CURRICULUM VITAE

Russell Schwartz

Professor of Biological Sciences and Computational Biology
Carnegie Mellon University

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Education

Massachusetts Institute of Technology (1991-2000)

Post-doctoral associate/fellow (2000), Supervisor: Jonathan King, Department of Biology

Ph.D. in Computer Science (2/00), Supervisor: Bonnie Berger, Department of Mathematics

Thesis: "The Local Rules Dynamics Model for Self-Assembly Simulation."

M.Eng. in Electrical Engineering and Computer Science (6/96)

Thesis: "A Multi-threaded Simulator for the Kinetics of Virus Shell Assembly."

B.S. in Computer Science and Engineering (6/96)

Employment History

Carnegie Mellon University

Co-Director, University if Pittsburgh/Carnegie Mellon Medical Scientist Training Program (August 2014-present)

Co-Director, Joint Carnegie Mellon University-University of Pittsburgh Ph.D. Program in Computational Biology (December 2009-present)

Co-Associate Director, Joint Carnegie Mellon University-University of Pittsburgh Ph.D. Program in Computational Biology (January, 2007 – 2009)

Professor of Biological Sciences and Computational Biology with additional appointments in the Computer Science Department and Machine Learning Department (July, 2011 – present)

Tenured Associate Professor of Biological Sciences (July, 2008 – June, 2011)

Untenured Associate Professor of Biological Sciences (July, 2007 – June, 2008)

Assistant Professor of Biological Sciences (September, 2002 – July, 2007)

Celera Genomics

Informatics Research Scientist (October, 2000 – July, 2002)

Publications and Presentations

Peer-reviewed research articles:

1. E.M. Gertz, S.A. Chowdhury, W.-J. Lee, D. Wangsa, K. Heselmeyer-Haddad, T. Ried, R. Schwartz, A.A. Schäffer. "FISHtrees 3.0: Tumor Phylogenetics Using a Ploidy Probe." *PLOS ONE*, 11(6): e0158569, 2016.
2. T. Roman, L. Xie, and R. Schwartz. "Automated deconvolution of structured mixtures from bulk tumor genomic data." *RECOMB Satellite Conference on Computational Cancer Biology* (published as *arXiv* preprint arXiv:1604.02487), 2016.

3. L. Xie, G. R. Smith, and R. Schwartz. "Derivative-free optimization of rate parameters of capsid assembly models from bulk in vitro data." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, published online before print, 2016.
4. G. R. Smith, L. Xie, and R. Schwartz. "Modeling effects of RNA on capsid assembly pathways via coarse-grained stochastic simulation." *PLoS ONE*, 5(11):e0156547, 2016.
5. T. Roman, L. Xie, and R. Schwartz. "Medoidshift clustering applied to genomic bulk tumor data." *BMC Genomics*, 17(S1):6, 2016.
6. D. Wangsa, S. A. Chowdhury, M. Ryott, E. M. Gertz, G. Elmberger, G. Auer, E. A. Lundqvist, S. Küffer, P. Ströbel, A. A. Schäffer, R. Schwartz, E. Munck-Wikland, T. Ried, K. Heselmeyer-Haddad. "Phylogenetic analysis of multiple FISH markers in oral tongue squamous cell carcinoma suggests that a diverse distribution of copy number changes in associated with poor prognosis." *International Journal of Cancer*, 138(1), 2016.
7. D. Catanzaro, S. Shackney, A. Schäffer, and R. Schwartz. "Classifying the progression of ductal carcinoma from single-cell sampled data via integer linear programming: a case study." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 13(4):643-655, 2016.
8. A. Subramanian and R. Schwartz. "Reference-free inference of tumor phylogenies from single-cell sequencing data." *BMC Genomics*, 16S11:S7, 2015.
9. T. Roman, B. Fasy, A. Nayyeri, and R. Schwartz. "A simplicial complex-based approach to unmixing tumor progression data." *BMC Bioinformatics*, 16:254, 2015.
10. SA Chowdhury, E Gertz, D Wangsa, K Heselmeyer-Haddad, T Ried, A Schaffer and R Schwartz. "Inferring models of multiscale copy number evolution for single-tumor phylogenetics." *Bioinformatics* (proceedings issue for *Intelligent Systems for Molecular Biology*), 31(12):i258-i267, 2015.
11. J Kang, KM Puskar, AJ Ehrlicher, PR LeDuc, and RS Schwartz. "Structurally governed cell mechanotransduction through multiscale modeling." *Scientific Reports*. 5, 2015.
12. S. E. Shackney, S. A. Chowdhury, R. Schwartz. “A novel subset of human tumors that simultaneously overexpress multiple E2F responsive genes found in breast, ovarian, and prostate cancer.” *Cancer Informatics*, 13(S5):89, 2014.
13. K. Heselmeyer-Haddad, L.Y. Berroa Garcia, A. Bradley, L. Hernandez, Y. Hu, J.K. Habermann, C. Dumke, C. Thorns, S. Perner, E. Pestova, C. Burke, S.A. Chowdhury, R. Schwartz, A.A. Schäffer, P. Paris, T. Ried. "Single-cell genetic analysis reveals insights into clonal development of prostate cancers and indicates loss of PTEN as a marker of poor prognosis", *American Journal of Pathology*, 184(10):2671-2686, 2014.
14. C. Tan, R. Schwartz, L. You. “Phenotypic signatures arising from unbalanced bacterial growth,” *PLoS Computational Biology*, 10(8):e1003751, 2014.
15. H. Ashktorab, M. Daremipouran, J. Devaney, S. Varma, H. Rahi, E., Lee, B. Shokrani, R. Schwartz, M. Nickerson, H. Brim. "Identification of novel mutations by exome sequencing in African American colorectal cancer patients", *Cancer*, 121(1):34-42, 2014.
16. S.A. Chowdhury, S.E. Shackney, K. Heselmeyer-Haddad, T. Ried, A. Schaffer, R. Schwartz. “Algorithms to model single gene, single chromosome, and whole genome copy number changes jointly in tumor phylogenetics,” *PLoS Computational Biology*, 10(7):e1003740, 2014.
17. G.R. Smith, L. Xie, B. Lee, and R. Schwartz. “Applying cellular crowding models to simulations of capsid assembly in vitro.” *Biophysical Journal*, 106(1):310-320, 2014.

18. M.-C. Tsai, G. Blelloch, R. Ravi, and R. Schwartz. "Coalescent-based method for learning parameters of admixture events from large-scale genetic variation data," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(5):1137-1149, 2013. (extended version of ACM-BCB conference paper below)
19. A. Subramanian, S. Shackney, and R. Schwartz. "Novel multi-sample scheme for inferring phylogenetic markers from whole genome tumor profiles." *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 10(6):1422-1431, 2013. (extended version of ISBRA conference paper below)
20. C. Tan, S. Saurabh, M. Bruchez, R. Schwartz, and P. LeDuc. "Molecular crowding shapes gene expression in synthetic cellular nanosystems." *Nature Nanotechnology*, 8(8):602-608, 2013.
21. S. A. Chowdhury, S. E. Shackney, K. Heselmeyer-Haddad, T. Ried, A. A. Schäffer, R. Schwartz. "Phylogenetic analysis of multiprobe fluorescence in situ hybridization data from tumor cell populations." *Bioinformatics* (proceedings issue for ISMB 2013), 29(13):i189-i198, 2013.
22. D. Catanzaro, R. Ravi, and R. Schwartz. "A mixed integer linear programming model to reconstruct phylogenies from single nucleotide polymorphism haplotypes under the maximum parsimony criterion." *Algorithms for Molecular Biology*, 8:3, 2013.
23. K. Heselmeyer-Haddad, L. Y. Berroa Garcia, A. Bradley, C. Ortiz-Melendez, W.-J. Lee, R. Christensen, S. A. Prindiville, K. A. Calzone, P. W. Soballe, Y. Hu, S. A. Chowdhury, R. Schwartz, A. A. Schäffer, and T. Ried. "Single-cell genetic analysis of ductal carcinoma in situ and invasive breast cancer reveals enormous tumor heterogeneity, yet conserved genomic imbalances and gain of MYC during progression." *American Journal of Pathology*, 181(11):1807-1822, 2012.
24. M.-C. Tsai, G. Blelloch, R. Ravi, and R. Schwartz. "Coalescent-based method for learning parameters of admixture events from large-scale genetic variation data." *ACM Conference on Computational Biology and Biomedicine (ACM-BCB)*, 90-97, 2012.
25. L. Xie, G. Smith, X. Feng, and R. Schwartz. "Surveying capsid assembly pathways through simulation-based data fitting." *Biophysical Journal*, 103:1545-1554, 2012.
26. W. C. Ruder, C.-P. D. Hsu, B. D. Edelman, R. Schwartz, and P. R. LeDuc "Biological colloid engineering: self-assembly of dipolar ferromagnetic chains in a functionalized biogenic ferrofluid." *Applied Physics Letters*, 101:063701, 2012.
27. A. Subramanian, S. Shackney, and R. Schwartz. "Novel multi-sample scheme for inferring phylogenetic markers from whole genome tumor profiles." *Lecture Notes in Computer Science 7292 (Proc. International Symposium on Bioinformatics Research and Applications)*, 250-262, 2012.
28. A. Subramanian, S. Shackney, and R. Schwartz. "Inference of tumor phylogenies from genomic assays on heterogeneous samples." *Journal of Biomedicine and Biotechnology*, 2012:798812, 2012. (extended version of 2011 ACM/BCB conference paper below)
29. H. Kuwahara and R. Schwartz. "Stochastic steady state gain in a gene expression process with mRNA degradation control." *Journal of the Royal Society Interface*, 9:1589-1598, 2012.
30. B. Lee, P. R. LeDuc, and R. Schwartz. "Three-dimensional stochastic off-lattice model of binding chemistry in crowded environments." *PLoS One*, 7(1): e30131, 2012.
31. N. S. Wren, R. Schwartz, and K. N. Dahl. "Modeling nuclear blebs in a nucleoskeleton of independent filament networks." *Cellular and Molecular Bioengineering*, 5(1):73-81, 2012.

32. C. E. Tsourakakis, R. Peng, M. A. Tsiarli, G. L. Miller, and R. Schwartz. “Approximation algorithms for speeding up dynamic programming and denoising aCGH data.” *Journal of Experimental Algorithmics*, 16:1.8, 2011.
33. B. Lee, P. R. LeDuc, and R. Schwartz. “Unified regression model of binding equilibria in crowded environments” *Scientific Reports*, 1:97, 2011.
34. N. Misra, G. Blelloch, R. Ravi, and R. Schwartz. “An optimization-based sampling scheme for phylogenetic trees.” *Journal of Computational Biology*, 18(11):1599-1609, 2011. (extended version of Misra et al. (2011) RECOMB conference paper below)
35. A. Subramanian, S. Shackney, and R. Schwartz. “Inference of tumor phylogenies from genomic assays on heterogeneous samples.” *Proceedings of the ACM Conference on Bioinformatics and Computational Biology*, 2011.
36. M.-C. Tsai, G. Blelloch, R. Ravi, and R. Schwartz. “A consensus-tree approach for reconstructing human evolutionary history and identifying population substructure.” *IEEE/ACM Transactions on Computational Biology and Bioinformatics.* 8(4):918-928, 2011. (extended version of Tsai et al. (2010) conference paper below)
37. J. Kang, R. Steward, R. Schwartz, P. R. Leduc, and K. Puskar. “Controlled response of actin filament networks under cyclic stress through a coarse grained Monte Carlo model.” *Journal of Theoretical Biology*, 274:109-119, 2011.
38. N. Misra, G. Blelloch, R. Ravi, and R. Schwartz. “An optimization-based sampling scheme for phylogenetic trees.” *Proc. International Conference on Research in Computational Molecular Biology (RECOMB 2011)*, 252-266, 2011.
39. G. L. Miller, R. Peng, R. Schwartz, and C. Tsourakakis. “Approximate dynamic programming using halfspace queries and multiscale Monge decomposition.” *ACM Symposium on Discrete Algorithms (SODA2011)*, 1675-1682, 2011.
40. N. Misra, G. Blelloch, R. Ravi, and R. Schwartz. “Generalized Buneman pruning for inferring the most parsimonious multi-state phylogeny.” *Journal of Computational Biology*, 18(3):445-457, 2011. (extended version of RECOMB 2010 paper, *Lecture Notes in Bioinformatics,* 6044:369-383, 2010)
41. M. S. Kumar and R. Schwartz. “A parameter estimation technique for stochastic self-assembly systems and its application to human papillomavirus self-assembly.” *Physical Biology*, 7:045005, 2010.
42. D. Tolliver, C. Tsourakakis, A. Subramanian, S. Shackney, and R. Schwartz. “Robust unmixing of tumor states in array comparative genomic hybridization data.” *Bioinformatics (*Proceedings Issue for *Intelligent Systems for Molecular Biology (ISMB 2010))*, 26(12):i106-i114, 2010.
43. G. Lancia, R. Rizzi, and R. Schwartz. “Tiling binary matrices in haplotyping: Complexity, models and algorithms.” *Proceedings of the Prague Stringology Conference* (*PSC 2010*), pp. 89-102, 2010.
44. M.-C. Tsai, G. Blelloch, R. Ravi, and R. Schwartz. “A consensus-tree approach for reconstructing human evolutionary history and identifying population substructure.” *Lecture Notes in Bioinformatics* (*Proc. International Symposium on Bioinformatics Research and Applications (ISBRA 2010)),* 6053:167-178, 2010.
45. R. Schwartz and S. Shackney. “Applying unmixing to gene expression data for tumor phylogeny inference.” *BMC Bioinformatics,* 11:42, 2010.
46. H. Gong, Y. Guo, A. D. Linstedt, and R. Schwartz. “Discrete, continuous, and stochastic models of protein sorting in the Golgi.” *Physical Review* E, 81:011914, 2010.

47. B. Lee, P. R. LeDuc, and R. Schwartz. “Parameter effects on binding chemistry in crowded media using a two-dimensional stochastic off-lattice model.” *Physical Review E*, 80:041918, 2009.
48. Y. Park, S. Shackney, and R. Schwartz. “Network-based inference of cancer progression from microarray data.” *IEEE Transactions on Computational Biology and Bioinformatics*, 6(2):200-212, 2009.
49. N. Misra and R. Schwartz. “Efficient stochastic sampling of first-passage times with applications to self-assembly simulations.” *Journal of Chemical Physics*, 129:204109, 2008.
50. S. Sridhar and R. Schwartz. “A human genome-wide library of local phylogeny predictions for whole-genome inference problems.” *BMC Genomics*, 9:389, 2008.
51. B. Lee, P. R. LeDuc, and R. Schwartz. “Stochastic off-lattice modeling of molecular self-assembly in crowded environments by Greens function reaction dynamics.“ *Physical Review E*, 78:031911, 2008.
52. N. Misra, D. Lees, T. Zhang, and R. Schwartz. “Pathway complexity of model virus capsid assembly systems.” *Computational and Mathematical Methods in Medicine*, 9(3):277-293, 2008.
53. H. Gong, D. Sengupta, A. D. Linstedt, and R. Schwartz. “Simulated *de novo* assembly of Golgi compartments by selective cargo capture during vesicle budding and targeted vesicle fusion.” *Biophysical Journal*, 95:1674-1688, 2008.
54. S. Sridhar, F. Lam, G. E. Blelloch, R. Ravi, and R. Schwartz. “Mixed integer linear programming for maximum parsimony phylogeny inference.” *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 5(3):323-331, 2008.
55. Y. Park, S. Shackney, and R. Schwartz. “Network-based inference of cancer progression from microarray data.” *International Symposium of Bioinformatics Research and Applications* (ISBRA08), pp. 268-279, 2008.
56. B. Sweeney, T. Zhang. and R. Schwartz. “Exploring the parameter space of complex self-assembly through virus capsid models.” *Biophysical Journal*, 94:772-783 2008.
57. S. Sridhar, F. Lam, G. E. Blelloch, R. Ravi, and R. Schwartz. “Direct maximum parsimony phylogeny reconstruction from genotype data.” *BMC Bioinformatics*, 8:472, 2007.
58. S. Sridhar, K. Dhamdhere, G. E. Blelloch, E. Halperin, R. Ravi, and R. Schwartz. “Algorithms for efficient near-perfect phylogenetic tree reconstruction in theory and practice.” *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 4(4):561-571, 2007.
59. K.M. Puskar, A. Parisi-Amon, S. Ta'asan, R. Schwartz, and P.R. LeDuc. “Modeling molecular interactions to understand spatial crowding effects on heterodimer formations.” *Physical Review E*, 76:e041904, 2007.
60. T. Zhang, W. Kim, and R. Schwartz. “Investigating scaling effects on virus capsid-like self-assembly using discrete event simulations.” *IEEE Transactions on Nanobioscience*, 6(3):235-241, 2007.
61. G. Pennington, C. E. Smith, S. Shackney, and R. Schwartz. “Reconstructing tumor phylogenies from single-cell data.” *Journal of Bioinformatics and Computational Biology*, 5(02A):407-427, 2007.
62. S. Sridhar, F. Lam, G. E. Blelloch, R. Ravi, and R. Schwartz. “Efficiently finding the most parsimonious phylogenetic tree via linear programming.” *Lecture Notes in Bioinformatics vol.* 4463 (*Proceedings of the International Symposium on Bioinformatics Research and Applications)*, 37-48, 2007.

63. A. P. Pfenning, R. Schwartz, and A. Barth. "A comparative genomics approach to identifying the plasticity transcriptome." *BMC Neuroscience*, 3:20, 2007.
64. D. R. Emlet, R. Schwartz, K. Brown, A. A. Pollice, C. A. Smith, and S. E. Schackney. "HER2 expression as a potential marker for response to therapy targeted to the EGFR." *British Journal of Cancer*, 94(8):1144-1153, 2006.
65. K. Puskar, S. Ta'asan, R. Schwartz, and P. LeDuc. "Evaluating spatial constraints in cellular assembly processes using a Monte Carlo approach." *Cell Biochemistry and Biophysics*, 45(2):195-202, 2006.
66. G. E. Blelloch, K. Dhamdhere, E. Halperin, R. Ravi, R. Schwartz, and S. Sridhar. "Fixed parameter tractability of binary near-perfect phylogenetic tree reconstruction." *Proceedings of the International Colloquium on Automata, Languages, and Computability (ICALP)*, pp. 667-678, 2006.
67. S. Sridhar, G. E. Blelloch, R. Ravi, and R. Schwartz. "Optimal imperfect phylogeny reconstruction and haplotyping." *Proceedings of the Computational Systems Bioinformatics Conference (CSB06)*, pp.199-210, 2006.
68. G. Pennington, C. A. Smith, S. Shackney, and R. Schwartz. "Expectation-maximization method for the reconstruction of tumor phylogenies from single-cell data." *Proceedings of the Computational Systems Bioinformatics Conference (CSB06)*, pp. 371-380, 2006.
69. S. Sridhar, K. Dhamdhere, G. E. Blelloch, E. Halperin, R. Ravi, and R. Schwartz. "Simple reconstruction of binary near-perfect phylogenetic trees." *Proc. International Workshop on Bioinformatics Research and Applications (IWBRA06)*, 2006.
70. N. Castellana, K. Dhamdhere, S. Sridhar, and R. Schwartz. "Relaxing haplotype block models for association testing." *Proceedings of the Pacific Symposium on Biocomputing* (*PSB06*), pp. 454-466, 2006.
71. T. Zhang and R. Schwartz. "Simulation study of the contribution of oligomer/oligomer binding to capsid assembly kinetics." *Biophysical Journal*, 90:57-64, 2006.
72. R. Schwartz and J. King. "Frequencies of hydrophobic and hydrophilic runs and alternations in proteins of known structure." *Protein Science*, 15:102-112, 2006.
73. T. Zhang, R. Rohlfs, and R. Schwartz. "Implementation of a discrete event simulator for biological self-assembly systems." *Proceedings of the INFORMS Winter Simulation Conference*, pp. 2223-2231, 2005.
74. F. Jamalyaria, R. Rohlfs, and R. Schwartz. "Queue-based method for efficient simulation of biological self-assembly systems." *Journal of Computational Physics*, 204(1):100-120, 2005.
75. R. Schwartz. "Haplotype parsing: methods for extracting information from human genetic variations." *Applied Bioinformatics* (special issue devoted to work presented at the First Biological Language Conference, 2003), 3:181-191, 2004.
76. R. Schwartz. "Algorithms for association study design using a generalized model of haplotype conservation." *Proceedings of the 3rd IEEE Computational Systems Biotechnology Conference*, 90-97, 2004.
77. R. Schwartz, A. G. Clark, and S. Istrail. "Inferring piecewise ancestral history from haploid sequences." *Proceedings of the 2002 DIMACS/RECOMB Satellite Workshop on SNPs and Haplotype Assembly* (published as *Lecture Notes in Bioinformatics* 2983), pp.62-73, 2004.
78. S. Istrail, L. Florea, B. Halldórsson, O. Kohlbacher, R. Schwartz, J. Yewdell, and S. Hoffman. "Comparative immuno-peptidomics of humans and their pathogens." *Proceedings of the National Academies of Science USA*, 101:13268-13272, 2004.

79. B. Halldórsson, V. Bafna, R. Lippert, R. Schwartz, F. De la Vega, A. Clark, and S. Istrail. "Optimal block-free selection of tagging SNPs for genome-wide association studies." *Genome Research*, 14:1633-1640, 2004.
80. K. Puskar, L. Apeltsin, S. Ta'asan, R. Schwartz, and P. R. LeDuc. "Understanding actin organization in cell structure through lattice Monte Carlo simulations." *Mechanics and Chemistry of Biosystems*, 1:123-131, 2004.
81. R. Schwartz, B. Halldórsson, V. Bafna, A. G. Clark, and S. Istrail. "Robustness of inference of haplotype block structure." *Journal of Computational Biology*, 10(1): 13-20, 2003.
82. L. Florea, B. Halldórsson, O. Kohlbacher, R. Schwartz, S. Hoffman, and S. Istrail. "Epitope prediction algorithms for peptide-based vaccine design." *Proceedings of the Second IEEE Computer Society Bioinformatics Conference*, pp. 17-26, 2003.
83. R. Schwartz. "Haplotype motifs: an algorithmic approach to locating evolutionarily conserved patterns in haploid sequences." *Proceedings of the Second IEEE Computer Society Bioinformatics Conference*, pp. 306-314, 2003.
84. V. Bafna, B. Halldórsson, R. Schwartz, A. Clark, and S. Istrail. "Haplotypes and informative SNP selection algorithms." In *Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology* (RECOMB 2003), pp. 19-27, 2003.
85. R. Lippert, R. Schwartz, G. Lancia, and S. Istrail. "Algorithmic strategies for the single nucleotide polymorphism haplotype assembly problem." *Briefings in Bioinformatics,* 3(1): 23-31, 2002.
86. R. Schwartz, A. G. Clark, and S. Istrail. "Methods for inferring block-wise ancestral history from haploid sequences: the haplotype coloring problem." *Proceedings of the Second Workshop on Algorithms in Bioinformatics* (published as *Lecture Notes in Computer Science 2452)*, 44-59, 2002.
87. G. Lancia, V. Bafna, S. Istrail, R. Lippert, and R. Schwartz. "SNPs problems, complexity, and algorithms." *Lecture Notes in Computer Science 2161* (*Proceedings of the Ninth Annual European Symposium on Algorithms*): 182-183, 2001.
88. R. J. Turner, K. Chaturvedi, N. J. Edwards, D. Fasulo, A. L. Halpern, D. H. Huson, O. Kohlbacher, J. R. Miller, K. Reinert, K. A. Remington, R. Schwartz, B. Walenz, S. Yooseph, and S. Istrail. "Visualization Challenges for a New Cyberpharmaceutical Computing Paradigm." In *Proceedings of the IEEE 2001 Symposium on Parallel and Large-Data Visualization and Graphics*, 2001.
89. R. Schwartz, C. Ting, and J. King. "Whole-proteome pI values correlate with sub-cellular localization for organisms in the three domains of life." *Genome Research*, 11(5):703-709, 2001.
90. J. C. Venter, M. A. Adams, E. W. Myers, *et al.* "The sequence of the human genome." *Science*, 291(5507):1304-1351, 2001.
91. R. Schwartz, S. Istrail, and J. King. "Frequencies of amino acid strings in globular protein sequences indicate suppression of blocks of consecutive hydrophobic residues." *Protein Science*, 10(5):1023-1031, 2001.
92. R. Schwartz, R. L. Garcea, and B. Berger. "`Local rules' theory applied to polyomavirus polymorphic capsid assemblies." *Virology*, 268(2):461-470, 2000.
93. B. Berger, J. A. King, R. Schwartz, and P. W. Shor. "Local rule mechanism for selecting icosahedral shell geometry." *Discrete Applied Mathematics*, 105:55-69, 2000.
94. S. Istrail, R. Schwartz, and J. King. "Lattice simulations of aggregation funnels for protein folding." *Journal of Computational Biology*, 6(2):143-162, 1999.

95. L. W. Hobbs, C. E. Jesurum, A. Coventry, V. Pulim, R. Schwartz, and B. Berger. “Towards a topological description of poorly-crystalline networks.” In *Advances in Materials for the 21st Century: The 1999 Julia R. Weertman Symposium*, 1999.
96. R. Schwartz, P. W. Shor, P. E. Prevelige, Jr., and B. Berger. “Local rules simulation of the kinetics of virus capsid self-assembly.” *Biophysical Journal*, 75:2626-2636, 1998.
97. R. Schwartz and B. Berger. “Applying multithreaded programming to the simulation of virus shell self-assembly.” *Proceedings of the Yale Multithreaded Programming Workshop*, 1998.

Review Articles:

1. M. Thomas and R. Schwartz. “Quantitative computational models of molecular self-assembly in systems biology.” *Physical Biology*, accepted for publication, 2017.
2. R. Schwartz and A. A. Schaffer. “The evolution of tumor phylogenetics: principles and practice.” *Nature Reviews Genetics*, 18(4):213-229, 2017.
3. J. Kang, R. Schwartz, J. Flickinger, and S. Beriwal. "Machine learning approaches to predicting radiotherapy outcomes: A clinician's perspective." *International Journal of Radiation Oncology, Biology, Physics*, 93(5), 2015.
4. R. Schwartz. “Theory and algorithms for the haplotype assembly problem.” *Communications in Information and Systems*, 10(1):23-38, 2010.
5. H. J. Greenberg, A. J. Holder, M.-Y. Leung, and R. Schwartz. “Computational biology and medical applications.” *OR/MS Today*, 36(3): 36-41, 2009.
6. P. LeDuc and R. Schwartz. “Computational models of molecular self-organization in cellular environments.” *Cell Biochemistry and Biophysics*, 48(1):16-31, 2007.
7. R. Schwartz, P. W. Shor, and B. Berger. “Local rule simulations of capsid assembly.” *Journal of Theoretical Medicine*, 6:81-86, 2005.

Education articles:

1. L. Welch, C. Brooksbank, R. Schwartz, S. L. Morgan, B. Gaeta, A. M. Kilpatrick, D. Mietchen, B. L. Moore, N. Mulder, M. Pauley, W. Pearson, P. Radivojac, N. Rosenberg, A. Rosenwald, G. Rustici, T. Warnow. "Applying, evaluating and refining bioinformatics core competencies (an update from the curriculum task force of ISCB's Education Committee." *PLoS Computational Biology, 12*(5): e1004943, 2016
2. L. Welch, F. Lewitter, R. Schwartz, C. Brooksbank. P. Radivojac, B. Gaeta, M.V. Schneider. “Bioinformatics curriculum guidelines: toward a definition of core competencies,” *PLoS Computational Biology, 10*(3): e1003496, 2014.
3. L. Welch, R. Schwartz, and F. Lewitter. “A report of the curriculum task force of the iscb education committee.” *PLoS Computational Biology*, 8(6): e1002570, 2012.

Unrefereed reports:

1. L. Xie, G. R. Smith, and R. Schwartz. "Derivative-free optimization of rate parameters of capsid assembly models from bulk in vitro data." *arXiv preprint arXiv:1507.02148* (2015).
2. C. Tsourakakis, D. Tolliver, M. A. Tsiarli, S. Shackney, and R. Schwartz. “CGHTrimmer: Discretizing noisy array CGH data.” arXiv:1002.4438v1, 2010.
3. N. Misra, G. Blelloch, R. Ravi, and R. Schwartz. “Generalized Buneman pruning for inferring the most parsimonious multistate phylogeny.” arXiv:0910.1830, 2009.
4. N. Misra and R. Schwartz. “Efficient stochastic sampling of first passage times for fracturing bond networks.“ *arXiv:0804.0448v1*, 2008.

5. G. Pennington, S. Shackney, and R. Schwartz. “Cancer phylogenetics from single-cell assays.” *CMU Computer Science Department Technical Report CMU-CS-06-103*, 2006.
6. K. Dhamdhere, S. Sridhar, G. E. Blelloch, E. Halperin, R. Ravi, and R. Schwartz. “A new algorithm for the reconstruction of near-perfect binary phylogenetic trees.” *CMU Computer Science Department Technical Report CMU-CS-05-119*, 2005.
7. S. Sridhar, K. Dhamdhere, G. E. Blelloch, E. Halperin, R. Ravi, and R. Schwartz. “FPT algorithms for binary near-perfect phylogenetic trees.” *CMU Computer Science Department Technical Report CMU-CS-05-181*, 2005.
8. S. Sridhar, K. Dhamdhere, G. E. Blelloch, R. Ravi, and R. Schwartz. “Evaluation of the haplotype motif model using the principle of minimum description.” *CMU Computer Science Department Technical Report CMU-CS-04-166*, 2004.
9. R. Schwartz. “The local rules dynamics model for self-assembly simulation.” *MIT Laboratory for Computer Science Technical Report 800*, 2000.
10. R. Schwartz, P. E. Prevelige, Jr., and B. Berger. “Local rules modeling of nucleation-limited virus capsid assembly.” *MIT Laboratory for Computer Science Technical Memo 584*, 1998.

Books and book chapters:

1. A. Subramanian, S. Shackney, and R. Schwartz. “Tumor phylogenetics in the NGS era: strategies, challenges, and future prospects,” *Applications of Next Generation Sequencing in Cancer Research*, Wei Wu and Hani Choudhry, eds., Springer, pp. 335-357, 2013.
2. L. Bleris, I. Mandoiu, R. Schwartz, and J. Wang, eds. “Proc. International Symposium on Bioinformatics Research and Applications.” *Lecture Notes in Bioinformatics* vol. 7292, Springer, 2012.
3. R. Schwartz. “Regulatory network inference.” In *Bioinformatics for Biologists*, R. Shamir and P. Pevzner, eds., Cambridge University Press, 2011.
4. R. Schwartz. *Biological Modeling and Simulation: A Survey of Practical Models, Algorithms, and Numerical Methods*. MIT Press: Cambridge, MA, 2008.
5. S. Shackney, D. R. Emlet, R. Schwartz, K. A. Brown, A. A. Pollice, and C.A. Smith. “Expression of HER-2 and epidermal growth factor receptor as clinical markers for response to targeted therapy.” in M.A. Hayat, ed. *Methods of Cancer Diagnosis, Therapy, and Prognosis: vol. 1, Breast Carcinoma*. Springer: Netherlands, 2008.

Invited Talks:

1. “Phylogenetics at the cellular level.” *Colloqium on Algorithms in Molecular Biology (CLIMB)*, 11/16, Laussanne, Switzerland.
2. “Computationally resolving heterogeneity in mixed genomic samples.” *IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS)*, 10/16, Atlanta, GA. (keynote talk)
3. "Applying core competencies to teaching bioinformatics engineers." *GLBIO 2016 Curriculum Workshop*, 5/16. Great Lakes Regional Bioinformatics Conference/Canadian Computational Biology Conference, Toronto, ON.
4. "Inferring evolution by copy number variations in tumor cell populations." *Simons Workshop on Computational Cancer Biology*, 2/16. Simons Institute for Theoretical Computer Science, Berkeley, CA.
5. "Reconstructing evolution by copy number variations in tumor cell populations." *Genetics Seminar Series*, 12/15, Rutgers University, Rutgers, NJ.

6. "How does a tumor evolve over time?", *HHMI Constellation Studio B* (education workshop), 11/15, Howard Hughes Medical Institute, Chevy Chase, MD.
7. "Applying core competencies to teaching bioinformatics scientists." *Education Workshop, Intelligent Systems for Molecular Biology*, 7/15, Dublin, Ireland.
8. "Bringing computational biology to every biology undergraduate." *Undergraduate Bioinformatics Education Conference*, 5/15, St. Vincent College, Latrobe, PA.
9. "What sequencing can and can't tell us about tumor evolution," *Great Lakes Regional Bioinformatics Conference (GLBIO)*, 5/15, Purdue University, West Lafayette, IN.
10. "Applying core competencies to teaching bioinformatics scientists," *Great Lakes Regional Bioinformatics Conference (GLBIO)*, 5/15, Purdue University, West Lafayette, IN.
11. "Reconstructing molecular self-assembly dynamics via simulation-based model fitting with application to virus capsid assembly" *Bioinformatics and Computational Biology Seminar Series*, 4/15, Iowa State University, Ames, IA.
12. "What sequencing can (and can't) tell us about tumor evolution." *Science 2014 Conference*, 10/14, University of Pittsburgh.
13. "Inferring fine-scale capsid assembly pathways from bulk in vitro data." *Mathematical Virology Conference*, 8/14, University of York, UK.
14. "Computational reconstruction of progression of tumor cell populations," *Developmental Systems Biology Symposium*, 7/2014, Children's Hospital of Pittsburgh UPMC.
15. "Making computational biology a requirement for biology undergraduates: The Carnegie Mellon Experience," *Intelligent Systems for Molecular Biology* (ISMB) Birds-of-a-Feather Education Session, 7/2014, International Society for Computational Biology.
16. "Understanding viral self-assembly pathways through stochastic simulation." Seminar for Interdisciplinary and Biomedical Sciences, 3/2014, University of New Mexico.
17. "Phylogenetic study of cancer progression at the cellular level." Department of Computer Science Student Research Symposium, 3/2014, University of New Mexico.
18. "Using Phylogenetics to Understand Cancer Progression at the Cellular Level." Bioinformatics Seminar Series, 11/2013, Indiana University.
19. "Reconstructing Evolution of Tumor Cells by Computer Algorithms." LaunchCMU Symposium, 11/2013, Carnegie Mellon University.
20. "Reconstructing Population-Level History from Genetic Variation Data." Computer Science Seminar Series, 10/2103, Ohio University.
21. "Phylogenetic Study of Tumor Progression from Single-Cell Data." Cancer Center Seminar Series, 10/13, West Virginia University.
22. "Model-based inference of virus capsid assembly pathways." *qBio Conference*, Santa Fe, NM, 8/2013 (short talk).
23. "Computer models of crowding effects on pathway selection in complex self-assembly." *Workshop on Macromolecular Crowding*, Telluride, CO, 6/2013, Telluride Science Research Conferences.
24. "Phylogenetic analysis of cancer progression at the single-cell level." *Computer Science Seminar Series*, Hong Kong, 4/2013, City University of Hong Kong.
25. "Algorithms for Cancer Phylogenetics at the Cellular Level." *INFORMS Computing Society Conference*, 1/2013, Institute for Operations Research and the Management Sciences (INFORMS).
26. "Understanding tumor development with phylogenetic algorithms." *Computer Science Seminar Series*, Detroit, MI, 12/2012, Wayne State University.

27. "Using phylogenetic algorithms to understand tumor evolution at the cellular level." *Bioinformatics Seminar*, Duarte, CA, 7/2012, City of Hope Comprehensive Cancer Center.
28. "From GWAS to personalized genomes: the fundamentals of analysis of genetic variations." *Intelligent Systems for Molecular Biology (ISMB)*, Long Beach, CA, 7/2012, International Society for Computational Biology (invited tutorial session, co-taught with Eleazar Eskin (UCLA)).
29. "Inferring physical parameters and assembly pathways from indirect measures of viral self-assembly." *SIAM Symposium on Discrete Mathematics*, Halifax, Canada, 6/2012, Society for Industrial and Applied Mathematics.
30. "Computational biology education at Carnegie Mellon University." *Great Lakes Regional Bioinformatics Conference (special session on Creating Teams for Bioinformatics)*. Ann Arbor, Michigan, 5/2012, International Society for Computational Biology.
31. "Learning population histories from genome variation data." *Great Lakes Regional Bioinformatics Conference*. Ann Arbor, Michigan, 5/2012, International Society for Computational Biology. (keynote talk)
32. "Unifying individual-level and population-level views of intraspecies phylogenetics." *Computer Science Seminar Series*, Lausanne, Switzerland, 5/2012, EPFL Lausanne.
33. "Using phylogenetics to understand tumor evolution at the cellular level." *Seminar Series*, Barcelona, Spain, 4/2012, Centro de Regulación Genómica.
34. "Understanding virus capsid assembly through stochastic simulation." *Department of Computer Science Seminar Series*, Orlando, FL 3/2012, University of Central Florida.
35. "Deciphering virus capsid assembly mechanisms through stochastic simulation." *Department of Molecular Biophysics and Structural Biology Seminar Series*, Pittsburgh, PA 2/2012, University of Pittsburgh.
36. "An optimization approach to efficient sampling over phylogenetic trees." *Triennial Conference for the International Federation of Operations Research Societies*, Melbourne, Australia, 2011.
37. "Phylogenetics of heterogeneous samples." *International Symposium on Bioinformatics Research and Applications*, Changsha, China 2011. (keynote talk)
38. "Computational inference of cancer progression pathways from heterogeneous samples." *Bioinformatics Seminar*, Shanghai, China 2011, Bioinformatics Department, Tongji University.
39. "Computational inference of cancer progression pathways from heterogeneous samples." *Computational Biology Seminar*, Shanghai, China 2011, Center for Computational Systems Biology, Fudan University.
40. "Computational inference of cancer progression pathways from heterogeneous samples." *Bioinformatics Seminar*, Beijing, China 2011, Center for Bioinformatics, Peking University.
41. "Computational inference of cancer progression pathways from heterogeneous samples." *Bioinformatics Seminar*, Beijing, China 2011, Dept. of Automation, Tsinghua University.
42. "Reconstructing tumor progression pathways from heterogeneous samples." Computational *Biology Seminar Series*, College Park, MD, 2011, University of Maryland.
43. "Accelerating ILP solutions for multi-state phylogenetics through generalized Buneman pruning." *INFORMS Annual Meeting*, Austin, TX, 2010, Institute for Operations Research and the Management Sciences (INFORMS).

44. "Exploring the space of virus capsid assembly pathways with stochastic simulations." *3rd Mathematical Virology Workshop*, Ambleside, UK, 2010, York Centre for Complex Systems Analysis.
45. "Understanding virus capsid assembly pathways with stochastic simulations." *Society for Mathematical Biology Annual Meeting*, Rio de Janeiro, Brazil, 2010, Society for Mathematical Biology.
46. "Computer simulation of compartment formation and maintenance in the Golgi." *Local Traffic*, Pittsburgh, PA 2010. Carnegie Mellon University.
47. "Principles of genetic regulatory network inference." *RECOMB Satellite Conference on Bioinformatics Education*, San Diego, CA 2010, University of California, San Diego.
48. "Cancer phylogenetics from mixed tumor samples." *CASB-16*, San Diego, CA, 2010. Center for Algorithmic and Systems Biology.
49. "Phylogenetic inference from mixed tumor samples." *Computational Biology Seminar Series*, Newark, DE, 2010. University of Delaware.
50. "Computational inference of tumor heterogeneity for cancer phylogenetics." *Computational Biology Seminar Series*, Cambridge, MA, 2010. Massachusetts Institute of Technology.
51. "Computer models of molecular self-assembly." *Pittsburgh Physical Virology Club*, Pittsburgh, PA, 2009. Carnegie Mellon University.
52. "Fast phylogenetic inference from genetic variation data." *Network Sciences Symposium*, Pittsburgh, PA, 2009. Carnegie Mellon University
53. "Applications of phylogenetic tree inference at genomics scales." *INFORMS Annual Meeting*. San Diego, CA, 2009. Institute for Operations Research and the Management Sciences (INFORMS).
54. "Exploiting tumor heterogeneity for phylogenetic inference." *National Center for Biotechnology Information (NCBI) Seminar Series*. Bethesda, MD, 2009. U.S. National Institutes of Health.
55. "Stochastic simulation of virus capsid assembly pathways." *Astbury Centre for Structural Molecular Biology Seminar Series*. Leeds, UK, 2009. University of Leeds.
56. "Stochastic simulation of virus capsid assembly pathways." *York Centre for Complex Systems Analysis Seminar Series*. York, UK, 2009. University of York.
57. "Phylogenetic inference from tumor samples." *Center for Bioinformatics Seminar Series*, Tübingen, Germany, 2009. Eberhard Karls University Tübingen.
58. "New computational methods for cancer phylogenetics." *Dipartimento di Mathematica e Informatica Seminar Series*, Udine, Italy, 2009. University of Udine.
59. "Stochastic simulations of virus capsid assembly pathways." *American Physical Society 2009 March Meeting, Focus Session on Physical Virology*. Pittsburgh, PA, 2009. The American Physical Society.
60. "Opportunities for operations research in genetic variation studies." *INFORMS Computing Society Conference*. Charleston, SC, 2009. INFORMS Computing Society.
61. "Accelerating stochastic models of self-assembly." *Pittsburgh Biophysical Theory Club*. Pittsburgh, PA, 2008. University of Pittsburgh.
62. "Applying computer models of evolution to cancer biology." *Carnegie Mellon Homecoming*. Pittsburgh, PA, 2008. Carnegie Mellon University.
63. "Studying cancer progression with computer models of evolution." *SACNAS National Conference*. Salt Lake City, UT, 2008, Society for the Advancement of Chicanos and Native Americans in Science (SACNAS).

64. “Applying computer models of evolution to cancer biology.” *Carnegie Mellon Volunteer Forum*, Pittsburgh, PA, 2008. Carnegie Mellon University.
65. “Stochastic simulation of capsid assembly pathways.” *FASEB Conference on Phage and Virus Assembly*, Saxtons River, VT, June, 2008. Federation of American Societies of Experimental Biology (FASEB).
66. “Using integer linear programming for genome-scale phylogenetics.” *SIAM Conference on Discrete Mathematics*, Burlington, VT, June, 2008. Society for Industrial and Applied Mathematics (SIAM).
67. “New algorithms for optimal maximum parsimony phylogenetics from SNP data.” *Genomics and Bioinformatics Seminar*, Philadelphia, PA, 2007. University of Pennsylvania.
68. “Exploring capsid assembly pathways through continuous-time discrete event simulation.” *Second Mathematical Virology Workshop*, Edinburgh, Scotland, 2007. International Center for Mathematical Sciences (ICMS).
69. “Mixed integer linear programming for haplotype-based phylogenetics.” *2007 INFORMS International Conference*, Rio Grande, Puerto Rico, 2007. Institute for Operations Research and the Management Sciences (INFORMS).
70. “Inferring phylogenies from ambiguous genetic variation data by integer linear programming.” *2007 INFORMS International Conference*, Rio Grande, Puerto Rico, 2007. Institute for Operations Research and the Management Sciences (INFORMS).
71. “Exploring virus capsid assembly pathways through stochastic simulation.” *Biophysics Seminar Series*, Columbus, OH, 2007. Ohio State University.
72. “Near-perfect phylogenetics and the human genome.” *RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes*, Los Angeles, CA, 2007. University of Southern California.
73. “Near-perfect phylogeny construction from genetic variation data.” *Computer Science Seminar Series*, Cleveland, OH, 2006. Case Western Reserve University.
74. “Modeling virus assembly.” *Systems Biology Seminar Series*, Pittsburgh, PA, 2006. University of Pittsburgh.
75. “Near-perfect phylogeny construction from genetic variation data.” *Computational Biology Seminar Series*, Cambridge, MA, 2006. Massachusetts Institute of Technology.
76. “Near-perfect phylogeny construction from genetic variation data.” *Computer Science Seminar Series*, Cambridge, MA, 2006. Tufts University.
77. “Near-perfect phylogenetics and the human genome.” *Workshop on Algorithms and Tools for Computational Genomics*, Providence, RI, 2006. Brown University.
78. “Efficient discrete-event simulations of molecular self-assembly.” *Computer Science Seminar Series*. Providence, RI, 2005. Brown University.
79. “Local rule simulations of virus capsid assembly.” *Third Biological Language Conference*. Pittsburgh, PA, 2005. Carnegie Mellon University.
80. “Conserved patterns of hydrophobicity in protein structures.” *Second Biological Language Conference*. Pittsburgh, PA, 2004. Carnegie Mellon University.
81. “Simulating self-assembly at cellular scales.” *INFORMS Annual Meeting*, Denver, CO, 2004. Institute for Operations Research and the Management Sciences (INFORMS).
82. “Efficient discrete event modeling of molecular self-assembly.” *Workshop on Computational Methodology in Modeling Complex Systems*, Pittsburgh, PA, 2004. University of Pittsburgh.
83. “Simulating capsid assembly kinetics with local rules models.” *Mathematical Virology Workshop*, Oxford, UK, 2004. Newton Institute.

84. "Haplotype parsing: methods for extracting information from human genetic variations." *First Biological Language Conference*, Pittsburgh, PA, 2003. University of Pittsburgh.
85. "Algorithms for extracting information from human genetic variations." *The Third Carnegie Mellon Computational Molecular Biology Symposium.* Pittsburgh, PA, 2003, Carnegie Mellon University
86. "Inferring piecewise ancestral history from haploid sequences." *DIMACS/RECOMB Satellite Workshop on SNPs and Haplotype Inference*, Rutgers, New Jersey, 2002. Center for Discrete Mathematics and Theoretical Computer Science.
87. "Haplotype separation of shotgun assembly fragments." *Baltimore-Washington Area Society of Industrial and Applied Mathematics (SIAM) Fall Meeting*, Baltimore, MD, 2001.
88. "Haplotype separation of shotgun assembly fragments." *Department Seminar Series*, Baltimore, MD, 2001. Johns Hopkins University Department of Mathematical Sciences.
89. "Comparative structural and functional genomics using weak prediction methods." DIMACS Workshop on Protein Structure and Structural Genomics: Prediction, Determination, Technology, and Algorithms. New Brunswick, NJ, 2001. Center for Discrete Mathematics and Theoretical Computer Science.
90. "The mathematics of virus shell assembly." *DIMACS Reconnect Conference*, New Brunswick, NJ, 1998. Center for Discrete Mathematics and Theoretical Computer Science.
91. "The mathematics of virus shell assembly." *Doing Science at the Interface*, Berkeley, CA, 1998. Program in Mathematics and Molecular Biology.

Grant Reviewing

Regular Member, Biodata Management and Analysis (DBMA) study section, U. S. National Institutes of Health, 2012-2018

Past ad hoc service for panels of the US NIH, US NSF, Cancer Research UK, Research Grants Council of Hong Kong, Israeli Science Foundation, Netherlands Science Foundation, Freiburg Institute for Advanced Studies, Science Foundation of Ireland

Journal Editorships

Associate Editor for Computational Biology, Medicine, and Healthcare Applications, *INFORMS Journal on Computing*

Member of the Editorial Board, *IEEE/ACM Transactions on Computational Biology and Bioinformatics*

Journal Reviewing

Reviews for *American Journal of Human Genetics, Acta Biotheoretica, Bioinformatics, Biophysical Journal, BMC Bioinformatics, BMC Genomics, Briefings in Bioinformatics, Cancer Informatics, Cancer Research, Cell Systems, Discrete Applied Mathematics, Entropy, FEBS Letters, Genome Biology, Genome Medicine, Genome Research, IEEE Transactions on Computers, IEEE/ACM Transactions on Computational Biology and Bioinformatics, IEEE Transactions on Nanobioscience, INFORMS Journal on Computing, International Journal of Molecular Sciences, Journal of Bioinformatics and Computational Biology, Journal of Chemical Information and Modeling, Journal of Chemical Physics, Journal of Computational Biology, Journal of Computational Physics, Journal of Mathematical Modeling and Algorithms, Journal of Molecular Biology, Journal of Physical Chemistry, Journal of Physics A, Journal of Physics: Condensed Matter, Journal of Structural Biology, Journal of Theoretical Biology, Journal of*

Theoretical Computer Science, Mathematical Biosciences, Molecular Simulation, Nature Communications, Nature Methods, Physical Biology, Physical Review E, Physical Review Letters, PLoS Computational Biology, PLoS One, Proceedings of the National Academy of Sciences (USA), Protein Science, Science, Scientific Reports, Theoretical Computer Science, Virology

Conference Organization

Treasurer, RECOMB 2002 Conference on Computational Molecular Biology
Organizer, 2004 RECOMB Satellite Workshop on SNPs and Haplotypes
Session Chair, Genetic Variation Analysis, INFORMS Annual Meeting, 2009
Cluster Chair, Computational Biology and Bioinformatics, INFORMS Annual Meeting, 2010
Co-Cluster Chair, Computational Biology and Bioinformatics, INFORMS Annual Meeting, 2011
Session Chair, Biological Self-Assembly, SIAM Conference on Discrete Mathematics, 2012
Intelligent Systems for Molecular Biology (ISMB): Co-chair of Population Genomics Track, 2012-13,2015; Co-chair of Proceedings, 2014; Co-Theme Chair for Genes, 2016; chair of Other Abstracts, 2017
Co-conference Chair, RECOMB 2014
Co-organizer, RECOMB Satellite Conference on Bioinformatics Education, 2014
Co-Proceedings Chair, Workshop on Algorithms in Bioinformatics (WABI), 2017
Co-Chair of Cancer Genomics, ACM Bioinformatics and Computational Biology (ACM-BCB), 2017
Co-Program Chair, International Symposium on Bioinformatics Research and Applications (ISBRA), 2012
Co-Conference Chair, Great Lakes Regional Bioinformatics Conference, 2013
Member of the Steering Committee, Great Lakes Regional Bioinformatics Conference, 2014-2017

Conference Program Committees

2004 RECOMB Satellite Workshop on SNPs and Haplotypes
IADIS Virtual Multi-Conference, 2005
International Conference on Models and Methods for Human Genomics, 2006
RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes, 2007
ISMB Bioinformatics of Disease Track, 2007-2009
ISMB Population Genomics Track, 2009-2010
ISMB Disease Models and Epidemiology Track, 2011
Ohio Bioinformatics Consortium (OCCBIO), 2009-2010
Research in Computational and Molecular Biology (RECOMB), 2009-2017
RECOMB-Seq, 2017
IEEE International Conference on Bioinformatics and Biomedicine (BIBM), 2009-2016
ACM Symposium on Applied Computing, BIO track, 2010-2011
IEEE International Conference on Computational Advances in Bio and medical Sciences (ICCABS), 2011-2015
Asia Pacific Bioinformatics Conference (APBC), 2013-17
Workshop on Algorithms in Bioinformatics (WABI), 2010-2017
ACM Bioinformatics and Computational Biology (ACM-BCB), 2015-2017
International Symposium on Bioinformatics Research and Applications (ISBRA), 2007-2017

European Conference on Computational Biology (ECCB), 2010,2012,2014,2016

Citations and Awards

Keynote speaker, IEEE International Conference on Computational Advances in Bio and Medical Sciences (ICCABS), 2016
Keynote speaker, Undergraduate Bioinformatics Education Conference (UBEC), 2015Best Paper in Translation Bioinformatics, ISMB 2013 (for Chowdhury et al., 2013)
Keynote speaker, Great Lakes Regional Bioinformatics Conference (GLBIO), 2012Best student paper award ACM-BCB Conference 2012 (for Tsai et al., 2012)
Keynote speaker, International Symposium on Bioinformatics Research and Education (ISBRA), 2011
Kavli Frontiers Fellow, 2007
Best paper award, International Symposium on Bioinformatics Research and Applications 2007 (for Sridhar et al., 2007)
Eberly Family Career Development Chair in Biological Sciences, 2005-2008
Presidential Early Career Award for Scientists and Engineers (PECASE), 2005
MIT EECS Dept.'s William A. Martin Award for best M.Eng. thesis in computer science, 1996
NSF graduate research fellow, 1995-1999