

## Sorin Istrail

Julie Nguyen Brown Professor of Computational and Mathematical Sciences  
Professor of Computer Science  
Department of Computer Science  
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16 Margrave Avenue  
Providence, RI 02906

### EDUCATION

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  
July 1, 2006 – Julie Nguyen Brown Professor of Computational and Mathematical Sciences  
July 1, 2005 – Professor of Computer Science  
September 1, 2006 – July 31, 2011 – Director, Center for Computational Molecular Biology

**Celera Genomics & Applied Biosystems, Rockville, MD**

*Applied Biosystems/Celera Genomics*

Advanced Research and Technology Division

Informatics Research Department

October 2003 – February 2005 Applied Biosystems Science Fellow, Informatics

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 Co-leader with Gene Myers of the Department

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 Project Leader, Computational Biology Project

1992 – 1993 Computational Scientist

**Wesleyan University, Middletown, CT**

Department of Mathematics

1985 – 1991 Assistant Professor of Computer Science

**University Al. I. Cuza, Iasi, Romania**

“Alexandru Myller” Mathematical Institute and University Computing Center

1979 – 1983 Computer Science Researcher

**Other Positions**

**DNA-NEXUS, Stanford, CA, Member, Computational Biology Advisory Board**

2013 - present

**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*

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

**Editor-in-Chief, Journal of Computational Biology** (co-EIC Michael Waterman)

*2006-present*

**Editor, Lecture Notes in Bioinformatics Book Series**, (co-Editor, together with Pavel Pevzner and Michael Waterman), Springer-Verlag *2003 – present*

**Editor, Computational Molecular Biology Book Series**, (co-Editor, together with Pavel Pevzner and Mike Waterman), MIT Press *1999 – present*

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

## **PUBLICATIONS**

### **Refereed Conference Proceedings Articles**

1. Derek Aguiar, Wendy S.W. Wong, Sorin Istrail, "Tumor haplotype assembly algorithms for cancer genomics.", *In Pacific Symposium on Biocomputing*, vol. 19, pp. 3-14, 2014
2. Derek Aguiar, Eric Morrow, Sorin Istrail, "Tractatus: an exact and subquadratic algorithm for inferring identity-by-descent multi-shared haplotype tracts", *In Proceedings of the 18<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB 2014)*, Lecture Notes in Bioinformatics, , pp. 158-173, Springer-Verlag 2014.
3. Derek Aguiar, Sorin Istrail, "Haplotype Assembly in Polyploid Genomes and Identical-by-Descent Shared Tracts," *Bioinformatics*, vol. 29, no. 13, pp. i352-i360, 2013.
4. 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, October 7-10, 2012.
5. L.N. Cooper and S. Istrail, Mental Experience and The Turing Test: This Double Face is the Face of Mathematics, CiE 2012: Turing Centenary Conference, Cambridge, UK, June 18-23, 2012.
6. S. Istrail and S. Marcus, "Turing and von Neumann's Brains and their Computers, CiE 2012: Turing Centenary Conference, Cambridge, UK, June 18-23, 2012.
7. S. Istrail, Computer Science Through Urn Games: A Unified Framework for a Hierarchy of Solvable and Unsolvable Problems, CiE 2012: Turing Centenary Conference, Cambridge, UK, June 18-23, 2012.

8. 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.
9. 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.
10. R. Tarpine, F. Lam, S. Istrail, Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-Loci Algorithms for Optimal Tagging SNP Selection, *Proceedings of the 15<sup>th</sup> Annual International Conference on Research in Computational Molecular Biology (RECOMB 2011)*, Lecture Notes in Bioinformatics, Springer-Verlag 2011.
11. B. Halldorsson, D. Aguiar, S. Istrail, Haplotype Phasing by Multi-Assembly of Shared Haplotypes: Phase-Dependent Interactions Between Rare Variants, *Proceedings of the Pacific Symposium on Biocomputing*, <http://psb.stanford.edu/psb-online/proceedings/psb11/>.
12. B. Halldorsson, D. Aguiar, R. Tarpine, S. Istrail, 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
13. 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)
14. 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
15. 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
16. 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
17. 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
18. 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
19. 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
20. 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
  21. Schwartz, R., A. Clark, S. Istrail, Methods for inferring block-wise ancestral history from haploid sequences: The haplotype coloring problem, Proceedings of the 2<sup>nd</sup> Workshop on Algorithms in Bioinformatics, (WABI02), Springer Lecture Notes in Computer Science, 44-59, 2002
  22. 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, p. 182-193, 2001
  23. 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
  24. 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 Eighth International Conference on Research on Computational Biology, (RECOMB 2001), ACM Press, p. 201-211, 2001
  25. 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, p. 87-96, Portland, Oregon, May 21-23, 2000
  26. 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
  27. S. Batzoglou, S. Istrail, Physical mapping with repeated probes: The hypergraph superstring problem, Journal of Discrete Algorithms 1(1):51-76, 2000
  28. 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
  29. 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 Lectures Notes in Computer Science 1645:66, Warwick, England, July 1999
  30. W. E. Hart, S. Istrail, Lattice and Off-Lattice Side Chain Models of Protein Folding: Linear Time Structure Prediction Better than 86% of Optimal (Extended Abstract), First International Conference on Computational Molecular Biology, (RECOMB 1997), ACM Press, January 20-23, pp. 137-146, 1997
  31. W. E. Hart, S. Istrail, Invariant Patterns in Crystal Lattices: Implications for Protein Folding Algorithms, Proceedings of the 7th Conference on Combinatorial Pattern Matching (CPM96), Springer Lecture Notes in Computer Science, pp. 288-303, June 1996

32. W. E. Hart, S. Istrail, Fast Protein Folding in the Hydrophobic-Hydrophilic Model Within Three-eighths of Optimal (Extended Abstract), Proceedings of 27th Annual ACM Symposium on Theory of Computation (STOC 1995), ACM Press, pp. 157-168, 1995
33. D. Zivkovic, S. Istrail, A non-probabilistic switching lemma for the Sipser function, Proceedings of the 10th Annual Symposium on Theoretical Aspects of Computer Science (STACS93), Springer Lecture Notes in Computer Science, No.665, pp. 566-575, 1993
34. S. Istrail, Constructing generalized universal traversal sequences of polynomial size for graphs of small diameter, Proceedings of the 31st Annual IEEE Symposium on Foundations of Computer Science (FOCS 1990), IEEE Computer Society Press pp. 439-448, 1990
35. S. Istrail, Polynomial universal traversal sequences for cycles are constructible, Proceedings of the 20th Annual ACM Symposium on Theory of Computing (STOC 1988), ACM Press, pp. 491-453, 1988
36. B. Bloom, S. Istrail, A. R. Meyer, Bisimulation can't be traced, Proceedings of the 15th Annual ACM Symposium on Principles of Programming Languages (POPL88), ACM Press, pp. 229-239, 1988
37. L. Heath, S. Istrail, The pagenumber of genus  $g$  graphs is  $O(g)$ , Proceedings of the 19th Annual ACM Symposium on Theory of Computing (STOC 1987), ACM Press, pp. 388-397, 1987
38. C. Masalagiu, S. Istrail, On protection in Nivat processing systems, Proceedings of the Colloquium of Automata and Programming (CAAP83), Springer Lecture Notes in Computer Science, No. 159, New York, pp. 255-268, 1983
39. S. Istrail, Chomsky-Schutzenger representations for families of languages and grammatical types, Proceeding of the International Conference on Automata, Languages and Programming (ICALP81) Springer Lecture Notes in Computer Science, No. 115, New York, pp. 333-347, 1981
40. S. Istrail, A fixed-point theorem for recursive-enumerable languages and some considerations about semantics of monadic programs, Proceeding of the International Conference on Automata, Languages and programming(ICALP79), Springer Lecture Notes in Computer Science, No. 71, New York, pp. 289-303, 1979

### **Refereed Journal Articles**

1. Atias N, Istrail S, Sharan R. "Pathway-based analysis of genomic variation data." In *Curr Opin Genet Dev.* 2013 Dec;23(6):622-6
2. 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
3. Alper Uzun, Andrew Dewan, Sorin Istrail, James Padbury, "Pathway-Based Genetic Analysis of Preterm Birth", *Genomics*, , vol. 101, Issue 3, 163-170 March 2013
4. 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.

5. 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.
6. 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.
7. 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.
8. 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.
9. 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
10. Derek Aguiar, Bjarni Halldorsson, Eric Morrow, Sorin Istrail, "DELISHUS: An Efficient and Exact Algorithm for Genome-Wide Detection of Deletion Polymorphism in Autism", *In Intelligent Systems for Molecular Biology*, Bioinformatics, 2012
11. Ryan Tarpine, Fumei Lam, Sorin Istrail, "Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-loci and Algorithms for Optimal Tagging SNP Selection", *Chapter in Research in Computational Molecular Biology*, Springer Berlin / Heidelberg, vol. 6577, pp. 468-482, 2011
12. Austin Huang, Rami Kantor, Allison DeLong, Leann Schreier, Sorin Istrail, "QColors: An algorithm for conservative viral quasispecies reconstruction from short and non-contiguous next generation sequencing reads", *In BIBM Workshops*, IEEE, pp. 130-136, 2011
13. Bjarni Halldorsson, Derek Aguiar, Ryan Tarpine, Sorin Istrail, "The Clark Phaseable Sample Size Problem: Long-Range Phasing and Loss of Heterozygosity in GWAS", *In Journal of Computational Biology*, vol. 18, no. 3, pp. 323-333, 2011
14. 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
15. 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
16. 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
- A. 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

17. 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
18. S. Istrail, S. Ben-Tabou de-Leon, E.H. Davidson. The Regulatory Genome and the Computer, *Developmental Biology*, vol. 310, pp. 187-195, 2007
19. 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
20. E. Sodergren, G. Weinstock, E. Davidson, ..., S. Istrail, ..., The Genome of the Sea Urchin *Strongylocentrotus purpuratus*, *Science*, vol. 314, pp. 941-952, 2006
21. 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
22. 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
23. 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
24. 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
25. 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
26. 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
27. 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
28. 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
29. 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
30. 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



31. 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
32. 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
33. 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. Ferreira, 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

34. 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.
35. S. Batzoglou, S. Istrail, Physical mapping with repeated probes: The hypergraph superstring problem, *Journal of Discrete Algorithms* 1(1):51-76, 2000
36. 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
37. 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
38. W. E. Hart, S. Istrail, Lattice and Off-Lattice Side Chain Models of Protein Folding: Linear Time Structure Prediction Better than 86% of Optimal, *Journal of Computational Biology*, vol. 4, no. 3, 1997
39. W. E. Hart, S. Istrail, Fast Protein Folding in the Hydrophobic-Hydrophilic Model Within Three-eighths of Optimal, *Journal of Computational Biology*, vol. 3, no. 1, pp. 53-96, 1996
40. D.S. Greenberg, S. Istrail, Physical Mapping by STS Hybridization: Algorithmic Strategies and the Challenge of Software Evaluation, *Journal of Computational Biology*, vol. 2, no. 2, pp. 219-274, 1995
41. B. Bloom, S. Istrail, A. R. Meyer, Bisimulation can't be traced, *Journal of the ACM*, vol. 42, no. 1, pp. 232-268, January 1995 (Also MIT tech. memo. TM-345, (1987) 21 pp. and Cornell University TR 1994)
42. D.S. Greenberg, S. Istrail, The Chimeric Mapping Problem: Algorithmic Strategies and Performance Evaluation on Synthetic Genomic Data, *Computers and Chemistry*, vol. 18, no.3, pp. 207-220, 1994
43. D. Zivkovic, S. Istrail, Bounded-width polynomial size Boolean formulas compute exactly those functions from AC0, *Information Processing Letters*, vol. 50 no. 4, pp. 211-216, 1994
44. L. Heath, S. Istrail, The pagenumber of genus  $g$  graphs is  $O(g)$ , *Journal of the ACM* 39, 479-501, 1992
45. S. Istrail, An arithmetical hierarchy in propositional dynamic logic, *Information and Computation*, vol. 81, no. 3, pp. 280-289, 1989
46. S. Istrail, An algorithm for embedding planar graphs in six pages, *Iasi University Annals, Mathematics-Computer Science*, vol. 34, no. 4, pp. 329-341, 1988
47. C. Masalagiu, S. Istrail, Nivat's processing systems: decision problems related to protection and synchronization, *Theoretical Computer Science*, vol. 26, pp. 83-103, 1983
48. S. Istrail, A programming exercise with some theoretical appeal, Part I and Part II, *Bulletin of the European Association for Theoretical Computer Science*, No. 20, pp. 70-97, 1983
49. S. Istrail, Some remarks on non-algebraic adherences, *Theoretical Computer Science*, vol. 21, pp. 341-349, 1982
50. S. Istrail, Generalizations of Ginsburg-Rice-Schutzemberger fixed-point theorem for context sensitive and recursive-enumerable sets, *Theoretical Computer Science*, no. 18, pp. 333-341, 1982
51. N. Xuang My, S. Istrail, N-contextual schemes, *Bulletin Mathematique*, Tome 26 (74) no. 3, pp. 241-249, 1982

52. S. Istrail, On a linear theory of recursive-enumerable sets, *Series in Mathematics*, no. 38 Incestr, Bucharest, 22 pp., 1981
53. C. Masalagiu, S. Istrail, Decision problems for languages associated with protection of systems, *Automatic Systems and Informatics, Polytechnic Institute of Bucharest*, pp. 306-312, 1981
54. S. Istrail, A fixed-point approach to contextual languages, *Revue Roumaine de Mathematiques Pures et Appliquees*, vol. 25, no. 6, pp. 861-869, 1980
55. L. Olaru, S. Istrail, An efficient data-structure for computer-graphics, *Artificial Intelligence and Information Control Systems of Robots*, ed. I. Plander, Slovak Academy of Sciences, pp. 83-85, 1980
56. S. Istrail, On complements of some bounded context-sensitive languages, *Information and Control*, vol. 42, no. 3, pp. 283-289, 1979
57. S. Istrail, On the complexity of program divergence, *Foundations of Control Engineering*, vol. 4, no. 1, pp. 19-26, 1979
58. S. Istrail, Contextual grammars with regular choice, *Studii si Cercetari Matematice*, vol. 30, no. 3, pp. 287-294, 1978
59. S. Istrail, D. Simovici, Computing grammars and context-sensitive languages, *Revue Francais D'Automatique, Informatique et Recherche Operationelle*, vol. 12, no. 1, pp. 33-48, 1978
60. S. Istrail, A problem about contextual grammars with choice, *Studii si Cercetari Matematice*, vol. 30, no. 4, pp. 401-408, 1978
61. S. Istrail, Elementary bounded languages, *Information and Control*, vol. 39, no. 2, pp. 177-191, 1978
62. S. Istrail, On irreducible languages and nonrational numbers, *Bulletin Mathematique*, vol. 21, no. 3-4, pp. 301-308, 1977
63. S. Istrail, On formal constructions of algebraic numbers of degree two, *Revue Roumaine de Mathematiques Pures et Appliquees*, vol. 22, no. 9, pp. 1235-1239, 1977
64. S. Istrail, On the weak equivalence problem of OL-systems with some generative devices, *Iasi University Annals*, vol. 23, no. 2, pp. 419-422, 1977
65. S. Istrail, On some symmetric operators on free semigroups, *Studii si Cercetari Matematice*, vol. 28, no. 1, pp. 111-121, 1976

## Posters

1. 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
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," The Gordon Research Conference on Human Genetics and Genomics, July 17-22, 2011, Salve Regina University, Newport, RI.
3. 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.

### **Editor of Books/Special Issues**

1. S. Istrail, P. Pevzner, R. Shamir, F. Sun (Editors), Special Issue Dedicated to Michael Waterman on the Occasion of his 67<sup>th</sup> 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 67<sup>th</sup> 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, Pages 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
6. D. Gusfield, P. Bourne, S. Istrail, P. Pevzner, M. Waterman (Editors), Proceedings of the 8th International Conference on Computational Molecular Biology (RECOMB 2004), ACM Press, San Diego, 2004
7. S. Istrail, M. Waterman, A. Clark (Editors) Proceedings of the 1st RECOMB Satellite Workshop Computational Methods for SNPs and Haplotype Inference, Piscataway, NJ November 21-22, 2004, Lecture Notes in Bioinformatics, (LNBI 2983), 2004
8. W. Miller, M. Vingron, S. Istrail, P. Pevzner, M. Waterman (Editors), Proceedings of the 7th International Conference on Computational Molecular Biology (RECOMB 2003), ACM Press, Washington, DC, 2003
9. C. Guerra, S. Istrail (Editors), Mathematical Methods for Protein Structure Analysis and Design, Advanced Lectures, CIME Summer School on Mathematical Methods for Protein Structure and Design, Marina Franca, Italy, July 9-15, 2000, Lecture Notes in Bioinformatics, (LNBI 2666), 2003
10. S. Istrail, P. Pevzner, R. Shamir (Editors), Volume IV on Computational Molecular Biology, DAM-CMB-Series, Discrete Applied Mathematics, Vol 127, No. 1, April 2003, North Holland/Elsevier.

11. S. Istrail, P. Pevzner, R. Shamir (Editors), Volume III on Computational Molecular Biology, DAM-CMB-Series, Discrete Applied Mathematics, Vol 101, No. 1, 2003, North Holland/Elsevier. The volume also appeared as a book with the same title in the "Topics in Discrete Mathematics" Book Series: No. 12, North Holland/Elsevier.
12. G. Myers, S.Hannenhalli, S. Istrail, P. Pevzner, M.Waterman (Editors), Proceedings of the 6th International Conference on Computational Molecular Biology (RECOMB 2002), ACM Press, Washington, DC, 2002
13. T. Lengauer, D. Sankoff, S. Istrail, P. Pevzner, M.Waterman (Editors), Proceedings of the 5th International Conference on Computational Molecular Biology (RECOMB 2001), ACM Press, Montreal, Canada, 2001
14. R. Shamir, S. Myanno, S. Istrail, P. Pevzner, M.Waterman (Editors) , Proceedings of the 4th International Conference on Computational Molecular Biology (RECOMB 2000), ACM Press, Tokyo, Japan, 2000
14. S. Istrail, P. Pevzner, R. Shamir (Editors), Volume II on Computational Molecular Biology, DAM-CMB Series, Discrete Applied Mathematics, Vol. 88, No.1-3, 2000, North Holland/Elsevier
14. S. Istrail, P. Pevzner, M.Waterman (Editors), Proceedings of the 3rd International Conference on Computational Molecular Biology (RECOMB 99), ACM Press, Lyon, France, 1999
14. S. Istrail, P. Pevzner, M.Waterman (Editors), Journal of Computational Biology, RECOMB 99 Special Issue, Vol.6, No. 3/4, 1999
15. S. Istrail, P. Pevzner, M.Waterman (Editors), Journal of Computational Biology, RECOMB 98 Special Issue, Vol.5, No. 3, 1998
16. S. Istrail, P. Pevzner, M.Waterman (Editors), Proceedings of the 2nd International Conference on Computational Molecular Biology (RECOMB 98), ACM Press, New York City, 1998
17. S. Istrail, P. Pevzner, M.Waterman (Editors), Proceedings of the 1st International Conference on Computational Molecular Biology (RECOMB 97), ACM Press, Santa Fe, New Mexico 1997
18. S. Istrail, P. Pevzner, M.Waterman (Editors), Journal of Computational Biology, RECOMB 97 Special Issues, Vol.4, No.3-4, 1997
19. S. Istrail, P. Pevzner, R. Shamir (Editors), Volume I on Computational Molecular Biology, DAM-CMB Series, Discrete Applied Mathematics, Vol. 71, No.1-3, 1996, North Holland/Elsevier

### Chapters in books

1. 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
2. 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
3. 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

4. L. Olaru, S. Istrail, Pictorial Grammars: Models for the syntax of the patterns of folk art textures, *The Mathematical Semiotics of Visual Arts*, S. Marcus ed., Editura Stiintifica si Enciclopedica, Bucharest, pp. 221-256, 1982

## Essays

1. Leon N. Cooper, Sorin Istrail, "Mental Experience and the Turing Test: This Double Face is the Face of Mathematics", *In Proceedings of the Turing Centenary Conference*, 2012
2. Sorin Istrail, Solomon Marcus, "Turing and von Neumann's Brains and their Computers", *Proceedings of the Turing Centenary Conference*, 2012
3. S. Istrail, Ode to Computational Biology: A letter in support of awarding the National Medal of Science to Professor Michael Waterman, 2012
4. 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
5. S. Istrail, Storytelling about Lighthouses: When Professor Dijkstra Slapped Me in the Quest for Beautiful Code, *Conduit*, Spring/Summer 2010, pp. 10-17
6. S. Istrail, Storytelling about Lighthouses: Criticizing Professor Dijkstra Considered Harmless, *Conduit*, Fall/Winter 2008, pp. 10-17
7. S. Istrail and Tracie Sweeney, Randomness is Beautiful: in Search of von Neumann, *Conduit*, Spring/Summer 2006, pp. 10-15
8. 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
1. 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
2. R. Schwartz, S. Istrail, J. King, Insights Into the Association of Partially Folded Chains Derived From Lattice Simulation Models, *Sandia Labs Technical Report*, 1999
3. 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
4. S. Istrail, R. Ravi, What is a Good Objective for Multiple Sequence Alignment?, *Sandia*

*Labs Technical Report*, 1998

5. S. Istrail, Multiple Sequence Alignment and Voting Paradoxes, *Sandia Labs Technical Report*, 1998
6. S. Istrail, Approximations Algorithms on Matroids Based on Cycle-Bases and Applications, *Sandia Labs Technical Report*, 1996
7. W. E. Hart, S. Istrail, Crystallographically universal approximation: A complexity theory of protein folding algorithms for crystal lattices, *Sandia Labs Technical Report*, 1995
8. S. Istrail, The Chimeric Clones Problem, *Sandia Labs Technical Report*, 1993
9. J. Zipoli, S. Istrail, On the impossibility of the crossover method for proving NP-completeness of the planar chromatic index problem, *Wesleyan University Technical Report*, 1991
10. S. Istrail, On the complexity of unpredictability, *Wesleyan University Technical Report*, 1990

### Invited lectures

1. "Grigore Moisil" Lecture, "Computer Science through Urn Games: An 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
1. "Genome-wide Haployppte Reconstruction and Beyond", **Keynote Speaker**, 20<sup>th</sup> International Computing and Combinatorics Conference (COCOON 2014) August 4-6, Atlanta, GA
2. "The Missing Heritability Problem: Disease Models, Algorithms and the Genome" University "Alexandru Ioan Cuza" Iasi, Romania, June 2013
3. "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
4. "Genome-wide Haplotype Assembly" - Tongji University, Department of Biotechnology, Shanghai, China, April 2013
5. "The Regulatory Genome and the Computer: Theory and Practice", **Distinguished Lecture**, Wayne St. University November 13, 2012
6. "The Linkage Disequilibrium Measures Unification Problem", RECOMB Satellite on Open Problems in Algorithmic Biology, St. Petersburg, Russia, August 28, 2012
7. "The Regulatory Genome and the Computer: Theory and Practice", Genopole Evry, France, April 18, 2012
8. "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 70<sup>th</sup> and Simon Tavaré's 60<sup>th</sup> birthday, "March 31, 2012
9. "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, " February 16, 2012
10. "Conservative Extensions of Linkage Disequilibrium Measures from Pairwise to Multi-Loci" UCLA Bioinformatics Seminar, November 28, 2011

11. "Long-Range Next-Gen Haplotype Phasing and Assembly: Phase-Dependent Interaction Between Rare Variants," Illumina, Inc., Essex, United Kingdom, September 1, 2011
12. "Human Genome and Medicine", "Alexandru Ioan Cuza" University, School of Medicine, Iasi, Romania, June 24, 2011
13. "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
14. "Cardiovascular Genomics and GWAS", Rhode Island Hospital, Providence, RI, Cardiovascular Research Center Seminar Series, May 9, 2011
15. "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
16. "The Regulatory Genome and the Computer: Theory and Practice", **Keynote Speaker**, Eighth Asia Pacific Bioinformatics Conference, Bangalore, India, January 2010
17. "The Regulatory Genome and the Computer", Indian Institute of Technology, Chennai, India, January 2010
18. "CYRENE: A cis-Lexicon and a cis-Browser for the Regulatory Genome", Annual Sea Urchin Meeting, Marine Biological Laboratory, Woods Hole, MA, September 2009
19. "The Regulatory Genome and the Computer," **Keynote Speaker**: Georgia Institute of Technology, Frontiers in Multiscale Systems Biology Symposium, "October 2008
20. "The Regulatory Genome and the Computer", University of Connecticut, November 2008
21. "The Regulatory Genome and the Computer", Boston University, September 2008
22. "The Regulatory Genome and the Computer", **Distinguished Lecture** University of Illinois at Urbana-Champaign, May 2008
23. "Towards Breaking the cis-Regulatory Code", Amsterdam **Distinguished Lecture**, Leiden University, December 2007
24. "The Regulatory Genome and the Computer", **Anton van Leeuwenhoek Distinguished Lecture**, Leiden University, Amsterdam, May 2007
25. "The Regulatory Genome and the Computer", **Distinguished Lecture**, Tufts University 2007
26. "Three lectures on Protein Folding and Regulatory Genomics", Lipari School, Italy, 2006
27. "Randomness is Beautiful", **Keynote Speaker**, NIH Graduate Student Symposium, Washington DC, MD, 2006
28. "Computational Challenges in Systems Biology", **Distinguished Lecture**, National Institute of Standards and Technology, Gaithersburg, MD, 2006
29. "Towards a Programming Language for Genomics: (G)", IBM, Yorktown Heights Research Center, July 21, 2004
30. "On the General and Logical Theory of Genomic Regulatory Systems," Institute for Pure and Applied Mathematics (IPAM), Functional Genomics Reunion Conference, UCLA June 2004
31. "Towards a Programming Language for Genomics (G)", Silicon Valley Software Development Forum, San Francisco, May 20, 2004
32. "On the General and Logical Theory of Genomic Regulatory Systems", Mathematics Department, MIT May 5, 2004
33. "Logical Circuitry of Genomic Regulatory Interactions: An Elemental Functional Repertoire" The Fourth International Conference on Systems Biology, St. Louis, November 2003



34. "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
35. "Epitope Prediction Algorithms for Peptide Based Vaccine Design", 2nd IEEE Computer Society Bioinformatics Conference, Stanford CA August 2003
36. "Combinatorial Problems Arising in SNP and Haplotype Analysis", Fourth International Conference on Discrete Mathematics and Theoretical Computer Science, Dijon France July 2003
37. "Principles of Computing in Genomic Regulatory Systems", Ninth International Meeting on DNA Based Computers, Madison WI, June 2003
38. "Inferring Gene Transcriptions Networks: The Davidson Model", **Keynote Speaker**: 13th International Conference on Genome Informatics (GWI02), Tokyo, Japan, December 16-18, 2002
39. "The Haplotype Phasing Problem", Maps, Sequences and Genomes: Workshop in Honor of Mike Waterman 60th birthday. University of Southern California, May 2002
40. "Haplotype Phasing, Blocking, and Mapping", Celera Diagnostics, March 2002
41. "Inferring Gene Transcription Networks: The Davidson Model", **Keynote Speaker**: University of Colorado at Denver, Center of Computational Biology, March 2002
42. "From First Assembly towards a new Cyberpharmaceutical Computing Paradigm", 2<sup>nd</sup> IEEE International Symposium on Bioinformatics and Bioengineering, November 2001
43. "Inferring Gene Transcription Networks: The Davidson Model", DIMACS Workshop on Analysis of Gene Expression Data, October 2001
44. "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
45. "SNPs, Haplotypes and Disease Association", Fifth Annual TIGR Conference on Computational Genomics, Baltimore, November 28–December 1, 2001
46. "From First Assembly Towards a New Cyberpharmaceutical Computing Paradigm", Supercomputing Conference, 2001
47. "From Genomics to Protein Folding: The Most Beautiful Algorithms (six lectures)", Academia Sinica, Taiwan, Summer Institute on Bioinformatics, August, 2001
48. "From First Assembly Towards a New Cyberpharmaceutical Computing Paradigm", **Keynote Speaker**: Compaq Corporation, Pharma Executive Meeting, June 2001
49. "SNPs, Assembly and Gene Hunting", Beyond Genome Conference, San Diego, June 2001
50. "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
51. "Five Lectures on: Computational Mathematics, Computational Biology, Computational Physics, Computational Chemistry, and Computational Materials", **Keynote Speaker - University Speaker**: University of Puerto Rico, Mayaguez, February 25- March 1, 2000
52. "Statistical Mechanics and Computational Complexity: The Rise and Fall of the Search for Exactly Solved Models", Department of Computer Science, University of New Mexico, February 22, 2000
53. "Algorithmic Strategies in Combinatorial Chemistry", Symposium on Discrete Algorithms, SODA 2000, San Francisco January 2000

54. "Protein Folding and Combinatorial Chemistry: Finding Better and Best Needles in Haystacks", Department of Computer Science, Purdue University December 1999
55. International School on Computational Biology, Lipari Island, Italy, "Three Lectures on Algorithms for Protein Structure Prediction," June 20-29, 1999
56. Department of Biology, MIT, "Computational Approaches to Predicting Structure of Amino Acid Sequences for Folding and Misfolding," June 16, 1999
57. Optimizations in Computational Chemistry and Molecular Biology, Princeton University "Algorithms in Molecular Recognition: Contact Map Structure Alignment and Combinatorial Chemistry," May 4-7, 1999
58. 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
59. Rutgers Center for Operations Research, "On the impossibility of exact solubility for the general 3D Ising model partitions functions," May 1999
60. University of California San Francisco, Department of Pharmaceutical Chemistry, Ken Dill Laboratory "Lectures on Statistical Physics and Computer Science," April 1999
61. 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," October 29, 1998
62. University of New Mexico Department of Mathematics "How To Take a Random Walk Deterministically," November 19, 1998
63. 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
64. Lawrence Berkeley National Laboratory, "Computational Short-Cuts for Computing Low Energy Conformations in Lattice Models," April 3, 1997
65. Lawrence Livermore National Laboratory, "Computational Short-Cuts for Computing Low Energy Conformations in Lattice Models," April 4, 1997
66. 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
67. A Day of Talks in Combinatorics, Smith College, "Protein Folding: Combinatorial Problems and Algorithms," Sept 12, 1996
68. Laboratory for Computer Science, MIT "Protein Folding: Combinatorial Problems and Algorithms," Sept 18, 1996
69. DIMACS, Rutgers University, "Protein Folding: Combinatorial Problems and Algorithms," Sept 22, 1996
70. 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
71. Workshop on Biopolymers: Sequence and Structure, Santa Fe Institute "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," Nov 5-8, 1995
72. Waksman Institute of Microbiology, Rutgers University, "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," September 20, 1995
73. Dartmouth University, Department of Computer Science, "Protein Folding Algorithms on Lattice Models and the Levinthal Paradox," September 15, 1995

74. 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
75. University of California San Francisco, Department of Pharmaceutical Chemistry, "Fast protein folding in the hydrophobic-hydrophilic model within three-eighths," February 15, 1995
76. 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," October 6-9, 1994
77. 4th International Workshop on Open Problems in Computational Molecular Biology, Telluride, CO, "Unresolved algorithmic questions occurring in genomic mapping," August 10-24, 1994
78. 3rd International Workshop on Open Problems in Computational Molecular Biology, Telluride, CO, "The chimeric clones problem," August 2-12, 1993
79. University of Rhode Island, Department of Computer Science, "Universal Traversal Sequences," October 1991
80. IBM Research Center, Yorktown Heights, NY, "Constructing Generalized Universal Traversal Sequences of Polynomial Size for Graphs with Small Diameter," October 1990
81. 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
82. Massachusetts Institute of Technology, Laboratory for Computer Science and Department of Mathematics "Polynomial Universal Traversal Sequences for Cycles are Constructible," December 1987
83. University of Massachusetts at Amherst, Department of Computer and Information Sciences "The Pagenumber of Genus  $g$  Graphs is  $O(g)$ ," April 1987
84. Massachusetts Institute of Technology, Laboratory for Computer Science, "The Expressive Power of a Game of Dijkstra: Predictability, Incompleteness, Complexity," March 1984

## **RESEARCH GRANTS**

### **Current Grants**

1. National Science Foundation 08/01/13 - 07/31/16  
IIS-Genome-Wide Haplotype Reconstruction and Beyond  
Role: PI
2. Brown University Inaugural Translational Seed Award 08/01/13 – 07/31/14  
"Development of New Computational and Point of Care Platforms for HIV Drug Resistance" Role: Co-PI (PI: Anubhav Tripathi).
3. National Institutes of Health 08/01/13-07/31/16

COBRE Center for Central Nervous System Function

Brown University Institute for Brain Science

Role: Mentor (PI: Jerome Sanes)

4. National Science Foundation – 08/01/10 – 07/31/15

IGERT: Reverse Ecology: Computational Integration of Genomes, Organisms, and Environments

Role: Co-PI (PI: David Rand)

### **Completed Grants**

1. National Science Foundation, “EAGER: Haplotype Phasing Algorithms and Clark Consistency Graphs,” Role: PI
2. National Science Foundation, “The *cis*-GRN Browser and Database: *cis*-Regulatory Information Behind the Network,” Role: PI
3. National Science Foundation, “Boot-camp Training at Brown in the Art of Asking Tough Scientific Questions”, Role: PI
4. March of Dimes Foundation, “Preterm Birth: A Novel Bioinformatics and Genomics Approach,” Role: Collaborator (PI: Jim Padbury)
5. Brown University OVPR Seed Fund Award, “The Cellarium Project: A Teaching and Research Environment for Computational Systems Biology,” Role-PI
6. Celera/Applied Biosystems, multi-million budget group (size of group varied over time 13-20 scientists)
7. Sandia National Laboratories – U.S. Department of Energy as well as internal funding: half-million funding project. DOE funding was part of the MICS – Applied Mathematics Program.
8. National Science Foundation “Semantics of Concurrency” at Wesleyan University.

### **SERVICE**

#### **University Service**

1. Member of the Faculty Committee on the Campaign (FCC), April 2009 – 2012

#### **Professional Service**

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, January 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 together with Fred Roberts (DIMACS) of 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, January 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.

## 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 four Fellows in a company of 800 scientists and 5500 employees. The other fellows are in the areas of biology, chemistry and materials science.
4. 2002: Manager of the Celera Sub-Team of the ClearForrest-Celera team that won the 2002 ACM Knowledge Discovery and Datamining Cup (ACM KDD Cup), arguably the top International Datamining/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 ranked in the top 10 most distinguished achievements in the “Advanced Scientific Computing Research” category and in the top 100 most important discoveries of the U.S. Department of Energy in its 25 years of existence.
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, SIAM. 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 this sort of 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”

## TEACHING

### Regular Courses

1. CSCI 1820 “Algorithmic Foundations of Computational Biology” (undergraduate course)
  - a. Spring 2006 – 28 students enrolled
  - b. Spring 2007 – 17 students enrolled
  - c. Spring 2008 – 16 students enrolled
  - d. Spring 2010 – 13 students enrolled
  - e. Spring 2011- 15 students enrolled
  - f. Spring 2013 -11 students enrolled
  - g. Spring 2014 -15 students enrolled
2. Algorithmic Foundations of Computational Biology II (graduate course)
  - a. Fall 2006 – 9 students enrolled
  - b. Fall 2007 – 3 students enrolled

3. Medical Bioinformatics: Disease Associations, Protein Folding and Immunogenomics (formerly Algorithmic Foundations of Computational Biology II) (graduate course)
  - a. Fall 2009 – 13 students enrolled
  - b. Fall 2010 – 6 students enrolled
  - c. Fall 2012 -- 10 students enrolled; three Brown Med faculty and one postdoctoral fellow audited
  - d. Fall 2013 -6 students enrolled
4. Advanced Algorithms in Computational Biology (graduate course)
  - a. Fall 2014 – 5 students enrolled

#### **Independent Studies Directed**

1. Spring 2008 – 2 students enrolled
2. Fall 2008 – 1 student enrolled
3. Spring 2009 – 2 students enrolled
4. Fall 2009 – 1 student enrolled
5. Spring 2010 – 1 student enrolled
6. Spring 2011 – 1 student enrolled
7. Spring 2012 -- 2 students enrolled
8. Spring 2013 – 1 student enrolled
9. Fall 2013 – 1 student enrolled
10. Spring 2014 – 2 students enrolled
11. Fall 2014 – 1 student enrolled

#### **Reading and Research Directed**

1. Fall 2005 – 1 student enrolled
2. Fall 2007 – 2 students enrolled
3. Spring 2008 – 1 student enrolled
4. Fall 2008 – 3 students enrolled
5. Spring 2009 – 2 students enrolled
6. Fall 2009 – 2 students enrolled
7. Spring 2010 – 2 students enrolled
8. Fall 2010 – 2 students enrolled
9. Spring 2011 – 2 students enrolled
10. Spring 2012 – 4 students enrolled
11. Spring 2013 – 1
12. Fall 2013 -2
13. Spring 2014 – 1 student enrolled

#### **Honors Theses Directed**

1. Lian Garton – “Population Substructure and MCMC”
2. Kyle Schutter – “The cis-Regulatory Genomics Quintessential Graph Problem”
3. Allan Stewart – “Protein Folding: The Lattice-to-off-Lattice Mapping Problem”
4. Tim Johnstone – “cis-Regulatory Genomics”
5. Jake Franco – “MCMC Algorithms for Haplotype Phasing”
6. James Weiss – “Bioenergy and Genomics”
7. Jeffrey Herman – “A Markov random field model for inferring population structure”
8. Douglas McErlean – “One Constraint to Rule Them All: How to simplify optimizations under constant variable sum, with applications for maximum likelihood”
9. Kshitij Lauria – “Bipole self-assembly and the biplane conjecture”
10. Ning Hou – “Two Problems Related to cis-Regulatory Architecture of Transcription Factor Encoding Genes: Homologous Translation and Evolutionary Conservation-Based cis-Module Inference”

### **Master’s Theses Directed**

1. Ryan Tarpine – “The CYRENE cisGRN Browser for the Regulatory Genome”
2. Derek Aguiar – “The ARIADNE Browser for Genome-Wide Association Studies”

### **Ph.D. Theses Directed**

1. Derek Aguiar – “Algorithmic Problems in Genome-Wide Association Studies” defended May 2014
2. Ryan Tarpine – “A database of causality-inferred structure-function information for genomic cis-regulatory architecture,” defended May 2012

### **Postdoctoral Students**

1. **Fumei Lam**
2. **Austin Huang**
3. **Alper Uzun**

### **Academic Advising**

1. Freshman Advisor (5 years)
2. Led Seminar on Brown University’s First Readings 2009-2010, “The Beak of the Finch,” by Jonathan Wiener

## ***Sorin's Honor Roll Students***

- *Derek Aguiar, his second PhD student at Brown, graduated May 2014 and is now Postdoctoral Fellow at Princeton University*
- *Ryan Tarpine, his first PhD student at Brown, graduated May 2012, now researcher at Google*



- **Austin Huang, Postdoctoral Fellow, co-advised with professor Rami Kantor, MD, Brown Medical School and professor Joe Hogan, School of Public Health, now at Pfizer Research**
- **Alper Uzun, Postdoctoral Fellow, co-advised with professor Jim Padbury, MD, Brown Medical School, now Assistant Professor at Brown Medical School**
- **Fumei Lam, Postdoctoral Fellow, now she is at IDA, Princeton**
- **Ning Hou, endowed and named UTRA award, the “Randy Pausch Computer UTRA” 2013 recipient, Honor Thesis and now she is a MS student in Computer Science at Brown**
- **Nick Goelz, UTRA award recipient 2014**
- **Doug McErlean, top Honor Thesis in the CS Department 2013, Magna Cum Laude, CRA Honorable Mention and now a Software Engineer at Google**
- **Kshitij Lauria, Honor Thesis and now at D. E. Shaw Research**
- **Jake Franco, Honor Thesis, now at Stony Brook Medical School**
- **Tim Johnstone, Leader of Cyrene Project biology team, Honor Thesis, Biology Prize, now at Yale University**
- **James Weis, Honor Thesis, now at MIT**
- **James Hart, Leader of the Cyrene Project biology team, now at U.C. Berkeley**
- **Kyle Schutter, Leader of the Cyrene Project biology team, Honor Thesis, Thesis Award, now business entrepreneur in Kenya**
- **William Allen, TA and Cyrene Project member, Marshall Fellowship, now at Stanford University**
- **Allan Stewart, endowed and named UTRA, the George I. Alden Trust UTRA Award, Honor Thesis, now at Facebook**
- **David Moskowitz endowed and named UTRA Award, Cyrene Project member, now at Stanford University**
- **Lian Garton, his first student at Brown; she received the SC Lamport Honor Thesis Award, now at Amazon**