Disorders from Croatia," in preparation for *PLoS Genetics*.
9. Li-San Wang, Shu-Kai Chang, Susan Leight, Malgorzata Knapik-Czajka, Leslie M. Shaw, Virginia M.-Y. Lee, John Q. Trojanowski, and Christopher M. Clark, "A comparison of multiplex xMAP Luminex and ELISA as CSF pathological peptide assays for diagnosis of Alzheimer's disease ," in preparation for *Archives of Neurology*.
10. Alena Y Zhang, Blaine W Robinson, Kajia Cao, Kathryn C Behling, Meenakshi Devidas, Todd A Alonzo, Susana C Raimondi, Andrew J Carroll, Cheryl L Willman, Li-San Wang, and Carolyn A Felix, "Cell death regulatory gene expression in acute leukemia in infants correlates with MLL rearrangement status and prognostic clinical covariates," in preparation for *Blood*.

#### Abstracts in Conference Proceedings:

1. Li-San Wang, Shu-Kai Chang, Susan Leight, Malgorzata Knapik-Czajka, Leslie M. Shaw, Virginia M.-Y. Lee, John Q. Trojanowski, and Christopher M. Clark, "A comparison of multiplex xMAP Luminex and ELISA as CSF pathological peptide assays for diagnosis of Alzheimer's disease ," Alzheimer's Disease Conference/ Parkinson's Disease Conference (AD/PD) 2009, March 11-15, Prague, Czech Republic.
2. Alena Y Zhang, Blaine W Robinson, Kajia Cao, Kathryn C Behling, Meenakshi Devidas, Todd A Alonzo, Susana C Raimondi, Andrew J Carroll, Cheryl L Willman, Li-San Wang, and Carolyn A Felix, "Cell death regulatory gene expression in acute leukemia in infants correlates with MLL rearrangement status and prognostic clinical covariates," American Society of Hematology (ASH) 2008, December 6-9, San Francisco, CA.
3. Blaine W. Robinson, Kajia Cao, Joanne M Hilden, Patricia A. Dinndorf, Nyla A. Heerema, Harland Sather, Ron McGlennen, Gregory H. Reaman, Li-San Wang, and Carolyn A. Felix, blast cell gene expression in MLL-rearranged infant ALL and MLL-AF4 directs a distinct gene expression profile related to CNS disease," American Society of Hematology (ASH) 2008, December 6-9, San Francisco, CA.
4. Alena Y. Zhang, Blaine W. Robinson, Li-San Wang, Kaija Cao, Lori Cory, Jeffrey S. Barrett, Susan B. Atlas, Cheryl L. Willman, Meenakshi Devidas, Andrew Carroll, Stephen P. Hunger, Jonni S. Moore, Craig B. Thompson, Mondira Kundu, and Carolyn A. Felix, "Pan-anti-apoptotic BCL-2 family inhibitor, obatoclax, activates autophagic cell death pathway and has potent cytotoxicity in infant and pediatric MLL rearranged leukemias," American Society of Hematology (ASH) 2008, December 6-9, San Francisco, CA.

5. Liying Cui, Jude E. Maul, Li-San Wang, David B. Stern, and Claude W. dePamphilis, "Unusual Gene Clustering in a Highly Rearranged Chloroplast Genome," *the Society for Molecular Biology and Evolution Annual Conference (SMBE)*, June 26-29, 2003.
6. Linda Raubeson, David Bader, Bernard M. E. Moret, Li-San Wang, Tandy Warnow, and Stacia K. Wyman, "Inferring phylogenies of photosynthetic organisms from chloroplast gene orders," *Botany* 2001, August 12 - 16, 2001.

#### Other Publications:

1. Li-San Wang, "Large-Scale Phylogenetic Analysis," *Ph.D. Dissertation*, University of Texas, May 2003.
2. Li-San Wang, "Design and Implementation of an Adaptive Modeling Unit for Multialphabet Arithmetic Compression," *Master's Thesis*, National Taiwan University, July 1996.

#### TALKS AND CONFERENCE PRESENTATIONS

1. "The impact of Multiple Protein Sequence Alignment on Phylogenetic Estimation," CIPRES All Hands Meeting, University of California at Berkeley, Berkeley, CA, July 22, 2009.
2. "Bioinformatic Approaches to Aging-Associated Gene Expression Modulation," Department of Pathology and Laboratory Medicine Grand Rounds, University of Pennsylvania, Philadelphia, PA, June 22, 2009.
3. "A Simple Introduction to Genome-Wide Association Studies," New York Academic Forum, Taipei Economic and Cultural Office, New York, NY, December 19, 2008.
4. "Genome-Wide Association Studies for Brain Disorders," Penn Center for Bioinformatics Annual Retreat, Philadelphia, PA, November 11, 2008.
5. "Introduction to NCBI and Other Online Bioinformatics Resources," Society for Developmental Biology Annual Meeting, Philadelphia, PA, July 28, 2008.
6. "Scaling Genome Rearrangement Phylogeny Reconstruction," Microsoft Research Workshop on Computational Aspects of Biological Information (CABI), Redmond, WA, December 6, 2007.
7. "Phylogenetic Estimation for Complex Evolutionary Processes," Center for Computational Biology and Bioinformatics, University of Maryland at College Park, November 15, 2007.
8. "Regulatory Module Discovery With Heterogeneous Data by Multipartite Cocustering," 39th Symposium on the Interface: Computing Science and Statistics: Systems Biology, Philadelphia, PA, May 25, 2007.
9. "Clustering in the Space of Phylogenies," Department of Computer and Information Science and Interdisciplinary Faculty Seminar on Biomedical Informatics, Fordham University, New York City, February 22, 2007.
10. "Phylogenetic Estimation for Complex Evolutionary Processes," Institute of Information Science, Academia Sinica, Taipei, Taiwan, January 4, 2007.
11. "Phylogenetic Estimation for Complex Evolutionary Processes," Department of Computer Science and Information Engineering, National Taiwan University, Taipei, Taiwan, December 22, 2006.
12. "Interaction and Progression Modeling from Functional Genomics Data," Institute on Aging and Department of Pathology and Laboratory Medicine, University of Pennsylvania, April 20, 2006.
13. "Phylogenetic Estimation for Complex Evolutionary Processes," School of Computer Science, University of New Mexico, Albuquerque, NM, March 30, 2006.

14. "Phylogenetic Estimation for Complex Evolutionary Processes," School of Computer Science, McGill University, Montreal, Canada, March 22, 2006.
15. "Phylogenetic Estimation for Complex Evolutionary Processes," Department of Computer Science, University of Pittsburgh, Pittsburgh, PA, February 28, 2006.
16. "Phylogenetic Estimation for Complex Evolutionary Processes," Department of Biology, Virginia Polytechnic Institute and State University, Blacksburg, VA, February 16, 2006.
17. "Genome Rearrangement Phylogeny," Department of Computer Science, Virginia Polytechnic Institute and State University, December 13, 2005.
18. "Improving Genome Rearrangement Phylogeny Using Sequence-Style Parsimony," conference presentation, *IEEE Fifth Symposium on Bioinformatics and Bioengineering (BIBE'05)*, University of Minnesota at Twin Cities, October 20, 2005.
19. "Enhanced position weight matrices using mixture models," conference presentation, *Thirteenth International Conference on Intelligent Systems for Molecular Biology (ISMB'05)*, Detroit, USA, June 28, 2005.
20. "Improving Genome Rearrangement Phylogeny Using Sequence-Style Parsimony," *Biocomplexity Workshop*, University of Texas at Austin, April 29, 2005.
21. "Genome Rearrangement Phylogeny," Department of Mathematics, Lehigh University, April 27, 2005.
22. "Genome Rearrangement Phylogeny," Department of Computer Science, University of Illinois at Urbana Champaign, April 4, 2005.
23. "Phylogenetic and Functional Analyses at the Genomic Scale," Department of Biostatistics and Medical Informatics, University of Wisconsin at Madison, March 9, 2005.
24. "Phylogenetic and Functional Analyses at the Genomic Scale," Department of Biomedical Informatics, Ohio State University, February 28, 2005.
25. "Semi-Parametric Gene Ranking for Microarray Experiments," *the Fourth Annual Emerging Information Technology Conference (EITC)*, Princeton University, October 28, 2004.
26. "Distance-Based Genome Rearrangement Phylogeny," *the Third Annual Emerging Information Technology Conference (EITC)*, Princeton University, October 31, 2003.
27. "Distance-Based Genome Rearrangement Phylogeny," *IMA/RECOMB Satellite Workshop on Comparative Genomics*, University of Minnesota, October 20 – 24, 2003.
28. "Distance-Based Genome Rearrangement Phylogeny," *Workshop on New Trends in Phylogenetics and Genomics, University of Tübingen, Germany*, July 1 – 4, 2003.
29. "A Simulation Study for Genome Rearrangement Phylogeny Using Beta-Splitting Models," *Biocomplexity Workshop*, University of Texas at Austin, April 12, 2003.
30. "Markovian Models for Genome Rearrangements," *Mathematics of Evolution and Phylogeny Workshop, Institut Henri Poincaré, France*, June 16-19, 2003.
31. "Distance-Based Genome Rearrangement Phylogeny Reconstruction," Department of Computer Science, Virginia Institute of Technology, April 30, 2003.
32. "Genome Rearrangement Phylogeny," *DIMACS Tree of Life Workshop*, Rutgers University, March 11 – 14, 2003.
33. "Distance-Based Genome Rearrangement Phylogeny," Department of Zoology, University of Chicago, January 30, 2003.

34. "Distance-Based Genome Rearrangement Phylogeny Reconstruction," Whitehead Institute, Massachusetts Institute of Technology, January 9, 2003.
35. "Genome Rearrangement Phylogeny Using Weighbor," conference presentation, *Second Workshop on Algorithms in Bioinformatics (WABI'02)*, Rome, Italy, September 17, 2002.
36. "Postprocessing of Phylogenetic Analysis Using Clustering," conference presentation, *Tenth International Conference on Intelligent Systems for Molecular Biology (ISMB'02)*, Edmonton, Canada, August 7, 2002.
37. "Computational Methods for Genome Rearrangement Phylogeny," *Biocomplexity Workshop*, University of Texas at Austin, April 12, 2002.
38. "Genome Rearrangement Phylogeny Estimation," *the Colloquium on Biosystematics and Evolution Biology*, hosted by Department of Biology, Stanford University and California Academy of Sciences, March 15, 2002.
39. "Fast Methods for Genome Rearrangement Phylogeny Estimation," Department of Ecology and Evolutionary Biology, Yale University, February 18, 2002.
40. "Clustering and Consensus for Phylogenetic Analysis," *DIMACS Bioconsensus 2 Workshop*, Rutgers University, October 4 – 7, 2001.
41. "New Polynomial Time Methods for Whole Genome Phylogeny Reconstruction," *DIMACS Whole Genome Comparison Workshop*, Rutgers University, February 28 – March 2, 2001.