

# CURRICULUM VITAE

LUAY K. NAKHLEH

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## CONTACT INFORMATION

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## PERSONAL INFORMATION

Birth date: 8 May 1974  
Citizenship: U.S.A. and Israel

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## EDUCATION

05/2004 Ph.D., Computer Sciences, University of Texas at Austin. (Advisor: Tandy Warnow)  
12/1998 M.S., Computer Science, Texas A&M University.  
06/1996 B.S., Computer Science, Technion–Israel Institute of Technology.

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## EMPLOYMENT

07/2018– J.S. Abercrombie Professor of Computer Science, Rice University.  
01/2017– Chair, Dept. of Computer Science, Rice University.  
07/2016– Full Professor, Dept. of Computer Science, Rice University.  
07/2016– Full Professor, Dept. of BioSciences, Rice University.  
07/2010–07/2016 Associate Professor (with Tenure), Dept. of Computer Science, Rice University.  
07/2014–07/2016 Associate Professor, Dept. of BioSciences, Rice University.  
07/2010–07/2014 Adjunct Associate Professor, Dept. of Systems Biology, UT M.D. Anderson Cancer Center.

09/2010–07/2014 Associate Professor, Dept. of Ecology and Evolutionary Biology, Rice University.  
07/2010–07/2014 Associate Professor, Dept. of Biochemistry and Cell Biology, Rice University.  
07/2004–06/2010 Assistant Professor, Dept. of Computer Science, Rice University.  
07/2008–07/2010 Assistant Professor, Dept. of Biochemistry and Cell Biology, Rice University.  
07/2007–01/2010 Adjunct Assistant Professor, Dept. of Systems Biology, UT M.D. Anderson Cancer Center.

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## RESEARCH INTERESTS

- Combinatorial optimization, statistical inference, and their applications to biological problems.
  - Phylogenomics and population genomics.
  - Evolution of biological networks (protein interaction networks and regulatory networks).
  - Modeling and analysis of biological networks (metabolic and regulatory networks)
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## RESEARCH AWARDS AND HONORS

07/2018 The J.S. Abercrombie Endowed Professorship.  
*Rice University.*

04/2018 The Outstanding Doctoral Thesis Adviser Award.  
*School of Engineering, Rice University.*

04/2015 The (T+R)<sup>2</sup> Excellence in Teaching and Research Award.  
*School of Engineering, Rice University.*

10/2013 Best Paper Award.  
*RECOMB Comparative Genomics, Lyon, France.*

04/2012 **Guggenheim Fellowship.**  
*The John Simon Guggenheim Memorial Foundation.*

02/2010 **Alfred P. Sloan Research Fellowship.**  
*The Alfred P. Sloan Foundation.*

01/2009 **Faculty Early Career Development (CAREER) Award.**  
*The National Science Foundation, USA.*

08/2006 **Early Career Principal Investigator 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 8<sup>th</sup> Annual Chinese American Frontiers of Science (CAFoS) Symposium, Xiamen, China.

07/2005	Best Paper Award. <i>The First IEEE Workshop on High Performance Computing in Medicine and Biology (HiPCoMP 2005)</i> , Fukuoka, Japan.
05/2005	Outstanding Dissertation Award (Mathematics, Physical Sciences, and Engineering category), The University of Texas at Austin.
04/2005	Computer Sciences Bert Kay Outstanding Dissertation Award.
03/2004	Travel fellowship, RECOMB 2004.
02/2004	James C. Browne Graduate Fellowship.
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.
01/2002	Travel fellowship, Department of Computer Sciences, The University of Texas at Austin.
01/2002	Travel fellowship, PSB 2002, National Library of Medicine, January 2002.

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## RESEARCH SUPPORT

- 07/2018—06/2021 “*IIS: Small: Models and Methods for Simultaneous Genotyping and Phylogeny Inference from Single-Cell DNA Data.*”  
**Principal Investigator.** \$499,804. National Science Foundation, USA.
- 07/2018—06/2022 “*AF: Medium: Algorithms for Scalable Phylogenetic Network Inference.*”  
**Principal Investigator.** \$960,000. National Science Foundation, USA.
- 08/2016—07/2019 “*RTG: Cross-Training in Statistics and Computer Science at Rice University.*”  
**Principal Investigator** (Other PI: Marina Vannucci). \$1,400,004. National Science Foundation, USA.
- 07/2015—06/2019 “*AF: Medium: Statistical Inference of Complex Evolutionary Histories.*”  
**Principal Investigator.** \$800,000. National Science Foundation, USA.
- 08/2014—08/2019 “*ABI Innovation: Algorithms and Models for Distributed Computation of Bayesian Phylogenetics.*”  
**co-PI.** \$1,150,888. National Science Foundation, USA. (PI: Christopher Jermaine). (2017-2019: No-cost extension)
- 04/2013—03/2019 “*AF: Medium: Algorithmic Foundations for Phylogenetic Networks.*”  
**Principal Investigator.** \$1,000,000. National Science Foundation, USA. (+\$25,725 in REU support) (2017-2019: No-cost extension)
- 07/2011—06/2015 “*ABI Innovation: Novel Methodologies for Genome-scale Evolutionary Analysis of Multi-locus Data.*”  
**Principal Investigator.** \$425,000 (Rice). National Science Foundation, USA. Total amount: \$1.2M; other institutions: Stanford (Noah Rosenberg) and UT Austin (Tandy Warnow). (2014-2015: No-cost extension)

- 07/2009—07/2015 “*CAREER: Computational Tools for Evolutionary Analysis of Biological Networks.*”  
**Principal Investigator.** \$500,000. National Science Foundation, USA. (2014-2015: No-cost extension) (+\$8,104 in REU support)
- 08/2008—08/2014 “*Evolutionary Analysis of Bacterial Genomes: High-throughput Computational Tools.*”  
**Principal Investigator.** \$1,325,790 (R01 mechanism). National Library of Medicine, National Institutes of Health, USA. (subcontractor: Hideki Innan)
- 09/2010—09/2012 Alfred P. Sloan Research Fellowship.  
**Principal Investigator.** \$50,000. The Alfred P. Sloan Foundation.
- 01/2010—12/2011 “*Network-guided Integration of Omics Data for Predicting Therapeutic Combinations.*”  
**Principal Investigator.** \$100,000. The Gulf Coast Center for Computational Cancer Research (GC4R), Rice University.
- 08/2008—07/2011 “*MRI: Acquisition of Cyberinfrastructure for Computational Research.*”  
**co-PI.** \$499,949. National Science Foundation, USA. (PI: John Mellor-Crummey).
- 04/2008—04/2011 “*Determinants of Signaling Network Regulation in Combinatorial Targeted Therapies.*”  
**co-PI.** \$168,671 (R01 mechanism. Total amount: \$1,070,544) National Institutes of Health, USA. (PI: Prahlad T. Ram, UT MD Anderson Cancer Center.)
- 09/2008—08/2009 “*SGER: NET HMMs and Their Applications to Biological Network Alignment.*”  
**Principal Investigator.** \$90,000. National Science Foundation, USA.
- 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)
- 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.

## PUBLICATIONS

- ‡: Nakhleh’s group members.
- **Computational conference proceedings are equivalent to journals; all conference proceeding papers listed below are peer-reviewed, long papers that are published in edited volumes.**

## NON-REFEREED ARTICLES

1. S. Kamoun, R. Lozano-Duran, and L. Nakhleh, “Stranger in a strange land: The experiences of immigrant researchers.” *Genome Biology* 18: 232, 2017.

2. L. Nakhleh, Review of “ReCombinatorics: The Algorithmics of Ancestral Recombination Graphs and Explicit Phylogenetic Networks” by Dan Gusfield, MIT Press. *SIAM Review*, 57(4): 638-642, 2015.
3. L. Nakhleh and D.A. Morrison, “Phylogenetic Networks.” In: Richard M. Kliman, editor. *The Encyclopedia of Evolutionary Biology*. Elsevier; 2015.
4. L. Nakhleh, “Evolutionary Trees.” In: Stanley Maloy and Kelly Hughes, editors. *Brenner’s Encyclopedia of Genetics*, 2nd Edition, Volume 2. San Diego: Academic Press; 2013. p. 549-550.

#### **PAPERS IN PEER-REVIEWED JOURNALS AND EDITED VOLUMES**

1. B.J. Grindel, J.R. Martinez, T.V. Tellman, D.A. Harrington, H. Zafar<sup>‡</sup>, L. Nakhleh, L.W. Chung, and M.C. Farach-Carson, “Matrilysin/MMP-7 cleavage of Perlecan/HSPG2 complexed with Semaphorin 3A supports FAK-mediated stromal invasion by prostate cancer cells.” *Scientific Reports* 8: 7262, 2018.
2. R.A.L. Elworth<sup>‡</sup>, C. Allen<sup>‡</sup>, T. Benedict<sup>‡</sup>, P. Dulworth<sup>‡</sup>, and L. Nakhleh, “ALPHA: A toolkit for automated local phylogenomic analyses.” *Bioinformatics* 34(16): 2848-2850, 2018.
3. G.A. Bravo, A. Antonelli, C.D. Bacon, K. Bartoszek, M. Blom, S. Huynh, G. Jones, L. Knowles, S. Lamichhaney, T. Marcussen, H. Morlon, L. Nakhleh, B. Oxelman, B. Pfeil, A. Schliep, N. Wahlberg, F. Werneck, J. Wiedenhoeft, S. Willows-Munro, and S.V. Edwards, “Embracing heterogeneity: Building the Tree of Life and the future of phylogenomics.” *PeerJ*. To appear, 2018.
4. Y. Wang<sup>‡</sup> and L. Nakhleh, “Towards an accurate and efficient heuristic for species/gene tree co-estimation.” *Bioinformatics* 34: i697-i705, 2018 (special issue for ECCB 2018 papers).
5. J. Zhu<sup>‡</sup> and L. Nakhleh, “Inference of species phylogenies from bi-allelic markers using pseudo-likelihood.” *Bioinformatics* 34: i376-i385, 2018 (special issue for ISMB 2018 papers).
6. D. Wen<sup>‡</sup>, Y. Yu<sup>‡</sup>, J. Zhu<sup>‡</sup>, and L. Nakhleh, “Inferring phylogenetic networks using PhyloNet.” *Systematic Biology* 67(4): 735-740, 2018.
7. J. Zhu<sup>‡</sup>, D. Wen<sup>‡</sup>, Y. Yu<sup>‡</sup>, H.M. Meudt, and L. Nakhleh, “Bayesian inference of phylogenetic networks from bi-allelic genetic markers.” *PLoS Computational Biology* 14(1): e1005932, 2018.
8. D. Wen<sup>‡</sup> and L. Nakhleh, “Co-estimating reticulate phylogenies and gene trees from multi-locus sequence data.” *Systematic Biology* 67(3): 439-457, 2018.
9. H. Zafar<sup>‡</sup>, N. Navin, L. Nakhleh, and K. Chen, “Computational approaches for inferring tumor evolution from single-cell genomic data.” *Current Opinion in Systems Biology* 7: 16-25, 2017.
10. H. Zafar<sup>‡</sup>, A. Tzen<sup>‡</sup>, N. Navin, K. Chen, and L. Nakhleh, “SiFit: A method for inferring tumor trees from single-cell sequencing data under finite-site models.” *Genome Biology* 18: 178, 2017.
11. X. Fan<sup>‡</sup>, M. Chaisson, L. Nakhleh, and K. Chen, “HySA: A hybrid structural variant assembly approach using next-generation and single-molecule sequencing technologies.” *Genome Research* 27: 793-800, 2017.
12. J. Zhu<sup>‡</sup>, Y. Yu<sup>‡</sup>, and L. Nakhleh, “In the light of deep coalescence: Revisiting trees within networks.” *BMC Bioinformatics* 17 (Suppl 14): 415, 2016.
13. Y. Yu<sup>‡</sup>, C. Jermaine, and L. Nakhleh, “Exploring phylogenetic hypotheses via Gibbs sampling on evolutionary networks.” *BMC Genomics* 17 (Suppl 10): 784, 2016.

14. D. Wen<sup>‡</sup>, Y. Yu<sup>‡</sup>, and L. Nakhleh, “Bayesian inference of species phylogenies under the multispecies network coalescent.” *PLoS Genetics* 12(5): e1006006, 2016.
15. H. Zafar<sup>‡</sup>, Y. Wang, L. Nakhleh, N. Navin, and K. Chen, “Monovar: single nucleotide variant detection in single cells.” *Nature Methods* 13(6): 505-507, 2016.
16. D. Wen<sup>‡</sup>, Y. Yu<sup>‡</sup>, M.W. Hahn, and L. Nakhleh, “Reticulate evolutionary history and extensive introgression in mosquito species revealed by phylogenetic network analysis.” *Molecular Ecology* 25: 2361-2372, 2016 (Special issue on Genomics of Hybridization).
17. M.W. Hahn and L. Nakhleh, “Irrational exuberance for resolved species trees.” *Evolution* 70(1): 7-17, 2016.
18. Y. Yu<sup>‡</sup> and L. Nakhleh, “A maximum pseudo-likelihood approach for phylogenetic networks.” *BMC Genomics*, 16(Suppl 10): S10, 2015.
19. K. Liu<sup>‡</sup>, E. Steinberg<sup>‡</sup>, A. Yozzo<sup>‡</sup>, Y. Song, M.H. Kohn, and L. Nakhleh, “Interspecific introgressive origin of genomic diversity in the house mouse.” *Proceedings of the National Academy of Sciences*, 112(1): 196-201, 2015.
20. Y. Yu<sup>‡</sup>, J. Dong<sup>‡</sup>, K. Liu<sup>‡</sup>, and L. Nakhleh, “Maximum likelihood inference of reticulate evolutionary histories.” *Proceedings of the National Academy of Sciences*, 111(46): 16448-16453, 2014.
21. G. Saxer, M.D. Krepps, E.D. Merkley, C.K. Ansong, B.L.D. Kaiser, M-T. Valovska, N. Ristic<sup>‡</sup>, T. Yeh, V. Prakash, O.P. Leiser, L. Nakhleh, H.S. Gibbons, H.W. Kreuzer, and Y. Shamoo, “Adaptation to complex environments consistently leads to metabolic selection via global regulators.” *PLoS Genetics*, 10(12): e1004872, 2014.
22. X. Fan<sup>‡</sup>, W. Zhou, Z. Chong, L. Nakhleh, and K. Chen, “Towards accurate characterization of clonal heterogeneity based on structural variation.” *BMC Bioinformatics*, 15: 299, 2014.
23. K. Liu<sup>‡</sup>, J. Dai<sup>‡</sup>, K. Truong<sup>‡</sup>, Y. Song, M.H. Kohn, and L. Nakhleh, “An HMM-based comparative genomic framework for detecting introgression in eukaryotes.” *PLoS Computational Biology*, 10(6): e1003649, 2014.
24. S. Iadevaia, L. Nakhleh, R. Azencott, and P.T. Ram, “Mapping motif tunability and robustness in the design of synthetic signaling networks.” *PLoS One*, 9(3): e91743, 2014.
25. N. Berestovsky<sup>‡</sup>, W. Zhou<sup>‡</sup>, D. Nagrath, and L. Nakhleh, “Modeling integrated cellular machinery using hybrid Petri-Boolean networks.” *PLoS Computational Biology*, 9(11): e1003306, 2013.
26. L. Nakhleh, “Computational approaches to species phylogeny inference and gene tree reconciliation.” *Trends in Ecology and Evolution*, 28(12): 719-728, 2013.
27. Y. Zhu<sup>‡</sup>, Z. Lin, and L. Nakhleh, “Evolution after whole-genome duplication: A network perspective.” *G3: Genes | Genomes | Genetics*, 3(11): 2049-2057, 2013.
28. Y. Yu<sup>‡</sup>, N. Ristic<sup>‡</sup>, and L. Nakhleh, “Fast algorithms and heuristics for phylogenomics under ILS and hybridization.” *BMC Bioinformatics*, 14(Suppl 16): S6, 2013.
29. Y. Yu<sup>‡</sup>, R.M. Barnett<sup>‡</sup>, and L. Nakhleh, “Parsimonious inference of hybridization in the presence of incomplete lineage sorting.” *Systematic Biology*, 62(5): 738-751, 2013.
30. E. Baptiste, L. van Iersel, A. Janke, S. Kelchner, S. Kelk, J.O. McInerney, D.A. Morrison, L. Nakhleh, M. Steel, L. Stougie, J. Whitfield, “Networks: Expanding evolutionary thinking.” *Trends in Genetics*, 29(8): 439-441, 2013.

31. T. Ruths<sup>‡</sup> and L. Nakhleh, “Boosting forward-time population genetic simulators through genotype compression.” *BMC Bioinformatics*, 14: 192, 2013.
32. T. Ruths<sup>‡</sup> and L. Nakhleh, “Quantifying neutral trends in the *E. coli* regulatory network.” *Proceedings of the National Academy of Sciences*, 110(19): 7754-7759, 2013.
33. N. Berestovsky<sup>‡</sup> and L. Nakhleh, “An evaluation of methods for inferring Boolean networks from time-series data.” *PLoS One*, 8(6): e66031, 2013.
34. F. Barbancon, S.N. Evans, L. Nakhleh, D. Ringe, and T. Warnow, “An experimental study comparing linguistic phylogenetic reconstruction methods.” *Diachronica*, 30(2): 143-170, 2013.
35. W. Zhou<sup>‡</sup> and L. Nakhleh, “Quantifying and assessing the effect of chemical symmetry in metabolic pathways.” *Journal of Chemical Information and Modeling*, 52(10): 2684-96, 2012.
36. T. Ruths<sup>‡</sup> and L. Nakhleh, “ncDNA and drift drive binding site accumulation.” *BMC Evolutionary Biology*, 12: 159, 2012.
37. W. Zhou<sup>‡</sup> and L. Nakhleh, “Convergent evolution of modularity in metabolic networks through different community structures.” *BMC Evolutionary Biology*, 12: 181, 2012.
38. Y. Zhu<sup>‡</sup>, P. Du, and L. Nakhleh, “Gene duplicability-connectivity-complexity across organisms and a neutral evolutionary explanation.” *PLoS One*, 7(9): e44491, 2012.
39. H.J. Park<sup>‡</sup> and L. Nakhleh, “Inference of reticulate evolutionary histories by maximum likelihood: The performance of information criteria.” *BMC Bioinformatics*, 13(Suppl 19): S12, 2012.
40. Y. Yu<sup>‡</sup>, J.H. Degnan, and L. Nakhleh, “The probability of a gene tree topology within a phylogenetic network with applications to hybridization detection.” *PLoS Genetics*, 8(4): e1002660, 2012.
41. S. Takuno, T. Kado, R.P. Sugino, L. Nakhleh, and H. Innan, “Population genomics in bacteria: A case study of *Staphylococcus aureus*.” *Molecular Biology and Evolution*, 29(2): 797-809, 2012.
42. Y. Yu<sup>‡</sup>, T. Warnow, and L. Nakhleh, “Algorithms for MDC-based multi-locus phylogeny inference: Beyond rooted binary gene trees on single alleles.” *Journal of Computational Biology*, 18(11): 1543-1559, 2011.
43. W. Zhou<sup>‡</sup> and L. Nakhleh, “The strength of chemical linkage as a criterion for pruning metabolic graphs.” *Bioinformatics*, 27(14): 1957-1963, 2011.
44. Y. Lu, M. Muller, D. Smith, B. Dutta, K. Kuomurov, S. Iadevaia, D. Ruths<sup>‡</sup>, J.T. Tseng, S. Yu, Q. Yu, L. Nakhleh, G. Balazsi, J. Donnelly, M. Schurdak, S. Morgan-Lappe, S. Fesik, P.T. Ram, and G.B. Mills, “Kinome siRNA-phosphoproteomic screen identifies networks regulating AKT signaling.” *Oncogene*, 30(45): 4567-4577, 2011.
45. W. Zhou<sup>‡</sup> and L. Nakhleh, “Properties of metabolic graphs: Biological organization or representation artifacts?” *BMC Bioinformatics*, 12: 132, 2011.
46. Y. Yu<sup>‡</sup>, C. Than<sup>‡</sup>, J.H. Degnan and L. Nakhleh, “Coalescent histories on phylogenetic networks and detection of hybridization despite lineage sorting.” *Systematic Biology*, 60(2): 138-149, 2011.
47. C. Than<sup>‡</sup> and L. Nakhleh, “Inference of parsimonious species phylogenies from multi-locus data by minimizing deep coalescences.” In *Estimating Species Trees: Practical and Theoretical Aspects*, L.L. Knowles and L.S. Kubatko (editors). Wiley-VCH, 79-98, 2010.

48. L. Nakhleh, "Evolutionary phylogenetic networks: models and issues." In *The Problem Solving Handbook for Computational Biology and Bioinformatics*, L. Heath and N. Ramakrishnan (editors). Springer, 125-158, 2010.
49. H.J. Park<sup>‡</sup>, G. Jin, and L. Nakhleh, "Bootstrap-based support of HGT inferred by maximum parsimony." *BMC Evolutionary Biology*, 10: 131, 2010.
50. L. Nakhleh, "A Metric on the Space of Reduced Phylogenetic Networks". *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 7(2): 218-222, 2010.
51. L. Nakhleh, D. Ruths<sup>‡</sup>, and H. Innan, "Gene Trees, Species Trees, and Species Networks." In *Meta-analysis and Combining Information in Genetics*, R. Guerra and D. Goldstein (editors). CRC Press, 275-293, 2009.
52. C. Than<sup>‡</sup> and L. Nakhleh, "Species tree inference by minimizing deep coalescences." *PLoS Computational Biology*, 5(9): e1000501, 2009.
53. T. Ruths<sup>‡</sup>, D. Ruths<sup>‡</sup>, and L. Nakhleh, "GS<sup>2</sup>: An efficiently computable measure of GO-based similarity of gene sets." *Bioinformatics*, 25(9): 1178-1184, 2009.
54. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, "Parsimony Score of Phylogenetic Networks: Hardness Results and a Linear-time Heuristic." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 6(3): 495-505, 2009.
55. C. Than<sup>‡</sup>, R. Sugino, H. Innan, and L. Nakhleh, "Efficient Inference of Bacterial Strain Trees From Genome-scale Multi-locus Data." *Bioinformatics*, 24: i123-i131, 2008. (Special Issue for ISMB 08 papers)
56. C. Than<sup>‡</sup>, D. Ruths<sup>‡</sup>, and L. Nakhleh, "PhyloNet: A Software Package for Analyzing and Reconstructing Reticulate Evolutionary Relationships." *BMC Bioinformatics*, 9: 322, 2008.
57. D. Ruths<sup>‡</sup>, L. Nakhleh, and P.T. Ram, "Rapidly Exploring Structural and Dynamic Properties of Signaling Networks Using PathwayOracle." *BMC Systems Biology*, 2: 76, 2008.
58. I. Kanj, L. Nakhleh, C. Than<sup>‡</sup>, and G. Xia, "Seeing the Trees and Their Branches in the Network is Hard." *Theoretical Computer Science (TCS)*, 401: 153-164, 2008.
59. D. Ruths<sup>‡</sup>, 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.
60. I. Kanj, L. Nakhleh, and G. Xia, "The Compatibility of Binary Characters on Phylogenetic Networks: Complexity and Parameterized Algorithms." *Algorithmica*, 51: 99-128, 2008.
61. C. Than<sup>‡</sup>, D. Ruths<sup>‡</sup>, 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.
62. 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.
63. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, "Maximum Likelihood of Phylogenetic Networks." *Bioinformatics*, 22(21): 2604-2611, 2006.
64. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, "Efficient Parsimony-based Methods for Phylogenetic Network Reconstruction." *Bioinformatics*, 23: e123-e128, 2006.



65. D. Ruths<sup>‡</sup>, 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.
66. 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.
67. 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.
68. 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.
69. 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.
70. D. Ruths<sup>‡</sup> and L. Nakhleh, “Recombination and Phylogeny: Effects and Detection.” *International Journal of Bioinformatics Research and Applications (IJBRA)*, 1(2): 202-212, 2005.
71. 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.
72. 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.
73. 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.
74. 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.
75. L. Nakhleh, U. Roshan, K. St. John, J. Sun, and T. Warnow, “Designing Fast Converging Phylogenetic Methods”. *Bioinformatics*, 17(90001), pp. S190-S198, 2001.

#### **PAPERS IN PEER-REVIEWED CONFERENCE PROCEEDINGS**

(\* indicates the conference proceedings were published as a special issue of a journal; the paper is listed above as well.)

1. X. Fan<sup>‡</sup>, Jie Xu, and L. Nakhleh, “Detecting large indels using optical map data.” *Proceedings of RECOMB Comparative Genomics*, 2018.
2. P. Du<sup>‡</sup> and L. Nakhleh, “Species tree and reconciliation estimation under a duplication-loss-coalescence model.” *The 9th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB)*, 2018.
3. R.A.L. Elworth<sup>‡</sup>, C. Allen<sup>‡</sup>, T. Benedict<sup>‡</sup>, P. Dulworth<sup>‡</sup>, and L. Nakhleh, “ $D_{\text{GEN}}$ : A test statistic for detection of general introgression scenarios.” *The 18th Workshop on Algorithms in Bioinformatics (WABI), LIPIcs 19:1 - 19:13*, 2018.
- \* 4. Y. Wang<sup>‡</sup> and L. Nakhleh, “Towards an accurate and efficient heuristic for species/gene tree co-estimation.” *The 17th European Conference on Computational Biology (ECCB)*, 2018. (published in the journal *Bioinformatics*)

- \* 5. J. Zhu<sup>‡</sup> and L. Nakhleh, “Inference of species phylogenies from bi-allelic markers using pseudo-likelihood.” The 26th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB), 2018. (published in the journal *Bioinformatics*)
- 6. R.A.L. Elworth<sup>‡</sup> and L. Nakhleh, “Inferring local genealogies on closely related genomes.” Proceedings of RECOMB Comparative Genomics, 2017. Lecture Notes in Bioinformatics #10562, 213-231, 2017.
- \* 7. J. Zhu<sup>‡</sup>, Y. Yu<sup>‡</sup>, and L. Nakhleh, “In the light of deep coalescence: Revisiting trees within networks.” RECOMB Comparative Genomics, 2016. (published in the journal *BMC Genomics*)
- \* 8. Y. Yu<sup>‡</sup>, C. Jermaine, and L. Nakhleh, “Exploring phylogenetic hypotheses via Gibbs sampling on evolutionary networks.” RECOMB Comparative Genomics, 2016. (published in the journal *BMC Genomics*)
- \* 9. Y. Yu<sup>‡</sup> and L. Nakhleh, “A maximum pseudo-likelihood approach for phylogenetic networks.” RECOMB Comparative Genomics, 2015. (published in the journal *BMC Genomics*)
- 10. Y. Yu<sup>‡</sup> and L. Nakhleh, “A distance-based method for inferring phylogenetic networks in the presence of incomplete lineage sorting.” Proceedings of ISBRA 2015, LNBI 9096, 378-389, 2015.
- \*11. Y. Zhu<sup>‡</sup>, Z. Lin, and L. Nakhleh, “Evolution after whole-genome duplication: A network perspective.” RECOMB/ISCB Conference on Regulatory and Systems Genomics, 2013. (published in the journal *G3: Genes | Genomes | Genetics*)
- \*12. Y. Yu<sup>‡</sup>, N. Ristic<sup>‡</sup>, and L. Nakhleh, “Fast algorithms and heuristics for phylogenomics under ILS and hybridization.” RECOMB Comparative Genomics, 2013. (published in the journal *BMC Bioinformatics*) (**Best paper award**)
- \*13. H.J. Park<sup>‡</sup> and L. Nakhleh, “Inference of reticulate evolutionary histories by maximum likelihood: The performance of information criteria.” RECOMB Comparative Genomics, 2012. (published in the journal *BMC Bioinformatics*)
- 14. Y. Zhu<sup>‡</sup> and L. Nakhleh, “Reconstructing the evolution of molecular interaction networks under the DMC and link dynamics models.” Proceedings of the Workshop on Algorithms in Bioinformatics (WABI), LNBI 7534, 57-68, 2012.
- 15. H.J. Park<sup>‡</sup> and L. Nakhleh, “MURPAR: A fast heuristic for inferring parsimonious phylogenetic networks from multiple gene trees.” Proceedings of the 8th International Symposium on Bioinformatics Research and Applications. Lecture Notes in Bioinformatics (LNBI #7292), pp. 213-224, 2012.
- 16. N. Berestovsky<sup>‡</sup>, R. Fukui<sup>‡</sup> and L. Nakhleh, “On the performance of particle swarm optimization for parameterizing kinetic models of cellular networks.” Proceedings of the IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology, 184-191, 2012.
- 17. Y. Yun<sup>‡</sup>, T. Warnow, and L. Nakhleh, “Algorithms for MDC-based multi-locus phylogeny inference.” Proceedings of the 15th Annual International Conference on Research in Computational Molecular Biology (RECOMB), LNBI 6577, 531-545, 2011.
- 18. H.J. Park<sup>‡</sup>, G. Jin, and L. Nakhleh, “Algorithmic strategies for estimating the amount of reticulation from a collection of gene trees.” Proceedings of the Ninth Annual International Conference on Computational Systems Biology, 114-123, 2010.
- 19. D. Ruths<sup>‡</sup> and L. Nakhleh, “Deriving predictive models of signaling network dynamics from qualitative experimental data.” Proceedings of the Ninth Annual International Conference on Computational Systems Biology, 136-145, 2010.

20. C. Than<sup>‡</sup>, G. Jin, and L. Nakhleh, “Integrating Sequence and Topology for Efficient and Accurate Detection of Horizontal Gene Transfer.” Proceedings of the Sixth RECOMB Comparative Genomics Satellite Workshop, 2008. Lecture Notes in Bioinformatics (LNBI #5267), pp. 113-127, 2008.
- \*21. C. Than<sup>‡</sup>, 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).
22. C. Than<sup>‡</sup> 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.
23. I. Kanj, L. Nakhleh, C. Than<sup>‡</sup>, 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.
24. 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.
25. D. Ruths<sup>‡</sup>, 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.
- \*26. G. Jin, L. Nakhleh, S. Snir, and T. Tuller, “Efficient Parsimony-based Methods for Phylogenetic Network Reconstruction.” The European Conference on Computational Biology (ECCB), 2006. (published in the journal Bioinformatics)
27. C. Than<sup>‡</sup>, D. Ruths<sup>‡</sup>, 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, 2006.
28. 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.
29. D. Ruths<sup>‡</sup> 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.
30. D. Ruths<sup>‡</sup> and L. Nakhleh, “RECOMP: A Parsimony-based Method for Detecting Recombination.” Proceedings of the Fourth Asia Pacific Bioinformatics Conference (APBC 06), 59-68, 2006.
31. 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.
32. 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.
33. L. Nakhleh, D. Ruths<sup>‡</sup>, 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.

34. 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), 2: 346-350, 2005. (**Best paper award.**)
35. 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.
36. 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.
37. 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).
38. 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.
39. 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.
40. 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.
41. 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.
42. 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.
43. 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.
- \*44. L. Nakhleh, U. Roshan, K. St. John, J. Sun, and T. Warnow, "Designing Fast Converging Phylogenetic Methods". The Ninth International Conference on Intelligent Systems for Molecular Biology (ISMB), 2001. (published in the journal Bioinformatics)

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## PRESENTATIONS AND INVITED TALKS

1. "Network Methods for Phylogenomics." The G10K/B10K Meeting, The Rockefeller University, New York, September 2018.
2. "Statistical Inference of Phylogenetic Networks from Multi-locus Data." The *Distinguishability in Genealogical Phylogenetic Networks* Workshop, Lorentz Center, Leiden, The Netherlands, August 2018.

3. "Phylogenetic network inference with PhyloNet." The 2018 Phylogenomics Software Symposium, Institut des Sciences de l'Evolution - Montpellier, France, August 2018.
4. "Inferring Evolutionary Histories of Species from Genome-wide Data." The Southeast Texas Evolutionary Genetics and Genomics Symposium (STEGG), Rice University, June 2018.
5. "Phylogenetic network inference with PhyloNet." The Species Tree Estimation Workshop (part of SSB 18), Ohio State University, June 2018.
6. "Computational Phylogenetics in the Post-genomic Era: From Cancer Cells to Populations and Species." University of Houston-Clear Lake, January 2018.
7. "Statistical Inference of Reticulate Evolutionary Histories from Multi-locus Data." The American Museum of Natural History, New York, November 2017.
8. "Phylogenetic Networks: From Simple Summaries to Probabilistic Models." Department of Organismal and Evolutionary Biology, Harvard University, November 2017.
9. "Statistical Inference of Reticulate Evolutionary Histories Using Data from Unlinked Loci." Department of Computational Biology, School of Computer Science, Carnegie Mellon University, November 2017.
10. "Phylogenetic Networks: From Displayed Trees to a Distribution of Gene Trees." Phyloseminar.org, October 2017.
11. "Phylogenetics in the Post-genomic Era: From Cancer Cells to Populations and Species." The Human Genetics Center, The University of Texas School of Public Health, Houston, October 2017.
12. "Phylogenetic Networks." The Canadian Discrete and Algorithmic Mathematics Conference (CanaDAM), Toronto, Canada, June 2017.
13. "The Multispecies Network Coalescent and Inference of Reticulate Evolutionary Histories." The University of California, Berkeley, June 2017.
14. "The Multispecies Network Coalescent and Inference of Reticulate Evolutionary Histories." The Phylogenomics and Phylogeography Workshop, The Gothenburg Centre of Advanced Studies in Science and Technology, Chalmers University and the University of Gothenburg, Gothenburg, Sweden, May 2017.
15. "Phylogenetics in the Post-genomics Era: In the Light of Population Genetics." The BioSciences Faculty Colloquium, Rice University, November 2016.
16. "Phylogenetics in the Post-genomics Era." The Research Exchange Seminar Series, Department of Genetics, MD Anderson Cancer Center, November 2016.
17. "The Multispecies Network Coalescent and Inference of Reticulate Evolutionary Histories." Ecology and Evolution Seminar, University of Chicago, November 2016.
18. "Statistical Phylogenomic Inference in the Presence of Incomplete Lineage Sorting and Hybridization." The School of Life Sciences, Arizona State University, November 2016.
19. "Statistical Inference of Reticulate Evolutionary Histories." Symposium on Advances in the Analysis of Reticulate Population Networks, Evolution 2016, Austin, Texas.
20. "The Multispecies Network Coalescent and Phylogenetic Network Inference." The Phylogenomics Symposium, Austin, Texas, June 2016.

21. "Statistical Phylogenomics in the Presence of Reticulation." The Bioinformatics Seminar Series, CSAIL, MIT, May 2016.
22. "Network Models for Evolutionary Analysis." Phylogenetic Models: Linguistics, Computation, and Biology, MIT, May 2016.
23. "Gene Tree Distributions in Species Trees and Networks." The Mathematics of Evolution Sectional Meeting of the American Mathematical Society, Loyola University, Chicago, October 2015.
24. "Statistical Inference of Reticulate Evolutionary Histories." The Evolution Seminar, The University of Wisconsin, Madison, September 2015.
25. "Statistical Inference of Phylogenetic Networks." Networks in Biological Sciences, the Institute for Mathematics Sciences, National University of Singapore, July 2015.
26. "Maximum Likelihood Inference of Reticulate Evolutionary Histories." The 2015 Phylogenomics Symposium and Software School, The University of Michigan at Ann Arbor, May 2015.
27. "New Methods for Inferring Reticulate Evolutionary Relationships." Department of Botany and Plant Pathology, Oregon State University, November 2014.
28. "Inference of Reticulate Evolutionary Histories from Multi-locus and Whole-genome Data." The Frontiers in Phylogenetics Symposium, National Museum of Natural History, Smithsonian Institution, Washington D.C., September 2014.
29. "Genomic Underpinnings for Network Patterns and Evolution." The Highlights Track at ISMB 2014, Boston, July 2014.
30. "Complexities in the Inference of Phylogenetic Networks." The "Utilizing Genealogical Phylogenetic Networks in Evolutionary Biology: Touching the Data" Workshop, The Lorentz Center, Leiden University, The Netherlands, July 2014.
31. "Inference of Reticulate Evolutionary Histories." The Phylogenomics Symposium, Evolution 2014, Raleigh, North Carolina, June 2014.
32. "On the Interplay Between Genome and Interactome Evolution." The 2014 PhyloLab Conference on Computational Biology, Department of Computer Science, University of Texas, Austin, May 2014.
33. "Phylogenomics in the Presence of ILS and Introgression." The 2014 Summer School for Big Data in Biology, University of Texas, Austin, May 2014.
34. "Modeling the Evolution of Genes and Genomes in the Presence of ILS and Hybridization." The Workshop on New Directions in Probabilistic Models of Evolution, The Program on Evolutionary Biology and the Theory of Computing, The Simons Institute for the Theory of Computing, University of California, Berkeley, April 2014.
35. "Hybridization Detection in the Presence of Incomplete Lineage Sorting." Botany 2013, New Orleans, July 2013.
36. "PhyloNet: A Software Package for Reconstructing Trees and Networks." iEvoBio 2013, Snowbird, Utah, June 2013.
37. "Elucidating Properties of Molecular Interaction Networks via Evolutionary Genomics." Mathematical and Computational Evolutionary Biology Conference, Hameau de l'Etoile, France, May 2013.

38. “Phylogeny Inference in the Presence of Hybridization and Incomplete Lineage Sorting.” Symposium on New Methods for Phylogenomics and Metagenomics, The University of Texas at Austin, Feb 2013.
39. “Phylogenomics and Population Genomics: Models, Algorithms, and Analytical Tools.” Tutorial given at the Pacific Symposium on Biocomputing, The Big Island of Hawaii, Jan 2013.
40. “From Gene Trees to Species Trees.” The Millican Colloquium, The Department of Mathematics, The University of North Texas, Denton, Nov 2012.
41. “Quantifying Homologous Recombination in *Staphylococcus aureus* Using Whole-genome Data.” The Center for Computational and Integrative Biomedical Research (CIBR) Seminar Series, Baylor College of Medicine, Houston, Nov 2012.
42. “Phylogenetic Networks and the Trees Within: A Probabilistic Framework.” The Future of Phylogenetic Networks Workshop, The Lorentz Center, Leiden University, The Netherlands, Oct 2012.
43. “Incomplete Lineage Sorting and Hybridization: Parsimony and Likelihood Approaches.” The Vigo Workshop on Statistical Phylogenetics, Vigo, Spain, Sep 2012.
44. “The Probability of Gene Trees in the Presence of Hybridization.” The Annual Meeting of the Society for Molecular Biology and Evolution, Dublin, Ireland, Jun 2012.
45. “Modeling With Fewer Parameters: Petri Nets and Boolean Networks.” The 28th Southern Biomedical Engineering Conference, MD Anderson Cancer Center, Houston, May 2012.
46. “Disentangling Vertical and Horizontal Evolution in Phylogenomic Studies.” The Workshop on Evolutionary Genomics, UCLA Institute for Pure and Applied Mathematics, Nov 2011.
47. “Disentangling Vertical and Horizontal Evolution in Phylogenomic Studies.” The Human Genetics Center Seminar, The University of Texas at Houston, Oct 2011.
48. “Reconciling Gene Trees in the Presence of Incomplete Lineage Sorting and Hybridization.” The Isaac Newton Institute for Mathematical Sciences (the Phylogenetics Workshop), The University of Cambridge, UK, Jun 2011.
49. “Inferring Species Phylogenies from Multi-locus Data: New Algorithmic Techniques.” Department of Biology, University of British Columbia, Vancouver, Canada, Mar 2011.
50. “Simulating the Evolution of Pathways in a Population Genetic Setting.” *From Networks to Pattern Formation — Evolution of Biological Function* Symposium, Rice University, Dec 2010.
51. “Inference of Phylogenetic Relationships from Multi-locus Data.” Department of Computer Science and Engineering, Texas A&M University, College Station, Oct 2010.
52. “Simulating Cellular Networks Using Petri Nets.” The Institutional Grand Grounds Series, MD Anderson Cancer Center, Houston, Sep 2010.
53. “Algorithmic strategies for estimating the amount of reticulation from a collection of gene trees.” CSB Conference, Stanford, CA, Aug 2010.
54. “Species Tree Inference by Minimizing Deep Coalescences.” The ISMB Highlights Track, Boston, MA, Jul 2010.
55. “Inference of Parsimonious Multi-locus Phylogenies.” Symposium on Integrative Phylogenomics: From Genes to Organismal History, The Annual Meeting of the Society for Molecular Biology and Evolution, Lyon, France, Jul 2010.

56. "Accurate Inference of Phylogenetic Relationships from Multi-locus Data." Bertinoro Computational Biology meeting, Bertinoro, Italy, May 2010.
57. "Accurate Inference of Phylogenetic Relationships from Multi-locus Data." College of Computing, Georgia Tech, Mar 2010.
58. "Accurate Inference of Phylogenetic Relationships from Multi-locus Data." Department of Computer Science, McGill University, Montreal, Canada, Mar 2010.
59. "Evolution and Networks." Department of Ecology and Evolutionary Biology, Rice University, Feb 2010.
60. "Accurate Inference of Phylogenetic Relationships from Multi-locus Data." Penn Bioinformatics Forum, University of Pennsylvania, Philadelphia, PA, Jan 2010.
61. "Accurate Inference of Phylogenetic Relationships from Multi-locus Data." University of Washington Computer Science Department, Seattle, WA, Nov 2009.
62. "Accurate Inference of Phylogenetic Relationships from Multi-locus Data." Stanford University Computational Biology Seminar, Stanford, CA, Nov 2009.
63. "Computational Techniques for Inferring Phylogenetic Relationships Using Multiple Loci." University of California Berkeley Mathematical and Computational Biology Seminar, Berkeley, CA, Nov 2009.
64. "Computational Techniques for Inferring Phylogenetic Relationships Using Multiple Loci." Department of Computer Science, University of Texas at Austin, Oct 2009.
65. "Computational Techniques for Inferring Phylogenetic Relationships Using Multiple Loci." University of Maryland Center for Bioinformatics and Computational Biology, College Park, MD, Oct 2009.
66. "Computational Techniques for Inferring Phylogenetic Relationships Using Multiple Loci." University of California Los Angeles Bioinformatics Program, Los Angeles, CA, Oct 2009.
67. "Computational Techniques for Inferring Phylogenetic Relationships Using Multiple Loci." University of Southern California Computational Biology Seminar, Los Angeles, CA, Oct 2009.
68. "Computational Techniques for Inferring Phylogenetic Relationships Using Multiple Loci." University of California San Diego, Los Angeles, CA, Oct 2009.
69. "From Gene Trees to Phylogenetic Networks: Computational Approaches." Symposium on Biological Networks from Genes to Populations, The 17<sup>th</sup> Annual Meeting of the Society for Molecular Biology and Evolution (SMBE 2009), Iowa City, IA, Jun 2009.
70. "From Gene Trees to Species Phylogenies: Computational Techniques." The Integrative Biology Seminar Series, School of Biological Sciences, The University of Texas at Austin, Feb 2009.
71. "Interdisciplinary Research." The Graduate student Advising Day, Department of Computer Sciences, The University of Texas at Austin, Feb 2009.
72. "Efficient Search for the Species Tree in the Compatibility Graph of Gene Trees." The *Estimating Species Trees* Workshop, The University of Michigan, Ann Arbor, Jan 2009.
73. "Network-guided Search for Biological Hypotheses in Large Data Sets." The *High Throughput Screening Large Scale Data Sets* Workshop, The Gulf Coast Consortium for Bioinformatics and the Gulf Coast Consortium for Chemical Genomics, Oct 2008.



74. "Network-guided Search for Biological Hypotheses." The Keck Annual Research Conference, The Gulf Coast Consortia, Oct 2008.
75. "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.
76. "Novel algorithmic techniques for gene tree reconciliation in bacterial genomes." The Evolution 2008 Conference, The University of Minnesota, Jun 2008.
77. "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.
78. "Phylogenetic Networks: Reconstruction and Evaluation." The ITES Networks Cluster Seminar, The University of Houston, Apr 2008.
79. "From Gene Trees to Species Phylogenies." Computational Aspects of Biological Information, Microsoft Research, Dec 2007.
80. "Petri Net Modeling of Signal Transduction Networks: Predicting Dynamics Without Prior Knowledge of Kinetics." Department of Biochemistry and Cell Biology, Rice University, Nov 2007.
81. "Efficient Reconstruction of Species Trees from Genome-scale Multi-locus Data Under the Coalescent." Department of Computational and Applied Mathematics, Rice University, Nov 2007.
82. "Graph-theoretic Modeling and Reasoning about Signaling Networks." Oklahoma Medical Research Foundation, Aug 2007.
83. "Horizontal Gene Transfer Detection: Issues and Algorithms." The 5th Bertinoro Computational Biology Meeting, Bertinoro, Italy, May 2007.
84. "Graph-Theoretic Techniques for Analyzing Signaling Networks." The 24th Annual Houston Conference on Biomedical Engineering Research, Houston, Texas, Feb 2007.
85. "Computational Hypothesis Generation in Signaling Networks ." Cancer Systems Biology Symposium, The University of Texas M.D. Anderson Cancer Center, Dec 2006.
86. "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.
87. "Computational Methodologies for Inferring and Analyzing Networks: Species, Individuals, and Molecules." Collaborative Research Symposium, Rice University and the Texas Medical Center, Nov 2006.
88. "Modeling and Reconstructing Non-treelike Evolutionary Relationships in Species and Populations." Keck Seminar, Gulf Coast Consortia/Keck Center, Rice University, Oct 2006.
89. "Phylogenetic Networks and Reconstruction of Horizontal Gene Transfer." Corporate Affiliates Meeting, Department of Computer, Rice University, Oct 2006.
90. "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.
91. "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.

92. "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.
93. "Phylogenetic networks and reconstruction of horizontal gene transfer." The Bioinformatics Program, The University of Michigan at Ann Arbor, Apr 2006.
94. "Alien genes, complex diseases, and targeted drugs: computational approaches." Computer and Information Technology Institute, Rice University, Dec 2005.
95. "Alien genes, complex diseases, and targeted drugs: computational approaches." Department of Computer Sciences, The University of Texas at Austin, Dec 2005.
96. "The gene tree and species network problem." Ecology and Evolutionary Biology, Rice University, Nov 2005.
97. "Computational phylogenetics in historical linguistics." The 8<sup>th</sup> Annual Chinese American Frontiers of Science (CAFoS) Symposium, Xiamen, China, Nov 2005.
98. "Phylogenetic networks: modeling and reconstruction." The 52<sup>nd</sup> Annual Systematics Symposium, Missouri Botanical Garden, St. Louis, Missouri, Oct 2005.
99. "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.
100. "Phylogenetic networks, trees, and clusters." IWBRA '05, Emory University, Atlanta, GA, May 2005. Co-authors: Li-San Wang.
101. "Phylogenetic networks: generation, reconstructibility, and comparison." DIMACS Workshop on Reticulated Evolution, Rutgers University, New Jersey, Sep 2004.
102. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, The University of Toronto, Toronto, Canada, Apr 2004.
103. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, Rice University, Houston, TX, Apr 2004.
104. "Reconstructing reticulate evolution in species – theory and practice." RECOMB '04, San Diego, CA, Mar 2004. Co-authors: T. Warnow and C.R. Linder.
105. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, Tufts University, Medford, MA, Mar 2004.
106. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, University of Maryland, College Park, MD, Mar 2004.
107. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." School of Informatics, Indiana University, Bloomington, IN, Mar 2004.
108. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, The University of Texas at Dallas, Richland, TX, Feb 2004.
109. "Reconstructing phylogenies: accuracy of methods and appropriateness of models." Dept. of Computer Science, George Washington University, Washington, D.C., Feb 2004.
110. "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.

111. “Reticulate evolution in biology and historical linguistics.” Dean Scholars Honor Program, The University of Texas at Austin, Austin, TX, May 2003.
  112. “Estimating deviation from a molecular clock.” WABI '02, Rome, Italy, Oct 2002. Co-authors: U. Roshan, L. Vawter, and T. Warnow.
  113. “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.
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## STUDENTS, POSTDOCS, AND RESEARCH STAFF

### CURRENT POSTDOCS

1. Huw Ogilvie. PhD from Australian National University, 2018 (PhD Advisors: Craig Moritz and Alexei Drummond).
2. Xian Fan. PhD from Rice University, 2018 (PhD Advisors: Luay Nakhleh and Ken Chen).

### CURRENT PH.D. AND MASTER'S COMMITTEE CHAIR

1. Peng Du. *Computer Science*, Rice University.  
Joined my group: Aug 2014.  
Master's thesis: waived (prior MSc degree).
2. Ryan (Leo) Elworth. *Computer Science*, Rice University.  
Joined my group: Aug 2014.  
Date of Master's defense: November 2016.  
Master's thesis title: Approximate Modeling of Recombination within the Multispecies Coalescent.
3. Jiafan Zhu. *Computer Science*, Rice University.  
Joined my group: Jan 2016.  
Date of Master's defense: November 2017.  
Master's thesis title: Statistical Inference of Phylogenetic Networks from Unlinked Bi-allelic Markers.
4. Yaxuan Wang. *Computer Science*, Rice University.  
Joined my group: Aug 2016.
5. Mohammad Edrisi. *Computer Science*, Rice University.  
Joined my group: May 2017.
6. Hunter Tidwell. *Computer Science*, Rice University.  
Joined my group: May 2017.
7. Shaoheng Liang. *Computer Science*, Rice University.  
Joined my group: Aug 2017.

### FORMER RESEARCH APPLICATION DEVELOPERS

1. R. Matt Barnett.

### FORMER POSTDOCS

1. Kevin Liu. Ph.D. from UT Austin, 2011 (PhD Advisor: Tandy Warnow). First position after post-doc (starting August 2014): Assistant Professor (tenure-track), Computer Science and Engineering, Michigan State University.

2. Jianrong Dong. Ph.D. from Iowa State University, 2012 (PhD Advisor: David Fernández-Baca). Currently a post-doc at Baylor College of Medicine.
3. Yun Yu. PhD from Rice University, 2014 (PhD Advisor: Luay Nakhleh). First position after post-doc (starting August 2016): Facebook.

#### PAST PH.D. AND MASTER'S COMMITTEE CHAIR

1. Derek Ruths. *Computer Science*, Rice University.  
 Joined my group: January 2005.  
 Date of Master's defense: November 2005.  
 Master's thesis title: Applications of Phylogenetic Incongruence to Detecting and Reconstructing Recombination and Horizontal Gene Transfer.  
 Date of PhD defense: April 2009.  
 PhD dissertation title: Deriving Executable Models of Biochemical Network Dynamics from Qualitative Data and Network Connectivity.  
 Current position: Associate Professor of Computer Science, McGill University.
2. Cuong Than. *Computer Science*, Rice University.  
 Joined my group: January 2006.  
 Date of Master's defense: May 2008.  
 Master's thesis title: Reconstruction of Phylogenetic Networks and Their Relationships with Trees and Branches.  
 Date of PhD defense: October 2009.  
 PhD dissertation title: Inference of Parsimonious Species Phylogenies from Multi-locus Data.  
 Current position: Axon Vietnam.
3. Jeff Kilpatrick. *Computer Science*, Rice University.  
 Joined my group: Aug 2007.  
 Date of Master's defense: December 2009.  
 Master's thesis title: Methods for Detecting Multi-locus Genotype-phenotype Association.  
 Current position: Tableau Software
4. Hyun Jung Park. *Computer Science*, Rice University.  
 Joined my group: Aug 2007.  
 Master's thesis: waived (prior MSc degree).  
 Date of PhD defense: Mar 2012.  
 PhD dissertation title: Towards Accurate Reconstruction of Phylogenetic Networks.  
 Current position: Assistant Professor, Department of Human Genetics, University of Pittsburgh.
5. Natalie Berestovsky. *Computer Science*, Rice University.  
 Joined my group: Aug 2008.  
 Date of Master's defense: April 2011.  
 Master's thesis title: On the Modeling of Signaling Networks with Petri Nets.  
 Date of PhD Defense: April 2013.  
 PhD dissertation title: Toward Integrated Computational Models of Cellular Networks.  
 Current position: Anadarko.
6. Wanding Zhou. *Bioengineering*, Rice University.  
 Joined my group: Jan 2009.  
 Master's thesis waived (non-CS student).  
 Date of PhD defense: March 2013.  
 PhD dissertation title: Graph-based Modeling and Evolutionary Analysis of Microbial Metabolism.  
 Current position: Post-doctoral fellow, Van Andel Institute.

7. Troy Ruths. *Computer Science*, Rice University.  
 Joined my group: Aug 2008.  
 Date of Master's defense: December 2010.  
 Master's thesis title: A Sequence-based, Population Genetic Model of Regulatory Pathway Evolution.  
 Date of PhD defense: Aug 2013.  
 PhD dissertation title: Population Regulomics: Applying Population Genetics to the *cis*-Regulome.  
 Current position: Founder and CEO of Ruths.ai
8. Yun Yu. *Computer Science*, Rice University.  
 Joined my group: Jul 2009.  
 Date of Master's defense: November 2011.  
 Master's thesis title: From Gene Trees to Species Trees: Algorithms for Parsimonious Reconciliation.  
 Date of PhD defense: Mar 2014.  
 PhD dissertation title: Models and Methods for Evolutionary Histories Involving Hybridization and Incomplete Lineage Sorting.  
 Current position: Facebook.
9. Yun (Angela) Zhu. *Computer Science*, Rice University.  
 Joined my group: Aug 2010.  
 Master's thesis waived (prior MSc degree).  
 Date of PhD defense: Apr 2014.  
 PhD dissertation title: Computational Analyses of Gene Duplication and Network Evolution.  
 Current position: Airbnb.
10. Nikola Ristic. *Computer Science*, Rice University.  
 Joined my group: Aug 2011.  
 Graduated in May 2014, with a professional Masters degree.
11. Jie Lv. *Ecology and Evolutionary Biology*, Rice University.  
 I became the committee chair, following the departure of Jie's advisor.  
 Date of PhD defense: April 2015.  
 PhD dissertation title: Evolution of Genome Organization in Animal and Yeast Species.  
 Current position: Post-doctoral fellow, Methodist Research Institute.
12. Dan Ye. *Computer Science*, Rice University.  
 Joined my group: Aug 2014.  
 Date of Master's defense: December 2016.  
 Master's thesis title: Gene Tree Distributions under Duplication, Loss, and Deep Coalescence.  
 Current position: Google.
13. Dingqiao Wen. *Computer Science*, Rice University.  
 Joined my group: Aug 2013.  
 Date of Master's defense: November 2015.  
 Master's thesis title: Bayesian Inference of Phylogenetic Networks.  
 Date of PhD defense: May 2017.  
 PhD dissertation title: Co-estimating Reticulate Phylogenies and Gene Trees from Multi-locus Sequence Data.  
 Current position: Facebook.
14. Xian Fan. *Computer Science*, Rice University.  
 Joined my group: Aug 2012. (co-advised by Prof. Ken Chen, MD Anderson Cancer Center)  
 Date of Master's defense: December 2014.

Master's thesis title: Calculating Variant Allele Fraction of Structural Variation in Next Generation Sequencing by Maximum Likelihood.

Date of PhD defense: April 2018.

PhD dissertation title: Detecting Structural Variations with Illumina, PacBio and Optical Maps Data by Computational Approaches.

Current position: Post-doc at Rice University.

15. Lee Chen. *Computer Science*, Rice University.

Joined my group: Jan 2016.

Date of Master's defense: April 2017.

Master's thesis title: Segmenting Genetic Sequences Based on Common Ancestry.

16. Hamim Zafar. *Computer Science*, Rice University.

Joined my group: Jan 2013. (co-advised by Prof. Ken Chen, MD Anderson Cancer Center)

Date of Master's defense: December 2014.

Master's thesis title: A SNP Calling and Genotyping Method for Single-cell Sequencing Data.

Date of PhD defense: April 2018.

PhD dissertation title: Statistical Methods for Elucidating Tumor Heterogeneity and Evolution from Single-cell DNA Sequencing Data.

Current position: Assistant Professor, Indian Institute of Technology, Kanpur.

#### ROTATING AND VISITING GRADUATE STUDENTS

1. Benjamin Bachman, SCBMB, Baylor College of Medicine.
2. Yu-Yu Cheng, BCB, Rice University.
3. Peng Du, Hokkaido University, Japan.
4. Shawn Luce, BCB, Rice University.
5. Wenshan Luo, BCB, Rice University.
6. Tatsuma Sakamoto, Hokkaido University, Japan.

#### CURRENT AND PAST UNDERGRADUATE STUDENT RESEARCHERS

1. Kyle Adams. Computer Science, Rice University.
2. Mustafa Al-Gamal. Computer Science, Rice University.
3. Chabrielle Allen. Computer Science, Rice University.
4. Daniela Arenas. Computer Science, Rice University.
5. Jeff Arenson. Computer Science, Rice University.
6. Travis Benedict. Computer Science, Rice University.
7. Melanie Beyt. Computer Science, Rice University.
8. Jingxuan Dai. Computer Science, Rice University.
9. Yi Dai. Computer Science, Rice University.
10. Gina De La Guardia. Computer Science, Rice University.

11. Jarrod Dunne. Computer Science, Rice University.
12. Peter Dulworth. Computer Science, Rice University.
13. Riya Fukui. Computer Science, Rice University.
14. Nicholas Hanson-Holtry. Computer Science, Rice University.
15. Skyler Johnson. Computer Science, Rice University.
16. Jan Li. Computer Science, Rice University.
17. Tianyi (Austin) Liu. Computer Science, Rice University.
18. Xinhao Liu. Computer Science, Rice University.
19. Alen Lukic. Computer Science, Rice University.
20. Richard Manning. Computer Science, Rice University.
21. Travis Martin. Computer Science, Rice University.
22. Noushin Quazi. Computer Science, Rice University.
23. Kunal Shah. Computer Science, Rice University.
24. Radhika Sharma. Computer Science, Rice University.
25. Aubrey Sirtautas. Computer Science, Rice University.
26. Richard Song. Computer Science, Rice University.
27. Ethan Steinberg. Computer Science, Rice University.
28. Zhiyuan Tang. Computer Science, Rice University.
29. Kathy Truong. Computer Science, Rice University.
30. Anthony Tzen. Computer Science, Rice University.
31. Kurt Warren. Computer Science, Rice University.
32. Lindsey Wohlfort. Biomedical Engineering, UT Austin.
33. Minghao Yan. Computer Science, Rice University.
34. Alexander Yozzo. Computer Science, Rice University.
35. Mayline Zhong. Computer Science, Rice University.

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## TEACHING

### MASSIVE OPEN ONLINE COURSES

- Algorithmic Thinking (Part of the Fundamentals of Computing specialization)
- Principles of Computing (Part of the Fundamentals of Computing specialization)

### COURSES AT RICE UNIVERSITY

- EEB Graduate Core Course (teach a module on Phylogenomics)
- COMP 182 Algorithmic Thinking
- COMP 481 Automata, Formal Languages, and Computability
- COMP 571 Bioinformatics: Sequence Analysis
- COMP 572 Bioinformatics: Network Analysis
- COMP 670 Graduate Seminar on Computational Biology
- COMP/STAT 496/696: RTG: Cross-training in Data Science

### COURSES AT UT AUSTIN

- CS 341 Automata Theory
- CS 328 Abstract Data Types
- CS 378 Contemporary Issues in Computer Science

### COURSES AT TEXAS A&M UNIVERSITY

- CPSC 629 Analysis of Algorithms

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## TEACHING AWARDS AND HONORS

04/2015	The (T+R) <sup>2</sup> Excellence in Teaching and Research Award. <i>School of Engineering, Rice University.</i>
04/2009	Winner, <i>The Phi Beta Kappa of Rice Teaching Prize. Rice University.</i>
04/2008	Finalist, <i>The Phi Beta Kappa of Rice Teaching Prize. Rice University.</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>



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## SERVICE

### DEPARTMENTAL SERVICE

- 01/2017— Chair, Department of Computer Science, Rice University.
- 08/2016—12/2016 Associate Chair, Department of Computer Science, Rice University.
- 2015—2016 Undergraduate Committee (chair), Department of Computer Science, Rice University.
- 2010—2015 Undergraduate Committee (member), Department of Computer Science, Rice University.
- 2011—2012 Graduate Committee, Department of Computer Science, Rice University.
- 2007—2009 Faculty Recruiting Committee, Department of Computer Science, Rice University.
- 2005—2008 Graduate Committee, Department of Computer Science, Rice University.

### UNIVERSITY SERVICE

- 2017—current Steering Committee member, The NLM Training Program (NLMTP) in Biomedical Informatics and Data Science.
- 2016 The Programming and Search Committee for the Data Science Initiative.
- 2016 The Curriculum Committee for the Data Science Initiative.
- 2016 School of Engineering Course Review Committee, member.
- 2015—2016 Graduate Honor Council, member.
- 2013—2016 Senator, Rice University.
- 2013—2014 Faculty Recruiting Committee, Department of Ecology and Evolutionary Biology, Rice University.
- 2011—2012 Member of The University Admissions Committee.
- 2011—2012 Triad Mentor Program, School of Engineering (mentoring assistant professors).
- 2011—2012 Faculty Mentoring Program (mentoring incoming freshmen).
- 2011 Member, Provost *ad hoc* committee on establishing a research distinction program for undergraduates.
- 2011 Member of the Huxley Faculty Search Committee, Department of Ecology and Evolutionary Biology, Rice University.
- 2007—2012 Faculty Associate, Wiess College, Rice University.
- 2007—2008 Faculty Recruiting Committee, Department of Biochemistry and Cell Biology, Rice University.

### OUTREACH ACTIVITIES

- Aug 31, 2013 Panelist, School Dialogue (an activity organized by Rice Empower) at the Yes Prep East End Academy, Houston.

## PROFESSIONAL SERVICE

1. Steering Committee member, RECOMB Comparative Genomics, 2017–current.
2. Guest Editor for BMC Genomics and BMC Bioinformatics issues dedicated to papers from RECOMB Comparative Genomics 2017.

## CONFERENCE PROGRAM COMMITTEE MEMBERSHIP

1. PC member, *The Twenty-sixth Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB 2018).
2. PC Chair, *RECOMB Comparative Genomics*, 2017.
3. PC member, *The 2016 ACM Conference on Bioinformatics, Computational Biology, and Health Informatics* (ACM-BCB 2016)
4. PC member, *The Sixteenth Workshop on Algorithms in Bioinformatics* (WABI 2016)
5. PC member, *The Twenty-third Annual International Conference on Intelligent Systems for Molecular Biology and the Fourteenth European Conference on Computational Biology* (ISMB/ECCB 2015)
6. Member of the Organizing Committee, *Networks in Biological Sciences*, The Institute of Mathematical Sciences, The National University of Singapore, 1 June - 31 July, 2015.
7. PC member, *The Fourteenth Workshop on Algorithms in Bioinformatics* (WABI 2014)
8. PC member, *The Twenty-second Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB 2014)
9. PC member, *The ACM Conference on Bioinformatics, Computational Biology and Biomedical Informatics* (ACM-BCB 2013).
10. PC member, *The Thirteenth Workshop on Algorithms in Bioinformatics* (WABI 2013)
11. Co-chair of the *Phylogenomics and Population Genomics: Models, Algorithms, and Analytical Tools* session at the *Pacific Symposium on Biocomputing* (PSB 2013).
12. PC member, *ISMB/ECCB 2013*.
13. PC member, *The ACM Conference on Bioinformatics, Computational Biology and Biomedicine* (ACM-BCB 2012)
14. PC member, *The Twelfth Workshop on Algorithms in Bioinformatics* (WABI 2012)
15. PC member, *The Twentieth Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB 2012)
16. PC member, *The Sixteenth International Conference on Research in Computational Molecular Biology* (RECOMB 2012)
17. PC member, *The Ninth European Conference on Computational Biology* (ECCB 2010)
18. PC member, *The Seventeenth Annual International Conference on Intelligent Systems for Molecular Biology & The Eighth European Conference on Computational Biology* (ISMB/ECCB 2009)
19. PC member, *The Ninth Annual Workshop on Algorithms in Bioinformatics* (WABI 2009)

20. PC member, *The Sixth Annual Conference on Theory and Applications of Models of Computation* (TAMC 2009)
21. PC member, *The Eighth Workshop on Algorithms in Bioinformatics* (WABI 2008)
22. PC member, *The Sixteenth Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB 2008)
23. PC member, *The Fifteenth Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB 2007)
24. PC member, *The Fourteenth Annual International Conference on Intelligent Systems for Molecular Biology* (ISMB 2006).
25. PC member, *The Sixth Workshop on Algorithms in Bioinformatics* (WABI 2006).
26. PC member, *The Fifth IEEE International Workshop on High Performance Computational Biology* (HiCOMB 2006).

#### REVIEWER

1. *Ad hoc* member of the “Genomics, Computational Biology and Technology” (GCAT) study section.
2. Mentor in the NSF AVATOL Idea Lab (one of five mentors chosen from across the United States).
3. Grant Proposals:
  - School of Computing, National University of Singapore.
  - City University of Hong Kong.
  - Big Data Panel, National Science Foundation.
  - Career Panel (IIS), National Science Foundation.
  - ABI (Advances in Biological Informatics) Panel, National Science Foundation.
  - CCF Panel, National Science Foundation.
  - Mentor for the AVAToL Ideas Lab, Directorate for Biological Sciences, National Science Foundation.
4. Book Proposals:
  - Wiley-Blackwell, MIT Press, Prentice-Hall, Springer-Verlag.
5. Journals:
  - Algorithmica, Bioinformatics, BMC Bioinformatics, BMC Evolutionary Biology, Communications of the ACM, Discrete Applied Mathematics, Evolution, Genome Research, INFORMS Journal on Computing, 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, Molecular Biology and Evolution, Molecular Phylogenetics and Evolution, Nature, PLoS Computational Biology, PLoS Genetics, Proceedings of the Royal Society B, Science, Systematic Biology, ACM/IEEE Transactions on Computational Biology and Bioinformatics.