

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

Professor: Department of Computer Science. Department of Human Genetics. *University of California, Los Angeles*. July 2014 - present.
Associate Professor: Department of Computer Science. Department of Human Genetics. *University of California, Los Angeles*. July 2009 - June 2014.
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.

TEACHING EXPERIENCE

Instructor: Computational Genetics.
University of California, Los Angeles, Spring 2007, Spring 2008, Spring 2009, Spring 2010, Spring 2011, Spring 2012, Winter 2013, Spring 2014, Spring 2015, Spring 2016.
Instructor: Algorithms in Systems Biology and Bioinformatics.
University of California, Los Angeles, Fall 2014, Winter 2016.
Instructor: Introduction to Bioinformatics.
University of California, Los Angeles, Fall 2010.
Instructor: Current Topics in Bioinformatics.
University of California, Los Angeles, Winter 2008, Fall 2008, Winter 2010, Fall 2011, Fall 2012.
Instructor: Research Training in Bioinformatics (undergraduate).
University of California, San Diego, Winter 2005, Spring 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.

JOURNAL EDITORIAL SERVICE

Genetics, Associate Editor, 2015-present.

American Journal of Human Genetics, Associate Editor, 2012-2015.

CONFERENCE PROGRAM COMMITTEE AND REVIEWING

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

Conference Program Committee: *The Thirteenth Workshop on Algorithms in Bioinformatics (WABI-2013)*, 2013.

The Twenty First Annual International Conference on Intelligent Systems in Molecular Biology (ISMB-2013), 2013 (**Area Chair**).

Population Quantitative Genetics Conference, 2012.

Second Annual RECOMB Satellite Meeting on Sequencing (RECOMB-seq), 2012 (**Chair**).

The Sixteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2012), 2012.

The Eleventh Workshop on Algorithms in Bioinformatics (WABI-2011), 2011.

The Nineteenth Annual International Conference on Intelligent Systems in Molecular Biology (ISMB-2011), 2011 (**Area Chair**).

First Annual RECOMB Satellite Workshop on Massively Parallel Sequencing (RECOMB-SEQ-2011), 2011.

The Fifteenth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2011), 2011.

The 2011 Pacific Symposium on Biocomputing (PSB-2011), 2011 (**Session Organizing Committee**).

NIPS 2010 workshop on Machine Learning in Computational Biology (MLCB-2010), 2010.

The Seventh Annual RECOMB Satellite Workshop on Regulatory Genomics, 2010.

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: *The Twentieth Annual International Conference on Research in Computational Molecular Biology (RECOMB-2016)*, 2016 **Conference Chair**.

Mathematical and Computational Approaches in High-Throughput Genomics, Institute of Pure and Applied Mathematics, University of California, Los Angeles, 2011.

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: *Annals of Applied Statistics*, 2012. *Gastroenterology*, 2012. *Communications of the ACM*, 2012. *Statistical Applications in Genetics and Molecular Biology*. 2011. *Genome Biology*. 2011. *Proceedings of the National Academy of Sciences*, 2007. *Nature Genetics*, 2007, 2008, 2010, 2011, 2012, 2013, 2014, 2015. *Nucleic Acids Research*, 2007. *Molecular Systems Biology*, 2007, 2008. *Genome Research*, 2004, 2005, 2007, 2008, 2011, 2012, 2013, 2014, 2015. *PLoS Genetics*, 2008, 2009, 2010, 2012, 2013, 2014, 2015. *Genetics*, 2009, 2010, 2011, 2013, 2014, 2015. *Genetic Epidemiology*, 2010, 2011. *Nature Methods*, 2009, 2011, 2014, 2015. *PLoS Computational Biology*, 2005, 2007, 2008, 2010, 2011, 2012, 2013. *American Journal of Human Genetics*, 2005, 2006, 2007, 2010, 2011, 2012, 2013, 2014, 2015. *Genes, Brain and Behavior*, 2011. *IEEE Transactions on Computational Biology and Bioinformatics*, 2005, 2006, 2007, 2008. *Journal of the American Statistical Association*, 2010. *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, 2010, 2011, 2014, 2015. *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 23 (NIPS-2010)*, 2010.

Advances in Neural Information Processing Systems 22 (NIPS-2009), 2009.

The 2013 Pacific Symposium on Biocomputing (PSB-2013), 2013.

The 2012 Pacific Symposium on Biocomputing (PSB-2012), 2012.

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. Michael Bilow, Fernando Crespo, Zhicheng Pan, Eleazar Eskin, and Susana Eyheramendy. “Simultaneous modeling of disease status and clinical phenotypes to increase power in GWAS.” **Genetics**, (In Press), 2017.
2. Matthew Buckley, Fernando Racimo, Morten E. Allentoft, Majken K. Jensen, Anna Jonsson, Hongyan Huang, Farhad Hormozdiari, Martin Sikora, Davide Marnetto, Eleazar Eskin, Marit E. Jrgensen, Niels Grarup, Oluf Pedersen, Torben Hansen, Peter Kraft, Eske Willerslev, Rasmus Nielsen. “Selection on the FADS region in Europeans.” **Molecular Biology and Evolution**, (In Press), 2017.
3. Serghei Mangul, Harry Yang, Farhad Hormozdiari, Elizabeth Tseng, Alex Zelikovsky, Eleazar Eskin. “HapIso : An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads.” **IEEE Transactions on NanoBioscience**, (In Press), 2017.
4. Jong Wha J Joo, Eun Yong Kang, Elin Org, Nick Furlotte, Brian Parks, Farhad Hormozdiari, Aldons J. Lusic, Eleazar Eskin. “Efficient and Accurate Multiple-Phenotype Regression Method for High Dimensional Data Considering Population Structure.” **Genetics**, (In Press), 2016.
5. Eun Yong Kang, Lisa Martin, Serghei Mangul, Warin Isvilanonda, Jennifer Zou, Eyal Ben-David, Buhm Han, Aldons J. Lusic, Sagiv Shifman, Eleazar Eskin . “Discovering SNPs Regulating Human Gene Expression Using Allele Specific Expression from RNA-Seq Data” **Genetics**, (In Press), 2016.

6. Tobias Marschall, Manja Marz, Thomas Abeel, Louis Dijkstra, Bas E. Dutilh, Ali Ghaffaari, Paul Kersey, Wigard P. Kloosterman, Veli Mkinen, Adam M. Novak, Benedict Paten, David Porubsky, Eric Rivals, Can Alkan, Jasmijn A. Baaijens, Paul I. W. De Bakker, Valentina Boeva, Raoul J. P. Bonnal, Francesca Chiaromonte, Rayan Chikhi, Francesca D. Ciccarelli, Robin Cijvat, Erwin Datema, Cornelia M. Van Duijn, Evan E. Eichler, Corinna Ernst, Eleazar Eskin, Erik Garrison, Mohammed El-Kebir, Gunnar W. Klau, Jan O. Korbelt, Eric-Wubbo Lameijer, Benjamin Langmead, Marcel Martin, Paul Medvedev, John C. Mu, Pieter Neerincx, Klaasjan Ouwers, Pierre Peterlongo, Nadia Pisanti, Sven Rahmann, Ben Raphael, Knut Reinert, Dick de Ridder, Jeroen de Ridder, Matthias Schlesner, Ole Schulz-Trieglaff, Ashley D. Sanders, Siavash Sheikhezadeh, Carl Shneider, Sandra Smit, Daniel Valenzuela, Jiayin Wang, Lodewyk Wessels, Ying Zhang, Victor Guryev, Fabio Vandin, Kai Ye, Alexander Schnhuth. "Computational pan-genomics: status, promises and challenges." **Briefings in Bioinformatics**, (In Press), 2016.
7. Farhad Hormozdiari, Martijn van de Bunt, Ayellet V. Segre, Xiao Li, Jong Wha Joo, Michael Bilow, Jae Hoon Sul, Sriram Sankararaman, Bogdan Pasaniuc, and Eleazar Eskin. "Colocalization of GWAS and eQTL Signals Detects Target Genes." **American Journal of Human Genetics** (In Press), 2016.
8. Bradley J Main, Yoosook Lee, Heather M Ferguson, Katharina S Kreppel, Anicet Kihonda, Nicodem J Govella, Travis C Collier, and others. "The Genetic Basis of Host Preference and Resting Behavior in the Major African Malaria Vector, *Anopheles Arabiensis*." **PLoS Genetics**.12(9), p. e1006303, 2016.
9. Joel Lavinsky, Marshall Ge, Amanda L Crow, Calvin Pan, Juemei Wang, Pehzaman Salehi Dermanaki, Anthony Myint, and others. "The Genetic Architecture of Noise-induced Hearing Loss: Evidence for a Gene-by-Environment Interaction." **G3: Genes—Genomes—Genetics**, (In Press), 2016.
10. Gleb Kichaev, Megan Roytman, Ruth Johnson, Eleazar Eskin, Sara Lindstrm, Peter Kraft, and Bogdan Pasaniuc. "Improved Methods for Multi-trait Fine Mapping of Pleiotropic Risk Loci." **Bioinformatics**, (In Press), 2016.
11. Hyejung Won, Luis de la Torre-Ubieta, Jason L. Stein, Jerry Huang, Carli K. Opland, Neelroop N. Parikshak, Michael Gandal, Daning Lu, Gavin J. Sutton, Farhad Hormozdiari, Changhoon Lee, Eleazar Eskin, Irina Voineagu, Jason Ernst, Daniel H. Geschwind. "Genome-wide chromosome conformation elucidates regulatory relationships in human brain evolution and disease." **Nature**, (In Press), 2016.
12. Alexander Artyomenko, Nicholas Wu, Serghei Mangul, Eleazar Eskin, Ren Sun and Alex Zelikovsky. "Long single-molecule reads can resolve the complexity of the Influenza virus composed of rare, closely related mutant variants." **Journal of Computational Biology**, (In Press), 2016.
13. Yehudit Hasin-Brumshtein, Arshad H Khan, Farhad Hormozdiari, Calvin Pan, Brian W Parks, Vladislav A Petyuk, Paul D Piehowski, Anneke Bruemmer, Matteo Pellegrini, Xinshu Xiao, Eleazar Eskin, Richard D Smith, Aldons J Lusk, Desmond J Smith. "Hypothalamic transcriptomes of 99 mouse strains reveal trans eQTL hotspots, splicing QTLs and novel non-coding genes." **eLife**, (In Press), 2016.
14. Regev Schweiger, Shachar Kaufman, Reijo Laaksonen, Marcus E. Kleber, Winfried Marz Eleazar Eskin, Saharon Rosset, Eran Halperin. "Fast and Accurate Construction of Confidence Intervals for Heritability" **American Journal of Human Genetics**. 98(6):1181-92, 2016.

15. Eun Yong Kang, Yurang Park, Xiao Li, Ayellet V. Segre, Buhm Han, Eleazar Eskin. "ForestPMPlot: a flexible tool for visualizing heterogeneity between studies in meta-analysis" **G3: Genes—Genomes—Genetics**. (In Press), 2016.
16. Farhad Hormozdiari, Eun Yong Kang, Michael Bilow, Eyal Ben-David, Chris Vulpe, Stela McLachlan, Aldons J. Lusk, Buhm Han, Eleazar Eskin. "Imputing phenotypes for genome-wide association studies" **American Journal of Human Genetics**. **99(1):89-103**, 2016.
17. Christine B. Peterson, Susan K. Service, Anna J. Jasinska, Fuying Gao, Ivette Zelaya, Terri M. Teshiba, Carrie E. Bearden, Rita M. Cantor, Victor I. Reus, Gabriel Macaya, Carlos Lpez-Jaramillo, Marina Bogomolov, Yoav Benjamini, Eleazar Eskin, Giovanni Coppola, Nelson B. Freimer, Chiara Sabatti. "Characterization of Expression Quantitative Trait Loci in Pedigrees from Colombia and Costa Rica Ascertained for Bipolar Disorder." **PLoS Genetics**, (In Press), 2016.
18. Dat Duong, Jennifer Zou, Farhad Hormozdiari, Jae-hoon Sul, Jason Ernst, Buhm Han, Eleazar Eskin. "Using genomic annotations increases statistical power to detect eGenes." **Bioinformatics**. **32(12):i156-i163**. *Special Issue of the Proceedings of the Nineteenth International Conference on Intelligent Systems in Molecular Biology (ISMB-2016): July 8th-12th, 2016*.
19. Aldons J. Lusk, Marcus Seldin, Hooman Allayee, Brian Bennett, Mete Civelek, Richard Davis, Eleazar Eskin, Charles Farber, Simon Hui, Margarete Mehrabian, Frode Norheim, Calvin Pan, Brian Parks, Christoph Rau, Desmond J. Smith, Thomas Vallim, Yibin Wang, Jessica Wang. "The Hybrid Mouse Diversity Panel: A Resource for Systems Genetics Analyses of Metabolic and Cardiovascular Traits." **Journal of Lipid Research**, (In Press), 2016.
20. Dan He, Zhanyong Wang, Laxmi Parida, Eleazar Eskin. "IPED2: Inheritance Path based Pedigree Reconstruction Algorithm for Complicated Pedigrees" **IEEE/ACM Transactions on Computational Biology and Bioinformatics**, (In Press), 2016.
21. Elior Rahmani, Noah Zaitlen, Yael Baran, Celeste Eng, Donglei Hu, Joshua Galanter, Sam Oh, Esteban G. Burchard, Eleazar Eskin, James Zou, Eran Halperin. "Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies." **Nature Methods**. **13(5):443-445**, 2016.
22. Buhm Han, Dat Duong, Jae Hoon Sul, Eleazar Eskin, Soumya Raychaudhuri. "A general framework for meta-analyzing dependent studies with overlapping subjects in association mapping." **Human Molecular Genetics**, (In Press), 2016.
23. Jae Hoon Sul, Michael Bilow, Wen-Yun Yang, Emrah Kostem, Nick Furlotte, Dan He, Eleazar Eskin. "Accounting for population structure in gene-by-environment interactions in genome-wide association studies using mixed models." **PLoS Genetics**. **12(3):e1005849**, 2016.
24. Dan He, Zhanyong Wang, Laxmi Parida, Eleazar Eskin. "IPED2: Inheritance Path based Pedigree Reconstruction Algorithm for Complicated Pedigrees." **ACM Transactions on Computational Biology and Bioinformatics**, (In Press), 2016.
25. Jong Wha J Joo, Farhad Hormozdiari, Eleazar Eskin, Buhm Han. "Multiple testing correction in linear mixed models" **Genome Biology**. **17(1):62**, 2016.
26. Brian J. Bennett, Richard C. Davis, Mete Civelek, Luz Orozco, Judy Wu, Hannah Qi, Calvin Pan, Ren R. Sevag Packard, Eleazar Eskin, Mujing Yan, Todd Kirchgesner, Zeneng Wang, Xinmin Li, Jill C. Gregory, Stanley L. Hazen, Peter Gargalovic,

- Aldons J. Lusis. "Genetic architecture of atherosclerosis in mice: A systems genetics analysis of common inbred strains." **PLoS Genetics**. **11(12):e1005711**, 2015.
27. Amanda L. Crow, Jeffrey Ohmen, Juemei Wang, Joel Lavinsky, Jaana Hartiala, Qingzhong Li, Xin Li, Pezhman Salehide, Eleazar Eskin, Calvin Pan, Aldons J. Lusis, Hooman Allayee, Rick A. Friedman. "The genetic architecture of hearing impairment in mice: evidence for frequency specific genetic determinants." **G3: GENES, GENOMES, GENETICS**. **5(11):2329-39**, 2015.
 28. Elin Org, Brian W. Parks, Jong Wha J Joo, Benjamin Emert, William Schwartzman, Eun Yong Kang, Margarete Mehrabian, Calvin Pan, Rob Knight, Robert Gunsalus, Thomas A. Drake, Eleazar Eskin, Aldons J. Lusis. "Genetic and environmental control of host-gut microbiota interactions" **Genome Research**. **25(10):1558-69**, 2015.
 29. Christoph D Rau, Brian Parks, Yibin Wang, Eleazar Eskin, Petr Simecek, Gary A Churchill, Aldons J Lusis. "High Density Genotypes of Inbred Mouse Strains: Improved Power and Precision of Association Mapping" **G3: GENES, GENOMES, GENETICS**. **5(10):2021-6**, 2015.
 30. Jae Hoon Sul, Towfique Raj, Simone de Jong, Paul I. W. de Bakker, Soumya Raychaudhuri, Roel A. Ophoff, Barbara E. Stranger, Eleazar Eskin, Buhm Han. "Accurate and fast multiple testing correction in eQTL studies" **American Journal of Human Genetics**. **96(6), 857-68**, 2015.
 31. Xiaoying Zhou, Amanda L. Crow, Jaana Hartiala, Tassja J. Spindler, Anatole Ghzalpour, Lora W. Barsky, Brian B. Bennett, Brian W. Parks, Eleazar Eskin, Rajan Jain, Jonathan A. Epstein, Aldons J. Lusis, Gregor B. Adams, Hooman Allayee. "The Genetic Landscape of Hematopoietic Stem Cell Frequency in Mice." **Stem Cell Reports**. **5(1):125-38**, 2015.
 32. Eleazar Eskin. "Discovering Genes Involved in Disease and the Mystery of Missing Heritability." **Communications of the ACM** (In Press), 2015.
 33. Joel Lavinsky, Amanda L Crow, Calvin Pan, Juemei Wang, Ksenia A Aaron, Maria K Ho, Qingzhong Li, Pezhman Salehide, Anthony Myint, Maya Monges-Hernandez, Eleazar Eskin, Hooman Allayee, Aldons J Lusis, and Rick A Friedman. "Genome-wide Association Study Identifies Nox3 As a Critical Gene for Susceptibility to Noise-induced Hearing Loss." **PLoS Genetics**. **11(4):e1005094**, 2015.
 34. Nicholas A Furlotte, Eleazar Eskin. "Efficient Multiple Trait Association and Estimation of Genetic Correlation Using the Matrix-Variate Linear Mixed-Model." **Genetics**. **200(1):59-68**, 2015.
 35. Farhad Hormozdiari, Gleb Kichaev, Wen-Yun Yang, Bogdan Pasaniuc, Eleazar Eskin. "Identification of causal genes for complex traits." **Bioinformatics**. **31(12):i206-i213** *Special Issue of the Proceedings of the Nineteenth International Conference on Intelligent Systems in Molecular Biology (ISMB-2015)*: July 10th-14th, 2015.
 36. Sarah Hiyari, Elisa Atti, Paulo M. Camargo, Eleazar Eskin, Aldons J. Lusis, Sotirios Tetradis, Flavia Q. Pirih. "Heritability of periodontal bone loss in mice." **Journal of Periodontal Research** (In Press), 2015.
 37. Jurjen Luykx, Steven Bakker, Wouter Visser, Nanda Verhoeven, Jonas Den Heijer, Marco Boks, Jae-Hoon Sul, Eleazar Eskin, Anil Ori, Rita Cantor, Jacob Vorstman, Eric Strengman, Joseph DeYoung, Teus Kappen, Esther Pariama, Eric Van Dongen, Paul Borgdorff, Peter Bruins, Tom De Koning, Rne S Kahn, Roel Ophoff. "Genome-Wide Association Study of NMDA Receptor Coagonists in Human Cerebrospinal Fluid and Plasma" **Molecular Psychiatry** (In Press), 2015.

38. Farhad Hormozdiari, Eleazar Eskin. "Memory Efficient Assembly of Human Genome." **Journal of Bioinformatics and Computational Biology** (In Press), 2015.
39. Wen-Yun Yang, Farhad Hormozdiari, Eleazar Eskin, and Bogdan Pasaniuc. "Spatial localization of recent ancestors for admixed individuals." **G3: GENES, GENOMES, GENETICS**. **4(12):2505-18**, 2014.
40. Gleb Kichaev, Wen-Yun Yang, Sara Lindstrom, Farhad Hormozdiari, Eleazar Eskin, Alkes L. Price, Peter Kraft and Bogdan Pasaniuc. "Integrating Functional Data to Prioritize Causal Variants in Statistical Fine-Mapping Studies." **PLoS Genetics**. **10(10): e1004722.**, 2014.
41. Dan He and Eleazar Eskin. "IPED2X: A Robust Pedigree Reconstruction Algorithm for Complicated Pedigrees." **Journal of Bioinformatics and Computational Biology**. **12(6):1442007**, 2014.
42. Zhanyong Wang, Jae Hoon Sul, Sagi Snir, Jose A. Lozano, and Eleazar Eskin. "Gene-Gene Interactions Detection Using A Two-stage Model." **Journal of Computational Biology**. **22(6), 563-76**, 2015.
43. Wen-Yun Yang, Farhad Hormozdiari, Eleazar Eskin, and Bogdan Pasaniuc. "A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation." **Journal of Computational Biology**. **22(5), 451-62**, 2014.
44. Farhad Hormozdiari, Emrah Kostem, Eun Yong Kang, Bogdan Pasaniuc, Eleazar Eskin. "Identifying causal variants at loci with multiple signals of association." **Genetics**. **198(2), 497-508**, 2014.
45. Farhad Hormozdiari, Jong Wha J Joo, Akshay Wadia, Feng Guan, Rafail Ostrosky, Amit Sahai, and Eleazar Eskin. "Privacy Preserving Protocol for Detecting Genetic Relatives Using Rare Variants." **Bioinformatics** **30(12):i204-i211**, *Special Issue of the Proceedings of the Nineteenth International Conference on Intelligent Systems in Molecular Biology (ISMB-2014)*: July 11th-15th, 2014.
46. Serghei Mangul, Nicholas C Wu, Nicholas Mancuso, Alex Zelikovsky, Ren Sun, and Eleazar Eskin. "Accurate Viral Population Assembly From Ultra-deep Sequencing Data." **Bioinformatics** **30(12):i329-i337**, *Special Issue of the Proceedings of the Nineteenth International Conference on Intelligent Systems in Molecular Biology (ISMB-2014)*: July 11th-15th, 2014.
47. Yehudit Hasin-Brumshtein, Farhad Hormozdiari, Lisa Martin, Atila van Nas, Eleazar Eskin, Aldons J Lusis, and Thomas A Drake. "Allele-specific Expression and eQTL Analysis in Mouse Adipose Tissue." **BMC Genomics** **15(1):471**, 2014.
48. Jong Wha J, Joo, Jae Hoon Sul, Buhm Han, Chun Ye, and Eleazar Eskin. "Effectively identifying regulatory hotspots while capturing expression heterogeneity in gene expression studies." **Genome Biol** **15 (4): R61**, 2014.
49. Dan He, Nicholas A Furlotte, Farhad Hormozdiari, Jong Wha J Joo, Akshay Wadia, Rafail Ostrovsky, Amit Sahai, and Eleazar Eskin. "Identifying Genetic Relatives Without Compromising Privacy." **Genome Research**. **4(4):664-72**, 2014.
50. Jeffrey Ohmen, Eun Yong Kang, Xin Li, Jong Wha Joo, Farhad Hormozdiari, Qing Yin Zheng, Richard C Davis, Aldons J Lusis, Eleazar Eskin, and Rick A Friedman. "Genome-Wide Association Study for Age-Related Hearing Loss (AHL) in the Mouse: A Meta-Analysis." **Journal of the Association of Research in Otolaryngology**. **15(3):335-52**, 2014.

51. Zhang, Kuixing, Matthew J Huentelman, Fangwen Rao, Eric I Sun, Jason J Corneveaux, Andrew J Schork, Zhiyun Wei, Jill Waalen, Jose Pablo Miramontes-Gonzalez, C Makena Hightower, Adam X Maihofer, Manjula Mahata, Tomi Pastinen, Georg B Ehret, Nicholas J Schork, Eleazar Eskin, Caroline M Nievergelt, Milton H Saier, and Daniel T O'Connor. "Genetic Implication of a Novel Thiamine Transporter in Human Hypertension." **Journal of the American College of Cardiology.** **63(15):1542-55**, 2014.
52. Eun Yong Kang, Buhm Han, Nicholas Furlotte, Jong Wha Joo, Diana Shih, Richard C. Davis, Aldons J. Lusk, Eleazar Eskin. "Meta-analysis identifies gene-by-environment interactions as demonstrated in a study of 4,965 mice." **PLoS Genetics.** **10.1 (January, 2014): e1004022** , 2014.
53. Clare D Marsden, Yoosook Lee, Katharina Kreppel, Allison Weakley, Anthony Cornel, Heather M Ferguson, Eleazar Eskin, Gregory C Lanzaro. "Diversity, Differentiation and Linkage Disequilibrium: Prospects for Association Mapping in the Malaria Vector, *Anopheles Arabiensis*." **G3: Genes, Genomes, Genetics.** **4(1):121-31**, 2013.
54. Buhm Han, Eun Yong Kang, Soumya Raychaudhuri, Paul I. W. de Bakker, Eleazar Eskin. "Fast Pairwise IBD Association Testing in Genome-wide Association Studies." **Bioinformatics.** **30(2):206-13**, 2013.
55. Itamar Eskin, Farhad Hormozdiari, Lucia Conde, Jacques Riby, Chris Skibola, Eleazar Eskin, Eran Halperin. "eALPS: Estimating Abundance Levels in Pooled Sequencing Using Available Genotyping Data." **Journal of Computational Biology.** **20(11):861-77**, 2013.
56. Dan He, Zhanyong Wang, Buhm Han, Laxmi Parida, Eleazar Eskin. "IPED: Inheritance Path-based Pedigree Reconstruction Algorithm Using Genotype Data." **Journal of Computational Biology.****20(2):780-91**, 2013.
57. Emrah Kostem, Eleazar Eskin. "Efficiently Identifying Significant Associations in Genome-wide Association Studies." **Journal of Computational Biology.****20(10):817-30**, 2013.
58. Sandrine Lagarrigue, Lisa J Martin, Farhad Hormozdiari, Pierre-Francois Roux, Calvin Pan, Atila van Nas, Olivier Demeure, Rita Cantor, Anatole Ghazalpour, Eleazar Eskin, Aldons J Lusk. "Analysis of Allele Specific Expression in Mouse Liver by RNA-Seq: A Comparison with "cis"-eQTL Identified Using Genetic Linkage." **Genetics.** **195(3):1157-66**, 2013.
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141. 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.
142. Martin Tompa, Nan Li, 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.
143. 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.
144. Eran Halperin and Eleazar Eskin. "Haplotypes Reconstruction from Genotype Data using Imperfect Phylogeny." **Bioinformatics**. **20(12):1842-9**. 2004.
145. 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.
146. 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.

147. Eleazar Eskin, William Stafford Noble, and Yoram Singer. "Protein Family Classification using Sparse Markov Transducers." **Journal of Computational Biology**. **10(2):187-213**. 2003.
148. 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.
149. 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.
150. 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

151. Elior Rahmani, Regev Schweiger, Liat Shenhav, Eleazar Eskin, Eran Halperin . "A Bayesian Framework for Estimating Cell Type Composition from DNA Methylation Without the Need for Methylation Reference." *In Proceedings of the Twenty First Annual Conference on Research in Computational Biology (RECOMB-2017)*. Hong Kong: May 3rd-7th, 2017.
152. Yue Wu, Farhad Hormozdiari, Jong Wha J Joo, Eleazar Eskin. "Improving imputation accuracy by inferring causal variants in genetic studies." *In Proceedings of the Twenty First Annual Conference on Research in Computational Biology (RECOMB-2017)*. Hong Kong: May 3rd-7th, 2017.
153. Serghei Mangul, Harry Yang, Farhad Hormozdiari, Elizabeth Tseng, Alex Zelikovsky, Eleazar Eskin. "HapIso : An Accurate Method for the Haplotype-Specific Isoforms Reconstruction from Long Single-Molecule Reads." *In Proceedings of the International Symposium on Bioinformatics Research and Applications (ISBRA-2016)*. Minsk, Belarus: June 5-8, 2016.
154. Alexander Artyomenko, Nicholas Wu, Serghei Mangul, Eleazar Eskin, Ren Sun and Alex Zelikovsky. "Long single-molecule reads can resolve the complexity of the Influenza virus composed of rare, closely related mutant variants." *In Proceedings of the Twentieth Annual Conference on Research in Computational Biology (RECOMB-2016)*. Santa Monica, CA : April 18th-21st, 2016.
155. Jong Wha J. Joo, Eun Yong Kang, Elin Org, Nick Furlotte, Brian Parks, Aldons J. Lusis, Eleazar Eskin. "Efficient and accurate multiple-phenotype regression method for high dimensional data considering population structure." *In Proceedings of the Nineteenth Annual Conference on Research in Computational Biology (RECOMB-2015)*. Warsaw, Poland : April 12th-15th, 2015.
156. Dan He and Eleazar Eskin. "IPED2X: A Robust Pedigree Reconstruction Algorithm for Complicated Pedigrees." *In Proceedings of the GIW/ISCB- ASIA 2014*, Tokyo, Japan: December 15th-17th, 2014.

157. Dan He, Zhanyong Wang, Laxmi Parida and Eleazar Eskin. "IPED2: Inheritance Path based Pedigree Reconstruction Algorithm for Complicated Pedigrees." *In Proceedings of the 5th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics*, Newport Beach, CA: September 20th-23rd, 2014.
158. Wen-Yun Yang, Farhad Hormozdiari, Eleazar Eskin, Bogdan Pasaniuc. "A Spatial-Aware Haplotype Copying Model with Applications to Genotype Imputation." *In Proceedings of the Eighteenth Annual Conference on Research in Computational Biology (RECOMB-2014)*. Pittsburgh, PA : April 2nd-5th, 2014.
159. Zhanyong Wang, Jae-Hoon Sul, Sagi Snir, Jose A. Lozano, Eleazar Eskin. "Gene-Gene Interactions Detection Using A Two-stage Model." *In Proceedings of the Eighteenth Annual Conference on Research in Computational Biology (RECOMB-2014)*. Pittsburgh, PA : April 2nd-5th, 2014.
160. Dan He, Eleazar Eskin. "IPEDX: An Exact Algorithm for Pedigree Reconstruction using Genotype Data." *Proceedings of the IEEE International Conference on Bioinformatics and Biomedicine (BIBM-2013)*. Shanghai, China: December 18th-21st, 2013.
161. Farhad Hormozdiari, Zhanyong Wang, Wen-Yun Yang, Eleazar Eskin. "Efficient Genotyping of Individuals using Overlapping Pool Sequencing and Imputation." *Proceedings of the Forty Sixth Asilomar Conference on Signals, Systems and Computers*, 1023-7, Asilomar, CA : November 4th-7th, 2012.
162. Emrah Kostem, Eleazar Eskin. "Efficiently Identifying Significant Associations in Genome-wide Association Studies." *In Proceedings of the Seventeenth Annual Conference on Research in Computational Biology (RECOMB-2013)*. Beijing, China : April 7th-10th, 2013.
163. Itamar Eskin, Farhad Hormozdiari, Lucia Conde, Chris Skibola, Jacques Riby, Eleazar Eskin, Eran Halperin "eALPS: Estimating Abundance Levels in Pooled Sequencing Using Available Genotyping Data." *In Proceedings of the Seventeenth Annual Conference on Research in Computational Biology (RECOMB-2013)*. Beijing, China : April 7th-10th, 2013.
164. Dan He, Zhanyong Wang, Laxmi Parida, Eleazar Eskin. "IPED: Inheritance Path based Pedigree Reconstruction Algorithm using Genotype Data." *In Proceedings of the Seventeenth Annual Conference on Research in Computational Biology (RECOMB-2013)*. Beijing, China : April 7th-10th, 2013.
165. Dan He, Buhm Han, Eleazar Eskin. "Optimal Algorithm for Haplotype Phasing with Imputation using Sequencing Data." *In Proceedings of the Sixteenth Annual Conference on Research in Computational Biology (RECOMB-2012)*. Barcelona, Spain : April 21st-24th, 2012.
166. Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin, Eleazar Eskin. "CNVeM: Copy Number Variation detection Using Uncertainty of Read Mapping." *In Proceedings of the Sixteenth Annual Conference on Research in Computational Biology (RECOMB-2012)*. Barcelona, Spain : April 21st-24th, 2012.
167. Jae Hoon Sul, Buhm Han, Eleazar Eskin. "Increasing Power of Groupwise Association Test with Likelihood Ratio Test." *In Proceedings of the Fifteenth Annual Conference on Research in Computational Biology (RECOMB-2011)*. Vancouver, BC : March 28th-31st, 2011.

168. Dan He, Eleazar Eskin. "Effective Algorithms for Fusion Gene Detection." *In Proceedings of the 10th Workshop on Algorithms in Bioinformatics (WABI-2010)*. Liverpool, United Kingdom: September 6-8, 2010.
169. Eun Yong Kang, Ilya Shpitser, Eleazar Eskin. "Respecting Markov Equivalence in Computing Posterior Probabilities of Causal Graphical Features." *In Proceedings of the 24th AAAI Conference on Artificial Intelligence (AAAI-10)*. Atlanta, GA: July 11-15, 2010.
170. 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.
171. 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.
172. 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
173. 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.
174. 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.
175. 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.
176. 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.
177. 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.
178. 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.
179. 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.

180. 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.
181. 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.
182. 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.
183. 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.
184. 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.
185. 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.
186. 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.
187. 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.
188. 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**)
189. 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.
190. 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.

191. 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.
192. 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.
193. 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.
194. 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.
195. 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

196. Michael Bilow, Eleazar Eskin, Susana Eyheramendy. "Simultaneous modeling of disease status and clinical phenotypes to increase power in GWAS." *In Proceedings of the Fourth RECOMB Satellite Workshop on Computational Methods in Genetics (RECOMB-Genetics)* Los Angeles, CA: April 16th-17th, 2016.
197. Yue Wu, Farhad Hormozdiari, Jong Wha J Joo, Eleazar Eskin. "Improving imputation accuracy by inferring causal variants in genetic studies." *In Proceedings of the Fourth RECOMB Satellite Workshop on Computational Methods in Genetics (RECOMB-Genetics)* Los Angeles, CA: April 16th-17th, 2016.
198. Lisa Gai, Serghei Mangul, Eun Yong Kang, Susana Eyheramendy, Eleazar Eskin. "Accounting for linkage disequilibrium when estimating the contribution of a genomic region." *In Proceedings of the Fourth RECOMB Satellite Workshop on Computational Methods in Genetics (RECOMB-Genetics)* Los Angeles, CA: April 16th-17th, 2016.
199. Dan He, Pratima Kunwar, Eleazar Eskin, Helen Horton, Peter Gilbert, Tomer Hertz. "Using HLA binding prediction algorithms for epitope mapping in HIV vaccine clinical trials." *In Proceedings of Second Immunoinformatics and Computational Immunology Workshop (ICIW-2011)*. Chicago, IL: August 1-3, 2011.
200. 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, BC, Canada: December 11th, 2009.
201. 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, BC, Canada: December 12th, 2008.
202. 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, BC, Canada: December 7th-8th, 2007.
 203. 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.
 204. 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, BC, Canada: December 8th-9th, 2006.
 205. 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, BC, Canada: December 9th-10th, 2005.
 206. 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.
 207. Eleazar Eskin, Eran Halperin, Roded Sharan. "Optimally Phasing Long Genomic Regions using Local Haplotype Predictions." *In Proceedings of the Second RECOMB Satellite Workshop on Computational Methods for SNPs and Haplotypes*. Pittsburg, PA: February 20th-21st, 2004.
 208. 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.
 209. 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.
 210. Eleazar Eskin, Matthew Miller, Zhi-Da Zhong, George Yi, Wei-Ang Lee, and Sal 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.
 211. 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.
 212. 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

213. Can Alkan, Emidio Capriotti, Eleazar Eskin, Fereydoun Hormozdiari, Maricel G. Kann. "PERSONAL GENOMICS - Session Introduction." Pacific Symposium in Biocomputing. 2011:229-30.
214. Buhm Han, Eleazar Eskin. "Multiple Testing in Genetic Epidemiology." Encyclopedia of Life Sciences, 2010.
215. 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.
216. 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.
217. 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.
218. 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.
219. 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.
220. 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 Undergraduate Bioinformatics Minor *Founder and Director* 2012-present.

Quantitative and Computational Biology Institute Search Committee, 2014-present

UCLA Biomedical Informatics Task Force *Chair*, 2013-2014.

UCLA Hellman Fellows Program Selection Committee, 2012-2013.

UCLA Physical Sciences, Life Sciences & Engineering Research Informatics Strategic Planning Committee. 2012-2013.

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 Biosciences Initiative Computational Biology Search Committee. 2010-2011.

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 Recruiting Committee *Chair* 2014-2015.

Computer Science Department Bioinformatics Minor Committee *Chair* 2012-present.

Computer Science Department Recruiting Committee 2010-2012.

Computer Science Department Academic Policy Committee 2009-2010, 2012-2014

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:

Jong Wha (Joanne) Joo UCLA Bioinformatics Ph.D. Program. 2011-.

Michael Bilow UCLA Computer Science Ph.D. Program. 2014-.

Lisa Gai UCLA Computer Science Ph.D. Program. 2014-.

Dat Duong UCLA Computer Science Ph.D. Program. 2014-.

PREVIOUS STUDENTS SUPERVISED

Ph.D. Theses Supervised:

Hyun Min Kang UCSD Computer Science and Engineering Ph.D. Program. 2004-2009. Now faculty at University of Michigan.

Sean O'Rourke UCSD Computer Science and Engineering Ph.D. Program. 2004-2009.

Noah Zaitlen UCSD Bioinformatics Ph.D. Program. 2004-2009. Now faculty at University of California, San Francisco.

Buhm Han UCSD Computer Science and Engineering Ph.D. Program. 2005-2009. Now faculty at Asan Medical Center, Korea.

Chun (Jimmie) Ye UCSD Bioinformatics Ph.D. Program. 2004-2009. Now faculty at University of California, San Francisco.

Dan He UCLA Computer Science Ph.D. Program. 2008-2012. Now researcher at IBM Research.

Emrah Kostem UCLA Computer Science Ph.D. Program. 2007-2013. Now researcher at Human Longevity Institute.

Nicholas Furlotte UCLA Computer Science Ph.D. Program. 2008-2013. Now researcher at 23andMe.

Jae-Hoon Sul UCLA Computer Science Ph.D. Program. 2008-2013. Now faculty at UCLA.

Eun Yong Kang UCLA Computer Science Ph.D. Program. 2008-2013. Now researcher at Human Longevity Institute.

Wen-Yun Yang UCLA Computer Science Ph.D. Program. 2010-2013. Now researcher at Human Longevity Institute.

Zhanyong Wang UCLA Computer Science Ph.D. Program. 2009-2014. Now at Google.

Jong Wha (Joanne) Joo UCLA Bioinformatics Ph.D. Program. 2010-2015. Now Post-Doc at UCLA.

Farhad Hormozdiari UCLA Computer Science Ph.D. Program. 2010-2016. Now Post-Doc at Harvard.

UCLA Masters Student Theses:

Nathan Parrish UCLA Masters Program. 2010-2012. Now at Microsoft.

UCLA Undergraduate Student Theses:

Greg Darnell. UCLA B.S. Computer Science '13. Now Ph.D. student at Princeton.

Dat Duong. UCLA B.S. Mathematics and Molecular, Cellular and Developmental Biology '11. Now Ph.D. student at UCLA.

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. Graduated Ph.D. program 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. Graduated Ph.D. program 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 ben-

effitted 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 Departmental 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

"Phenotype Imputation In Genetics Studies" *University of California, Los Angeles*, November 20th, 2015

"Computational Challenges in Identifying Genetic Variants Involved in Common Diseases" *University of California, Los Angeles*, November 16th, 2015

"Searching for a sequence needle in a genome haystack" *RECOMB Satellite Workshop on Bioinformatics Education, HHMI*, November 15th, 2015

"Known and Unknown Confounding in Genetic Studies" *Daniel O'Connor Memorial Lecture, Genetics, Bioinformatics and Systems Biology Colloquium, University of California, Los Angeles*, October 15th, 2015

"Correcting for Population Structure using Mixed Models" *Short Course on Systems Genetics, Jackson Laboratory, Bar Harbor, Maine*. October 1st, 2015.

"Heterogeneity in Genetic Studies." *Gordon Meeting on Human Genetics*, July 22nd, 2015.

"Introduction to Quantitative Genetics" *Lorentz Workshop on Pan-Genomics*, June 9th, 2015.

"Association of Genomic Data" *Symposium on Advances in Genomics, Epidemiology, and Statistics (SAGES)*, May 29th, 2015.

"Known and Unknown Confounding in Genetic Studies" *Bertinoro Computational Biology, Bertinoro, Italy*, September 30th, 2014.

“Gene-be-Environment Interactions and Heterogeneity.” *Emerging Statistical Challenges and Methods For Analysis of Massive Genomic Data in Complex Human Disease Studies*, Banff, Canada, June 24th, 2014.

“Identifying Genetic Relatives while Preserving Privacy” *UCLA Big Data to Knowledge Symposium* March 28th, 2014.

“Known and Unknown Confounding in Genetic Studies” *University Chicago Statistics Seminar*, March 3rd, 2014.

“Known and Unknown Confounding in Genetic Studies” *Duke University Machine Learning Seminar*, February 26th, 2014.

“Known and Unknown Confounding in Genetic Studies” *Simons Institute, University of California, Berkeley*, February 21st, 2014.

“Personalized Genomics and Medicine” *2014 UCLA Engineering Tech Forum*. February 6th, 2014.

“Identifying Genetic Relatives while Preserving Privacy” *Protecting Genomic Data Privacy while Accelerating Scientific Progress, Banbury Center of Cold Spring Harbor Laboratory, Long Island, NY* December 12, 2013.

“Correcting for Population Structure using Mixed Models” *Short Course on Systems Genetics, Jackson Laboratory, Bar Harbor, Maine*. September 12th, 2013.

“Personalized Genomics and Medicine” *Google Los Angeles*. May 30th, 2013.

“Personalized Genomics and Medicine” *2013 UCLA Engineering Tech Forum*. March 8th, 2013.

“Known and Unknown Confounding in Genetic Studies” *University of Southern California*, March 28th, 2013.

“Spatial Structure in Genetic Data” *UCLA Bioinformatics Retreat*. February 7th, 2013.

“Known and Unknown Confounding in Genetic Studies” *Hong Kong University*, January 29th, 2013.

“Allele Specific Expression Mapping” *American Society of Human Genetics*. November 7th, 2012.

“Correcting for Population Structure using Mixed Models” *Short Course on Systems Genetics, Jackson Laboratory, Bar Harbor, Maine*. November 2nd, 2012.

“Known and Unknown Confounding in Genetic Studies” *Penn Bioinformatics Forum, University of Pennsylvania*, October 10th, 2012.

“Spatial Structure in Genetic Data” *Mathematical Biology Seminar, University of California, Berkeley*. September 12th, 2012.

“Known and Unknown Confounding in Genetic Studies” *2012 Joint Statistical Meetings*, July 31st, 2012.

“Incorporating Prior Information into Association Studies” *Intelligent Systems in Molecular Biology*. July 15th, 2012.

“From GWAS to Personal Genomes: The Fundamentals of Analysis of Genetic Variation” *ISBM Tutorial*, July 14th, 2012.

“Spatial Structure in Genetic Data” *Haifa University*. March 25th, 2012.

“Allele Specific Expression Mapping” *Safra Distinguished Speaker, Tel Aviv University*. March 25th, 2012.

“Identifying expression quantitative trait loci using allele specific expression” *Neurogenetics Affinity Group Seminar, University of California, Los Angeles*. March 1st, 2012.

“Identifying expression quantitative trait loci using allele specific expression” *Genome Sciences Seminar Series, University of Virginia*. February 27th, 2012.

“Allele Specific Expression Mapping” *Human Genetics Seminar Series, University of Michigan, Ann Arbor, MI*. February 6th, 2012.

“Computational challenges in genome-wide association studies” *Bioinformatics Program, University of California, Los Angeles*. February 3rd, 2012.

“The computational challenges of personal genomes” *European Union-United States Frontiers of Engineering, National Academy of Engineering, University of California, Irvine*. November 4th, 2011.

“Computational Genetics Tutorial” *Institute for Pure and Applied Mathematics, University of California, Los Angeles*. September 16th, 2011.

“Allele Specific Expression Mapping” *Wellcome Trust Centre for Human Genetics, Oxford, UK*. September 5th, 2011.

“Computational Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Meeting with Zhejiang University School of Medicine, University of California, Los Angeles*. August 29th, 2011.

“Known and Unknown Confounding in Genetic Studies” *Keynote Talk for Machine Learning in System Biology Workshop, Intelligent Systems in Molecular Biology, Vienna, Austria*, July 20th, 2011.

“Efficient algorithms for tandem copy number variation reconstruction in repeat-rich regions” *HiTSeq 2011: Conference on High Throughput Sequencing Analysis and Algorithms Special Interest Group of ISMB 2011, Vienna, Austria*, July 16, 2011.

“Personalized Genomics and Medicine” *UCLA / PKU Joint Research Institute Mini-Symposium, Beijing, China*. April 25th, 2011.

“Simulations and Replications to verify GWAS experiments” *Systems Biology Verification*, March 24th, 2011.

“Personalized Genomics and Medicine” *2011 UCLA Engineering Tech Forum*. March 1st, 2011.

“Statistical Methods for Association Studies with Rare Variants” *School of Public Health Seminar, Harvard*. February 8th, 2011.

“Computational challenges in genome-wide association studies” *Bioinformatics Program, University of California, Los Angeles*. February 3rd, 2011.

“Computational challenges in genome-wide association studies” *UCLA-Institute of Psychiatry Conference, University of California, Los Angeles*. January 31st, 2011.

“Computational challenges in genome-wide association studies” *IBM Research, Tel Aviv*. January 23rd, 2011.

“Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains” *The Institute of Evolution, Haifa University*. January 19th, 2011.

“Computational challenges in genome-wide association studies” *Computer Science Department Seminar, Tel Aviv University*. January 16th, 2011.

“Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains” *Genetics Seminar, The Hebrew University, Jerusalem, Israel*. January 12th, 2011.

“Computational Challenges in Combining Genome-Wide Association Studies” *The Successes, Challenges and Prospects for Next Generation GWAS analyses for Complex Diseases Workshop, Edinburgh, UK*. October 15th, 2010.

“Correcting for Population Structure using Mixed Models” *Short Course on Systems Genetics, Jackson Laboratory, Bar Harbor, Maine*. September 21st, 2010.

“Accounting for sample structure in Genome-Wide Association Studies” *International Bioinformatics and Systems Biology Workshop, Kyoto University*. July 29th, 2010.

“Accounting for sample structure in Genome-Wide Association Studies” *Computational Biology Seminar, Hebrew University*. June 29th, 2010.

“Leveraging Linkage Disequilibrium in Genome-Wide Association Studies”. *Computational Biology Seminar, Brown University*. March 3rd, 2010.

“Computational Challenges in Discovering the Genetic Basis of Complex Traits in Inbred Mouse Strains”. *Bioinformatics Program, University of California, Los Angeles*. February 18th, 2010.

“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”. *Tranla-*

tional 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.