

# Mukul S. Bansal

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## CONTACT INFORMATION

Department of Computer Science & Engineering  
University of Connecticut  
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Storrs, CT, USA

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*Lab Website:* <http://compbio.engr.uconn.edu/>

## RESEARCH INTERESTS

**Computational biology** and **bioinformatics**, with a focus on computational phylogenetics and comparative genomics; **Algorithms** and **combinatorial optimization** in general.

## EDUCATION

**Postdoctoral Associate**, January 2011 – August 2013  
Computer Science and Artificial Intelligence Laboratory  
Massachusetts Institute of Technology, Cambridge, USA  
*Postdoc Advisors:* Manolis Kellis and Eric J. Alm

**Postdoctoral Fellow**, July 2009 – December 2010  
The Blavatnik School of Computer Science  
Tel Aviv University, Tel Aviv, Israel  
*Postdoc Advisor:* Ron Shamir

**M.S. and Ph.D.** in Computer Science, Fall 2004 – Summer 2009  
Department of Computer Science  
Iowa State University, Ames, Iowa, USA  
*Advisors:* David Fernández-Baca and Oliver Eulenstein

B.Tech. in Computer Science, 2000 – 2004  
Department of Computer Science and Engineering  
International Institute of Information Technology, Hyderabad, India

## EMPLOYMENT HISTORY

**Assistant Professor:** *August 2013 – Present;* Department of Computer Science and Engineering, University of Connecticut, USA.

**Postdoctoral Associate:** *January 2011 – August 2013;* Computational Biology Research Group, Computer Science and Artificial Intelligence Laboratory, Massachusetts Institute of Technology, USA.

**Postdoctoral Fellow:** *July 2009 – December 2010;* Algorithms for Computational Genomics Group, The Blavatnik School of Computer Science, Tel Aviv University, Israel.

**Visiting Graduate Student:** *Summer 2007;* Michael Sanderson's Lab, Department of Ecology and Evolutionary Biology, University of Arizona, USA.

**Research/Teaching Assistant:** *Fall 2004 – Summer 2009;* Department of Computer Science, Iowa State University, USA.

## OTHER APPOINTMENTS AND AFFILIATIONS

- **Faculty Member:** The Institute for Systems Genomics (ISG), University of Connecticut.
- **Faculty Affiliate:** The Center for Microbial Systems, Ecology and Evolution (CMSEE), University of Connecticut.

## RESEARCH FUNDING

- 2/2016–1/2021** Principal Investigator, *CAREER: Algorithms for Domain-Level Analysis of Gene Family Evolution*. \$499,576, National Science Foundation, USA.
- 8/2016–8/2019** Principal Investigator, *Understanding Horizontal Gene Transfer in Bacteria and Archaea: Units of Transfer and Modes of Integration*. \$598,801, National Science Foundation, USA.
- 8/2016–7/2019** Co-Principal Investigator (PI: Ion Mandoiu), *Collaborative Research: Algorithmic Techniques for Inferring Transmission Networks from Noisy Sequencing Data*. \$199,999, National Science Foundation, USA.
- 9/2016–8/2019** Principal Investigator, *Collaborative Research: Integrating the geological and genomic records: time-calibrating Earth's dynamic biogeochemical history*. \$316,714, National Science Foundation, USA.

## SELECTED RECENT AWARDS AND HONORS

- 2/2016** Recipient of NSF CAREER award
- 7/2016** Named *UTC professor of engineering innovation* for research excellence
- 2015, 2016** Received UConn provost's commendation for teaching excellence

## JOURNAL PUBLICATIONS

- [1] M. Kordi and M. S. Bansal, "Exact Algorithms for Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees", *IEEE/ACM Transactions on Computational Biology and Bioinformatics*: in press.
- [2] M. Kordi and M. S. Bansal, "On the Complexity of Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees", *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 2017, 14(3): 587–599.
- [3] Roadmap Epigenomics Consortium, A. Kundaje, W. Meuleman, J. Ernst, M. Bilenky, A. Yen, A. Heravi-Moussavi, P. Kheradpour, Z. Zhang, J. Wang, M. J. Ziller, V. Amin, J. W. Whitaker, M. D. Schultz, L. D. Ward, A. Sarkar, G. Quon, R. S. Sandstrom, M. L. Eaton, Y. Wu, A. R. Pfenning, X. Wang, M. Claussnitzer, Y. Liu, C. Coarfa, R. A. Harris, N. Shores, C. B. Epstein, E. Gjoneska, D. Leung, W. Xie, R. D. Hawkins, R. Lister, C. Hong, P. Gascard, A. J. Mungal, R. Moore, E. Chuah, A. Tam, T. K. Canfield, R. S. Hansen, R. Kaul, P. J. Sabo, M. S. Bansal, A. Carles, J. R. Dixon, K. Farh, S. Feizi, R. Karlic, A. Kim, A. Kulkarni, D. Li, R. Lowdon, T. R. Mercer, S. J. Neph, V. Onuchic, P. Polak, N. Rajagopa, P. Ray, R. C. Sallari, K. T. Siebenthal, N. A. Sinnott-Armstrong, M. Stevens, R. E. Thurman, J. Wu, B. Zhang, X. Zhou, A. E. Beaudet, L. Boyer, P. De Jager, P. J. Farnham, S. J. Fisher, D. Haussler, S. Jones, W. Li, M. Marra, M. T. McManus, S. Sunyaev, J. A. Thomson, T. D. Tlsty, L. Tsai, W. Wang, R. A. Waterland, M. Zhang, L. H. Chadwick, B. E. Bernstein, J. F. Costello, J. R. Ecker, M. Hirst, A. Meissner, A. Milosavljevic, B. Ren, J. A. Stamatoyannopoulos, T. Wang, and M. Kellis, "Integrative analysis of 111 reference human epigenomes", *Nature* 2015, 518: 317–330.
- [4] M. S. Bansal, Y. Wu, E. J. Alm, and M. Kellis, "Improved Gene Tree Error Correction in the Presence of Horizontal Gene Transfer", *Bioinformatics* 2015, 31(8): 1211–1218.

- [5] F. Yue, Y. Cheng, A. Breschi, J. Vierstra, W. Wu, T. Ryba, R. Sandstrom, Z. Ma, C. Davis, B. Pope, Y. Shen, D. Pervouchine, S. Djebali, R. E. Thurman, R. Kaul, E. Rynes, A. Kirilusha, G. K. Marinov, B. A. Williams, D. Trout, H. Amrhein, K. Fisher-Aylor, I. Antoshechkin, G. DeSalvo, L. H. See, M. Fastuca, J. Drenkow, C. Zaleski, A. Dobin, P. Prieto, J. Lagarde, G. Bussotti, A. Tanzer, O. Denas, K. Li, M. A. Bender, M. Zhang, R. Byron, M. T. Groudine, D. McCleary, L. Pham, Z. Ye, S. Kuan, L. Edsall, Y. Wu, M. D. Rasmussen, M. S. Bansal, M. Kellis, C. A. Keller, C. S. Morrissey, T. Mishra, D. Jain, N. Dogan, R. S. Harris, P. Cayting, T. Kawli, A. P. Boyle, G. Euskirchen, A. Kundaje, S. Lin, Y. Lin, C. Jansen, V. S. Malladi, M. S. Cline, D. T. Erickson, V. M. Kirkup, K. Learned, C. A. Sloan, K. R. Rosenbloom, B. L. de Sousa, K. Beal, M. Pignatelli, P. Flicek, J. Lian, T. Kahveci, D. Lee, W. J. Kent, M. R. Santos, J. Herrero, C. Notredame, A. Johnson, S. Vong, K. Lee, D. Bates, F. Neri, M. Diegel, T. Canfield, P. J. Sabo, M. S. Wilken, T. A. Reh, E. Giste, A. Shafer, T. Kutuyavin, E. Haugen, D. Dunn, A. P. Reynolds, S. Neph, R. Humbert, R. S. Hansen, M. De Bruijn, L. Selleri, A. Rudensky, S. Josefowicz, R. Samstein, E. E. Eichler, S. H. Orkin, D. Levasseur, T. Papayannopoulou, K. H. Chang, A. Skoultschi, S. Gosh, C. Disteché, P. Treuting, Y. Wang, M. J. Weiss, G. A. Blobel, X. Cao, S. Zhong, T. Wang, P. J. Good, R. F. Lowdon, L. B. Adams, X. Q. Zhou, M. J. Pazin, E. A. Feingold, B. Wold, J. Taylor, A. Mortazavi, S. M. Weissman, J. A. Stamatoyannopoulos, M. P. Snyder, R. Guigo, T. R. Gingeras, D. M. Gilbert, R. C. Hardison, M. A. Beer, B. Ren; Mouse ENCODE Consortium, “A Comparative Encyclopedia of DNA Elements in the Mouse Genome”, *Nature* 2014, 515: 355–364.
- [6] Y. Wu, M. D. Rasmussen, M. S. Bansal, and M. Kellis, “Most Parsimonious Reconciliation in the Presence of Gene Duplication, Loss, and Deep Coalescence Using Labeled Coalescent Trees”, *Genome Research* 2014, 24: 475–486.
- [7] M. S. Bansal, E. J. Alm, and M. Kellis, “Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss”, *Journal of Computational Biology* 2013, 20(10): 738–754.
- [8] M. S. Bansal and O. Eulenstein, “Algorithms for Genome-Scale Phylogenetics Using Gene Tree Parsimony”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 2013, 10(4): 939–956.
- [9] M. S. Bansal, G. Banay, T. J. Harlow, J. P. Gogarten, and R. Shamir, “Systematic Inference of Highways of Horizontal Gene Transfer in Prokaryotes”, *Bioinformatics* 2013, 29(5): 571–579.
- [10] Y. Wu, M. D. Rasmussen, M. S. Bansal, and M. Kellis, “TreeFix: statistically informed gene tree error correction using species trees”, *Systematic Biology* 2013, 62(1): 110–120.
- [11] M. S. Bansal, G. Banay, J. P. Gogarten, and R. Shamir, “Detecting Highways of Horizontal Gene Transfer”, *Journal of Computational Biology* 2011, 18(9): 1087–1114.
- [12] M. S. Bansal, J. Dong, and D. Fernández-Baca, “Comparing and Aggregating Partially Resolved Trees”, *Theoretical Computer Science* 2011, 412: 6634–6652.
- [13] M. S. Bansal and R. Shamir, “A Note on the Fixed Parameter Tractability of the Gene-Duplication Problem”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 2011, 8(3): 848–850.
- [14] J. G. Burleigh, M. S. Bansal, O. Eulenstein, S. Hartmann, A. Wehe, and T. J. Vision, “Genome-Scale Phylogenetics: Inferring the Plant Tree of Life from 18,896 Gene Trees”, *Systematic Biology* 2011, 60(2): 117–125.
- [15] R. Chaudhary, M. S. Bansal, A. Wehe, D. Fernández-Baca, and O. Eulenstein, “iGTP: A software package for large-scale gene tree parsimony analysis”, *BMC Bioinformatics* 2010, 11:574.
- [16] M. S. Bansal, J. G. Burleigh, O. Eulenstein, and D. Fernández-Baca, “Robinson-Foulds Supertrees”, *Algorithms for Molecular Biology* 2010, 5:18.
- [17] M. S. Bansal, O. Eulenstein, and A. Wehe, “The Gene-Duplication Problem: Near-Linear Time Algorithms for NNI Based Local Searches”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 2009, 6(2): 221–231.
- [18] J. G. Burleigh, M. S. Bansal, A. Wehe, and O. Eulenstein, “Locating Large-Scale Gene Duplication Events Through Reconciled Trees: Implications For Identifying Ancient Polyploidy Events In Plants”, *Journal of Computational Biology* 2009, 16(8): 1071–1083.

- [19] M. S. Bansal and D. Fernández-Baca, “Computing Distances Between Partial Rankings”, *Information Processing Letters* 2009, 109(4): 238–241.
- [20] M. S. Bansal and O. Eulenstein, “An  $\Omega(n^2/\log n)$  Speed-Up of TBR Heuristics for the Gene-Duplication Problem”, *IEEE/ACM Transactions on Computational Biology and Bioinformatics* 2008, 5(4): 514–524.
- [21] A. Wehe, M. S. Bansal, J. G. Burleigh, and O. Eulenstein, “DupTree: A program for large-scale phylogenetic analyses using gene tree parsimony”, *Bioinformatics* 2008, 24(13): 1540–1541.
- [22] D. Chen, J. G. Burleigh, M. S. Bansal, and D. Fernández-Baca, “PhyloFinder: An Intelligent Search Engine for Phylogenetic Tree Databases”, *BMC Evolutionary Biology* 2008, 8:90.

## REFEREED CONFERENCE PUBLICATIONS

(Including conference proceedings published in journal special issues, not listed above.)

- [23] S. Kundu and M. S. Bansal, “On the Impact of Uncertain Gene Tree Rooting on Duplication-Transfer-Loss Reconciliation”. *Thirteenth International Symposium on Bioinformatics Research and Applications (ISBRA 2017)*, *LNCS 10330*: L–LI. (short paper)
- [24] M. Kordi and M. S. Bansal, “Exact Algorithms for Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees”. *Seventh ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM-BCB 2016)*; *Proceedings*: 297–306.
- [25] Misagh Kordi and Mukul S. Bansal, “On the Complexity of Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees”. *Eleventh International Symposium on Bioinformatics Research and Applications (ISBRA 2015)*, *LNCS 9096*: 187–198.
- [26] R. Libeskind-Hadas, Y. Wu, M. S. Bansal, and M. Kellis, “Pareto-Optimal Phylogenetic Tree Reconciliation”. *22nd Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2014)*; *Bioinformatics* 2014, 30: i87–i95.
- [27] M. S. Bansal, E. J. Alm, and M. Kellis, “Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss”. *Seventeenth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2013)*, *LNCS 7821*: 1–13.
- [28] M. S. Bansal, E. J. Alm, and M. Kellis, “Efficient Algorithms for the Reconciliation Problem with Gene Duplication, Horizontal Transfer, and Loss”. *Twentieth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2012)*; *Bioinformatics* 2012, 28: i283–i291.
- [29] M. S. Bansal, J. P. Gogarten, and R. Shamir, “Detecting Highways of Horizontal Gene Transfer”. *Eighth Annual RECOMB Comparative Genomics Workshop (RECOMB-CG 2010)*, *LNCS 6398*: 109–120.
- [30] H. Narayanappa, M. S. Bansal, and H. Rajan, “Property-Aware Program Sampling”, *Ninth ACM SIGPLAN-SIGSOFT Workshop on Program Analysis for Software Tools and Engineering (PASTE 2010)*: 45–52.
- [31] J. G. Burleigh, M. S. Bansal, O. Eulenstein, and T. J. Vision, “Inferring Species Trees From Gene Duplication Episodes”. *First ACM International Conference on Bioinformatics and Computational Biology (ACM-BCB 2010)*: 198–203.
- [32] M. S. Bansal, J. G. Burleigh, and O. Eulenstein, “Efficient genome-scale phylogenetic analysis under the duplication-loss and deep coalescence cost models”, *Eighth Asia-Pacific Bioinformatics Conference (APBC 2010)*; *BMC Bioinformatics* 2010, 11(Suppl 1): S42.
- [33] M. S. Bansal, W. Chang, O. Eulenstein, and D. Fernández-Baca, “Generalized Binary Tanglegrams: Algorithms and Applications”. *First International Conference on Bioinformatics and Computational Biology (BICoB 2009)*, *LNCS 5462*: 114–125. This paper won the **Best Paper Award**.
- [34] M. S. Bansal and O. Eulenstein, “The Multiple Gene Duplication Problem Revisited”, *Sixteenth Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2008)*; *Bioinformatics* 2008, 24(13): i132–i138.

- [35] M. S. Bansal and O. Eulenstein, “The Gene-Duplication Problem: Near-Linear Time Algorithms for NNI Based Local Searches”, *Fourth International Symposium on Bioinformatics Research and Applications (ISBRA 2008)*, LNCS 4983: 14–25.
- [36] J. G. Burleigh, M. S. Bansal, A. Wehe, and O. Eulenstein, “Locating Multiple Gene Duplications Through Reconciled Trees”, *Twelfth Annual International Conference on Research in Computational Molecular Biology (RECOMB 2008)*, LNCS 4955: 273–284.
- [37] M. S. Bansal, J. Dong, and D. Fernández-Baca, “Comparing and Aggregating Partially Resolved Trees”, *Eighth Latin American Theoretical Informatics Symposium (LATIN 2008)*, LNCS 4957: 72–83.
- [38] M. S. Bansal and O. Eulenstein, “An  $\Omega(n^2/\log n)$  Speed-Up of TBR Heuristics for the Gene-Duplication Problem”, *Seventh Workshop on Algorithms in Bioinformatics (WABI 2007)*, LNCS 4645: 124–135.
- [39] M. S. Bansal, J. G. Burleigh, O. Eulenstein, and A. Wehe, “Heuristics for the Gene-Duplication Problem: A  $\Theta(n)$  Speed-Up for the Local Search”, *Eleventh Annual International Conference on Research in Computational Molecular Biology (RECOMB 2007)*, LNCS 4453: 238–252.

## TECHNICAL REPORTS

- [40] Y. Wu, M. S. Bansal, M. D. Rasmussen, J. Herrero, and M. Kellis, “Phylogenetic Identification and Functional Characterization of Orthologs and Paralogs across Human, Mouse, Fly, and Worm”, *Technical Report 2014*, *BioRxiv*.
- [41] M. S. Bansal and V. Ch. Venkaiah, “Improved Fully Polynomial Time Approximation Scheme for the 0-1 Multiple-Choice Knapsack Problem”, *Technical Report 2004*, *IIIT-H, India*.

## MANUSCRIPTS UNDER REVIEW

- [42] L. Li and M. S. Bansal, “An Integrated Reconciliation Framework for Domain, Gene, and Species Level Evolution: Algorithms and Applications”.
- [43] M. S. Bansal, M. Kellis, M. Kordi, and S. Kundu “RANGER-DTL 2.0: Rigorous Reconstruction of Gene-Family Evolution by Duplication, Transfer, and Loss”.
- [44] M. Kordi and M. S. Bansal “Handling Gene Tree Uncertainty in Duplication-Transfer-Loss Reconciliation: Algorithms and Applications”.
- [45] S. Kundu and M. S. Bansal, “On the Impact of Uncertain Gene Tree Rooting on Duplication-Transfer-Loss Reconciliation”.

## SOFTWARE PACKAGES

- **RANGER-DTL**: (<http://compbio.engr.uconn.edu/software/RANGER-DTL/>) Short for Rapid ANalysis of Gene family Evolution using Reconciliation-DTL, this is a software package for inferring gene family evolution by speciation, gene duplication, horizontal gene transfer, and gene loss. RANGER-DTL v2.0 implements the algorithms presented in refs. [28],[7], [23], and [24], and makes it possible to perform rigorous evolutionary analyses of even large gene families with thousands of taxa while accounting for confounding factors such as gene tree uncertainty, uncertain rooting, and multiple optima.
- **RF-Supertrees**: (<http://genome.cs.iastate.edu/CBL/RFsupertrees/>) This is a fast and accurate supertree program for rooted phylogenetic trees. RF-supertrees implements efficient search algorithms described in ref. [16] and constructs a supertree that minimizes the total Robinson-Foulds distance between the supertree and the input trees.

- **DupTree**: (<http://genome.cs.iastate.edu/CBL/DupTree/>) This is a tool box for constructing species phylogenies from genome-scale multi-locus data using gene tree parsimony. DupTree implements the fast local search algorithm from ref. [39] and was programmed jointly with André Wehe.
- **TreeFix**: (<http://compbio.mit.edu/treefix/>) This is a program for very accurate reconstruction of eukaryotic gene trees. It takes as input a maximum likelihood gene tree topology, a known species tree, and a multiple sequence alignment for the gene family and computes a more accurate gene tree topology using the approach described in ref. [10]. TreeFix was programmed by Yi-Chieh Wu.
- **TreeFix-DTL**: (<http://compbio.mit.edu/treefix-dtl/>) This is a program for very accurate reconstruction of prokaryotic gene trees. Like the program TreeFix above, it takes as input a maximum likelihood gene tree topology, a known species tree, and a multiple sequence alignment for the gene family and computes a more accurate gene tree topology while accounting for horizontal gene transfer, gene duplication, and gene loss as described in ref. [4]. TreeFix-DTL was programmed by Yi-Chieh Wu.
- **DupLoss** and **DeepC**: (<http://genome.cs.iastate.edu/CBL/iGTP/>) These programs extend on the program DupTree and make it possible to construct species phylogenies, from genome-scale multi-locus data, under the duplication-loss and deep coalescence cost models respectively. They implement the local search algorithms described in ref. [32] and are available as part of the iGTP [15] package.
- **HiDe**: (<http://acgt.cs.tau.ac.il/hide/>) Short for Highway Detection, HiDe is a software package for inferring highways of horizontal gene transfer (representing large-scale horizontal transfer of genes) in the evolutionary history of a set of species. HiDe implements the highway detection method described in ref. [9] and was programmed by undergraduate summer student Guy Banay under my supervision.

## SELECTED PRESENTATIONS AND INVITED TALKS

1. “Inferring Microbial Gene Family Evolution Despite Phylogenetic Uncertainty”; *Evolution meeting, Portland, OR, USA. June 2017*
2. “Phylogenetic Uncertainty and Transmission Network Inference: Lessons from Phylogenetic Reconciliation”; *Workshop on Computational Advances in Molecular Epidemiology (CAME), Atlanta, USA. October 2016.*
3. “Deciphering microbial evolution using phylogenetic reconciliation”; *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), Atlanta, USA. October 2016. Invited.*
4. “Exact Algorithms for Duplication-Transfer-Loss Reconciliation with Non-Binary Gene Trees”; *ACM Conference on Bioinformatics, Computational Biology, and Health Informatics (ACM BCB), Seattle, USA. October 2016.*
5. “Using Phylogenetic Reconciliation to Decipher Microbial Evolution: Theory and Practice”; *Evolution meeting, Austin, USA. June 2016*
6. “Deciphering Reticulate Evolution Using Phylogenetic Reconciliation”; *Networks in Biological Sciences, Singapore. July 2015. Invited.*
7. “Deciphering Reticulate Evolution Using Phylogenetic Reconciliation”; *Utilizing Genealogical Phylogenetic Networks in Evolutionary Biology: Touching the Data, Leiden, Netherlands. July 2014. Invited.*
8. “Deciphering Microbial Evolution Using Phylogenetic Reconciliation”; *Computational Biology and Bioinformatics Organization meeting, Broad Institute of MIT and Harvard, Cambridge, USA. March 2014. Invited.*
9. “Deciphering Microbial Evolution Using Phylogenetic Reconciliation”; *Biomedical Engineering Seminar, University of Connecticut, Storrs, USA. March 2014.*
10. “Reconciliation Revisited: Handling Multiple Optima when Reconciling with Duplication, Transfer, and Loss”; *International Conference on Research in Computational Molecular Biology (RECOMB), April 2013, Beijing, China.*

11. “Accurate gene tree reconstruction using TreeFix and TreeFix-DTL”; *Symposium and Workshop on New Methods for Phylogenomics and Metagenomics, University of Texas, Austin, USA. February 2013. Invited.*
12. “Reconciliation revisited: Towards faster and more accurate inference of gene family evolution by duplication, transfer, and loss”; *Computational and Statistical Phylogenomics Meeting, Vigo, Spain. September 2012. Invited.*
13. “Efficient Algorithms for the Reconciliation Problem with Gene Duplication, Horizontal Transfer, and Loss”; *International Conference on Intelligent Systems for Molecular Biology (ISMB), July 2012, Long Beach, USA.*
14. “Reconciliation revisited: Towards more accurate inference of gene family evolution”; *Mathematical and Computational Evolutionary Biology (MCEB), June 2012, Montpellier, France.*
15. “Reconstructing gene family evolution by speciation, duplication, horizontal transfer & loss”; *Boston Evolutionary Genomics Supergroup Meeting, August 2011, Cambridge, USA.*
16. “Systematic Detection of Large-Scale Horizontal Gene Transfer Events on the Tree of Life”; *Computer Science Colloquium, Iowa State University, Ames, USA. April 2011. Invited.*
17. “Detecting Highways of Horizontal Gene Transfer”; *RECOMB Comparative Genomics Workshop (RECOMB-CG), October 2010, Ottawa, Canada.*
18. “Inferring Species Trees and Large-Scale Horizontal Gene Transfer from Discordant Gene Trees”; *Computational Biology Group and Laboratory for Microbiology, Massachusetts Institute of Technology, Cambridge, USA. October 2010. Invited.*
19. “Inferring Species Trees and Large-Scale Horizontal Gene Transfer from Discordant Gene Trees”; *Evolutionary Genomics Research Group, NCBI, National Institutes of Health, Bethesda, USA. July 2010. Invited.*
20. “Detecting Highways of Horizontal Gene Transfer”; *Bertinoro Computational Biology Meeting, May 2010, Bertinoro, Italy.*
21. “Detecting Highways of Horizontal Gene Transfer”; *Stringology Research Workshop, May 2010, Tel-Aviv, Israel.*
22. “Genome-Scale Phylogenetic Analyses using Gene Tree Parsimony”; *Asia-Pacific Bioinformatics Conference (APBC), January 2010, Bangalore, India.*
23. “Generalized Binary Tanglegrams”; *International Conference on Bioinformatics and Computational Biology (BICoB), April 2009, New Orleans, USA.*
24. “The Gene-Duplication Problem”; *Computational Genomics Research Group, Tel Aviv University, Tel Aviv, Israel. February 2009. Invited.*
25. “The multiple gene duplication problem revisited”; *International Conference on Intelligent Systems for Molecular Biology (ISMB), July 2008, Toronto, Canada.*
26. “The Gene-Duplication Problem: Near-Linear Time Algorithms for NNI Based Local Searches”; *International Symposium on Bioinformatics Research and Applications (ISBRA), May 2008, Atlanta, USA.*
27. “Heuristics for the Gene-Duplication Problem: A  $\Theta(n)$  Speed-up of the Local Search”; *International Conference on Research in Computational Molecular Biology (RECOMB), April 2007, San Francisco, USA.*

## TEACHING

Department of Computer Science & Engineering, University of Connecticut, USA.

1. CSE 3502 Theory of Computation: *Fall 2016, Fall 2017*
2. CSE 2500 Introduction to Discrete Systems: *Fall 2015, Spring 2016*
3. CSE 5500 Algorithms (graduate level): *Spring 2015, Fall 2015, Fall 2016, Fall 2017*
4. CSE 3800/CSE 5800/BME 4800 Bioinformatics: *Fall 2014*

5. CSE 3500 Algorithms and Complexity: *Spring 2014*
6. CSE 5095 Approximation, Randomized, and Fixed Parameter Algorithms: *Fall 2013*

## STUDENTS

### **Current lab members:**

1. Lei Li (PhD student)
2. Misagh Kordi (PhD student)
3. Lina Kloub (PhD student)
4. Soumya Kundu (undergraduate research assistant)
5. Chengchen Zhang (undergraduate research assistant)
6. Samuel Sledzieski (undergraduate research assistant)
7. Eric van Heel (undergraduate research assistant)
8. Alex Masi (undergraduate research assistant)
9. Hannah Reed (undergraduate research assistant)

### **Previous lab members:**

1. Kevin Grabowski (undergraduate research assistant)
2. Maryzyrene Adao (undergraduate research assistant)
3. James Boivie (undergraduate research assistant)

## PROFESSIONAL SERVICE

### **Conference program committees:**

- ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2017.
- International Symposium on Bioinformatics Research and Applications (ISBRA) 2017
- International Conference on Bioinformatics and Computational Biology (BICoB) 2017
- International Symposium on Bioinformatics Research and Applications (ISBRA) 2016
- International Conference on Intelligent Systems for Molecular Biology (ISMB) 2016
- International Conference on Bioinformatics and Computational Biology (BICoB) 2016
- International Conference on Intelligent Systems for Molecular Biology and European Conference on Computational Biology (ISMB/ECCB) 2015
- International Symposium on Bioinformatics Research and Applications (ISBRA) 2015
- International Conference on Bioinformatics and Computational Biology (BICoB) 2015
- International Conference on Research in Computational Molecular Biology (RECOMB) 2014
- International Conference on Applied Algorithms (ICAA) 2014
- International Conference on Intelligent Systems for Molecular Biology (ISMB) 2013
- International Conference on Bioinformatics and Computational Biology (BICoB) 2013
- ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB) 2012
- International Workshop on Data Mining in Bioinformatics (BIOKDD) 2012
- International Conference on Bioinformatics and Computational Biology (BICoB) 2012

### **Conference/workshop organizing:**

- Co-chair for "Inferring Phylogenies and Haplotypes" track of the ACM Conference on Bioinformatics, Computational Biology and Biomedicine (ACM-BCB). August 2017

- Co-organizer and host for "Biogeochemical Dating in Deep Time" workshop. May 2017
- Finance chair for IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS). 2014, 2015, 2016

**Selected journal and conference reviewing:**

- IEEE/ACM Transactions on Computational Biology and Bioinformatics (TCBB)
- Proceedings of the National Academy of Sciences (PNAS)
- Journal of Computational Biology (JCB)
- Journal of Theoretical Biology (JTB)
- PLoS Computational Biology
- Systematic Biology
- Nature Ecology & Evolution
- Mathematical Biosciences
- Information Processing Letters (IPL)
- Bioinformatics
- BMC Bioinformatics
- Molecular Biology and Evolution (MBE)
- Molecular Phylogenetics and Evolution (MPE)
- Methods in Ecology and Evolution
- BMC Evolutionary Biology
- Journal of Mathematical Biology (JOMB)
- Theoretical Computer Science (TCS)
- Algorithms for Molecular Biology (AMB)
- Cladistics
- Theoretical Population Biology (TPB)
- International Conference on Research in Computational Molecular Biology (RECOMB)
- ACM-SIAM Symposium on Discrete Algorithms (SODA)
- Pacific Symposium on Biocomputing (PSB)
- Combinatorial Pattern Matching (CPM)
- Latin American Theoretical Informatics (LATIN)
- International Symposium on Bioinformatics research and Applications (ISBRA)
- RECOMB Comparative Genomics (RECOMB-CG)
- Workshop on Algorithms in Bioinformatics (WABI)

**PROFESSIONAL MEMBERSHIPS**

- International Society for Computational Biology (ISCB)
- Society for Molecular Biology and Evolution (SMBE)
- Society of Systematic Biologists (SSB)