

CURRICULUM VITAE

LUAY K. NAKHLEH

CONTACT INFORMATION

Department of Computer Science
Rice University
6100 Main Street, MS 132
Houston, Texas 77005

Office: Duncan Hall 3119
Phone: 713-348-3959
Fax: 713-348-5930

Email: nakhleh@cs.rice.edu
Homepage: <http://www.cs.rice.edu/~nakhleh/>

PERSONAL INFORMATION

Citizenship: Israel (permanent resident of the United States)

EDUCATION

05/2004 Ph.D., Computer Sciences, University of Texas at Austin. (Advisor: Tandy Warnow)
Thesis title: Phylogenetic Networks

12/1998 M.S., Computer Science, Texas A&M University.

06/1996 B.S., Computer Science, Technion–Israel Institute of Technology.

EMPLOYMENT

07/2004–Present Assistant Professor, Dept. of Computer Science, Rice University.

08/2001–07/2004 Research Assistant, Dept. of Computer Sciences, The University of Texas at Austin.

06/2001–08/2001 Assistant Instructor, Dept. of Computer Sciences, The University of Texas at Austin.
(Automata Theory)

09/2000–05/2001 Teaching Assistant, Dept. of Computer Sciences, The University of Texas at Austin.
(Automata Theory)

05/2000–08/2000 Summer Intern, Intel Corporation, Austin, TX.

- 01/1999–05/2000 Teaching Assistant, Dept. of Computer Sciences, The University of Texas at Austin. (Abstract Data Types, Contemporary Issues in Computer Science)
- 08/1998–12/1998 Teaching Assistant, Dept. of Computer Science, Texas A&M University. (Graduate Algorithms)
- 05/1998–08/1998 Summer Intern, Texas Instruments, Dallas, TX.
- 08/1997–05/1998 Research Assistant, Dept. of Computer Science, Texas A&M University.
-

AFFILIATIONS, MEMBERSHIPS, AND OTHER POSITIONS

- Adjunct Assistant Professor, Department of Systems Biology, UT M.D. Anderson Cancer Center.
 - Faculty member, The Graduate Program in Structural and Computational Biology and Molecular Biophysics (SCBMB), Baylor College of Medicine.
 - Faculty member, The W.M. Keck Center for Interdisciplinary Bioscience Training, Rice University.
 - Faculty member, The Institute of Biosciences and Bioengineering (IBB), Rice University.
 - Faculty member, The Center for High Performance Software Research (HiPerSoft), Rice University.
 - Faculty member, The Computer and Information Technology Institute (CITI), Rice University.
 - Member, The International Society for Computational Biology (ISCB).
 - Member, The American Association for the Advancement of Science (AAAS).
-

RESEARCH INTERESTS

- Computational biology and bioinformatics: phylogenetics, comparative genomics, multi-locus genotype-phenotype associations, biological network analysis.
 - Algorithm design and analysis.
 - Experimental and empirical performance studies.
 - Computational phylogenetics in Historical Linguistics.
-

COURSES TAUGHT

- COMP 572 Bioinformatics: Network Analysis (every Spring semester since 2008, Rice University)
- COMP 571 Bioinformatics: Sequence Analysis (every Fall semester since 2004, Rice University)
- COMP 481 Automata, Formal Languages, and Computability (every Spring semester since 2005, Rice University)
- CS 341 Automata Theory (Fall 2000, Spring 2001, Summer 2001, UT Austin)
- CS 328 Abstract Data Types (Spring 2000, UT Austin)
- CS 378 Contemporary Issues in Computer Science (Spring 1999, Fall 1999, UT Austin)
- CPSC 629 Analysis of Algorithms (Fall 1998, Texas A&M University)

UNIVERSITY SERVICE

- 2007—Current Faculty Associate, Wiess College, Rice University.
- 2007—Current Faculty Recruiting Committee, Department of Computer Science, Rice University.
- 2007—Current Faculty Recruiting Committee, Department of Biochemistry and Cell Biology, Rice University.
- 2005—Current Graduate Committee, Department of Computer Science, Rice University.
-

PROFESSIONAL SERVICE

CONFERENCE PROGRAM COMMITTEE MEMBERSHIP

1. PC member, *The Eighth Workshop on Algorithms in Bioinformatics (WABI 2008)*.
2. PC member, *The Sixteenth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2008)*
3. PC member, *The Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2007)*
4. PC member, *The Fourteenth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2006)*.
5. PC member, *The Sixth Workshop on Algorithms in Bioinformatics (WABI 2006)*.
6. PC member, *The Fifth IEEE International Workshop on High Performance Computational Biology (HiCOMB 2006)*.

REVIEWER (since July 2004)

1. Publishers:
Prentice-Hall, Springer-Verlag.
 2. Journals and Conferences:
Algorithmica, Bioinformatics, BMC Evolutionary Biology, Discrete Applied Mathematics, Evolution, Journal of Bioinformatics and Computational Biology, Journal of Computational Biology, Journal of Graph Algorithms and Applications, Journal of Theoretical Biology, Journal of Theoretical Computer Science, Language & Linguistics Compass, Systematic Biology, ACM/IEEE Transactions on Computational Biology and Bioinformatics, ISMB, RECOMB, PSB, WABI.
 3. Others:
School of Computing, National University of Singapore.
National Science Foundation.
-

RESEARCH SUPPORT

- 07/2008—06/2011 “*MRI: Acquisition of Cyberinfrastructure for Computational Research.*”
co-PI. \$500,000. National Science Foundation, USA. (PI: John Mellor-Crummey).

- 09/2008—09/2013 “*Evolutionary Analysis of Bacterial Genomes: High-throughput Computational Tools.*”
Principal Investigator. \$1,552,236 (R01 mechanism). National Library of Medicine, National Institutes of Health, USA. (subcontractor: Hideki Innan)
- 04/2008—04/2013 “*Determinants of Signaling Network Regulation in Combinatorial Targeted Therapies.*”
co-PI. \$500,479 (R01 mechanism. Total amount: \$2,482,995) National Institutes of Health, USA. (PI: Prahlad T. Ram, UT MD Anderson Cancer Center.)
- 05/2007—05/2008 The Collaborative Advances in Biomedical Computing (CABC) Program.
Principal Investigator. \$50,000. The Gulf Coast Center for Computational Cancer Research (GC4R), Rice University.
- 05/2006—05/2009 The Roy E. Campbell Faculty Development Award.
Principal Investigator. \$21,000. The George R. Brown School of Engineering, Rice University.
- 08/2006—08/2009 “*Tools for Accurate and Efficient Analysis of Complex Evolutionary Mechanisms in Microbial Genomes.*”
Principal Investigator. \$300,000. Department of Energy, USA.
- 09/2006—09/2009 “*Efficient Techniques for Reconstructing Horizontal Gene Transfer in Bacteria.*”
Principal Investigator. \$600,000. National Science Foundation, USA. (subcontractor: Hideki Innan)

AWARDS AND HONORS

- 04/2008 Finalist, *The Phi Beta Kappa of Rice Teaching Prize.*
Rice University.
- 08/2006 Early Career Award.
The Department of Energy, USA.
- 05/2006 The Roy E. Campbell Faculty Development Award.
The George R. Brown School of Engineering, Rice University.
- 11/2005 Invited speaker, The 8th Annual Chinese American Frontiers of Science (CAFoS) Symposium, Xiamen, China.
- 07/2005 Best Paper Award.
The First IEEE Workshop on High Performance Computing in Medicine and Biology (HiPCoMP 2005), Fukuoka, Japan.
- 05/2005 Outstanding Dissertation Award (Mathematics, Physical Sciences, and Engineering category), The University of Texas at Austin.
This award is presented annually at UT Austin to four students in four different categories in recognition of the outstanding PhD dissertations in each of these categories.
- 04/2005 Computer Sciences Bert Kay Outstanding Dissertation Award.
This award is presented annually at the Department of Computer Sciences, UT Austin, in recognition of the outstanding PhD dissertation.
- 03/2004 Travel fellowship.
Paid for attending the Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB 04).

02/2004	James C. Brown Graduate Fellowship. <i>This award is presented annually to one graduate student in the Department of Computer Sciences at the University of Texas at Austin, for outstanding academic achievements.</i>
05/2003	Invited speaker, The Dean Scholars Honor Program, College of Natural Sciences, The University of Texas at Austin.
04/2003	The George H. Mitchell/University Co-op Graduate Award for Research, The University of Texas at Austin. <i>This award was given to eight out of two hundred graduate student applicants in 2003.</i>
01/2002	Travel fellowship, Department of Computer Sciences, The University of Texas at Austin.
01/2002	Travel fellowship, National Library of Medicine, January 2002. <i>Paid for attending the Pacific Symposium on Biocomputing (PSB 02).</i>
03/2001	One of my lectures was videotaped and archived by the Center for Teaching Effectiveness at the University of Texas at Austin.
02/2001	Texas Excellence Teaching Award, College of Natural Sciences, The University of Texas at Austin. <i>This award is given annually to one professor and one graduate instructor in each college at The University of Texas at Austin.</i>
12/2000	Outstanding Teaching Assistant Award, Department of Computer Sciences, The University of Texas at Austin. <i>This award is given annually to one Teaching Assistant in the Department of Computer Sciences at the University of Texas at Austin.</i>

PRESENTATIONS AND INVITED TALKS

1. "Exploiting Biological Networks for Identifying Drug Targets and Understanding Genetic Causes of Disease." Pathways to Personalized Medicine: Rate-limiting Factors in Delivering the Promise, Rice University and the Texas Medical Center, Jun 2008. (*Invited talk.*)
2. "Novel algorithmic techniques for gene tree reconciliation in bacterial genomes." The Evolution 2008 Conference, The University of Minnesota, Jun 2008. (*Invited talk.*)
3. "Petri Net Modeling of Signal Transduction Networks: Qualitative Characterizations Based on the Network Connectivity." The Graduate Program in Structural and Computational Biology and Molecular Biophysics, Baylor College of Medicine, May 2008. (*Invited talk.*)
4. "Phylogenetic Networks: Reconstruction and Evaluation." The ITES Networks Cluster Seminar, The University of Houston, Apr 2008. (*invited talk.*)
5. "From Gene Trees to Species Phylogenies." Computational Aspects of Biological Information, Microsoft Research, Dec 2007. (*Invited talk.*)
6. "Petri Net Modeling of Signal Transduction Networks: Predicting Dynamics Without Prior Knowledge of Kinetics." Department of Biochemistry and Cell Biology, Rice University, Nov 2007. (*Invited talk.*)

7. "Efficient Reconstruction of Species Trees from Genome-scale Multi-locus Data Under the Coalescent." Department of Computational and Applied Mathematics, Rice University, Nov 2007. (*Invited talk.*)
8. "Graph-theoretic Modeling and Reasoning about Signaling Networks." Oklahoma Medical Research Foundation, Aug 2007. (*Invited talk.*)
9. "Horizontal Gene Transfer Detection: Issues and Algorithms." The 5th Bertinoro Computational Biology Meeting, Bertinoro, Italy, May 2007. (*Invited talk.*)
10. "Graph-Theoretic Techniques for Analyzing Signaling Networks." The 24th Annual Houston Conference on Biomedical Engineering Research, Houston, Texas, Feb 2007. (*Invited talk.*)
11. "Computational Hypothesis Generation in Signaling Networks ." Cancer Systems Biology Symposium, The University of Texas M.D. Anderson Cancer Center, Dec 2006. (*Invited talk.*)
12. "De Novo Signaling Pathway Predictions Based on Protein Interactions, Targeted Therapy, and Protein Microarray Analysis." Symposium on Data Integration in Bioinformatics and Computational Biology, Gulf Coast Consortium, Rice University, Dec 2006. (*Invited talk.*)
13. "Computational Methodologies for Inferring and Analyzing Networks: Species, Individuals, and Molecules." Collaborative Research Symposium, Rice University and the Texas Medical Center, Nov 2006. (*Invited talk.*)
14. "Modeling and Reconstructing Non-treelike Evolutionary Relationships in Species and Populations." Keck Seminar, Gulf Coast Consortia/Keck Center, Rice University, Oct 2006. (*Invited talk.*)
15. "Phylogenetic Networks and Reconstruction of Horizontal Gene Transfer." Corporate Affiliates Meeting, Department of Computer, Rice University, Oct 2006. (*Invited talk.*)
16. "Identifiability Issues in Phylogeny-based Detection of Horizontal Gene Transfer." RECOMB Comparative Genomics, Montreal, Canada, Sep 2006. Co-authors: C. Than, D. Ruths, and H. Innan. (*Presentation.*)
17. "Phylogeny-based Detection of Horizontal Gene Transfer: Challenges and Computational Approaches." The Graduate Program in Structural and Computational Biology and Molecular Biophysics, Baylor College of Medicine, May 2006. (*Invited talk.*)
18. "Phylogeny-based Detection of Reticulate Evolution: Identifiability and Computational Methods ." The Center for Genomics and Bioinformatics, and the Department of Biology, Indiana University, Bloomington, Apr 2006. (*Invited talk.*)
19. "Phylogenetic networks and reconstruction of horizontal gene transfer." The Bioinformatics Program, The University of Michigan at Ann Arbor, Apr 2006. (*Invited talk.*)
20. "Alien genes, complex diseases, and targeted drugs: computational approaches." Computer and Information Technology Institute, Rice University, Dec 2005. (*Invited talk.*)
21. "Alien genes, complex diseases, and targeted drugs: computational approaches." Department of Computer Sciences, The University of Texas at Austin, Dec 2005. (*Invited talk.*)
22. "The gene tree and species network problem." Ecology and Evolutionary Biology, Rice University, Nov 2005. (*Invited talk.*)
23. "Computational phylogenetics in historical linguistics." The 8th Annual Chinese American Frontiers of Science (CAFoS) Symposium, Xiamen, China, Nov 2005. (*Invited talk.*)

24. "Phylogenetic networks: modeling and reconstruction." The 52nd Annual Systematics Symposium, Missouri Botanical Garden, St. Louis, Missouri, Oct 2005. (*Invited talk.*)
25. "Reconstructing phylogenetic networks using maximum parsimony." CSB '05, Stanford University, Palo Alto, CA, Aug 2005. Co-authors: G. Jin, F. Zhao, and J. Mellor-Crummey. (*Presentation.*)
26. "Phylogenetic networks, trees, and clusters." IWBRA '05, Emory University, Atlanta, GA, May 2005. Co-authors: Li-San Wang. (*Presentation.*)
27. "Phylogenetic networks: generation, reconstructibility, and comparison." DIMACS Workshop on Reticulated Evolution, Rutgers University, New Jersey, Sep 2004. (*Invited talk.*)
28. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, The University of Toronto, Toronto, Canada, Apr 2004. (*Invited talk.*)
29. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, Rice University, Houston, TX, Apr 2004. (*Invited talk.*)
30. "Reconstructing reticulate evolution in species – theory and practice." RECOMB '04, San Diego, CA, Mar 2004. Co-authors: T. Warnow and C.R. Linder. (*Presentation.*)
31. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, Tufts University, Medford, MA, Mar 2004. (*Invited talk.*)
32. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, University of Maryland, College Park, MD, Mar 2004. (*Invited talk.*)
33. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." School of Informatics, Indiana University, Bloomington, IN, Mar 2004. (*Invited talk.*)
34. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, The University of Texas at Dallas, Richland, TX, Feb 2004. (*Invited talk.*)
35. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, George Washington University, Washington, D.C., Feb 2004. (*Invited talk.*)
36. "Network (Reticulate) Evolution: Biology, Models, and Algorithms." PSB '04, The Big Island, Hawaii, Jan 2004. Co-authors: C.R. Linder, B.M.E. Moret, and T. Warnow. (*Presentation.*)
37. "Reticulate evolution in biology and historical linguistics." Dean Scholars Honor Program, The University of Texas at Austin, Austin, TX, May 2003. (*Invited talk.*)
38. "Estimating deviation from a molecular clock." WABI '02, Rome, Italy, Oct 2002. Co-authors: U. Roshan, L. Vawter, and T. Warnow. (*Presentation.*)
39. "The performance of phylogenetic methods on trees of bounded diameter." WABI '01, Aarhus, Denmark, Oct 2001. Co-authors: U. Roshan, K. St. John, J. Sun, and T. Warnow. (*Presentation.*)

STUDENTS

PH.D. AND MASTER'S COMMITTEE CHAIR

1. Derek Ruths. *Computer Science*, Rice University. (Joined my group: Jan 2005. Expected date of PhD: May 2009.)

2. Cuong Than. *Computer Science*, Rice University. (Joined my group: Jan 2006. Expected date of PhD: May 2010.)
3. Evan Huston. *Computer Science*, Rice University. (Joined my group: Jan 2007. Expected date of PhD: May 2011.)
4. Jeff Kilpatrick. *Computer Science*, Rice University. (Joined my group: Aug 2007. Expected date of PhD: May 2012.)
5. Justin Park. *Computer Science*, Rice University. (Joined my group: Aug 2007. Expected date of PhD: May 2012.)

PH.D. AND MASTER'S COMMITTEE MEMBER

1. Seth Fogarty. *Computer Science*, Rice University. (Advisor: Moshe Vardi)
2. Alan R. Harris. Baylor College of Medicine. (Advisor: Aleksandar Milosavljevic)
3. Allison Heath. *Computer Science*, Rice University. (Advisor: Lydia Kavraki)
4. Sara Kalla. *Ecology and Evolutionary Biology*, Rice University. (Advisors: Joan Strassmann and David Queller)
5. Christopher A. Miller. Baylor College of Medicine. (Advisor: Aleksandar Milosavljevic)
6. Niv Sabath. *Department of Biology and Chemistry*, University of Houston. (Advisor: Dan Graur)
7. Amarda Shehu. *Computer Science*, Rice University. (Advisor: Lydia Kavraki)
8. David Schwarz. *Computer Science*, Rice University. (Advisor: Lydia Kavraki)
9. Hernan Stamati. *Computer Science*, Rice University. (Advisor: Lydia Kavraki)
10. Deian Tabakov. *Computer Science*, Rice University. (Advisor: Moshe Vardi)
11. Jen-Te Tseng. *Systems Biology*, UT M.D. Anderson Cancer Center. (Advisor: Prahlad T. Ram)
12. Konstantinos I. Tsianos. *Computer Science*, Rice University. (Advisor: Lydia Kavraki)

PUBLICATIONS

[[‡]: **Nakhleh's students.**]

UNDER REVIEW

1. C. Than[‡], D. Ruths[‡], and L. Nakhleh, "PhyloNet: A Software Package for Analyzing and Reconstructing Reticulate Evolutionary Relationships."
2. L. Nakhleh, "A Metric for Comparing Phylogenetic Network Topologies".
3. C. Than[‡], G. Jin, and L. Nakhleh, "Integrating Sequence and Topology for Efficient and Accurate Detection of Horizontal Gene Transfer."
4. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, "On Approximating the Parsimony Score of Phylogenetic Networks."

BOOKS AND BOOK CHAPTERS

1. L. Nakhleh, D. Ruths[‡], and H. Innan, “Gene Trees, Species Trees, and Species Networks.” In *Meta-analysis and Combining Information in Genetics*, R. Guerra and D. Allison (editors). In press, 2007.

PAPERS IN PEER-REVIEWED JOURNALS AND EDITED VOLUMES

1. D. Ruths[‡], L. Nakhleh, and P.T. Ram, “Rapidly Exploring Structural and Dynamic Properties of Signaling Networks Using PathwayOracle.” *BMC Systems Biology*. In press, 2008.
2. I. Kanj, L. Nakhleh, C. Than[‡], and G. Xia, “Seeing the Trees and Their Branches in the Network is Hard.” *Theoretical Computer Science (TCS)*, 401: 153-164, 2008.
3. D. Ruths[‡], M. Muller, J.T. Tseng, L. Nakhleh, and P.T. Ram, “The Signaling Petri Net-based Simulator: A Non-parametric Strategy for Characterizing the Dynamics of Cell-specific Signaling Networks.” *PLoS Computational Biology*, 4(2): e1000005, 2008.
4. I. Kanj, L. Nakhleh, and G. Xia, “The Compatibility of Binary Characters on Phylogenetic Networks: Complexity and Parameterized Algorithms.” *Algorithmica*, 51: 99-128, 2008.
5. C. Than[‡], D. Ruths[‡], H. Innan, and L. Nakhleh, “Confounding Factors in HGT Detection: Statistical Error, Coalescent Effects, and Multiple Solutions.” *Journal of Computational Biology*, 14(4): 517-535, 2007.
6. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, “Inferring Phylogenetic Networks by the Maximum Parsimony Criterion: A Case Study.” *Molecular Biology and Evolution*, 24(1): 324-337, 2007.
7. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, “Maximum Likelihood of Phylogenetic Networks.” *Bioinformatics*, 22(21): 2604-2611, 2006.
8. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, “Efficient Parsimony-based Methods for Phylogenetic Network Reconstruction.” *Bioinformatics*, 23: e123-e128, 2006. (Proceedings of the European Conference on Computational Biology (ECCB 06)).
9. D. Ruths[‡], L. Nakhleh, M.S. Iyengar, S.A.G. Reddy, and P.T. Ram, “Graph-theoretic Hypothesis Generation in Biological Signaling Networks.” *Journal of Computational Biology*, 13(9): 1546-1557, 2006.
10. T. Shigaki, I. Rees, L. Nakhleh, and K. Hirschi, “Identification of Three Distinct Phylogenetic Groups of CAX Cation/Proton Antiporters.” *Journal of Molecular Evolution*, 63:815-825, 2006.
11. Y. Dotsenko, C. Coarfa, L. Nakhleh, J. Mellor-Crummey, and U. Roshan, “PRec-I-DCM3: A Parallel Framework for Fast and Accurate Large Scale Phylogeny Reconstruction.” *International Journal of Bioinformatics Research and Applications (IJBRA)*, 2(4): 407-419, 2006.
12. T. Warnow, S.N. Evans, D. Ringe, and L. Nakhleh, “A Stochastic model of language evolution that incorporates homoplasy and borrowing.” In *Phylogenetic Methods and the Prehistory of Languages*, P. Forster and C. Renfrew (editors), 75-87. McDonald Institute for Archaeological Research, Cambridge, UK, 2006.
13. L. Nakhleh and L.S. Wang, “Phylogenetic Networks: Properties and Relationship to Trees and Clusters.” *Transactions on Computational Systems Biology II*, LNBI 3680, 82-99, 2005.
14. D. Ruths[‡] and L. Nakhleh, “Recombination and Phylogeny: Effects and Detection.” *International Journal of Bioinformatics Research and Applications (IJBRA)*, 1(2): 202-212, 2005.
15. L. Nakhleh, T. Warnow, D. Ringe, and S.N. Evans, “A Comparison of Phylogenetic Reconstruction Methods on an IE Dataset.” *Transactions of the Philological Society*, 3(2): 171-192, 2005.

16. L. Nakhleh, T. Warnow, C.R. Linder, and K. St. John, "Reconstructing Reticulate Evolution in Species – Theory and Practice." *Journal of Computational Biology*, 12(6-7):796-811, 2005.
17. L. Nakhleh, D. Ringe, and T. Warnow, "Perfect Phylogenetic Networks: A New Methodology for Reconstructing the Evolutionary History of Natural Languages." *LANGUAGE, Journal of the Linguistic Society of America*, 81(2): 382-420, 2005.
18. B.M.E. Moret, L. Nakhleh, T. Warnow, C.R. Linder, A. Tholse, A. Padolina, J. Sun, and R. Timme, "Phylogenetic networks: modeling, reconstructibility, and accuracy." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 1(1):13-23, 2004.
19. L. Nakhleh, U. Roshan, K. St. John, J. Sun, and T. Warnow, "Designing Fast Converging Phylogenetic Methods". *Bioinformatics*, 17(90001), pp. S190-S198, 2001. Proceedings of the Ninth International Conference on Intelligent Systems for Molecular Biology (ISMB 2001).

PAPERS IN PEER-REVIEWED CONFERENCE PROCEEDINGS

1. C. Than[‡], R. Sugino, H. Innan, and L. Nakhleh, "Efficient Inference of Bacterial Strain Trees From Genome-scale Multi-locus Data." The 16th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB). *Bioinformatics*, 24: i123-i131, 2008.
2. C. Than[‡] and L. Nakhleh, "SPR-based Tree Reconciliation: Non-binary Trees and Multiple Solutions." Proceedings of the Sixth Asia Pacific Bioinformatics Conference (APBC 08), 251-260, 2008.
3. I. Kanj, L. Nakhleh, C. Than[‡], and G. Xia, "Seeing the Trees and Their Branches in the Network is Hard." Proceedings of the Tenth Italian Conference on Theoretical Computer Science (ICTCS '07), 82-93, 2007.
4. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, "A New Linear-time Heuristic Algorithm for Computing the Parsimony Score of Phylogenetic Networks: Theoretical Bounds and Empirical Performance." Proceedings of the International Symposium on Bioinformatics Research and Applications (ISBRA'07). *Lecture Notes in Bioinformatics (LNBI #4463)*, pp. 61-72, 2007.
5. D. Ruths[‡], J.T. Tseng, L. Nakhleh, and P.T. Ram, "De novo Signaling Pathway Predictions based on Protein-Protein Interaction, Targeted Therapy and Protein Microarray Analysis." Proceedings of the RECOMB Satellite Workshop on Systems Biology and Proteomics. *Lecture Notes in Bioinformatics (LNBI #4532)*, pp. 109-119, 2007.
6. C. Than[‡], D. Ruths[‡], H. Innan, and L. Nakhleh, "Identifiability Issues in Phylogeny-based Detection of Horizontal Gene Transfer." Proceedings of the Fourth RECOMB Comparative Genomics Satellite Workshop, 2006. *Lecture Notes in Bioinformatics (LNBI #4205)*, pp. 215-229.
7. I. Kanj, L. Nakhleh, and G. Xia, "Reconstructing Evolution of Natural Languages: Complexity and Parameterized Algorithms." Proceedings of the Twelfth Annual International Computing and Combinatorics Conference (COCOON'06). *Lecture Notes in Computer Science (LNCS #4112)*, 299-308, 2006.
8. D. Ruths[‡] and L. Nakhleh, "Techniques for Assessing Phylogenetic Branch Support: A Comparative Study." Proceedings of the Fourth Asia Pacific Bioinformatics Conference (APBC 06), 187-196, 2006.
9. D. Ruths[‡] and L. Nakhleh, "RECOMP: A Parsimony-based Method for Detecting Recombination." Proceedings of the Fourth Asia Pacific Bioinformatics Conference (APBC 06), 59-68, 2006.
10. Z. Du, A. Stamatakis, F. Lin, U. Roshan, and L. Nakhleh, "Parallel divide-and-conquer phylogeny reconstruction by maximum likelihood." Proceedings of the 2005 International Conference on High Performance Computing and Communications (HPCC 05), 2:346-350, 2005.

11. L. Nakhleh, G. Jin, F. Zhao, and J. Mellor-Crummey, "Reconstructing Phylogenetic Networks Using Maximum Parsimony." Proceedings of the 2005 IEEE Computational Systems Bioinformatics Conference (CSB 05), 93-102, 2005.
12. L. Nakhleh, D. Ruths[‡], and L.-S. Wang, "RIATA-HGT: A Fast and Accurate Heuristic for Reconstructing Horizontal Gene Transfer." Proceedings of the Eleventh International Computing and Combinatorics Conference (COCOON 05). Lecture Notes in Computer Science (LNCS #3595), pp. 84-93.
13. C. Coarfa, Y. Dotsenko, J. Mellor-Crummey, L. Nakhleh, and U. Roshan, "PRec-I-DCM3: A Parallel Framework for Fast and Accurate Large Scale Phylogeny Reconstruction." Proceedings of the First IEEE Workshop on High Performance Computing in Medicine and Biology (HiPCoMP 2005). In press, 2005. (**Best paper award.**)
14. L. Nakhleh and L.-S. Wang, "Phylogenetic Networks, Trees, and Clusters." Proceedings of the International Workshop on Bioinformatics Research and Applications, The International Conference on Computational Science, 2: 919-926, 2005.
15. L. Nakhleh, T. Warnow, and C.R. Linder, "Reconstructing Reticulate Evolution in Species – Theory and Practice". Proceedings of the Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB), 337-346, 2004.
16. L. Nakhleh, D. Miranker, F. Barbancon, W.H. Piel, and M.J. Donoghue, "Requirements of Phylogenetic Databases". Proceedings of the Third IEEE Symposium on Bioinformatics and Bioengineering (BIBE 2003). IEEE Press, pp. 141-148.
17. E. Erdem, V. Lifschitz, L. Nakhleh, and D. Ringe, "Reconstructing the Evolutionary History of Indo-European Languages using Answer Set Programming". Proceedings of the Fifth International Symposium on Practical Aspects of Declarative Languages (PADL 2003). Lecture Notes in Computer Science (LNCS #2562), pp. 160-176.
18. L. Nakhleh, J. Sun, T. Warnow, C.R. Linder, B.M.E. Moret, and A. Tholse, "Towards the Development of Computational Tools for Evaluating Phylogenetic Network Reconstruction Methods". Proceedings of the Eighth Pacific Symposium on Biocomputing (PSB 2003), 8:315-326.
19. L. Nakhleh, U. Roshan, L. Vawter, and T. Warnow, "Estimating the Deviation from a Molecular Clock". Proceedings of the Second International Workshop on Algorithms in Bioinformatics (WABI 2002). Lecture Notes in Computer Science (LNCS #2452), pp. 287-299.
20. L. Nakhleh, B.M.E. Moret, U. Roshan, K. St. John, J. Sun, and T. Warnow, "The Accuracy of Phylogenetic Methods for Large Datasets". Proceedings of the Seventh Pacific Symposium on Biocomputing (PSB 2002), 7:211-222.
21. L. Nakhleh, U. Roshan, K. St. John, J. Sun, and T. Warnow, "The Performance of Phylogenetic Methods on Trees of Bounded Diameter". Proceedings of the First International Workshop on Algorithms in Bioinformatics (WABI 2001). Lecture Notes in Computer Science (LNCS #2149), pp. 214-226.

SURVEYS AND POSTERS

1. C.R. Linder, B.M.E. Moret, L. Nakhleh, and T. Warnow, "Network (Reticulate) Evolution: Biology, Models, and Algorithms." A tutorial presented at The Ninth Pacific Symposium on Biocomputing (PSB 2004).
2. R. Kalra, K. St. John, L. Nakhleh, and T. Warnow, "Applications of Clustering and Visualization to Phylogeny." Poster at the European Conference on Computational Biology (ECCB 2003).
3. L. Nakhleh, T. Warnow, and C.R. Linder, "Reconstructing Reticulate Evolution in Species." Poster at the IMA Workshop on Comparative Genomics, Minneapolis, MN, October 2003.

COLLABORATORS

(in Alphabetical order)

1. F. Barbancon, Dept. of Computer Sciences, UT Austin.
2. C. Coarfa, Dept. of Computer Science, Rice University.
3. M. Donoghue, Dept. of Ecology and Evolutionary Biology, Yale University.
4. Y. Dotsenko, Dept. of Computer Science, Rice University.
5. Z. Du, Bioinformatics Research Center, Nanyang Technological University (Singapore).
6. E. Erdem, Dept. of Computer Science, Vienna University of Technology.
7. S.N. Evans, Dept. of Statistics, UC Berkeley.
8. K. Hirschi, Baylor College of Medicine.
9. S. Iadevai, UT M.D. Anderson Cancer Center.
10. H. Innan, School of Advanced Sciences, Graduate University for Advanced Studies (Japan).
11. M.S. Iyengar, UT Health Sciences, Houston.
12. G. Jin, Dept. of Computer Science, Rice University.
13. I. Kanj, School of Computer Science, Telecommunications, and Informatics Systems, DePaul University.
14. R. Kalra, Dept. of Computer Science, CUNY.
15. V. Lifschitz, Dept. of Computer Sciences, UT Austin.
16. C.R. Linder, School of Biological Sciences, UT Austin.
17. F. Lin, Bioinformatics Research Center, Nanyang Technological University (Singapore).
18. J. Mellor-Cummey, Dept. of Computer Science, Rice University.
19. G. Mills, UT M.D. Anderson Cancer Center.
20. D. Miranker, Dept. of Computer Sciences, UT Austin.
21. B.M.E. Moret, Dept. of Computer Science, University of New Mexico.
22. M. Muller, UT M.D. Anderson Cancer Center.
23. A. Padolina, School of Biological Sciences, UT Austin.
24. W.H. Piel, Dept. of Biological Sciences, University of Buffalo.
25. P.T. Ram, UT M.D. Anderson Cancer Center.
26. S.A.G. Reddy, UT M.D. Anderson Cancer Center.
27. I. Rees, Baylor College of Medicine.

28. D. Ringe, Dept. of Linguistics, UPenn.
29. U. Roshan, Dept. of Computer Science, Illinois Institute of Technology.
30. D. Ruths, Dept. of Computer Science, Rice University.
31. T. Shigaki, Baylor College of Medicine.
32. S. Snir, Dept. of Mathematics, UC Berkeley.
33. K. St. John, Dept. of Computer Science, CUNY.
34. A. Stamatakis, Institute of Computer Science, Foundation for Research and Technology-Hellas (Greece).
35. R. Sugino, School of Advanced Sciences, Graduate University for Advanced Studies (Japan).
36. J. Sun, Dept. of Computer Science, U Colorado, Boulder.
37. C. Than, Dept. of Computer Science, Rice University.
38. A. Tholse, Dept. of Computer Science, University of New Mexico.
39. R. Timme, School of Biological Sciences, UT Austin.
40. J.T. Tseng, UT M.D. Anderson Cancer Center.
41. T. Tuller, School of Computer Science, Tel Aviv University.
42. L. Vawter, Aventis Pharmaceuticals.
43. L.-S. Wang, Dept. of Biology, UPenn.
44. T. Warnow, Dept. of Computer Science, UT Austin.
45. G. Xia, Dept. of Computer Science, Texas A&M University.
46. F. Zhao, Dept. of Computer Science, Rice University.