

Eleazar Eskin

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EDUCATION Ph.D., Computer Science, **Columbia University**, October 2002.
M.S., Computer Science, **Columbia University**, May 2000.
B.S., Computer Science (with Honors), **University of Chicago**, May 1997.
B.A., Economics (with Honors), **University of Chicago**, May 1997.
B.S., Mathematics, **University of Chicago**, May 1997.

WORK EXPERIENCE

Associate Professor: Department of Computer Science. Department of Human Genetics. *University of California, Los Angeles*. July 2009 - present.
Assistant Professor: Department of Computer Science. Department of Human Genetics. *University of California, Los Angeles*. October 2006 - June 2009.
Assistant Professor in Residence: Department of Computer Science and Engineering. *University of California, San Diego*. July 2003 - October 2006.
Post Doctoral Researcher: School of Computer Science and Engineering. *The Hebrew University*. October 2002 - July 2003.
Consultant and Co-Founder: *System Detection*. Commercial entity to transition DARPA sponsored research in Intrusion Detection at Columbia University to government and industry. 2001-present.
Consultant: *Arcsight*. Consultant on Security and Intrusion Detection Systems. 2000-2001.
Graduate Research Assistant: Department of Computer Science. *Columbia University*. 1997 - 2002.

TEACHING EXPERIENCE

Instructor: Computational Genetics. University of California, Los Angeles, Spring 2009.
Instructor: Current Topics in Bioinformatics. University of California, Los Angeles, Fall 2008.
Instructor: Computational Genetics. University of California, Los Angeles, Spring 2008.
Instructor: Current Topics in Bioinformatics. University of California, Los Angeles, Winter 2008.
Instructor: Computational Genetics. University of California, Los Angeles, Spring 2007.
Instructor: Research Training in Bioinformatics (undergraduate). University of California, San Diego, Spring 2005.
Instructor: Research Training in Bioinformatics (undergraduate). University of California, San Diego, Winter 2005.
Instructor: Introduction to Computer Programming in Java. Columbia University, Spring 1999.

Instructor: Introduction to Computers.
Barnard College Pre-College Program, Summers 1998, 1999, 2000.
Teaching Assistant: Columbia University, 1997-1998.
Machine Learning, Speech Processing.
Teaching Assistant: University of Chicago, 1994-1997.
Junior Tutor for Calculus.

CONFERENCE PROGRAM COMMITTEE AND REVIEWING

Conference Steering Committee: *RECOMB Satellite Workshop on Regulatory Genomics*, 2004-2007 (**Chair**).

Conference Program Committee: *The 2011 Pacific Symposium on Biocomputing (PSB-2011)*, 2011 (**Area Chair**).

The Eighteenth Annual International Conference on Intelligent Systems in Molecular Biology (ISMB-2010), 2010 (**Area Chair**).

The Fourteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2010), 2010.

NIPS 2009 workshop on Machine Learning in Computational Biology, 2009.

The Sixth Annual RECOMB Satellite Workshop on Regulatory Genomics, 2009.

The Ninth Workshop on Algorithms in Bioinformatics (WABI-2009), 2009.

The Seventeenth Annual International Conference on Intelligent Systems in Molecular Biology (ISMB-2009), 2009 (**Area Chair**).

The Thirteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2009), 2009.

Advances in Neural Information Processing Systems 21 (NIPS-2008), 2008 (**Area Chair**).

The Fifth Annual RECOMB Satellite Workshop on Regulatory Genomics, 2008.

The Eighth Workshop on Algorithms in Bioinformatics (WABI-2008), 2008.

The Twelfth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2008), 2008.

NIPS 2007 New Problems and Methods in Computational Biology Workshop, 2007.

The Fourth Annual RECOMB Satellite Workshop on Regulatory Genomics, 2007.

The Fifteenth Annual International Conference on Intelligent Systems in Molecular Biology (ISMB-2007), 2007.

The Twenty Fourth International Conference on Machine Learning (ICML-2007), 2007.

The Eleventh Annual International Conference on Research in Computational Molecular Biology (RECOMB-2007), 2007.

NIPS 2006 New Problems and Methods in Computational Biology Workshop, 2006.

The Twenty Third International Conference on Machine Learning (ICML-2006), 2006.

The Third Annual RECOMB Satellite Workshop on Regulatory Genomics, 2006.

NIPS 2005 New Problems and Methods in Computational Biology Workshop, 2005.

The Second Annual RECOMB Satellite Workshop on Regulatory Genomics, 2005 (**Chair**).

The Twenty Second International Conference on Machine Learning (ICML-2005), 2005.

The Ninth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2005), 2005.

NIPS 2004 New Problems and Methods in Computational Biology Workshop, 2004.

The First Annual RECOMB Satellite Workshop on Regulatory Genomics, 2004 (**Chair**).

The Twenty First International Conference on Machine Learning (ICML-2004), 2004.

The Twentieth International Conference on Machine Learning (ICML-2003), 2003.

Workshop on Data Mining for Computer Security (DMSEC-2004), 2004.

Workshop on Data Mining for Computer Security (DMSEC-2003), 2003.

Conference Organizing Committee: *RECOMB Satellite Workshop on Regulatory Genomics*, 2004-2006 (**Chair**).

The Tenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2006), 2006 (**Tenth Year Anniversary Committee Chair**).

Journal Referee: *Proceedings of the National Academy of Sciences*, 2007. *Nature Genetics*, 2007, 2008. *Nucleic Acids Research*, 2007. *Molecular Systems Biology*, 2007, 2008. *Genome Research*, 2004, 2005, 2007, 2008. *PLoS Genetics*, 2008, 2009, 2010. *Genetics*, 2009. *Nature Methods*, 2009. *PLoS Computational Biology*, 2005, 2007, 2008. *American Journal of Human Genetics*, 2005, 2006, 2007. *IEEE Transactions on Computational Biology and Bioinformatics*, 2005, 2006, 2007, 2008. *Pharmacogenomics*, 2008. *Journal of Neuroscience Methods*, 2007. *Journal of Molecular Genetics*, 2007. *IEEE Transactions on Knowledge and Data Engineering*, 2005. *BMC Bioinformatics*, 2004, 2005, 2007, 2008, 2009. *BMC Medical Genetics*, 2008. *Human Molecular Genetics*, 2005, 2006. *Bioinformatics*, 2003, 2004, 2005, 2006, 2007, 2008. *Nature Molecular Systems Biology*, 2006. *Journal of Computational Biology*, 2004, 2005, 2007, 2009. *Journal of Bioinformatics and Computational Biology*, 2003, 2007, 2008. *IEEE Transactions on Systems, Man and Cybernetics*, 2002, 2003.

Conference Reviewer: *Advances in Neural Information Processing Systems 22 (NIPS-2009)*, 2009.

The 2007 Pacific Symposium on Biocomputing (PSB-2007), 2007.

Advances in Neural Information Processing Systems 20 (NIPS-2007), 2007.

The ACM-SIAM Symposium on Discrete Algorithms (SODA-2007), 2007

The Tenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2006), 2006.

The Thirteenth Annual International Conference on Intelligent Systems in Molecular Biology (ISMB-2005), 2005.

The Eighth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2004), 2004.

The 2004 Pacific Symposium on Biocomputing (PSB-2004), 2004.

Advances in Neural Information Processing Systems 16 (NIPS-2003), 2003.

The 2003 European Conference on Computational Biology (ECCB-2003), 2003.

The Ninth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD-2003), 2003.

The Nineteenth Conference on Uncertainty in Artificial Intelligence (UAI-2003), 2003.

The Seventh Annual International Conference on Research in Computational Molecular Biology (RECOMB-2003), 2003.

The Eighth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD-2002), 2002.

The 2002 ACM SIGMOD International Conference on Management of Data (SIGMOD-2002), 2002.

The Sixth ACM SIGKDD International Conference on Knowledge Discovery and Data Mining (KDD-2000), 2000.

PUBLICATIONS

Refereed Journal Papers

1. Dan He, Arthur Choi, Knot Pipatsrisawat, Adnan Darwiche, Eleazar Eskin. "Op-

timal Algorithms for Haplotype Assembly From Whole-Genome Sequence Data.” **Bioinformatics** (In Press) *Special Issue Proceedings of the Eighteenth International Conference on Intelligent Systems for Molecular Biology (ISMB-2010)* Boston, MA: July 11-13, 2010.

2. Andrew Kirby, Hyun Min Kang, Claire M. Wade, Chris Cotsapas, Emrah Kostem, Buhm Han, Nick Furlotte, Eun Yong Kang, Manuel Rivas, Molly A. Bogue, Kelly A. Frazer, Frank M. Johnson, Erica J. Beilharz, David R. Cox, Eleazar Eskin, Mark J. Daly. “Fine mapping in 94 inbred mouse strains using a high-density haplotype resource.” **Genetics** (In Press), 2010.
3. Noah Zaitlen, Eleazar Eskin. “Imputation Aware Meta-Analysis of Genome Wide Association Studies.” **Genetic Epidemiology** (In Press), 2010.
4. Kuixing Zhang, Alan B. Weder, Eleazar Eskin, Daniel T. O’Connor. “Genome-wide case/control studies in hypertension: only the ‘tip of the iceberg’.” **Journal of Hypertension** (In Press), 2010.
5. Hyun Min Kang, Noah Zaitlen, Buhm Han, Eleazar Eskin. “An Adaptive and Memory Efficient Algorithm for Genotype Imputation.” **Journal of Computational Biology** (In Press), 2010.
6. Eun Yong Kang, Ilya Shpitser, Chun Ye, Eleazar Eskin. “Detecting the Presence and Absence of Causal Relationships Between Expression of Yeast Genes with Very Few Samples.” **Journal of Computational Biology** (In Press), 2010.
7. Jason L. Stein, Xue Hua, Jonathan H. Morra, Suh Lee, Derrek P. Hibar, April J. Ho, Alex D. Leow, Arthur W. Toga, Jae Hoon Sul, Hyun Min Kang, Eleazar Eskin, Andrew J. Saykin, Li Shen, Tatiana Foroud, Nathan Pankratz, Matthew J. Huentelman, David W. Craig, Jill D. Gerber, April N. Allen, Jason J. Corneveaux, Dietrich A. Stephan, Jennifer Webster, Bryan M. DeChairo, Steven G. Potkin, Clifford R. Jack Jr., Michael W. Weiner, Paul M. Thompson, and the Alzheimer’s Disease Neuroimaging Initiative. “Genome-wide analysis reveals novel genes influencing temporal lobe structure with relevance to neurodegeneration in Alzheimer’s disease.” **Neuroimage** (In Press), 2010.
8. Hyun Min Kang, Jae Hoon Sul, Susan K Service, Noah A Zaitlen, Sit-yeek Kong, Nelson B Freimer, Chiara Sabatti, Eleazar Eskin. “Variance component model to account for sample structure in genome-wide association studies.” **Nature Genetics** (In Press), 2010.
9. Brian J. Bennett, Charles R. Farber, Luz Orozco, Hyun Min Kang, Anatole Ghazalpour, Nathan Siemers, Michael Neubauer, Isaac Neuhaus, Roumyana Yordanova, Bo Guan, Amy Truong, Wen-pin Yang, Aiqing He, Paul Kayne, Peter Gargalovic, Todd Kirchgessner, Calvin Pan, Lawrence W. Castellani, Emrah Kostem, Nicholas Furlotte, Thomas A. Drake, Eleazar Eskin, Aldons J. Lusis. “A High Resolution Association Mapping Panel for the Dissection of Complex Traits in Mice.” **Genome Research**. **20(2):281-90**, 2010.
10. Ivana V. Yang, Claire M. Wade, Hyun Min Kang, Scott Alper, Holly Rutledge, Brad Lackford, Eleazar Eskin, Mark J. Daly, and David A. Schwartz. “Identification of Novel Genes that Mediate Innate Immunity Using Inbred Mice.” **Genetics**. **183(4):1535-44**, 2009.
11. Brinda K. Rana, Jennifer Wessel, Vafa Mahboubi, Fangwen Rao, Jeannine Haeller, Jiaur R. Gayen, Eleazar Eskin, Anne Valle, Madhusudan Das, Sushil K. Mahata,

- Laurent Taupenot, Mats Stridsberg, Todd Talley, Michael Ziegler, Douglas W. Smith, Nicholas J. Schork, Daniel T. O'Connor, Palmer Taylor. "Natural variation within the neuronal nicotinic acetylcholine receptor cluster on human chromosome 15q24: Influence on heritable autonomic traits in twin pairs." **Journal of Pharmacology And Experimental Therapeutics**. **331(2):419-28**, 2009.
12. Smith, E. N., Bloss, C. S., Badner, J. A., Barrett, T., Belmonte, P. L., Berrettini, W., et al. (2009). "Genome-Wide association study of bipolar disorder in european american and african american individuals." **Molecular Psychiatry**.**14(8):755-63**, 2009.
 13. Buhm Han, Hyun Min Kang, Eleazar Eskin. "Rapid and Accurate Multiple Testing Correction and Power Estimation for Millions of Correlated Markers." **PLoS Genetics**. **5:4, e1000456**, 2009.
 14. Chun Ye, Simon J. Galbraith, James C. Liao, Eleazar Eskin. "Using Network Component Analysis to Dissect Regulatory Networks Mediated by Transcription Factors in Yeast." **PLoS Computational Biology**. **5(3):e1000311**, 2009.
 15. Noah Zaitlen, Hyun Min Kang, Eleazar Eskin. "Linkage Effects and Analysis of Finite Sample Errors in the HapMap." **Human Heredity**. **68:2, 73-86**, 2009.
 16. Hyun Min Kang, Chun Ye, Eleazar Eskin. "Accurate discovery of expression quantitative trait loci under confounding from spurious and genuine regulatory hotspots." **Genetics**. **180(4):1909-25**, 2008.
 17. Anatole Ghazalpour, Sudheer Doss, Hyun Kang, Charles Farber, Ping-Zi Wen, Alec Brozell, Ruth Castellanos, Eleazar Eskin, Desmond J. Smith, Thomas A. Drake, Aldons J. Lusis. "High Resolution Mapping of Gene Expression Using Association in an Outbred Mouse Stock." **PLoS Genetics**. **4(8):e1000149**, 2008.
 18. Buhm Han, Hyun Min Kang, Myeong Seong Seo, Noah Zaitlen, Eleazar Eskin. "Efficient Association Study Design via Power-Optimized Tag SNP Selection." **Annals of Human Genetics**. **72(Pt 6):834-47**, 2008.
 19. Eleazar Eskin. "Increasing Power in Association Studies by using Linkage Disequilibrium Structure and Molecular Function as Prior Information." **Genome Research**. **18(4):653-60** *Special Issue Proceedings of the 12th Annual Conference on Research in Computational Biology (RECOMB-2008)*, 2008.
 20. Adam B Olshen , Bert Gold , Kirk E Lohmueller , Jeffrey P Struewing , Jaya Satagopan , Stefan A Stefanov , Eleazar Eskin , Tomas Kirchhoff , James A Lautenberger , Robert J Klein , Eitan Friedman , Larry Norton , Nathan A Ellis , Agnes Viale , Catherine S Lee , Patrick I Borgen , Andrew G Clark , Kenneth Offit and Jeff Boyd. "Analysis of genetic variation in Ashkenazi Jews by high density SNP genotyping." **BMC Genetics**. **9:14**, 2008.
 21. Hyun Min Kang, Noah A. Zaitlen, Claire M. Wade, Andrew Kirby, David Heckerman, Mark J. Daly, and Eleazar Eskin. "Efficient Control of Population Structure in Model Organism Association Mapping." **Genetics**. **178(3):1709-23**, 2008.
 22. Thomas B. Barrett, John E. Emberton, Caroline M. Nievergelt, Sherri G. Liang, Richard L. Hauger, Eleazar Eskin, Nicholas J. Schork, John R. Kelsoe. "Further evidence for association of GRK3 to bipolar disorder suggests a second disease mutation." **Psychiatric Genetics**. **17(6):315-22.**, 2007.
 23. Kelly A. Frazer, Eleazar Eskin, Hyun Min Kang, Molly A. Bogue, David A. Hinds, Erica J. Beilharz, Robert V. Gupta, Julie Montgomery, Matt M. Morenzoni, Geoffrey

- B. Nilsen, Charit L. Pethiyagoda, Laura L. Stuve, Frank M. Johnson, Mark J. Daly, Claire M. Wade, David R. Cox. "A sequence-based variation map of 8.27 million SNPs in inbred mouse strains." **Nature**. **448(7157):1050-3**. 2007.
24. Eleazar Eskin, Sagi Snir. "Incorporating Homologues into Sequence Embeddings for Protein Analysis." **Journal of Bioinformatics and Computational Biology**. **5(3):717-38**. 2007.
 25. Fangwen Rao, Gen Wen, Jiur R. Gayen, Madhusudan Das, Sucheta M. Vaingankar, Brinda K. Rana, Manjula Mahata, Brian P. Kennedy, Rany M. Salem, Mats Stridsberg, Kenneth Abel, Douglas W. Smith, Eleazar Eskin, Nicholas J. Schork, Bruce A. Hamilton, Michael G. Ziegler, Sushil K. Mahata, Daniel T. O'Connor. "Catecholamine Release Inhibitory Peptide Catestatin (Chromogranin A352-372). Naturally Occurring Amino Acid Variant Gly364Ser Causes Profound Changes in Human Autonomic Activity and Alters Risk for Hypertension." **Circulation**. **115(17):2271-81**. 2007.
 26. Noah Zaitlen, Hyun Min Kang, Eleazar Eskin, Eran Halperin. "Leveraging the HapMap Correlation Structure in Association Studies." **American Journal of Human Genetics**. **80(4):683-91**. 2007.
 27. Chun Ye, Eleazar Eskin. "Discovering Tightly Regulated and Differentially Expressed Gene Sets in Whole Genome Expression Data." **Bioinformatics** **23(2):e84-90**. *Special Issue Proceedings of the 5th European Conference on Computational Biology (ECCB-2006)*. Eilat, Israel: January 21st-24th, 2007.
 28. Eleazar Eskin, Eran Halperin, Roded Sharan. "A Note on Optimally Phasing Long Genomic Regions using Local Haplotype Predictions." **Journal of Bioinformatics and Computational Biology**. Vol. 4, No. 3 **639-647**. 2006.
 29. Sean O'Rourke, Gal Checkik, Robin Friedman, Eleazar Eskin. "Discrete profile alignment via constrained information bottleneck." **BMC Bioinformatics**. **7 Suppl 1:S1-8**. 2006.
 30. Jonathan Marchini, David Cutler, Nick Patterson, Matthew Stephens, Eleazar Eskin, Eran Halperin, Shin Lin, Steve Qin, Goncalo Abecassis, Heather Munro, Peter Donnelly. "A comparison of phasing algorithms for trios and unrelated individuals." **American Journal of Human Genetics**. **78(3):437-50**. 2006.
 31. Evan L. Riddle, Kenton K. Murthy, Eleazar Eskin, Daniel T. O'Connor, Brinda K. Rana, Paul A. Insel "Single Nucleotide Polymorphisms and Ethnic-specific Haplotypes of the Regulator of G-Protein Signaling-2 (RGS2) Gene in Hypertensive and Normotensive Subjects" **Hypertension**. **47(3):415-20**. 2006.
 32. Tiffany A. Greenwood, Nicholas J. Schork, Eleazar Eskin, and John R. Kelsoe. "Identification of Additional Variants within the Human Dopamine Transporter Gene Provides Further Evidence for an Association with Bipolar Disorder" **Mol Psychiatry**. **11(2):115**. 2006.
 33. Noah Zaitlen, Hyun Min Kang, Michael Feolo, Stephen Sherry, Eran Halperin, Eleazar Eskin. "Inference and Analysis of Haplotypes from Combined Genotyping Studies Deposited in dbSNP." **Genome Research**. **15(11):1594-600**. 2005.
 34. Shaojie Zhang, Brian Haas, Eleazar Eskin, Vineet Bafna. "Searching genomes for non-coding RNA using FastR." **IEEE/ACM Transactions on Computational Biology and Bioinformatics**. **2(4):366-379**. 2005.

35. Salvatore J. Stolfo, Frank Apap, Eleazar Eskin, Katherine Heller, Shlomo Hershkop, Andrew Honig, and Krysta Svore. "A Comparative Evaluation of Two Algorithms for Windows Registry Anomaly Detection." **Journal of Computer Security**. **13(4):659-693**. 2005.
36. David A. Hinds, Laura L. Stuve, Geoffrey B. Nilsen, Eran Halperin, Eleazar Eskin, Dennis G. Ballinger, Kelly A. Frazer, David R. Cox. "Whole-Genome Patterns of Common DNA Variation in Three Human Populations" **Science** **18 February: 307(5712):1072-1079**. 2005.
37. Martin Tompa, Nan Li1, Timothy L. Bailey, George M. Church, Bart De Moor, Eleazar Eskin, Alexander V. Favorov, Martin C. Frith, Yutao Fu, W. James Kent, Vsevolod J. Makeev, Andrei A. Mironov, William Stafford Noble, Giulio Pavesi, Graziano Pesole, Mireille Regnier, Nicolas Simonis, Saurabh Sinha, Gert Thijs, Jacques van Helden, Mathias Vandenbogaert, Zhiping Weng, Christopher Workman, Chun Ye, Zhou Zhu. "An Assessment of Computational Tools for the Discovery of Transcription Factor Binding Sites." **Nature Biotechnology**. **23(1):137-44**. 2005.
38. Alkes L. Price, Eleazar Eskin, Pavel A. Pevzner. "Whole genome analysis of Alu repeat elements reveals complex evolutionary history." **Genome Research**. **14(11):2245-2252**. 2004.
39. Eran Halperin and Eleazar Eskin. "Haplotypes Reconstruction from Genotype Data using Imperfect Phylogeny." **Bioinformatics**. **20(12):1842-9**. 2004.
40. Christina Leslie, Eleazar Eskin, Adiel Cohen, Jason Weston and William Stafford Noble. "Mismatch String Kernels for SVM Protein Classification." **Bioinformatics**. **20(4):467-476**. 2004.
41. Eleazar Eskin, Eran Halperin and Richard M. Karp. "Efficient Reconstruction of Haplotype Structure via Perfect Phylogeny" **Journal of Bioinformatics and Computational Biology**. **1(1):1-20**. 2003.
42. Eleazar Eskin, William Stafford Noble, and Yoram Singer. "Protein Family Classification using Sparse Markov Transducers." **Journal of Computational Biology**. **10(2):187-213**. 2003.
43. Eleazar Eskin, William Stafford Noble and Yoram Singer. "Using Substitution Matrices to Estimate Probability Distributions for Biological Sequences." **Journal of Computational Biology**. **9(6):775-91**. 2002.
44. Eleazar Eskin and Pavel Pevzner. "Finding Composite Regulatory Patterns in DNA Sequences." **Bioinformatics** **18 Supplement 1:S354-63**. *Special Issue Proceedings of the Tenth International Conference on Intelligent Systems for Molecular Biology (ISMB-2002)*. Edmonton, Canada: August 3-7, 2002.
45. Eleazar Eskin, William Noble Grundy and Yoram Singer. "Using Mixtures of Common Ancestors for Estimating the Probabilities of Discrete Events in Biological Sequences." **Bioinformatics** **17 Supplement 1:S65-73**. *Special Issue Proceedings of the Ninth International Conference on Intelligent Systems for Molecular Biology (ISMB-2001)*. Copenhagen, Denmark: July 21-25, 2001.

Refereed Conference Papers

46. Eun Yong Kang, Eleazar Eskin. "Respecting Markov Equivalence in Identification of Causal Graphical Features." *In Proceedings of the 24th AAAI Conference on Artificial Intelligence (AAAI-10)*. Atlanta, GA: July 11-15, 2010.

47. Hyun Min Kang, Noah Zaitlen, Buhm Han, Eleazar Eskin. "An Adaptive and Memory Efficient Algorithm for Genotype Imputation." *In Proceedings of the Thirteenth Annual Conference on Research in Computational Biology (RECOMB-2009)*. Tucson, AZ: May 18th-21st, 2009.
48. Eun Yong Kang, Ilya Shpitser, Chun Ye, Eleazar Eskin. "Detecting the Presence and Absence of Causal Relationships Between Expression of Yeast Genes with Very Few Samples." *In Proceedings of the Thirteenth Annual Conference on Research in Computational Biology (RECOMB-2009)*. Tucson, AZ: May 18th-21st, 2009.
49. Arthur Choi, Noah Zaitlen, Buhm Han, Knot Pipatsrisawat, Adnan Darwiche, Eleazar Eskin. "Efficient Genome Wide Tagging by Reduction to SAT." *In Proceedings of the 8th Workshop on Algorithms in Bioinformatics (WABI-2008)*. Universitt Karlsruhe, Germany: September 15-17, 2008
50. Erik Corona, Benjamin Raphael, Eleazar Eskin. "Identification of Deletion Polymorphisms from Haplotypes." *In Proceedings of the Eleventh Annual Conference on Research in Computational Biology (RECOMB-2007)*. Oakland, CA: April 21st-25th, 2007.
51. Sean O'Rourke, Noah Zaitlen, Nebojsa Jojic, Eleazar Eskin. "Reconstructing the Phylogeny of Mobile Elements." *In Proceedings of the Eleventh Annual Conference on Research in Computational Biology (RECOMB-2007)*. Oakland, CA: April 21st-25th, 2007.
52. Eleazar Eskin, Sagi Snir. "The Homology Kernel: A Biologically Motivated Sequence Embedding into Euclidean Space." *In Proceedings of the 2005 IEEE Symposium on Computational Intelligence in Bioinformatics and Computational Biology (CIBCB-2005)*. 179-186. La Jolla, CA: November 14th-15th, 2005.
53. Sean O'Rourke, Gal Chechik, Robin Friedman, Eleazar Eskin. "Discrete profile alignment via constrained information bottleneck." *In Proceedings of Advances in Neural Information Processing Systems 17 (NIPS-2004)*. Vancouver, Canada: December 13-18, 2004.
54. Eleazar Eskin. "From Profiles to Patterns and Back Again: A Branch and Bound Algorithm for Finding Near Optimal Motif Profiles." *In Proceedings of the Eight Annual International Conference on Research in Computational Molecular Biology (RECOMB-2004)*. 115-124. San Diego, CA: March 27-31, 2004.
55. Eleazar Eskin and Eugene Agichtein. "Combining Text Mining and Sequence Analysis to Discover Protein Functional Regions." *In Proceedings of the Pacific Symposium on Biocomputing (PSB-2004)*. 566-575. Kaua'i, Hawaii: January 6-10, 2004.
56. Alex Smola, S. V. Vishwanathan, and Eleazar Eskin. "Laplace Propagation." *In Proceedings of Advances in Neural Information Processing Systems 16 (NIPS-2003)*. Vancouver, Canada: December 8-13, 2003.
57. Eleazar Eskin, Eran Halperin, and Richard M. Karp. "Large Scale Reconstruction of Haplotypes from Genotype Data" *In Proceedings of the Seventh Annual International Conference on Research in Computational Molecular Biology (RECOMB-2003)*. 104-113. Berlin, Germany: April 10-13, 2003.
58. Eleazar Eskin, Uri Keich, Mikhail Gelfand and Pavel Pevzner. "Genome-Wide Analysis of Bacterial Promoter Regions." *In Proceedings of the Pacific Symposium on Biocomputing (PSB-2003)*. 29-40. Kaua'i, Hawaii: January 3-7, 2003.

59. Christina Leslie, Eleazar Eskin, Jason Weston and William Stafford Noble. "Mismatch String Kernels for SVM Protein Classification." *In Proceedings of Advances in Neural Information Processing Systems 15 (NIPS-2002)*. 1417-1424. Vancouver, Canada: December 9-14, 2002.
60. Frank Apap, Andrew Honig, Shlomo Hershkop, Eleazar Eskin and Salvatore Stolfo. "Detecting Malicious Software by Monitoring Anomalous Windows Registry Accesses." *In Proceedings of the Fifth International Symposium on Recent Advances in Intrusion Detection (RAID-2002)*. 36-53. Zurich, Switzerland: October 16-18, 2002.
61. Bernhard Schölkopf, Jason Weston, Eleazar Eskin, Christina Leslie and William Stafford Noble. "A Kernel Approach for Learning from Almost Orthogonal Patterns." *In Proceedings of the 13th European Conference on Machine Learning (ECML'2002)* 511-528 and *Proceedings of the 6th European Conference on Principles and Practice of Knowledge Discovery in Databases (PKDD'2002)* 494-511. Helsinki, Finland: August 19th-23rd, 2002.
62. Christina Leslie, Eleazar Eskin and William Stafford Noble. "The Spectrum Kernel: A String Kernel for SVM Protein Classification." *In Proceedings of the Pacific Symposium on Biocomputing (PSB-2002)*. 566-575. Kaua'i, Hawaii: January 2-7, 2002.
63. Eleazar Eskin, Wenke Lee and Salvatore J. Stolfo. "Modeling System Calls for Intrusion Detection with Dynamic Window Sizes." *In Proceedings of DARPA Information Survivability Conference and Exposition II (DISCEX II)*. 165-174. Anaheim, CA: June 12-14, 2001.
64. Wenke Lee, Salvatore J. Stolfo, Philip K. Chan, Eleazar Eskin, Wei Fan, and Matthew Miller, Shlomo Hershkop and Junxin Zhang. "Real Time Data Mining-based Intrusion Detection." *In Proceedings of DARPA Information Survivability Conference and Exposition II (DISCEX II)*. 89-101. Anaheim, CA: June 12-14, 2001.
65. Matthew G. Schultz, Eleazar Eskin, Erez Zadok, Manasi Bhattacharyya, and Salvatore J. Stolfo. "Malicious Email Filter - A UNIX Mail Filter that Detects Malicious Windows Executables." *In Proceedings of USENIX Annual Technical Conference - FREENIX Track*. 245-252. Boston, MA: June 2001. (**Best Student Paper Award**)
66. Matthew G. Schultz, Eleazar Eskin, Erez Zadok, and Salvatore J. Stolfo. "Data Mining Methods for Detection of New Malicious Executables." *In Proceedings of 2001 IEEE Symposium on Security and Privacy (IEEE S&P-2001)*. 38-49. Oakland, CA: May 2001.
67. Eleazar Eskin, William Noble Grundy, and Yoram Singer. "Protein Family Classification using Sparse Markov Transducers." *In Proceedings of the Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB-2000)*, San Diego, CA: August 20-23, 2000.
68. Eleazar Eskin. "Anomaly Detection over Noisy Data using Learned Probability Distributions." *In Proceedings of the 2000 International Conference on Machine Learning (ICML-2000)*. 255-262. Palo Alto, CA: July, 2000.
69. Eleazar Eskin. "Detecting Errors within a Corpus using Anomaly Detection." *In Proceedings of 2000 North American Chapter of the Association of Computational Linguistics (NAACL-2000)*. 148-153. Seattle, WA: April 29-May 4, 2000.

70. Vasileios Hatzivassiloglou, Judith Klavans, and Eleazar Eskin. "Detecting Text Similarity over Short Passages: Exploring Linguistic Feature Combinations via Machine Learning." *In Proceedings of the Joint SIGDAT Conference on Empirical Methods in Natural Language Processing and Very Large Corpora (EMNLP/VLC-1999)*. 203-212. College Park, MD: June 21-22, 1999.
71. Kathy McKeown, Judith Klavans, Vasileios Hatzivassiloglou, Regina Barzilay, and Eleazar Eskin. "Towards Multidocument Summarization by Reformulation: Progress and Prospects." *In Proceedings of the Sixteenth National Conference on Artificial Intelligence (AAAI-1999)*. 453-460. Orlando, FL: July 18-22, 1999.
72. Eleazar Eskin and Eric Siegel. "Genetic Programming Applied to Othello: Introducing Students to Machine Learning Research." *In Proceedings of the 30th Technical Symposium of the ACM Special Interest Group in Computer Science Education (SIGCSE-1999)*. 242-246. New Orleans, LA: March 24-28, 1999.

Refereed Workshop Papers

73. Buhm Han, Chun Ye, Ted Choi and Eleazar Eskin. "Leveraging joint test status distribution for an optimal significance testing." *In Proceedings of the NIPS 2009 Workshop on Machine Learning in Computational Biology*. Whistler, CA: December 11th, 2009.
74. Eun Yong Kang, Ilya Shpitser, Hyun Min Kang, Chun Ye and Eleazar Eskin. "Detecting the Presence and Absence of Causal Relationships Between Expression of Yeast Genes with Very Few Samples." *In Proceedings of the NIPS 2009 Workshop on Machine Learning in Computational Biology*. Whistler, CA: December 12th, 2008.
75. Sean O'Rourke, Eleazar Eskin. "A finite state transducer approach to haplotype phasing" *In Proceedings of the NIPS 2007 Workshop on Machine Learning in Computational Biology*. Whistler, CA: December 7th-8th, 2007.
76. Chun Ye, Matthew A. Zapala, Hyun Min Kang, Jennifer Wessel, Eleazar Eskin, Nicholas Schork. "High-Density QTL Mapping to Identify Phenotypes and Loci Influencing Gene Expression Patterns in Entire Biochemical Pathways" *In Proceedings of the Second RECOMB Satellite Workshop of Systems Biology*. San Diego, CA: December 1st-2nd, 2006.
77. Sean O'Rourke, Noah Zaitlen, Nebojsa Jojic, Eleazar Eskin. "Reconstructing the Phylogeny of Mobile Elements" *In Proceedings of the NIPS 2006 Workshop on New Problems and Methods in Computational Biology*. Whistler, CA: December 8th-9th, 2006.
78. Sean O'Rourke, Gal Chechik, Eleazar Eskin. "Separation of overlapping subpopulations by mutual information" *In Proceedings of the NIPS 2005 Workshop on Computational Biology and the Analysis of Heterogeneous Data*. Whistler, CA: December 9th-10th, 2005.
79. Chaya Ben-Zaken Zilberstein, Eleazar Eskin, Zohar Yakhini. "Using Expression Data to Discover RNA and DNA Regulatory Sequence Motifs." *In Proceedings of the First RECOMB Satellite Workshop on Regulatory Genomics 2004*. 65-78. San Diego, CA: March 26th-27th, 2004.

80. Eleazar Eskin, Eran Halperin, Roded Sharan. "Optimally Phasing Long Genomic Regions using Local Haplotype Predictions." *In Proceedings of the Second RE-COMB Satellite Workshop on Computational Methods for SNPs and Haplotypes*. Pittsburg, PA: February 20th-21st, 2004.
81. Manasi Bhattacharyya, Matthew G. Schultz, Eleazar Eskin, Shlomo Hershkop, and Salvatore J. Stolfo. "MET: An Experimental System for Malicious Email Tracking." *In Proceedings of the 2002 New Security Paradigms Workshop (NSPW-2002)*. 3-10. Virginia Beach, VA: September 23rd-26th, 2002.
82. Leonid Portnoy, Eleazar Eskin and Salvatore J. Stolfo. "Intrusion Detection with Unlabeled Data using Clustering." *In Proceedings of ACM CCS Workshop on Data Mining Applied to Security (DMSA-2001)*. Philadelphia, PA: November 8, 2001.
83. Eleazar Eskin, Matthew Miller, Zhi-Da Zhong, George Yi, Wei-Ang Lee, and Salvatore J. Stolfo. "Adaptive Model Generation for Intrusion Detection." *In Proceedings of the 2000 ACM CCS Workshop on Intrusion Detection and Prevention (WIDS-2000)*. Athens, Greece: November 1, 2000.
84. Eugene Agichtein, Eleazar Eskin and Luis Gravano. "Combining Strategies for Extracting Relations from Text Collections." *In Proceedings of 2000 ACM SIGMOD Workshop on Research Issues in Data Mining and Knowledge Discovery (DMKD-2000)*. 86-95. Dallas, TX: May 14, 2000.
85. Eleazar Eskin and Matthew Bogosian. "Classifying Text Documents using Modular Categories and Linguistically Motivated Indicators". *In Proceedings of the AAAI-1998 Workshop on Machine Learning for Text Classification (MLTC-98)*. Madison, WI: July 26-30, 1998.

Invited Papers

86. Buhm Han, Eleazar Eskin. "Multiple Testing in Genetic Epidemiology." *Encyclopedia of Life Sciences*. (In Press), 2010.
87. Sarah J. Aerni, Eleazar Eskin. "10 Years of the International Conference on Research in Computational Molecular Biology (RECOMB)." *In Proceedings of the Tenth Annual Conference on Research in Computational Biology (RECOMB 2006)*. 546-562. Venice, Italy: April 2nd-5th, 2006.
88. Christina Leslie, Rui Kuang and Eleazar Eskin. "Inexact Matching String Kernels for Protein Classification." *Kernel Methods in Computational Biology*. Bernhard Schoelkopf, Koji Tsuda and Jean-Phillip Vert, ed. MIT Press. 95-112. 2004.
89. Bernhard Schölkopf, Jason Weston, Eleazar Eskin, Christina Leslie and William Stafford Noble. "A Kernel Approach for Learning from Almost Orthogonal Patterns." *Principles of Data Mining and Knowledge Discovery*, Springer LNCS 243, 2002.
90. Eleazar Eskin, Andrew Arnold, Michael Prerau, Leonid Portnoy and Salvatore Stolfo. "A Geometric Framework for Unsupervised Anomaly Detection: Detecting Intrusions in Unlabeled Data." *Data Mining for Security Applications*. Kluwer, 2002.
91. Andrew Honig, Andrew Howard, Eleazar Eskin, and Salvatore Stolfo. "Adaptive Model Generation: An Architecture for the Deployment of Data Mining-based Intrusion Detection Systems." *Data Mining for Security Applications*. Kluwer, 2002.

92. Salvatore J. Stolfo, Wenke Lee, Philip K. Chan, Wei Fan, and Eleazar Eskin. "Data Mining-based Intrusion Detection: An Overview of the Columbia IDS Project". **ACM SIGMOD RECORD** 30(4):5-14, December 2001.

DISSERTATION

Title: Sparse Sequence Modeling with Applications to Computational Biology and Intrusion Detection

Summary: Sequence models have been studied for some time in different contexts including language parsing and analysis, genomics, and recently in computer security in the area of intrusion detection. Many of these sequences can be characterized as "sparse", that is only a fraction of the elements of the sequence have meaningful value. The thesis presents a new efficient framework for approaching sparse sequence modeling problems. The thesis presents techniques using this framework to address three computational problems: classification or transduction, outlier detection, and signal finding. These techniques are applied to protein family classification, regulatory pattern discovery in DNA sequences, and detection of intrusions in audit streams.

Advisor: Salvatore J. Stolfo.

HONORS AND AWARDS

Alfred P. Sloan Foundation Research Fellowship February 2009.

Okawa Foundation Research Grant August 2008.

William J. von Liebig Center for Entrepreneurism and Technology Advancement Award: University of California, San Diego (UCSD). January 2005.

Paul Charles Michaelman Memorial Departmental Service Award: Columbia University Computer Science Department. May 2002.

Best Student Paper Award: USENIX Technical Symposium. FREENIX Track. June 2001.

All-Conference 2nd Team: New York Division. Collegiate Water Polo Association. Fall 2001.

DEPARTMENTAL/UNIVERSITY SERVICE

University Committees: UCLA Bioinformatics Inter-Departmental Ph.D. Program Steering Committee. 2007-present.

UCLA Burroughs Wellcome Fund Inter-school Training Program in Metabolic Diseases. Program Steering Committee. 2009-present.

UCLA Center for High Throughput Biology. Steering Committee. 2010-present.

Undergraduate/Masters Bioinformatics Research Program Coordinator: Founded and served in position to encourage undergraduate and masters students to participate in bioinformatics research groups. 2004-2006.

<http://www.cs.ucsd.edu/~eeskin/projects/>

Departmental Committees: Computer Science Department Publicity Committee 2007-2009.

Computer Science Undergraduate Committee 2004-2006.

Bioinformatics Undergraduate Committee 2004-2006.

Research Project Liaison: Instituted and served in position to encourage undergraduate and masters students to participate in departmental research groups. 1998-2002.

Graduate School Advisory Committee: Served as departmental representative to student

government for Ph.D. students within the Graduate School of Arts and Sciences (GSAS). 1998-2002.

CURRENT STUDENTS SUPERVISED

Ph.D. Students Supervised:

Daniel He UCLA Computer Science Ph.D. Program. 2008-.

Nicholas Furlotte UCLA Computer Science Ph.D. Program. 2008-.

Olivera Grujic UCLA Computer Science Ph.D. Program. 2007-.

Buhm Han UCSD Computer Science and Engineering Ph.D. Program. 2005-.

Christophen Jones UCLA Computer Science Ph.D. Program. 2007-.

Eun Yong Kang UCLA Computer Science Ph.D. Program. 2008-.

Hyun Min Kang UCSD Computer Science and Engineering Ph.D. Program. 2004-.

Emrah Kostem UCLA Computer Science Ph.D. Program. 2007-.

Sean O'Rourke UCSD Computer Science and Engineering Ph.D. Program. 2004-.

Jae-Hoon Sul UCLA Computer Science Ph.D. Program. 2008-.

Chun (Jimmie) Ye UCSD Bioinformatics Ph.D. Program. 2004-.

Noah Zaitlen UCSD Bioinformatics Ph.D. Program. 2004-.

PREVIOUS STUDENTS SUPERVISED

UCSD Undergraduate Student Theses:

Erik Corona. UCSD B.S. CSE Bioinformatics '07. Undergraduate Thesis, "Identification of Deletion Polymorphisms using Haplotypes." Thesis work published at RECOMB-2007. Current Ph.D. student at Stanford.

Robin Friedman. UCSD B.S. CSE Bioinformatics '05. Undergraduate Thesis, "Discrete profile alignment via constrained information bottleneck." Thesis work published at NIPS-2004. Winner of Honorable Mention from Computer Research Association national Undergraduate Research Award. Current Ph.D. student at MIT.

UCSD Undergraduate/Masters Bioinformatics Research Program: 2004-2006. Supervised many students in context of undergraduate bioinformatics research program.

Columbia University Students Supervised:

Intrusion Detection Systems Project: Spring 2000-Spring 2002. Organized large project on Intrusion Detection Systems. Typically around 30 students are registered for course credit to perform research on the project. Students range from sophomores in college to masters students and have various levels experience and ability. Designed and instituted a management structure where students are broken up into sub-project teams. Students benefitted with research experience and course credit. Many students successfully completed an undergraduate or masters thesis.

Columbia University Undergraduate and Masters Theses Supervised:

Andrew Arnold. Columbia University B.A. '03. Undergraduate Thesis. "Using One-Class SVM for Computer Forensics". Thesis work published in DMSA-2002. Current Ph.D. student at CMU.

Frank Apap. Columbia University B.A. '02. Undergraduate Thesis. "Registry Anomaly Detection". Thesis work published in RAID-2002. Winner of Honorable Mention from Computer Research Association national Undergraduate Research Award.

Andrew Honig. Columbia University B.A. '02. Undergraduate Thesis. "Adaptive Model Generation". Thesis work published in DMSA-2002. Winner of Honorable Mention from Computer Research Association national Undergraduate Research Award. Winner of De-

partmental Undergraduate Research Award.

Andrew Howard. Columbia University B.A. '02. Undergraduate Thesis. "Adaptive Model Generation". Thesis work published in DMSA-2002. Current Ph.D. student at Columbia University.

Michael Prerau. Columbia University B.A. '02. Undergraduate Thesis. "Unsupervised Anomaly Detection using K-Nearest Neighbor". Thesis work published in DMSA-2002. Current Ph.D. student at Boston College.

Manasi Bhattacharyya. Columbia University B.A. '01, M.S. '02. Masters Thesis. "Malicious Email Tracking". Thesis work published in NSPW-2002. Winner of Best Student Paper Award at USENIX-FREENIX 2001.

Matthew Schultz. Columbia University B.A. '01. Undergraduate Thesis. "Data Mining Methods for Detection of New Malicious Executables". Thesis work published in IEEE S&P-2001. Winner of Best Student Paper Award at USENIX-FREENIX 2001. Winner of Departmental Undergraduate Research Award.

Leonid Portnoy. Columbia University B.A. '00. Undergraduate Thesis. "Intrusion detection with unlabeled data using clustering". Thesis work published in DMSA-2001.

INVITED TALKS AND CONFERENCE PRESENTATIONS

"Leveraging joint test status distribution for an optimal significance testing". *The Fifth Annual Information Theory and Applications Workshop (ITA-2010)*. February 5th, 2010.

"Leveraging joint test status distribution for an optimal significance testing". *P. Universidad Catlica de Chile, Santiago, Chile*. December 16th, 2009.

"Leveraging joint test status distribution for an optimal significance testing". *NIPS 2009 Machine Learning in Computational Biology Workshop (MLCB-2009)*. December 11th, 2009.

"Leveraging Linkage Disequilibrium Structure in Association Studies". *10th International Symposium on Genetic Epidemiology, Seoul, Korea*. November 11th, 2009.

"Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains". *Tsinghua University, Beijing, China*. November 6th, 2009.

"Multiple testing in genome-wide association studies". *The Fourth Annual Information Theory and Applications Workshop (ITA-2009)*. February 13th, 2009.

"Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains". *Bioinformatics Program, University of California, Los Angeles*. February 2nd, 2009.

"Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains". *Bioinformatics Program, University of California, San Diego*. January 22nd, 2009.

"Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains". *University of California, Riverside*. January 12th, 2009.

"Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains". *Biostatistics and Medical Informatics, University of Wisconsin, Madison*. November 7th, 2008.

"Increasing Power in Association Studies by using Linkage Disequilibrium Structure and Molecular Function as Prior Information". *University of the Basque Country, San Sebastian*. September 24th, 2008.

"Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains". *CardioMet Symposium, Lausanne, Switzerland*. September 19th, 2008.

"Increasing Power in Association Studies by using Linkage Disequilibrium Structure and

Molecular Function as Prior Information”. *DIMACS Workshop on Computational Issues in Genetic Epidemiology, Rutgers University*. August 22nd, 2008.

“Computational Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Southern California Bioinformatics Institute, California State University, Los Angeles*. August 1st, 2008.

“Computational Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Bioinformatics Program Retreat, University of California, Los Angeles*. May 23rd, 2008.

“Computational Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Computer Science Department Seminar, University of California, Los Angeles*. May 22nd, 2008.

“Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Computational Life Sciences Seminar, Emory University*. April 11th, 2008.

“Increasing Power in Association Studies by using Linkage Disequilibrium Structure and Molecular Function as Prior Information”. *The Twelfth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2008)*. April 2nd, 2008.

“A Sequence-Based Variation Map of 8.27 Million SNPs in Inbred Mouse Strains”. *Keystone Symposium on Complex Traits: Biologic and Therapeutic Insights*. March 1st, 2008.

“Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Computational Biology Seminar, University of California, Los Angeles*. February 20th, 2008.

“Computational and Statistical Challenges in Design and Analysis of Association Studies”. *The Fourth Annual Information Theory and Applications Workshop (ITA-2009)*. February 1st, 2008.

“Computational and Statistical Challenges in Design and Analysis of Association Studies”. *Cedar-Sinai Medical Genetics Institute*. November 29th, 2007.

“Computational and Statistical Challenges in Design and Analysis of Association Studies”. *VanBUG Seminar, Vancouver, BC*. November 8th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *Google Research*. September 6th, 2007.

“Leveraging the HapMap to Increase the Power of Association Studies”. *Carnegie Mellon University*. July 12th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *GRIB, University Pompeu Fabra*. July 5th, 2007.

“Leveraging the HapMap to Increase the Power of Association Studies”. *University of the Basque Country, San Sebastian*. June 28th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *Graybill Bioinformatics Workshop*. June 11th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *The Second Annual Information Theory and Applications Workshop (ITA-2007)*. January 30th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *Weizmann Institute*. January 30th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *Tel Aviv University*. January 29th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *Hebrew University*. January 28th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *The Second Annual Imaging Genetics Congress*. January 15th, 2007.

“Whole Genome Associations in Inbred Mouse Strains”. *NIEHS Center for Rodent Genetics Annual Conference*. September 27th, 2006.

“Whole Genome Associations in Inbred Mouse Strains”. *University of Washington*. July 26th, 2006.

“Whole Genome Associations in Inbred Mouse Strains”. *Fourth Bertinoro Computational Biology Meeting*. June 29th, 2006.

“Whole Genome Associations in Inbred Mouse Strains”. *3rd International HapMap Project Community Analysis Meeting*. May 10th, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *Carnegie Mellon University*. May 4th, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *University of California, Los Angeles*. April 25th, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *Cornell University*. April 18th, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *University of California, San Diego*. April 5th, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *Translational Genomics Research Institute (TGen)*. March 29th, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *Brown University*. March 22nd, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *University of California, Irvine*. March 1st, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *Memorial Sloan-Kettering Cancer Center*. February 22nd, 2006.

“Genomic Approaches to Understanding the Genetic Basis of Human Disease”. *Columbia University*. February 20th, 2006.

“Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *University of Southern California*. January 26th, 2006.

“Integrated Genomics Approaches to Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *University of California, San Diego*. January 18th, 2006.

“Integrated Genomics Approach to Modeling Complex Traits in Inbred Mouse Strains”. *University of Michigan*. November 11th, 2005.

“Human Disease and Human Variation”. *Columbia University*. May 24th, 2005.

“Incorporating Function of Variation into Whole Genome Association Studies”. *Broad Institute*. May 20th, 2005.

“Incorporating Function of Variation into Whole Genome Association Studies”. *Whole Genome Association Symposium*. April 15th, 2005.

“The Structure of Human Variation”. *UCSD Jabobs School of Engineering Research-EXPO*. February 25th, 2005.

“Identifying Associated Haplotype Regions by Phylogenetic Analysis”. *HapMap Consortium Meeting 2004*. April 20th, 2004.

“From Profiles to Patterns and Back Again: A Branch and Bound Algorithm for Finding Near Optimal Motif Profiles”. *The Eight Annual International Conference on Research in Computational Molecular Biology (RECOMB-2004)*. March 29th, 2004.

“Optimally Phasing Long Genomic Regions using Local Haplotype Predictions”. *Perlegen Sciences*. March 21st, 2004.

“Optimally Phasing Long Genomic Regions using Local Haplotype Predictions”. *Second RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes*. February 21st, 2004.

“The Homology Kernel: A Biologically Motivated Sequence Embedding”. *Columbia University*. January 27th, 2004.

“Combining Text Mining and Sequence Analysis To Discover Protein Functional Regions”. *The 2004 Pacific Symposium on Biocomputing (PSB-2004)*. January 8th, 2004.

“The Homology Kernel: A Biologically Motivated Sequence Embedding”. *University of California, San Diego*. October 20th, 2003.

“Genome Wide Analysis of Transcription Factor Binding Sites”. *Moscow Conference on Computational Molecular Biology*. July 22nd, 2003.

“The Homology Kernel: A Biologically Motivated Sequence Embedding”. *The Hebrew University*. June 26th, 2003.

“Genome Wide Analysis of Transcription Factor Binding Sites”. *Compugen, Israel*. June 25th, 2003.

“A Unified Framework for Motif Finding: Finding Position Specific Scoring Matrices using Patterns with Mismatches”. *Bertinoro Computational Biology Workshop*. June 8th, 2003.

“Large Scale Reconstruction of Haplotypes from Genotype Data”. *The Seventh Annual International Conference on Research in Computational Molecular Biology (RECOMB-2003)*. April 13th, 2003.

“A Unified Framework for Motif Finding: Finding Position Specific Scoring Matrices using Patterns with Mismatches”. *University of Queensland*. March 14th, 2003.

“Large Scale Recovery of Haplotypes from Genotype Data using Imperfect Phylogeny”. *University of Newcastle*. March 11th, 2003.

“Large Scale Recovery of Haplotypes from Genotype Data using Imperfect Phylogeny”. *Australian National University*. March 5th, 2003.

“A Unified Framework for Motif Finding: Finding Position Specific Scoring Matrices using Patterns with Mismatches”. *Australian National University*. February 26th, 2003.

“Biological Sequence Analysis using String Kernels”. *Machine Learning Summer School, Australian National University*. February 12-13th, 2003.

“A Unified Framework for Motif Finding: Finding Position Specific Scoring Matrices using Patterns with Mismatches”. *University of California, Berkeley*. January 24th, 2003.

“A Unified Approach to Modeling Sequences using String Kernels”. *Stanford University*. January 23rd, 2003.

“A Unified Framework for Motif Finding: Finding Position Specific Scoring Matrices using Patterns with Mismatches”. *University of California, San Diego*. January 13th, 2003.

“Genome Wide Analysis of Bacterial Promoter Regions”. *The 2003 Pacific Symposium on Biocomputing (PSB-2003)*. January 4th, 2003.

“Genome Wide Analysis of Bacterial Regulatory Patterns”. *The Hebrew University*. December 22nd, 2002.

“A Unified Approach to Modeling Sequences using String Kernels”. *Ben Gurion University*. December 18th, 2002.

“String Kernels applied to Biological Sequence Analysis”. *The Hebrew University*. December 8th, 2002.

“Genome Wide Analysis of Bacterial Regulatory Patterns”. *Tel Aviv University*. December 4th, 2002.

“Large Scale Recovery of Haplotypes from Genotype Data using Imperfect Phylogeny”. *The Hebrew University*. November 24th, 2002.

“Large Scale Recovery of Haplotypes from Genotype Data using Imperfect Phylogeny”. *Technion*. November 21st, 2002.

“Genome Wide Analysis of Bacterial Regulatory Patterns”. *Columbia University*. September 24th, 2002.

“Genome Wide Analysis of Bacterial Regulatory Patterns”. *University of California, San*

Diego. August 31st, 2002.

“Finding Composite Regulatory Patterns in DNA Sequences”. *Tenth International Conference on Intelligent Systems in Molecular Biology (ISMB-2002)*. August 7th, 2002.

“Finding Composite Regulatory Patterns in DNA Sequences”. *New York University*. June 5th, 2002.

“Finding Composite Regulatory Patterns in DNA Sequences”. *University of California, Berkeley*. May 14th, 2002.

“Finding Composite Regulatory Patterns in DNA Sequences”. *Stanford University*. May 13th, 2002.

“Finding Composite Regulatory Patterns in DNA Sequences”. *Cornell University*. May 8th, 2002.

“Finding Composite Regulatory Patterns in DNA Sequences”. *University of Pennsylvania*. May 3rd, 2002.

“Sparse Sequence Modeling with Applications to Computational Biology and Intrusion Detection”. *University of California, San Diego*. April 17th, 2002.

“Unsupervised Anomaly Detection: Intrusion Detection over Unlabeled Data.”. *University of California, San Diego*. April 17th, 2002.

“Sparse Sequence Modeling with Applications to Computational Biology and Intrusion Detection”. *University of Chicago*. April 15th, 2002.

“Unsupervised Anomaly Detection: Intrusion Detection over Unlabeled Data.”. *DARPA*. April 10th, 2002.

“Sparse Sequence Modeling with Applications to Computational Biology and Intrusion Detection”. *Dartmouth College*. March 1st, 2002.

“Genome-Wide Analysis for Finding Composite Signals in DNA Sequences”. *University of Southern California*. January 10th, 2002.

“Modeling Sparse Sequences.” *Columbia University*. December 10th, 2001.

“Finding Composite Signals in DNA Sequences.” *The Hebrew University*. November 28th, 2001.

“Unsupervised Anomaly Detection with Clustering.” *ACM CCS Workshop on Data Mining Applied to Security (DMSA-2001)*. November 8th, 2001.

“Finding Composite Signals in DNA Sequences.” *University of California, San Diego*. August 29th, 2001.

“Using Mixtures of Common Ancestors for Estimating the Probabilities of Discrete Events in Biological Sequences.” *Ninth International Conference on Intelligent Systems for Molecular Biology (ISMB-2001)*. July 25th, 2001.

“Sparse Markov Transducers for Protein Family Classification.” *The Hebrew University*. July 7th, 2001.

“Detecting Malicious Software with Data Mining Methods.” *2001 IEEE Symposium on Security and Privacy (IEEE S&P-2001)* May 14th, 2001.

“Modeling System Calls with Dynamic Window Sizes.” *National Research Lab*. March 25th, 2001.

“Data Mining-based Intrusion Detection.” *Arcsight*. December 22nd, 2001.

“Adaptive Model Generation for Intrusion Detection Systems.” *2000 ACM CCS Workshop on Intrusion Detection and Prevention (WIDS-2000)*. November 1st, 2001.

“Sparse Markov Transducers.” *University of California, San Diego*. August 19th, 2000.

“Protein Family Classification using Sparse Markov Transducers.” *Eighth International Conference on Intelligent Systems for Molecular Biology (ISMB-2000)*. August 22nd, 2000.

“Anomaly Detection over Noisy Data.” *International Conference on Machine Learning*

(*ICML-2000*). June 29th, 2000.

“Detecting Errors in the Penn Treebank.” *2000 North American Chapter of the Association of Computational Linguistics (NAACL-2000)*. May 2nd, 2000.

“Teaching Students Machine Learning with Genetic Programming Applied to Othello.” *30th Technical Symposium of the ACM Special Interest Group in Computer Science Education (SIGCSE-1999)*. March 26th, 1999.

“Text Classification using Linguistically Motivated Indicators.” *AAAI-1998 Workshop on Machine Learning for Text Classification (MLTC-98)* July 27th, 1998.