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HONORS AND AWARDS

SERVICE TO UNIVERSITY

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EDUCATION

California Institute of Technology, Division of Biological Engineering

2004-2007 Postdoctoral studies

Logic Functions of the Genomics cis-Regulatory Code

Advisor: Professor Eric Davidson

Massachusetts Institute of Technology, Laboratory for Computer Science

1986-1989 Postdoctoral studies

Theory of Programming Languages for Concurrency

Advisor: Professor Albert Meyer

University of Bucharest, Bucharest, Romania

1979 Ph.D. in Computer Science

Thesis: *Context Sensitive Languages with Applications to Semantics of Programs and Number Theory*

Advisors: Professors Solomon Marcus and Sergiu Rudeanu

Al. I. Cuza University, Iasi, Romania

1975 B.S. in Computer Science

Honors: *Summa Cum Laude*; three awards for research

PROFESSIONAL APPOINTMENTS

Brown University, Providence, RI

Department of Computer Science

Center for Computational Molecular Biology

September 1, 2006 – July 31, 2011: Director, Center for Computational Molecular Biology

July 1, 2006: Julie Nguyen Brown Professor of Computational and Mathematical Sciences

July 1, 2005: Professor of Computer Science

Celera Genomics & Applied Biosystems, Rockville, MD

Applied Biosystems

Advanced Research and Technology Division

Informatics Research Department

October 2003 – February 2005: Science Fellow (one of six in a company of 800 scientists)

February 2003 – February 2005: Senior Director and Department Head

Celera Genomics

Informatics Research Department

September 2002 – February 2003: Senior Director and Department Head

July 2001 – September 2002: Department Co-leader with Gene Myers

April 2000 – July 2001: Senior Director

Sandia National Laboratories, Albuquerque, NM

Massively Parallel Computing Research Laboratory

1998 – April 2000: Principal Senior Member of the Technical Staff

1994 – 1998: Senior Member of the Technical Staff

1992 – 2000: Founder and Project Leader, Computational Biology Project

1992 – 1993: Computational Scientist

Wesleyan University, Middletown, CT

Department of Mathematics

1985 – 199: Assistant Professor of Computer Science

University Al. I. Cuza, Iasi, Romania

Alexandru Myller Mathematical Institute and University Computing Center

1979 – 1983: Computer Science Researcher

PUBLICATIONS

1. Sorin Istrail, “Davidson Causality: The Unreasonable Effectiveness of Mathematics in the Regulatory Genome,” 2021
2. Doug McEearlean, Sorin Istrail, “The Maximum-Likelihood Haplotype Phasing Problem: Practical Globally Optimal Solutions via Likelihood Graph Homomorphism,” 2021
3. Sorin Istrail, “Statistical Mechanics, Three-Dimensionality and NP-Completeness II: Universality of the Intractability of the Partition Function of the Two-Coupling Constants Ising Model Across Lattices,” 2021
4. Sorin Istrail, “Zero-Knowledge-SNPs and Zero-Knowledge-Haplotypes: An information theory-based genome privacy (non-cryptographic) algorithm for summary statistics in GWAS,” 2020
5. Hammurabi Mendes, Sorin Istrail, “Thermodynamic Hypothesis as Social Choice: An Arrow Impossibility Theorem for Protein Folding,” 2020
6. Alpay, Bert, Demetci, Pinar, Istrail, Sorin, Aguiar, Derek, “Combinatorial and Statistical Predictions of Gene Expression from Haplotype Sequence,” International Conference on Intelligent Systems in Molecular Biology (ISMB 2020), *Bioinformatics* 2020 Bioinformatics Jul 1; 36 (Supplement 1):i94-i202
7. D. Armanious, J. Schuster, G. Tellefson, A. Agudelo, A. DeWan, S. Istrail, J. Padbury, A. Uzun, “Proteinarium: Multi-sample Protein-Protein Interaction

- Analysis and Visualization Tool," *Genomics*, Vol. 112, Issue 6, Nov. 2020, pp. 4288-4296
8. Sorin Istrail, "Eric Davidson's Regulatory Genome for Computer Science: Causality, Logic and Proof Principles of the Genomic cis-Regulatory Code," *Journal of Computational Biology*, Vol. 26, No. 7, 10/19/2019
 9. Istrail, Sorin, Peter, Isabelle S., "How Does the Regulatory Genome Work?," *Journal of Computational Biology*, Vol. 26, No. 7, pp. 685-695, Oct. 19, 2019
 10. Sorin Istrail, "Computer Science Through Urn Games: A Game of Dijkstra and a Hierarchy of Complete Problems for NL, P, NP, PSPACE, PSPACE, EXPTIME and Unsolvability," Springer, Volume for Solomon Marcus, in Memoriam, 2018
 11. Sorin Istrail, "An Approximation Algorithm with Mathematically Guaranteed Error Bounds for the Cycle-basis Local Optimization Problems on Graphs and Matroids," Springer, Solomon Marcus 90th Birthday Celebration Volume, 2016
 12. Sorin Istrail, "Computational Complexity in Biology, Physics and Chemistry: Biology 100, Physics 10, Chemistry 1 (Uses and Misuses of NP-completeness)", 2015
 13. Derek Aguiar, Wendy S.W. Wong, Sorin Istrail, "Tumor Haplotype Assembly Algorithms for Cancer Genomics," *Pacific Symposium on Biocomputing*, Vol. 19, pp. 3-14, 2015
 14. Derek Aguiar, Eric Morrow, Sorin Istrail, "Tractatus: An Exact and Subquadratic Algorithm for Inferring Identity-by-Descent Multi-shared Haplotype Tracts," Proceedings of the 18th Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014), *Lecture Notes in Bioinformatics*, pp. 158-173, Springer-Verlag 2014
 15. Ian C. McDowell, Chamilani Nikapitiya, Derek Aguiar, Christopher E. Lane, Sorin Istrail, Marta Gomez-Chiarri, "Transcriptome of American Oysters, *Crassostrea virginica*, in Response to Bacterial Challenge: Insights into Potential Mechanisms of Disease Resistance," *PLoS ONE* 9(8): (2014)
 16. Atias N, Istrail S, Sharan R. "Pathway-Based Analysis of Genomic Variation Data," *Curr Opin Genet Dev.* 2013 Dec;23(6):622-6
 17. Ece D Gamsiz, Emma W Viscidi, Shailender Nagpal, Stephan J Sanders, Michael T Murtha, Elizabeth W Triche, Matthew W State, Sorin Istrail, Edwin H Cook, Bernie Devlin, Eric M. Morrow, "Intellectual Disability Is Associated With Increased Runs-of-Homozygosity in Simplex Autism," *The American Journal of Human Genetics*, Vol. 93, Issue 1, 103-109, 03 July 2013
 18. Derek Aguiar, Sorin Istrail, "Haplotype Assembly in Polyploid Genomes and Identical-by-Descent Shared Tracts," ISMB 2013 and *Bioinformatics*, Vol. 29, No. 13, pp. i352-i360, 2013
 19. Alper Uzun, Andrew Dewan, Sorin Istrail, James Padbury, "Pathway-Based Genetic Analysis of Preterm Birth," *Genomics*, Vol. 101, Issue 3, 163-170 March 2013

20. Sarah Tulin, Derek Aguiar, Sorin Istrail, Joel Smith, "A Quantitative Reference Transcriptome for *Nematostella vectensis* Early Embryonic Development: A Pipeline for de novo Assembly in Emerging Model Systems," in *EvoDevo*, Vol. 4, No. 16, 2013
21. Huang, J.W. Hogan, S. Istrail, A. DeLong, D.A. Katzenstein, R.Kantor, "Global Analysis of Sequence Diversity Within HIV-1 Subtypes Across Geographic Regions," *Future Virology* Vol. 7, No. 5, pp. 505-517, 2012
22. Uzun, A. Aliberte, J. Park, C. Andrew, E. Winterrowd, S. Sharma, S. Istrail, J. Padbury, "dbPTB: A Database for Preterm Birth," *Database*, Vol. 2012, doi 10.1093/database/bar069
23. D. Aguiar and S. Istrail, "HAPCOMPASS: A Fast Cycle Basis Algorithm for Accurate Haplotype Assembly of Sequence Data," *Journal of Computational Biology*, Vol. 19, No. 6, pp. 577-590, 2012
24. Sorin Istrail, "Computer Science Through Urn Games: An Unified Framework for a Hierarchy of Solvable and Unsolvable Problems," in *Proceedings of the Turing Centenary Conference*, 2012
25. Austin Huang, Joseph W Hogan, Sorin Istrail, Allison DeLong, David A Katzenstein, Rami Kantor, "Global Analysis of Sequence Diversity within HIV-1 Subtypes Across Geographic Regions," in *Future Virology*, Vol. 7, No. 5, pp. 505-517, 2012
26. D. Aguiar, B. Halldorsson, E.M. Morrow, S. Istrail, "DELISHUS: An Efficient and Exact Algorithm for Genome-Wide Detection of Hemizygous Deletion Polymorphism in Autism." *Bioinformatics* 2012, special issue devoted to the papers presented at the 20th Annual International Conference on Intelligent Systems for Molecular Biology (ISMB 2012), Long Beach, CA July 15-17, 2012
27. L.N. Cooper and S. Istrail, "Mental Experience and the Turing Test: This Double Face is the Face of Mathematics," CiE 2012: Proceedings of the Turing Centenary Conference, Cambridge, UK, June 18-23, 2012
28. S. Istrail and S. Marcus, "Turing and von Neumann's Brains and Their Computers," CiE 2012: Proceedings of the Turing Centenary Conference, Cambridge, UK, June 18-23, 2012
29. S. Istrail, "Computer Science Through Urn Games: A Unified Framework for a Hierarchy of Solvable and Unsolvable Problems," CiE 2012: Proceedings of the Turing Centenary Conference, Cambridge, UK, June 18-23, 2012
30. H. Shatkay, R. Narayanaswamy, S. Nagaral, N. Harrington, D. Blostein, R. Tarpine, K. Schutter, R. Mv, G. Somanath, S. Istrail, and C. Kambahmettu, "OCR-based Image Features for Biomedical Image and Article Classification: Identifying Documents Relevant to Cis-Regulatory Elements," accepted to ACM Conference on Bioinformatics, Computational Biology, and Biomedicine, Orlando, FL, Oct. 7-10, 2012
31. Ryan Tarpine, Fumei Lam, Sorin Istrail, "Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-loci and Algorithms for Optimal Tagging SNP Selection," RECOMB 2011, Springer Berlin /

- Heidelberg, Vol. 6577, pp. 468-482, 2011
32. A. Huang, R. Kantor, A. DeLong, L. Schreier, S. Istrail, "QColors: An Algorithm for Conservative Viral Quasispecies Reconstruction from Short and Non-Contiguous Next Generation Sequencing Reads," *Proceedings of the 2011 IEEE Conference on Bioinformatics and Biomedicine, Workshop on Computational Advances in Molecular Epidemiology*, 1:130-136, 2011
 33. Bjarni Halldorsson, Derek Aguiar, Sorin Istrail, "Haplotype Phasing by Multi-Assembly of Shared Haplotypes: Phase-Dependent Interactions Between Rare Variants," in *Pac Symp Biocomput.*, pp. 88-99, 2011
 34. Halldorsson, D. Aguiar, R. Tarpine, S. Istrail, "The Clark Phase-able Sample Size Problem: Long-range Phasing and Loss of Heterozygosity in GWAS," *Journal of Computation Biology*, March 2011, 18(3): 323-333 and "The Clark Phase-able Sample Size Problem: Long-range Phasing and Loss of Heterozygosity in GWAS," in *Proceedings of the 14th Annual International Conference (RECOMB 2010)*, Lecture Notes in Bioinformatics 6044, pp. 158-173, Springer Verlag 2010
 35. J. Nam, P. Dong, R. Tarpine, S. Istrail and E. Davidson, "Functional cis-regulatory genomics for systems biology," *Proceedings of the National Academy of Sciences*, Vol. 107, No. 8, pp. 3930-3935, 2010
 36. S. Istrail, R. Tarpine, K. Schutter, and D. Aguiar, "Practical Computational Methods for Regulatory Genomics: A cis-Lexicon and cis-Browser for Gene Regulatory Networks," in I. Ladunga (ed.) *Computational Biology of Transcription Factor Binding*, Methods in Molecular Biology 674, pp. 369-399, Springer/Humana Press, 2010
 37. F. Lam, R. Tarpine and S. Istrail, "The Imperfect Ancestral Recombination Graph Reconstruction Problem: A Hierarchy of Upper Bounds," *Journal of Computational Biology*, Vol. 17, No. 6, pp. 767-781, 2010
 38. Tarpine, R., Istrail, S. "On the Concept of Cis-Regulatory Information: From Sequence Motifs to Logic Functions," *Algorithmic Bioprocesses*, Springer-Verlag, Berlin Heidelberg, pp. 731-742, 2009
 39. S. Istrail, F. Lam, "Combinatorial Algorithms for Protein Folding in Lattice Models: A Survey of Mathematical Results," *Communications in Information and Systems*, Vol. 9, No. 4, pp. 303-346, 2009
 40. S. Istrail, S. Ben-Tabou de-Leon, E.H. Davidson, "The Regulatory Genome and the Computer," *Developmental Biology*, Vol. 310, pp. 187-195, 2007
 41. M. Samanta, W. Tongprasit, S. Istrail, A. Cameron. Q. Tu, E. Davidson, V. Stolc, "The Transcriptome of the Sea Urchin Embryo," *Science*, Vol. 314, pp. 960-962, 2006
 42. E. Sodergren, G. Weinstock, E. Davidson, ..., S. Istrail, ..., "The Genome of the Sea Urchin *Strongylocentrotus purpuratus*," *Science*, Vol. 314, pp. 941-952, 2006
 43. R. Sharan, B.V. Halldorsson, S. Istrail, "Islands of Tractability for Parsimony Haplotyping," *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, Vol. 3, pp. 303-311, 2006

44. B.V. Halldorsson, S. Istrail, F.M. De La Vega, "Optimal Selection of SNP Markers for Disease Association Studies," *Human Heredity*, Vol. 58, pp. 190-202, 2006
45. S. Istrail and E. Davidson, "Logic Functions of the Genomic cis-Regulatory Code", *Proceedings of the National Academy of Sciences*, vol. 102, no. 14, 4954-4959, 2005
46. F.M. De La Vega, H. Isaac, A. Collins, C.R. Scafe, B.V. Halldorsson, X. Su, R.A. Lippert, F. Kalush, S.J. O'Brian, A. Clark, S. Istrail, M.W. Hunkapiller, E.G. Spier and D. Gilbert, "The Linkage Disequilibrium Maps of Three Human Chromosomes Across Four Populations Reflect Their Demographic History and a Common Underlying Recombination Pattern," *Genome Research*, March 21, 2005
47. L. Florea, V. Di Francesco, J. Miller, R. Turner, C. Mobarry, A. Yao, M. Harris, B. Walenz, I. Dew, G. Merkulov, R. Charlab, Z. Deng, S. Istrail, P. Li, G. Sutton, "Gene and Alternative Splicing Annotation with AIR," *Genome Research*, Vol. 15, No. 1, 54-66, 2005
48. Bjarni Halldorsson, Roded Sharan, and Sorin Istrail, "Islands of Tractability for Parsimony Haplotyping," *Proceedings of the Stanford Computational Systems Biology 2005*, pp. 65-72 (IEEE/ACM Transactions on Computational Biology and Bioinformatics)
49. S. Istrail, L. Florea, B.V. Halldorsson, O. Kohlbacher, R.S. Schwartz, V.B. Yap, J. Yewdell, S. Hoffman, "Comparative Immuno-Peptidomics of Humans and their Pathogens," *Proceedings of the National Academy of Sciences*, Vol. 101, No. 36, pp. 13268-13272, 2004
50. Lippert, R., X. Zhao, L. Florea, C. Mobarry, S. Istrail (2004), "Finding Anchors for Genomic Sequence Comparison," *Proceedings of the 8th Annual International Conference on Research in Computational Biology (RECOMB 2004)*, ACM Press 2004
51. B.V. Halldorsson, V. Bafna, R. Lippert, R.S. Schwartz, F.M. De La Vega, A.G. Clark, S. Istrail, "Optimal Haplotype Block Free Selection of Tagging SNPs for Genome-wide Association Studies," *Genome Research*, Vol. 14, pp. 1633-1640, August 2004
52. S. Istrail, G.G. Sutton, L. Florea, A.L. Halpern, C.M. Mobarry, R. Lippert, B. Walenz, H. Shatkay, I. Dew, J.R. Miller, M.J. Flanigan, N.J. Edwards, R. Bolanos, D. Fasulo, B.V. Halldorsson, S. Hannenhalli, R. Turner, S. Yooseph, F. Lu, D.R. Nusskern, B.C. Shue, X. H. Zheng, F. Zhong, A.L. Delcher, D.H. Huson, S.A. Kravitz, L. Mouchard, K. Reinert, K.A. Remington, A.G. Clark, M.S. Waterman, E.E. Eichler, M.D. Adams, M.W. Hunkapiller, E.W. Myers, J.C. Venter, "Whole Genome Shotgun Assembly and Comparison of Human Genome Assemblies," *Proceedings of the National Academy of Sciences*, Vol. 101, pp. 1916-21, 2004
53. Caprara, R. Carr, S. Istrail, G. Lancia, and B. Walenz, "1001 Optimal PDB Structure Alignments: Integer Programming Methods for Finding the Maximum Contact Map Overlap," *Journal of Computational Biology*, Vol. 11,

- No. 1, pp. 27-52, 2004
54. Vineet Bafna, Bjarni V. Halldorsson, Russell S. Schwartz, Andrew G. Clark, Sorin Istrail, "Haplotypes and Informative SNP Selection Algorithms: Don't Block Out Information," *Proceedings of the 7th Annual International Conference on Computational Molecular Biology (RECOMB 2003)*, ACM Press, pp. 19-27, 2003
 55. Bjarni V. Halldorsson, Vineet Bafna, Nathan Edwards, Ross Lippert, Shibu Yooseph, Sorin Istrail, "A Survey of Computational Methods for Determining Haplotypes," *Proceedings of the First RECOMB Satellite on Computational Methods for SNPs and Haplotype Inference (RECOMB SNP&HAP03)*, Springer Lecture Notes in Bioinformatics, LNBI 2983, pp. 26-47, 2003
 56. Liliana Florea, Bjarni V. Halldorsson, Oliver Kohlbacher, Russell S. Schwartz, Stephen Hoffman, Sorin Istrail, "Epitope Prediction Algorithms for Peptide-based Vaccine Design," *Proceedings of the Second Annual IEEE Computer Society Bioinformatics Conference (CSB03)*, IEEE Press, pp. 17-26, 2003
 57. R.S. Schwartz, B.V. Halldorsson, V. Bafna, A.G. Clark, S. Istrail, "Robustness of Inference of Haplotype Block Structure," *Journal of Computational Biology*, Vol. 10, pp. 13-19, 2003
 58. Bjarni V. Halldorsson, Vineet Bafna, Nathan Edwards, Ross Lippert, Shibu Yooseph, Sorin Istrail, "Combinatorial Problems Arising in SNP and Haplotype Analysis," *Proceedings of the Fourth International Conference on Discrete Mathematics and Theoretical Computer Science (CDMTCS03)*, Springer Lecture Notes in Computer Science, pp. 26-47, 2003
 59. R. Schwartz, A. Clark, S. Istrail, "Inferring Piecewise Ancestral Sequences from Haploid Sequences," *Proceedings of the First RECOMB Satellite on Computational Methods for SNPs and Haplotype Inference (RECOMB SNP&HAP03)*, Springer Lecture Notes in Bioinformatics, LNBI 2983, 2003
 60. G. Lancia, S. Istrail, "Protein Structure Comparison: Algorithms and Applications," pp. 1-33, LNBI 2666, *Mathematical Methods for Protein Structure Analysis and Design, Lecture Notes in Bioinformatics*, Springer Verlag, 2003
 61. R. Lippert, R. Schwartz, G. Lancia, S. Istrail, "Algorithmic Strategies for the SNP Haplotype Assembly Problem," *Briefings in Bioinformatics*, Vol. 3, No. 1, pp. 1-9, March 2002
 62. Rizzi, R., V. Bafna, S. Istrail, G. Lancia, "Practical Algorithms and Fixed-Parameter Tractability for the Single Individual SNP Haplotyping Problem," *Proceeding of the 2nd Workshop on Algorithms in Bioinformatics (WABI02)*, Springer Lecture Notes in Computer Science, 29-43, 2002
 63. Schwartz, R., A. Clark, S. Istrail, "Methods for Inferring Block-wise Ancestral History from Haploid Sequences: The Haplotype Coloring Problem," *Proceedings of the 2nd Workshop on Algorithms in Bioinformatics (WABI02)*, Springer Lecture Notes in Computer Science, 44-59, 2002
 64. R.S. Schwartz, S. Istrail, J. King, "Frequencies of Amino-acid Strings in Globular Proteins Sequences Indicate Suppression of Blocks of Consecutive

- Hydrophobic Residues," *Protein Science* Vol. 10, pp. 1023-1031, 2001
65. J.C. Venter, M.D. Adams, E.W. Myers, P. Li, R.J. Mural, G.G. Sutton, H.O. Smith, M. Yandell, C.A. Evans, R.A. Holt, J.D. Gocayne, P. Amanatides, R.M. Ballew, D.H. Huson, J. Russo Wortman, Q. Zhang, C. Kodira, X.H. Zheng, L. Chen, M. Skupski, G. Subramanian, P.D. Thomas, J. Zhang, G.L. Gabor Miklos, C. Nelson, S. Broder, A.G. Clark, J. Nadeau, V.A. McKusick, N. Zinder, A.J. Levine, R.J. Roberts, M. Simon, C. Slayman, M. Hunkapiller, R. Bolanos, A. Delcher, I. Dew, D. Fasulo, M. Flanigan, L. Florea, A. Halpern, S. Hannenhalli, S. Kravitz, S. Levy, C. Mobarry, K. Reinert, K. Remington, J. Abu-Threideh, E. Beasley, K. Biddick, V. Bonazzi, R. Brandon, M. Cargill, I. Chandramouliswaran, R. Charlab, K. Chaturvedi, Z. Deng, V. Di Francesco, P. Dunn, K. Eilbeck, C. Evangelista, A.E. Gabrielian, W. Gan, W. Ge, F. Gong, Z. Gu, P. Guan, T.A. Heiman, M.E. Higgins, R-R. Ji, Z. Ke, K.A. Ketchum, Z. Lai, Y. Lei, Z. Li, J. Li, Y. Liang, X. Lin, F. Lu, G.V. Merkulov, N. Milshina, H.M. Moore, A.K. Naik, V.A. Narayan, B. Neelam, D. Nusskern, D.B. Rusch, S. Salzberg, W. Shao, B. Shue, J. Sun, Z. Yuan Wang, A. Wang, X. Wang, J. Wang, M-H. Wei, R. Wides, C. Xiao, C. Yan, A. Yao, J. Ye, M. Zhan, W. Zhang, H. Zhang, Q. Zhao, L. Zheng, F. Zhong, W. Zhong, S. C. Zhu, S. Zhao, D. Gilbert, S. Baumhueter, G. Spier, C. Carter, A. Cravchik, T. Woodage, F. Ali, H. An, A. Awe, D. Baldwin, H. Baden, M. Barnstead, I. Barrow, K. Beeson, D. Busam, A. Carver, A. Center, M. Lai Cheng, L. Curry, S. Danaher, L. Davenport, R. Desilets, S. Dietz, K. Dodson, L. Doup, S. Ferriera, N. Garg, A. Gluecksmann, B. Hart, J. Haynes, C. Haynes, C. Heiner, S. Hladun, D. Hostin, J. Houck, T. Howland, A. Chinyere Ibegwam, J. Johnson, F. Kalush, L. Kline, S. Koduru, A. Love, F. Mann, D. May, S. McCawley, T. McIntosh, I. McMullen, M. Moy, L. Moy, B. Murphy, K. Nelson, C. Pfannkoch, E. Pratts, V. Puri, H. Qureshi, M. Reardon, R. Rodriguez, Y-H. Rogers, D. Romblad, B. Ruhfel, R. Scott, C. Sitter, M. Smallwood, E. Stewart, R. Strong, E. Suh, R. Thomas, N. Ni Tint, S. Tse, C. Vech, G. Wang, J. Wetter, S. Williams, M. Williams, S. Windsor, E. Winn-Deen, K. Wolfe, J. Zaveri, K. Zaveri, J.F. Abril, R. Guigo, M.J. Campbell, K.V. Sjolander, B. Karlak, A. Kejariwal, H. Mi, B. Lazareva, T. Hatton, A. Narechania, K. Diemer, A. Muruganujan, N. Guo, S. Sato, V. Bafna, S. Istrail, R. Lippert, R. Schwartz, B. Walenz, S. Yooseph, D. Allen, J. Baxendale, L. Blick, M. Caminha, J. Carnes-Stine, P. Caulk, Y-H. Chiang, M. Coyne, C. Dahlke, A. Deslattes Mays, M. Dombroski, M. Donnelly, D. Ely, S. Esparham, C. Fosler, H. Gire, S. Glanowski, K. Glasser, A. Glodek, M. Gorokhov, K. Graham, B. Gropman, M. Harris, J. Heil, S. Henderson, J. Hoover, D. Jennings, C. Jordan, J. Jordan, J. Kasha, L. Kagan, C. Kraft, A. Levitsky, M. Lewis, X. Liu, J. Lopez, D. Ma, W. Majoros, J. McDaniel, S. Murphy, M. Newman, T. Nguyen, N. Nguyen, M. Nodell, S. Pan, J. Peck, W. Rowe, R. Sanders, J. Scott, M. Simpson, T. Smith, A. Sprague, T. Stockwell, R. Turner, E. Venter, M. Wang, M. Wen, D. Wu, M. Wu, A. Xia, A. Zandieh, X. Zhu, "The Sequence of the Human Genome," *Science*, Vol. 291, pp. 1304-1351, 2001
66. G. Lancia, V. Bafna, S. Istrail, R. Lippert, R. Schwartz, "SNPs Problems: Complexity and Algorithms," *Proceedings of the 3rd European Symposium on*

Algorithms (EAS01) Springer Lecture Notes in Computer Science, 2161, pp. 182-193, 2001

67. R. Turner, K. Chaturvedi, N. Edwards, D. Fasulo, A. Halpern, D. Huson, O. Kohlbacher, J. Miller, K. Reinert, K. Remington, R. Schwartz, B. Walenz, S. Yooseph, S. Istrail, "Visualization Challenges for a New Cyberpharmaceutical Computing Paradigm," *Proceedings of the Symposium on Large-Data Visualization and Graphics*, San Diego, California, October 22-23, 2001
68. G. Lancia, R. Carr, B. Walenz, S. Istrail, "101 Optimal PDB Structure Alignments: A Branch-and-Cut Algorithm for the Maximum Contact Map Overlap Problem," *Proceeding of the Eight International Conference on Research on Computational Biology (RECOMB 2001)*, ACM Press, pp. 201-211, 2001
69. S. Istrail, "Statistical Mechanics, Three-Dimensionality and NP-Completeness: I. Universality of Intractability of the Partition Functions of the Ising Model Across Non-Planar Lattices," *Proceedings of the 32nd ACM Symposium on the Theory of Computing (STOC 2000)*, ACM Press, pp. 87-96, Portland, Oregon, May 21-23, 2000
70. D. Goldman, S. Istrail, G. Lancia, A. Piccolboni, B. Walenz, "Algorithmic Strategies in Combinatorial Chemistry," *Proceedings of the ACM-SIAM Symposium on Discrete Algorithms (SODA 2000)*, ACM Press, January 2000
71. Sorin Istrail, Alan Hurd, Ross A. Lippert, Brian Walenz, Serafim Batzoglou, John H. Conway, Fredrick W. Peyerl, "Prediction of Self-Assembly of Energetic Tiles and Dominos: Experiments, Mathematics and Software," *Sandia Labs Technical Report 2000-0875*, 2000
72. W.E. Hart, S. Istrail, "Invariant Patterns in Crystal Lattices: Implications for Protein Folding Algorithms," *Journal of Universal Computer Science*, Vol. 6, No. 6, pp. 560-579, 2000
73. S. Batzoglou, S. Istrail, "Physical Mapping with Repeated Probes: The Hypergraph Superstring Problem," *Journal of Discrete Algorithms* 1(1):51-76, 2000
74. D. Goldman, S. Istrail, C. Papadimitriou, "Algorithmic Aspects of Protein Structure Similarity," *Proceedings of the IEEE Symposium on Foundations of Computer Science (FOCS 1999)*, IEEE Computer Society Press, October 1999
75. S. Batzoglou, S. Istrail, "Physical Mapping with Repeated Probes: The Hypergraph Superstring Problem," *Proceedings of the 10th Conference on Combinatorial Pattern Matching (CPM 1999)*, Springer Lecture Notes in Computer Science 1645:66, Warwick, England, July 1999
76. S. Istrail, R. Schwartz, J. King, "Lattice Simulations of Aggregation Funnels of Protein Folding," *Journal of Computational Biology*, Vol. 6, No. 2, pp. 143-162, 1999
77. W. E. Hart, S. Istrail, "Robust Proofs of NP-Hardness for Protein Folding: General Lattices and Energy Potentials," *Journal of Computational Biology*, Vol. 4, No. 1, pp. 1-22, 1997
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Posters

1. D. McEarlean, S. Istrail, "CorePhase: Reducing maximum likelihood phasing problems of 2^{100} variables or more to EM-practical sizes without loss of optimality via graph-theoretic symmetries of the likelihood function," Probabilistic Modeling in Genomics, Cold Spring Harbor Laboratory, September 2018
2. D. Aguiar, R. Tarpine, F. Lam, B. Halldorsson, E. Morrow, and S. Istrail, "Long-Range Haplotype Phasing by Multi-Assembly of Shared Haplotypes: Phase-Dependent Interactions Between Rare Variants," Genomics of Common Disease, Wellcome Trust Sanger Genome Center, Cambridge UK, December 2011
3. D. Aguiar, R. Tarpine, F. Lam, B. Halldorsson, E. Morrow, and S. Istrail, "Long-Range Haplotype Phasing by Multi-Assembly of Shared Haplotypes: Phase-Dependent Interactions Between Rare Variants," The Gordon Research Conference on Human Genetics and Genomics, July 17-22, 2011, Salve Regina University, Newport, RI
4. R. Tarpine, J. Hart, T. Johnstone, D. Aguiar, S. Istrail, "Report on the Cyrene Project: A cis-Lexicon Containing the Regulatory Architecture of 557 Regulatory

Genes Experimentally Validated Using the ‘Davidson Criteria,’” The Developmental Biology of the Sea Urchin Meeting, April 27-30, 2011, Woods Hole, MA

Books/Special Issues Editor

1. S. Istrail, P. Pevzner, R. Shamir, F. Sun (Editors), Special Issue Dedicated to Michael Waterman on the Occasion of his 67th Birthday: Parts III-IV, *Communications in Information and Systems*, Vol. 10, Nos. 3-4, pp. 1-115, The Institute of Mathematical Sciences, The Chinese University of Hong Kong, International Press, 2010
2. S. Istrail, P. Pevzner, R. Shamir, F. Sun (Editors), Special Issue Dedicated to Michael Waterman on the Occasion of his 67th Birthday: Parts I-II, *Communications in Information and Systems*, Vol. 9, Nos. 1-2, pp. 235-347, The Institute of Mathematical Sciences, The Chinese University of Hong Kong, International Press, 2009
3. S. Istrail, P. Pevzner, R. Shamir (Editors), Volume V on Computational Molecular Biology, DAM-CMB-Series, *Discrete Applied Mathematics*, Volume 155, Issues 6-7, pp. 673-888 (April 1, 2007)
4. Apostolico, T. Guerra, S. Istrail, P. Pevzner, M. Waterman (Editors), *Proceedings of the 10th International Conference on Computational Molecular Biology (RECOMB 2006)*, *Lecture Notes in Bioinformatics*, Springer-Verlag, Venice, Italy, 2006
5. S. Miyano, J. Mesirov, S. Kasif, S. Istrail, P. Pevzner, M. Waterman (Editors), *Proceedings of the 9th International Conference on Computational Molecular Biology (RECOMB 2005)*, *Lecture Notes in Bioinformatics*, Springer-Verlag, Boston, 2005
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7. S. Istrail, M. Waterman, A. Clark (Editors) *Proceedings of the 1st RECOMB Satellite Workshop Computational Methods for SNPs and Haplotype Inference*, Piscataway, NJ, Nov. 21-22, 2004, *Lecture Notes in Bioinformatics*, (LNBI 2983), 2004
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Essays

1. Sorin Istrail, Eric Davidson: Master of the Universe, *Developmental Biology* 412, S47–S54, 2016
2. Leon N. Cooper, Sorin Istrail, "Mental Experience and the Turing Test: This Double Face is the Face of Mathematics," *Proceedings of the Turing Centenary Conference*, 2012

3. Sorin Istrail, Solomon Marcus, "Turing and von Neumann's Brains and their Computers," *Proceedings of the Turing Centenary Conference*, 2012
4. S. Istrail, Ode to Computational Biology: A letter in support of awarding the National Medal of Science to Professor Michael Waterman, 2012
5. S. Istrail, Professor Solomon Marcus' Axioms, *Intilniri cu / Meetings with Solomon Marcus: 85th Birthday Celebration of Professor Solomon Marcus*, Editura Academiei Romane, and Editura Spandugino/Colectia Distinguo, 2011
6. S. Istrail, Storytelling about Lighthouses: When Professor Dijkstra Slapped Me in the Quest for Beautiful Code, *Conduit*, Spring/Summer 2010, pp. 10-17
7. S. Istrail, Storytelling about Lighthouses: Criticizing Professor Dijkstra Considered Harmless, *Conduit*, Fall/Winter 2008, pp. 10-17
8. S. Istrail and Tracie Sweeney, Randomness is Beautiful: In Search of von Neumann, *Conduit*, Spring/Summer 2006, pp. 10-15
9. On the scientific activity of Laurent Chottin (1947 - 1979), *Bulletin of the European Association for Theoretical Computer Science*, No. 15, pp. 139-146, 1981

Technical Reports

1. S. Istrail, The Haplotype Phasing Problem, *Celera Genomics Technical Report*, 2002
2. M. Li, R. Lippert, R. Schwartz, M. Waterman, S. Istrail, Haplotype Reconstruction from SNP Alignment, *Celera Genomics Technical Report*, 2001
3. R. Lippert, S. Istrail, A. Hurd, Prediction of Energetic Tiles Self-Assembly, *Sandia Labs Technical Report*, 1999
4. B. Carr, G. Lancia, S. Istrail, Branch-and-Bound LP-algorithms for Protein Structure Alignment Based on Contact Map Overlap, *Sandia Labs Technical Report*, 1999
5. R. Schwartz, S. Istrail, J. King, Insights Into the Association of Partially Folded Chains Derived From Lattice Simulation Models, *Sandia Labs Technical Report*, 1999
6. Sorin Istrail, Alan Hurd, Ross A. Lippert, Brian Walenz, Serafim Batzoglou, John H. Conway, Fredrick W. Peyerl, "Prediction of Self-Assembly of Energetic Tiles and Dominos: Experiments, Mathematics and Software," *Sandia Labs Technical Report 2000-0875*, 2000
7. S. Istrail, R. Ravi, What is a Good Objective for Multiple Sequence Alignment?, *Sandia Labs Technical Report*, 1998
8. S. Istrail, Multiple Sequence Alignment and Voting Paradoxes, *Sandia Labs Technical Report*, 1998
9. S. Istrail, Approximations Algorithms on Matroids Based on Cycle-Bases and Applications, *Sandia Labs Technical Report*, 1996

10. W. E. Hart, S. Istrail, Crystallographically universal approximation: A complexity theory of protein folding algorithms for crystal lattices, *Sandia Labs Technical Report*, 1995
11. S. Istrail, The Chimeric Clones Problem, *Sandia Labs Technical Report*, 1993
12. S. Istrail, On the impossibility of the crossover method for proving NP-completeness of the planar chromatic index problem, *Wesleyan University Technical Report*, 1991
13. S. Istrail, On the complexity of unpredictability, *Wesleyan University Technical Report*, 1990

SERVICE TO THE COMPUTATIONAL BIOLOGY COMMUNITY

Co-Founder, the RECOMB Conference “The Annual International Conference on Research in Computational Molecular Biology” (with Mike Waterman and Pavel Pevzner) in 1997-present

Co-Editor-in-Chief, Journal of Computational Biology (with Michael Waterman) 2000-2020

Editor, Springer, Lecture Notes in Bioinformatics book series (co-editor with Pavel Pevzner and Michael Waterman), 2003 – present

Editor, MIT Press, Computational Molecular Biology book series (co-editor with Pavel Pevzner and Mike Waterman), 1999 – present

Editor, North-Holland/Elsevier, Discrete Applied Mathematics, (co-editor with Pavel Pevzner and Ron Shamir), Series on Computational Molecular Biology 1996 – present

SYMPOSIA

1. Eric Davidson Memorial Lecture Series, 2016-present

2. Brown University 250th Anniversary Symposium: The Next 250 Years

May 12-15, 2015

14 John von Neumann Lectures on Economics, Physics, Computer Science, and Brain and Neuroscience unified by John von Neumann's vision of "Computation as a Scientific Lens". Organized by the von Neumann Professors "cluster" at Brown and the Office of President Christina Paxson, and hosted by the Department of Computer Science (Symposium Chair)

“Grigor Moisil” Institute for Computer Science and Applications, University Al. I. Cuza Iasi, Romania 2011- present (Co-Founder and International Director)

3. **John von Neumann Days and The Genome and the Computational Sciences: The Next Paradigms**, organized together by Center for Computational Molecular Biology and Office of President Ruth Simmons May 3–7, 2010, Brown University (Symposium Chair)
4. **John von Neumann Distinguished Lectures Series at Brown University**
5. **The Genome and the Computational Sciences: The Next Paradigms**, organized together with the Office of President Ruth Simmons, December 6-8, 2006, Brown University (Symposium Chair)

INVITED LECTURES

0. “Causality and Computational Biology” ECODAM Lecture, University Al. I Cuza Iasi, Doctoral Summer School in Computer Science, (Evolutionary Computing in Optimization and Data Mining) 2019
1. “Eric Davidson’s ‘Regulatory Genome’ for Computer Science,” Distinguished Lecture Series, Department of Computer Science at the University of Illinois at Chicago, October 2018
2. “Eric Davidson’s ‘Regulatory Genome’ for Computer Science,” Distinguished Lecture Series, School of Computer Science at Tel Aviv University in Israel, December 2018
3. “Eric Davidson’s ‘Regulatory Genome’ for Computer Science,” 9th International Conference “Genomic Regulation: Experiments, Computational Modeling, and Philosophy” at the Jacques Loeb Centre for the History and Philosophy of the Life Sciences, Ben-Gurion University, Israel, December 2018
4. Chinese National Academy of Sciences, Shanghai Institute for Computational Biology Lecture 1 “Algorithmic Strategies for Haplotype Reconstruction: Humans, Plants and Disease;” Lecture 2 “Regulatory Genomics: the cis-GRN Lexicon” 2018
5. University Al I Cuza, Iasi, School of Medicine, “Medical Bioinformatics: SNPs, Haplotypes and the search for meaning in GWAS,” June 2010
6. Talk, Alberto Apostolico Memorial Conference, Venice, Italy, 2016
7. “Logic Functions of the Genomic cis-regulatory Code,” Eric Davidson memorial conference, Marine Biological Laboratory, Woods Hole, MA, 2016
8. Keynote at 26 International Conference on Combinatorial Pattern Matching, Ischia Island, Italy, 2015
9. Lecture 8th International Congress of Romanian Mathematicians, University of Iasi, 2015

10. "Grigore Moisil" Lecture, "Computer Science through Urn Games: A Unified Framework for a Hierarchy of Solvable and Unsolvable Problems," presented at the conference opening the Grigore Moisil Institute, University Al. I. Cuza Iasi, Romania, June 2014
11. "Genome-wide Haploypye Reconstruction and Beyond," **keynote speaker**, 20th International Computing and Combinatorics Conference (COCOON 2014) Aug. 4-6, Atlanta, GA
12. "The Missing Heritability Problem: Disease Models, Algorithms and the Genome" University Alexandru Ioan Cuza Iasi, Romania, June 2013
13. "The Regulatory Genome and the Computer: Theory and Practice," Chinese Academy of Sciences, Shanghai Institute for Biological Sciences, Partner Institute for Computational Biology, Shanghai, China, April 2013
14. "Genome-wide Haplotype Assembly," Tongji University, Department of Biotechnology, Shanghai, China, April 2013
15. "The Regulatory Genome and the Computer: Theory and Practice," **Distinguished Lecture**, Wayne St. University, Nov. 13, 2012
16. "The Linkage Disequilibrium Measures Unification Problem," RECOMB Satellite on Open Problems in Algorithmic Biology, St. Petersburg, Russia, Aug. 28, 2012
17. "The Regulatory Genome and the Computer: Theory and Practice," Genopole Evry, France, April 18, 2012
18. "The Haplotype Phasing Problem: New Algorithms for Long-Range Phasing and Haplotype Assembly from Next-Generation Sequencing Data," University of Southern California, 30 Years of Computational Biology at USC: In honor of Mike Waterman's 70th and Simon Tavaré's 60th birthday, March 31, 2012
19. "The CYRENE Project: A cis-Lexicon containing the regulatory architecture of 586 regulatory genes (393 are transcription factors) experimentally validated using the 'Davidson Criteria,'" University of Rhode Island INBRE seminar, Feb. 16, 2012
20. "Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-Loci," UCLA Bioinformatics Seminar, Nov. 28, 2011
21. Developmental Biology of the Sea Urchin XX Meeting, Marine Biological Laboratory, April 27-30, 2011, Ryan Tarpine presented "Report on the Cyrene Project: A cis-Lexicon containing the regulatory architecture of 557 regulatory genes experimentally validated using the 'Davidson Criteria'"
22. "Long-Range Next-Gen Haplotype Phasing and Assembly: Phase-Dependent Interaction Between Rare Variants," Illumina, Inc., Essex, United Kingdom, Sept. 1, 2011

23. "Human Genome and Medicine," Alexandru Ioan Cuza University, School of Medicine, Iasi, Romania, June 24, 2011
24. "Genome Assembly Algorithms," Alexandru Ioan Cuza University, Faculty of Computer Science, Iasi, Romania, Doctoral Summer School on Meta-heuristics in optimization and intelligent data analysis and Evolutionary Computing in Optimization and Data Mining (ECODAM), June 22, 2011
25. "Cardiovascular Genomics and GWAS," Rhode Island Hospital, Providence, RI, Cardiovascular Research Center Seminar Series, May 9, 2011
26. "Concepts of Mathematical Rigor for Algorithms in De-randomization, Statistical Physics, and Molecular Biology," Alexandru Ioan Cuza University, Iasi, Romania, Centennial Conference of the Alexandru Myller Mathematical Seminar, June 2010
27. "The Regulatory Genome and the Computer: Theory and Practice," **keynote speaker**, Eighth Asia Pacific Bioinformatics Conference, Bangalore, India, January 2010
28. "The Regulatory Genome and the Computer," Indian Institute of Technology, Chennai, India, January 2010
29. "CYRENE: A cis-Lexicon and a cis-Browser for the Regulatory Genome," Annual Sea Urchin Meeting, Marine Biological Laboratory, Woods Hole, MA, September 2009
30. "The Regulatory Genome and the Computer," **keynote speaker**, Southern Methodist University, April 22, 2009
31. "The Regulatory Genome and the Computer," **keynote speaker**, Georgia Institute of Technology, Frontiers in Multiscale Systems Biology Symposium, "October 2008
32. "The Regulatory Genome and the Computer," University of Connecticut, November 2008
33. "The Regulatory Genome and the Computer," Boston University, September 2008
34. "The Regulatory Genome and the Computer," **Distinguished Lecture** University of Illinois at Urbana-Champaign, May 2008
35. "Towards Breaking the cis-Regulatory Code," **Distinguished Lecture**, Leiden University, Amsterdam, December 2007
36. "The Regulatory Genome and the Computer," **Anton van Leeuwenhoek Distinguished Lecture**, Leiden University, Amsterdam, May 2007
37. "The Regulatory Genome and the Computer," **Distinguished Lecture**, Tufts University 2007

38. "Three Lectures on Protein Folding and Regulatory Genomics," Lipari School, Italy, 2006
39. "Randomness is Beautiful," **keynote speaker**, NIH Graduate Student Symposium, Washington DC, 2006
40. "Computational Challenges in Systems Biology," **Distinguished Lecture**, National Institute of Standards and Technology, Gaithersburg, MD, 2006
41. "Towards a Programming Language for Genomics: (G)," IBM, Yorktown Heights Research Center, July 21, 2004
42. "On the General and Logical Theory of Genomic Regulatory Systems," Institute for Pure and Applied Mathematics (IPAM), Functional Genomics Reunion Conference, UCLA, June 2004
43. "Towards a Programming Language for Genomics (G)," Silicon Valley Software Development Forum, San Francisco, May 20, 2004
44. "On the General and Logical Theory of Genomic Regulatory Systems," Mathematics Department, MIT, May 5, 2004
45. "Logical Circuitry of Genomic Regulatory Interactions: An Elemental Functional Repertoire," Fourth International Conference on Systems Biology, St. Louis, MO, November 2003
46. "The Minimum Informative Subset Problem," **keynote speaker**, Conference on Biological Knowledge Discovery and Data-mining (BIOKD03) - 3rd Workshop on Data Mining in Bioinformatics, Washington DC, August 2003
47. "Epitope Prediction Algorithms for Peptide Based Vaccine Design," 2nd IEEE Computer Society Bioinformatics Conference, Stanford, CA, August 2003
48. "Combinatorial Problems Arising in SNP and Haplotype Analysis," Fourth International Conference on Discrete Mathematics and Theoretical Computer Science, Dijon, France, July 2003
49. "Principles of Computing in Genomic Regulatory Systems," Ninth International Meeting on DNA Based Computers, Madison, WI, June 2003
50. "Inferring Gene Transcriptions Networks: The Davidson Model," **keynote speaker**, 13th International Conference on Genome Informatics (GWI02), Tokyo, Japan, Dec. 16-18, 2002
51. "The Haplotype Phasing Problem," Maps, Sequences and Genomes: Workshop in Honor of Mike Waterman 60th birthday, University of Southern California, May 2002
52. "Haplotype Phasing, Blocking, and Mapping," Celera Diagnostics, March 2002
53. "Inferring Gene Transcription Networks: The Davidson Model," **keynote speaker**, University of Colorado at Denver, Center of Computational Biology, March 2002

54. "From First Assembly towards a new Cyberpharmaceutical Computing Paradigm," 2nd IEEE International Symposium on Bioinformatics and Bioengineering, November 2001
55. "Inferring Gene Transcription Networks: The Davidson Model," DIMACS Workshop on Analysis of Gene Expression Data, October 2001
56. "Visualization challenges for a new cyberpharmaceutical computing paradigm," **keynote speaker**, IEEE 2001 Symposium on Parallel and Large-Data Visualization and Graphics, San Diego, CA, October 2001
57. "SNPs, Haplotypes and Disease Association," Fifth Annual TIGR Conference on Computational Genomics, Baltimore, Nov. 28–Dec. 1, 2001
58. "From First Assembly Towards a New Cyberpharmaceutical Computing Paradigm," Supercomputing Conference, 2001
59. "From Genomics to Protein Folding: The Most Beautiful Algorithms (six lectures)," Academia Sinica, Taiwan, Summer Institute on Bioinformatics, August 2001
60. "From First Assembly Towards a New Cyberpharmaceutical Computing Paradigm," **keynote speaker**, Compaq Corporation, Pharma Executive Meeting, June 2001
61. "SNPs, Assembly and Gene Hunting", Beyond Genome Conference, San Diego, June 2001
62. "101 PDB Structural Alignments: A Branch-and-Cut Algorithm for Maximum Contact Map Overlap Problem," DIMACS Workshop on Protein Structure and Structural Genomics: Determination, Technology and Algorithms, August 2001
63. "Five Lectures on: Computational Mathematics, Computational Biology, Computational Physics, Computational Chemistry, and Computational Materials," **keynote speaker / university speaker**, University of Puerto Rico, Mayaguez, Feb. 25 - March 1, 2000
64. "Statistical Mechanics and Computational Complexity: The Rise and Fall of the Search for Exactly Solved Models," Department of Computer Science, University of New Mexico, Feb. 22, 2000
65. "Algorithmic Strategies in Combinatorial Chemistry," Symposium on Discrete Algorithms, SODA 2000, San Francisco January 2000
66. "Protein Folding and Combinatorial Chemistry: Finding Better and Best Needles in Haystacks," Department of Computer Science, Purdue University December 1999
67. International School on Computational Biology, Lipari Island, Italy, "Three Lectures on Algorithms for Protein Structure Prediction," June 20-29, 1999

68. Department of Biology, MIT, "Computational Approaches to Predicting Structure of Amino Acid Sequences for Folding and Misfolding," June 16, 1999
69. Optimizations in Computational Chemistry and Molecular Biology, Princeton University, "Algorithms in Molecular Recognition: Contact Map Structure Alignment and Combinatorial Chemistry," May 4-7, 1999
70. American Mathematical Society Conference on Combinatorial Methods in Statistical Physics, Georgia Tech, "On the impossibility of exact solubility for the general 3D Ising model partitions functions," May 1999
71. Rutgers Center for Operations Research, "On the impossibility of exact solubility for the general 3D Ising model partitions functions," May 1999
72. University of California San Francisco, Department of Pharmaceutical Chemistry, Ken Dill Laboratory, "Lectures on Statistical Physics and Computer Science," April 1999
73. U.S. Department of Energy Mathematics, Information and Computer Science (MICS) Workshop, Albuquerque, "Computational Complexity as a Source of Uncertainty for Three-Dimensional Statistical Mechanics Models," Oct. 29, 1998
74. University of New Mexico Department of Mathematics, "How to Take a Random Walk Deterministically," Nov. 19, 1998
75. Workshop on Physics via High Performance Computing: Approaches and Tools, University of New Mexico, Physics Department, "The Search for Computationally Tractable Lattice-Protein Folding Models," 1998
76. Lawrence Berkeley National Laboratory, "Computational Shortcuts for Computing Low Energy Conformations in Lattice Models," April 3, 1997
77. Lawrence Livermore National Laboratory, "Computational Shortcuts for Computing Low Energy Conformations in Lattice Models," April 4, 1997
78. 1st International Conference on Computational Biology (RECOMB 97), Santa Fe, NM, "Lattice and Off-Lattice Side Chain Models of Protein Folding: Linear Time Structure Prediction Better than 86% of Optimal," 1997
79. A Day of Talks in Combinatorics, Smith College, "Protein Folding: Combinatorial Problems and Algorithms," Sept. 12, 1996
80. Laboratory for Computer Science, MIT, "Protein Folding: Combinatorial Problems and Algorithms," Sept. 18, 1996
81. DIMACS, Rutgers University, "Protein Folding: Combinatorial Problems and Algorithms," Sept. 22, 1996
82. Third German-Israeli Workshop on Computer Science Aspects in Molecular Biology, Tel-Aviv, Israel, "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," Nov. 24-26, 1995

83. Workshop on Biopolymers: Sequence and Structure, Santa Fe Institute, "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," Nov. 5-8, 1995
84. Waksman Institute of Microbiology, Rutgers University, "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," Sept. 20, 1995
85. Dartmouth University, Department of Computer Science, "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," Sept. 15, 1995
86. DIMACS Special Year on Mathematical Support for Molecular Biology, Workshop on Sequence Based Protein Structure Prediction, Rutgers-Princeton U., "Protein Folding in the Hydrophobic-Hydrophilic Model: Achieving Speed and Near-Optimal Stability through Plausible Folding Pathways," March 26, 1995
87. University of California San Francisco, Department of Pharmaceutical Chemistry, "Fast protein folding in the hydrophobic-hydrophilic model within three-eighths," Feb. 15, 1995
88. DIMACS Special Year on Mathematical Support for Molecular Biology, Workshop on Combinatorial Methods in DNA Mapping and Sequencing, Rutgers-Princeton U., "Algorithmic strategies for handling errors in physical mapping: chimerism and deletions," Oct. 6-9, 1994
89. 4th International Workshop on Open Problems in Computational Molecular Biology, Telluride, CO, "Unresolved algorithmic questions occurring in genomic mapping," Aug. 10-24, 1994
90. 3rd International Workshop on Open Problems in Computational Molecular Biology, Telluride, CO, "The chimeric clones problem," Aug. 2-12, 1993
91. University of Rhode Island, Department of Computer Science, "Universal Traversal Sequences," October 1991
92. IBM Research Center, Yorktown Heights, NY, "Constructing Generalized Universal Traversal Sequences of Polynomial Size for Graphs with Small Diameter," October 1990
93. University of Massachusetts at Amherst, Department of Computer and Information Sciences, "Constructing Generalized Universal Traversal Sequences of Polynomial Size for Graphs with Small Diameter," October 1990
94. Massachusetts Institute of Technology, Laboratory for Computer Science and Department of Mathematics, "Polynomial Universal Traversal Sequences for Cycles are Constructible," December 1987
95. University of Massachusetts at Amherst, Department of Computer and Information Sciences, "The Page Number of Genus g Graphs is $O(g)$," April 1987

96. Massachusetts Institute of Technology, Laboratory for Computer Science, “The Expressive Power of a Game of Dijkstra: Predictability, Incompleteness, Complexity,” March 1984

Other Positions

Johns Hopkins University, External Review Committee member, Computer Science Department, 2017

DNA-NEXUS, Stanford, CA, member, Computational Biology Advisory Board, 2013 – 2018

University of Connecticut, Storrs CT, member, External Advisory Board, Computer Science and Engineering Department, 2008 – present

Reykjavik University, Reykjavik, Iceland, member, Advisory Board, Icelandic Centre of Excellence in Theoretical Computer Science, 2008 – present

Mathematical Biosciences Institute, Columbus, OH, member, Scientific Advisory Committee, 2007 – 2012

University of Southern California, Los Angeles, CA, member of the External Advisory Board of the Center for Excellence in Genomics, 2003 – 2007

Virginia Polytechnic Institute, Blacksburg, VA, member, Board of Directors of the School of Computing, 2002 – 2004

University of Colorado at Boulder, Boulder, CO, member, Board of Directors of the Center for Computational Biology, 2001– 2005

California Institute of Technology, Pasadena, CA, Visiting Associate in Biology, Division of Biology, November 2004 – present

George Washington University, Washington, DC, Adjunct Professor of Biochemistry and Molecular Biology, George Washington Medical School, September 2002 – 2010

University of New Mexico, Albuquerque, NM, Adjunct Associate Professor of Biology, Department of Biology, 1998 – 2000

Massachusetts Institute of Technology, Cambridge, MA, Visiting Scientist, Laboratory for Computer Science and Department of Mathematics, 1986 – 1992

RESEARCH GRANTS

Submitted

AI Institute: (M3I) Mechanistic Modeling of Multi-scale Interactomics
UCONN-Brown-Yale, S. I. (Co-PI), submitted Dec 2020

Current

Brown University Seed Fund Award: “A learning healthcare system in Rhode Island for COVID-19,” 2020-2021

NIH/NLM BD2K Research Education Curriculum Development: Data Science Overview for Biomedical Scientists (R25) – “Training and Teaching for Transforming Big Data to Knowledge,” 09/01/2019 - 08/31/2020 (co-PI; Neil Sarkar PI)

Completed

1. National Science Foundation, III: Small: Genome-Wide Algorithms for Haplotype Reconstruction and Beyond: A Combined Haplotype Assembly and Identical-by-Descent Tracts Approach; Award Date: 10/01/2014 – 09/01/2018 (PI)
2. OVPR Brown Seed Award 2014: Genome-wide sequence analysis in severe autism and intellectual disability (co-PI; Eric Morrow PI)
3. Brown University Inaugural Translational Seed Award: “Development of New Computational and Point-of-Care Platforms for HIV Drug Resistance” (co-PI; Anubhav Tripathi PI) 08/01/13 – 07/31/15;
4. National Institutes of Health, COBRE: “Center for Central Nervous System Function,” Brown University Institute for Brain Science (Role: Mentor to Eric Morrow, MD, PhD; Jerome Sanes PI) 08/01/13-07/31/16
5. National Science Foundation, IGERT: “Reverse Ecology: Computational Integration of Genomes, Organisms, and Environments” (David Rand PI; Co-PI: Johanna Schmitt, Zoe Cardon, Mitchell Sogin, Sorin Istrail, Erika Edwards) Award Date: 08/01/2010 – 08/01/2016
6. National Science Foundation, “EAGER: Haplotype Phasing Algorithms and Clark Consistency Graphs” (PI) 09/01/2011 – 09/01/2015
7. National Science Foundation, “The *cis*-GRN Browser and Database: *cis*-Regulatory Information Behind the Network” (PI) 09/01/2007 – 09/01/2011

8. National Science Foundation, “The Genome and the Computational Sciences: Boot Camp Training at Brown in the Art of Asking Tough Scientific Questions” (PI) 2008
9. March of Dimes Foundation, “Preterm Birth: A Novel Bioinformatics and Genomics Approach” (Collaborator; Jim Padbury PI)
10. Brown University OVPR Seed Fund Award, “The Cellarium Project: A Teaching and Research Environment for Computational Systems Biology” (PI)
11. National Science Foundation, “Structural Operational Semantics of Concurrency” 09/01/1988 – 09/01/1991

TEACHING

Courses at Brown University

1. CSCI 1810 “Computational Molecular Biology”
2. CSCI 1820 “Algorithmic Foundations of Computational Biology”
3. CSCI 2820 Advanced Algorithms in Computational Biology and Medical Bioinformatics (graduate course)
4. CSCI 2950-L Algorithmic Foundations of Computational Biology II (graduate course)
5. CSCI 2950-L Medical Bioinformatics: Disease Associations, Protein Folding and Immunogenomics (graduate course)

STUDENTS

Ph.D. Theses

- Pinar Demetci, current Ph.D. student, co-adviser
- Derek Aguiar – “Genome-wide Algorithms for Haplotype Assembly, Haplotype Phasing and Identical-by-Descent Inference.” Ph.D. thesis defended in May 2014; postdoctoral student at Princeton University; now assistant professor of computer science at the University of Connecticut
- Ryan Tarpine – “A database of causality-inferred structure-function information for genomic cis –regulatory architecture,” Ph.D. thesis defended in May 2012, now software engineer at Google
- Dejan Zivkovic “Bounded-width polynomial size Boolean formulas compute exactly those functions from AC^0 .” May 1994, now professor at Belgrade University.

Postdoctoral Students

- Fumei Lam – now at UC Davis/UC Berkeley
- Austin Huang – researcher at Pfizer Research Center; now Vice President, Artificial Intelligence and Machine Learning at Fidelity Investments
- Alper Uzun – now Assistant Professor Research, Department of Pediatrics, Brown Medical School

Master's Theses

- Ryan Tarpine – “The CYRENE cisGRN Browser for the Regulatory Genome;” now software engineer at Google
- Derek Aguiar – “The ARIADNE Browser for Genome-Wide Association Studies;” now assistant professor of computer science at UCONN
- Ning Hou – “Two Problems Related to cis-Regulatory Architecture of Transcription Factor Encoding Genes Homologous Translation and Evolutionary Conservation-Based cis-Module Inference” (2014); now at Amazon
- Lan Nguyen, MS thesis – “Survey on Protein Folding Algorithms of HP model and Proposal of a Hybrid Heuristic Algorithm” (2019); now at a startup software company

Honors Theses

- Lian Garton – “Population Substructure and MCMC” (S.C. Lamport Honor Thesis Award) (2008); now at Amazon
- Kyle Schutter – “The cis-Regulatory Genomics Quintessential Graph Problem” (2010); now at a startup
- Allan Stewart “Face-centered cubic (FCC) lattice models for protein folding: energy function inference and biplane packing” (2010); now at Facebook
- Tim Johnstone – “Gene Networks: An Algorithm to Discover Causal Relationships Through Systematic Experimentation” (Senior Prize for Biology) (2012); now a Ph.D. student at Yale University
- Jake Franco – “MCMC Algorithms for Haplotype Phasing” (2012); now at Stony Brook Medical School
- James Weiss – “Computational Genomics and Bioenergy: Modeling and Clustering of RNA-seq Data” (2012); now Ph.D. student at MIT
- Jeffrey Herman – “A Markov Random Field Model for Inferring Population Structure” (2012); now at Google
- Andy Ly – “Towards Unifying Tagging SNP Selection Algorithms” (2016)

- Sudheesha Perera – “A Haplotype-Based Predictive Model for Genotype/Expression Datasets” (2017); now at Brown Medical School
- Nick Goelz – “Exact Backtracking Algorithms for Optimal Bipole Packing in HP Model of Protein Folding” (2015)
- Alex Gillmore – “Linear Models for SNPs selection” (2012); now at Yelp
- Douglas McErlean – “One Constraint to Rule Them All: How to Simplify Optimizations under Constant Variable Sum, with Applications for Maximum Likelihood” (Top Honor Thesis, CS Department, 2014); now at Google
- Kshitij Lauria – “Bipole Self-assembly and the Biplane Conjecture” (2015)
- Ning Hou – “Two Problems Related to cis-Regulatory Architecture of Transcription Factor Encoding Genes: Homologous Translation and Evolutionary Conservation-Based cis-Module Inference” (2017); now at Amazon
- Daniel Seidman – “LumberTracts: A Method for Time Efficient Determination of Identical by Descent Tracts Between Unphased Genotypes” (2016); now Ph.D. student at Cornell University
- Sam Crosanto – “HapROSEA Software Package for Long Range Haplotype Phasing” (2016); now at Microsoft
- Youn Kim – “Algebraic Connectivity of Graphs, with applications” (2016); now Ph.D. student at MIT with Presidential Fellowship
- Marko Fejzo – “Spectral graph theory and Markov Chains” (2019); now at TwoSigma
- Shivam Nadimpalli – “Discrete Isoperimetry and Protein Folding” (2019); now Ph.D. student at Columbia University
- Sam Hinthorn – “Cis-Lexicon Ontology Search Engine for Gene Regulatory Networks” (2020); now Ph.D. student at Brown University
- Bethany Dubois – “Metropolis-Coupled Monte Carlo in Application to Protein Structure Prediction” (2018); D.E. Shaw; now at Mount Sinai Medical School
- Adrian Turcu – “Protein Folding Prediction and Visualization Techniques Based on Hydrophobic Side Chain Interactions” (2019); now at Brown Medical School
- Min Jean Cho – “Genomic privacy algorithms based on information theory” (2020); now 5th year MS in computer science at Brown University
- Arun Das – “Approaches to Genomic privacy” (2018); now Ph.D. at Johns Hopkins University
- Daniel Ben-Isvy – “Combinatorial methods for the discovery of GWAS SNPs” (2020)

HONORS AND AWARDS

1. 2010: *Professor Honoris Causa*, Alexandru Ioan Cuza University, Iasi, Romania
2. 2006: Endowed Chair Professor, Brown University
3. 2003: Applied Biosystems Science Fellow, Informatics “Best in Class” – Highest distinction for individual technical contributions in Applied Biosystems. One of six Fellows in a company with 800 scientists.
4. 2002: Manager of the Celera Sub-Team of the ClearForrest-Celera team that won the 2002 ACM Knowledge Discovery and Data Mining Cup (ACM KDD Cup), arguably the top International Data Mining/Machine Learning Competition. Theme: automatic genomic annotation of *Drosophila* literature that matches human expert genomic annotation.
5. 2001: Work on the Computational Complexity of the Three-Dimensional Ising Model was listed in the top 100 most important discoveries of the U.S. Department of Energy in its 25 years of existence, being ranked 7th top achievement in the “Advanced Scientific Computing” category.
6. 2000: Graduation speaker for the Mathematics and Physics Class of 2000, University of New Mexico
7. 2000: ACM Service Recognition, ACM General Chair of the RECOMB Conference
8. 2000: Work on computational statistical mechanics selected as the basis for a major theoretical computer science challenge for the 21st century by the “Workshop on Challenges for Theoretical Computer Science at the Beginning of the 21st Century;” workshop sponsored by National Science Foundation, ACM/SIGACT, DIMACS, and SIAM.

Citation:

“Challenge: Computational Statistical Mechanics

In recent years there have been an increasing number of collaborations between theoretical computer scientists and physicists interested in statistical mechanics. Microsoft Research has an entire department devoted to such work. The synergy is due to the fact that both groups of researchers are interested in the same sorts of problems, but bring different sets of tools and ways of thought to them. The classical physics problem that serves as a motivation is the behavior of matter (from gases to crystal lattices) in the presence of heat, magnetism, or other external forces. One fundamental quantity that physicists are interested in is the “partition function” for a given model, which is needed if probabilities are to be normalized. For one well-studied model, the Ising model for spin

glasses, we now have almost completely characterized the complexity of computing the partition function. It has long been known to be polynomial-time computable for planar lattices, and now, due to results of Istrail (STOC 2000) it is known to be NP-hard for any non-planar lattice. One challenge is to extend this work to other important models.”

9. 1999: Keynote speaker for the New Mexico Mathematics Olympiad Finalists
10. 1998: Scientific American “Best of 1998” included the Supercomputing Simulation of Protein Misfolding Project, done by my Sandia Labs group in collaboration with Jonathan King (MIT)
11. 1995: The STOC95 Program Committee referred to our STOC95 paper – the first protein folding algorithms in the literature generating provable near-optimal folds – as a “seminal contribution.”
12. 1995: Sandia National Laboratories Award for Excellence for “the first protein-folding prediction algorithm with guaranteed error bounds”

SERVICE TO BROWN UNIVERSITY

1. **Director, Center for Computational Molecular Biology (CCMB), 2006-2011.**
Asked by Provost Robert Zimmer to take over as Director of CCMB in 2006.
Reported to Provost Robert Zimmer and Provost David Kertzer.

Top Achievements

1. Hired two strong junior faculty: Dan Weinreich, Sohini Ramachandran
2. Established the Brown University Ph.D. Program in Computational Biology
3. Revised the Undergraduate Computational Biology concentration – the longest-running program of its kind in the U.S.
4. Renovated CCMB space, transforming the SWIG Boardroom/CCMB Conference Room into a classroom for the 21st century
5. Organized and ran two world-class symposia, including “The Genome and the Computational Sciences: The Next Paradigms,” which put the Center on the scientific world map
6. Mentored CCMB junior faculty – Dan Weinreich, Jean Wu, Sohini Ramachandran – and four assistant professors in medical school for K awards
7. CCMB faculty published 10 articles in the top three journals: Science, Nature, PNAS
8. President Simmons selects CCMB as the lead story in the 2010 Brown Annual Report

Research Initiatives and Collaborations

1. Genome Assembly Special Forces Workshop – jointly organized with Assistant Professor Casey Dunn (EEB)
2. Molecular Epidemiology through the Bioinformatics Lens – cp-designed with a director and a chief biologist from two NIH institutes, IBM and the Venter Institute (also an IGERT pre-proposal)
3. COBRE proposal on cancer genomics with John Sedivy, Constantine Gatsonis and Chip Lawrence
4. Universal cis-Regulatory Genomics with the MBL

Faculty/Student/Academic/Mentoring Initiatives

In addition to items mentioned above:

1. CCMB Seed Award for Junior Faculty
2. Grad Student/Postdoc Recognition Awards for papers presented at top conferences
3. Grad Student/Postdoc Discussion Lunches
4. DUG for Computational Biology concentrators
5. Grantsmanship Lecture Series, featuring presentations by program managers from NIH and other government agencies who came to campus to discuss their programs and advise Brown PIs
6. The NSF-funded “Sweat-Box Training Camp at Brown in the Art of Asking Tough Scientific Questions,” which was cited by the Provost for its “innovation in teaching”
7. Supported the Artemis Project, which brought high school girls from RI to campus to participate in a science camp
8. Supported the Brown iGEM team

Events

In addition to items mentioned above:

1. John von Neumann Distinguished Lecture Series organized with Leon Cooper (Physics), Stu Geman (Applied Mathematics), Roberto Serrano (Economics)
2. Ernst Ising Distinguished Lecture Series with colleagues from Chemistry and Physics departments
3. CCMB Distinguished Lecture Series
4. CCMB Industry Leaders Lecture Series

Personal achievements while serving as director

1. Was the co-author and/or senior author of 30% of the papers published by CCMB faculty in the top three journals (Science, PNAS and Nature)

2. Winner of top papers (co-authored with my students) in the RECOMB Conference, annual research competition in computational molecular biology
3. As the single PI, brought to Brown two NSF grants totaling \$1M in NSF funding
4. Served as co-PI of the IGERT “Computational Reconstruction of Genomes/Ecology”
5. Oversaw 32 students in my lab: 3 postdocs, 2 Ph.D. students, 5 MS, 20 undergraduates; 2 endowed UTRAs
6. Oversaw 4 honor theses, one of which received a University Award
7. Lab collaborations with the following: Eric Davidson, biology (Caltech); Multiple Sclerosis Consortium GWAS Analysis Group; Eric Morrow, autism (Brown Med); Rami Kantor, AIDS (Brown Med); Jim Padbury, preterm labor (Brown Med)
8. Hosted 80% of all the CCMB visitors and speakers (about 25 per year)
9. Built research bridges among CCMB and Brown Medical School, IBM, Venter Institute, NIH/NIAID, MBL, 454, DOE/Oakridge, FDA, and NIST
10. Member of the Faculty Committee on the Campaign, April 2009 – 2012

SERVICE TO THE COMMUNITY

1. Member of the NSF Algorithmic Foundations (Large) Panel, February 2011
2. Member of the NSF Medical Bioinformatics Program Panel, November 2010
3. Member of the NSF Career Panel, September 2010
4. Member of the NSF Career Panel, September 2009
5. Member of the DOE Early Career Research Program Panel, December 2009
6. Member of the NSF Data-Intensive Computing Panel for the Cluster Exploratory Program
7. Co-organized the Protein Folding Workshop at the University of Minnesota, Jan. 14-18, 2008
8. Member of the DOE INCITE FY 2008 Peer Review Panel
9. Member of 2005 DOE Human Genome to Life Panel
10. Member of 2005 NSF Biological Databases and Informatics Panel
11. Conference started with support from Sloan Foundation and the U.S. Department of Energy. The DOE support was part of the Applied Mathematics Program, Fred Howes, Program Director; program started at DOE by John von Neumann
12. Initiated, with Fred Roberts (DIMACS), the DIMACS-Celera/Applied Biosystems Award for Distinguished Ph.D. Achievement in Computational Biology, 2000-2004

13. Member of the Advisory Committee of the DIMACS Special Years in Computational Biology, 2001-2004
14. Member of the Board of Directors of the International Society for Computational Biology, 1999-2002
15. Member of DOE Human Genome Program Advisory Panels
16. Member of NSF Computer Science Advisory Panels
17. Member of NSF Computer Science and Engineering Advisory Panels
18. Member of NSF Computational Biology Advisory Panels
19. Co-organizer of the DIMACS Workshop on Protein Structure and Structural Genomics: Determination, Technology and Algorithms, Rutgers University, August 2001
20. School Co-Director, International Summer School on Mathematical Methods in Protein Structure Prediction, Italy, July 2000
21. Member of the Program Committee of the 31st ACM Symposium on the Theory of Computing, (STOC 99)
22. Chair of Sandia National Laboratories Workshops on Computational Molecular Biology, Albuquerque, June 20, 21, 24, 1994, and March 4-6, 1996
23. Program Committee Member, 4th Israel Symposium on Theory on Computing and Systems, Jan. 4-6, 1996
24. Program Committee Member DIMACS International Implementation Challenge in Computational Biology: DNA Fragment Assembly and Genomic Rearrangements, Rutgers University, September 20-21, 1995