

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 and Chair: Department of Computational Medicine. *University of California, Los Angeles*. December 2017 - present.

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.

PROFESSIONAL AND LEADERSHIP ACTIVITIES

UCLA Department of Computational Medicine, Founding Chair. 2017- present.

- The Department of Computational Medicine is a department that spans the Henry Samueli School of Engineering, the David Geffen School of Medicine and the UCLA Health System with the goal of developing a data science community that will leverage advances in genomic and artificial intelligence to improve patient care in the UCLA Health System.
- Expanded scope of existing Department of Biomathematics to broader scope encompassing the research areas of Computational Genomics, Medical Imaging, Machine Learning in Health Data and Mathematical Modeling.
- Since 2017, appointed 18 faculty to the department through external recruitments and appointment of existing UCLA faculty covering all departmental research areas. Many of the faculty have won awards including appointment as Sloan Research Fellowships and International Society of Computational Biology Fellows.
- Developed the AI in Medicine research program which provides access to UCLA Health System data to UCLA researchers enabling data science collaborations with clinical units.

UCLA Bioinformatics.

- Co-authored the original proposal for creating the UCLA Bioinformatics Ph.D. program in 2007
- Founded the Undergraduate Bioinformatics Minor academic degree program in 2012 and currently serves as Co-director of the minor
- Developed the rigorous computational core curriculum for the program including authoring the curriculum for 3 of the core courses and guiding the curriculum for the remaining by serving as chair of the curriculum committee since the inception of the program. Taught over 20 core courses in the program.
- Played a role in recruiting 22 faculty who are now members of the Bioinformatics community turning UCLA into a powerhouse in the area.

Computational Genomics Summer Institute.

- The Computational Genomics Summer Institute is an annual program four week program at UCLA held each summer that brings more than 50 faculty and 100 advanced graduate student and postdoc trainees to UCLA. The program was held in person from 2016-2019 and resumes in 2022.
- Co-founded the annual CGSI in 2016 currently serving as Co-director.
- Obtained NIH R25 funding to support 10 years of the program (two 5 year grants) with funding through 2026.

Bruins In Genomics Undergraduate Research Program.

- Co-founded the Bruins in Genomics Undergraduate Research Program in 2016 which recruits dozens of undergraduate students into summer research experiences hosted at UCLA.
- Goals of the program include developing recruitment pipelines for the UCLA Bioinformatics Ph.D. program as well as increase the diversity in the field
- Serves as PI on multiple NIH R25 grants funding the program.

UCLA SwabSeq COVID-19 Diagnostic Technology.

- Leads the UCLA SwabSeq COVID-19 Diagnostic Laboratory which developed novel next-generation sequencing based diagnostic test and deployed technology within 6 months.
- Core technology developed in April 2020 in collaboration with small group of faculty at UCLA and FDA Emergency Use Authorization obtained in October 2020.
- Provides testing for multiple universities including UCLA, UCSB, UCSC, Caltech, Pepperdine, and Cal States. Additional partnerships with the Los Angeles Unified School District and California Department of Public Health.
- Performed over 1,500,000 diagnostic tests with revenues of over \$40,000,000.
- Principal Investigator on \$13.3 million NIH Rapid Acceleration of Diagnostics (RADx) to expand the laboratory testing capacity.

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.
Fall 2021

Instructor: Algorithms in Systems Biology and Bioinformatics.

University of California, Los Angeles, Fall 2014, Winter 2016. Winter 2017. Winter 2018.
Spring 2019. Spring 2020.

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: *Research in Computational Molecular Biology (RECOMB)*, 2017-present.

RECOMB Satellite Workshop on Genetics, 2016-present.

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: *Computational Genomics Summer Institute 2016 - present*, (**Co-Director**).

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, 2017. *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, 2016, 2017. *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. Hilary A Collier, Stacey Beggs, Samantha Andrews, Jeff Maloy, Alec Chiu, Sriram Sankararaman, Matteo Pellegrini, Nelson Freimer, Tracy Johnson, Jeanette Papp, Eleazar Eskin, Alexander Hoffmann. “Bruins-in-Genomics: Evaluation of the impact of a UCLA undergraduate summer program in computational biology on participating students.” **PLoS One**.**17(5):e0268861**, 2022.
2. Fernando Meyer, Adrian Fritz, Zhi-Luo Deng, David Koslicki, Till Robin Lesker, Alexey Gurevich, Gary Robertson, Mohammed Alser, Dmitry Antipov, Francesco Beghini, Denis Bertrand, Jaqueline J Brito, C Titus Brown, Jan Buchmann, Aydin Bulu, Bo Chen, Rayan Chikhi, Philip T L C Clausen, Alexandru Cristian, Piotr Wojciech Dabrowski, Aaron E Darling, Rob Egan, Eleazar Eskin, Evangelos Georganas, Eugene Goltsman, Melissa A Gray, Lars Hestbjerg Hansen, Steven Hofmeyr, Pingqin Huang, Luiz Irber, Huijue Jia, Tue Sparholt Jrgensen, Silas D Kieser, Terje Klemetsen, Axel Kola, Mikhail Kolmogorov, Anton Korobeynikov, Jason Kwan, Nathan LaPierre, Claire Lemaitre, Chenhao Li, Antoine Limasset, Fabio Malcher-Miranda, Serghei Mangul, Vanessa R Marcelino, Camille Marchet, Pierre Marijon, Dmitry Meleshko, Daniel R Mende, Alessio Milanese, Niranjan Nagarajan, Jakob Nissen, Sergey Nurk, Leonid Olikier, Lucas Paoli, Pierre Peterlongo, Vitor C Piro, Jacob S Porter, Simon Rasmussen, Evan R Rees, Knut Reinert, Bernhard Renard, Espen Mikal Robertsen, Gail L Rosen, Hans-Joachim Ruscheweyh, Varuni Sarwal, Nicola Segata, Enrico Seiler, Lizhen Shi, Fengzhu Sun, Shinichi Sunagawa, Sren Johannes Srensen, Ashleigh Thomas, Chengxuan Tong, Mirko Trajkovski, Julien Tremblay, Gherman Uritskiy, Riccardo Vicedomini, Zhengyang Wang, Ziye Wang, Zhong Wang, Andrew Warren, Nils Peder Willassen, Katherine Yelick, Ronghui You, Georg Zeller, Zhengqiao Zhao, Shanfeng Zhu, Jie Zhu, Ruben Garrido-Oter, Petra Gastmeier, Stephane Hacquard, Susanne Huler, Ariane Khaledi, Friederike Maechler, Fantin Mesny, Simona Radutoiu, Paul Schulze-Lefert, Nathiana Smit, Till Strowig, Andreas Bremges, Alexander Sczyrba, Alice Carolyn McHardy. “Critical Assessment of Metagenome Interpretation: the second round of challenges.” **Nat Methods**. **19(4):429-440**, 2022.
3. Longhua Guo, James Boockock, Evann E Hilt, Sukantha Chandrasekaran, Yi Zhang, Chetan Munugala, Laila Sathe, Noah Alexander, Valerie A Arboleda, Jonathan Flint, Eleazar Eskin, Chongyuan Luo, Shangxin Yang, Omai B Garner, Yi Yin, Joshua S Bloom, Leonid Kruglyak. “Genomic epidemiology of the Los Angeles COVID-19 outbreak and the early history of the B.1.43 strain in the USA” **BMC Genomics**. **23(1):260**, 2022.
4. Cinelli, Carlos, Nathan LaPierre, Brian L. Hill, Sriram Sankararaman, Eleazar Eskin. Robust Mendelian Randomization in the Presence of Residual Population Stratification, Batch Effects and Horizontal Pleiotropy. *Nature Communications* 13 (1): 1093, 2022.
5. LaPierre, Nathan, Kodi Taraszka, Helen Huang, Rosemary He, Farhad Hormozdiari, and Eleazar Eskin. Identifying Causal Variants by Fine Mapping across Multiple Studies. *PLoS Genetics* 17 (9): e1009733, 2021.
6. Bloom, Joshua S., Laila Sathe, Chetan Munugala, Eric M. Jones, Molly Gasperini, Nathan B. Lubock, Fauna Yarza, Erin M Thompson, Kyle M Kovary, Jimin Park,

Dawn Marquette, Stephania Kay, Mark Lucas, TreQuan Love, A Sina Booeshaghi, Oliver F Brandenburg, Longhua Guo, James Boockock, Myles Hochman, Scott W Simpkins, Isabella Lin, Nathan LaPierre, Duke Hong, Yi Zhang, Gabriel Oland, Bianca Judy Choe, Sukantha Chandrasekaran, Evann E Hilt, Manish J Butte, Robert Damoiseaux, Clifford Kravit, Aaron R Cooper, Yi Yin, Lior Pachter, Omai B Garner, Jonathan Flint, Eleazar Eskin, Chongyuan Luo, Sriram Kosuri, Leonid Kruglyak, Valerie A Arboleda. Massively Scaled-up Testing for SARS-CoV-2 RNA via next-Generation Sequencing of Pooled and Barcoded Nasal and Saliva Samples. *Nature Biomedical Engineering* 5 (7): 65765, 2021.

7. Hormozdiari, Farhad, Junghyun Jung, Eleazar Eskin, and Jong Wha J Joo. MARS: Leveraging Allelic Heterogeneity to Increase Power of Association Testing. *Genome Biology* 22, no. 1: 128, 2021.
8. Goede, Olivia M. de, Daniel C. Nachun, Nicole M. Ferraro, Michael J. Gloudemans, Abhiram S. Rao, Craig Smail, Tiffany Y. Eulalio, et al. Population-Scale Tissue Transcriptomics Maps Long Non-Coding RNAs to Complex Disease. *Cell* 184, no. 10: 263348.e19, 2021.
9. Timothy S Chang, Yi Ding, Malika K Freund, Ruth Johnson, Tommer Schwarz, Julie M Yabu, Chad Hazlett, Jeffrey N Chiang, David A Wulf, UCLA Precision Health Data Discovery Repository Working Group; Daniel H Geschwind, Manish J Butte, Bogdan Pasaniuc. “Pre-existing conditions in Hispanics/Latinxs that are COVID-19 risk factors.” *iScience*. **24(3):102188.**, 2021.
10. Cue Hyunkyu Lee, Huwenbo Shi, Bogdan Pasaniuc, Eleazar Eskin, Buhm Han. “PLEIO: a method to map and interpret pleiotropic loci with GWAS summary statistics.” *Am J Hum Genet*. **108(1):36-48.**, 2021.
11. Kiflai Bein, Koustav Ganguly, Timothy M Martin, Vincent J Concel, Kelly A Brant, Y P Peter Di, Swapna Upadhyay, James P Fabisiak, Louis J Vuga, Naftali Kaminski, Emrah Kostem, Eleazar Eskin, Daniel R Prows, Ann-Soo Jang, George D Leikauf. “Genetic determinants of ammonia-induced acute lung injury in mice.” *Am J Physiol Lung Cell Mol Physiol*. **320(1):L41-L62.**, 2021.
12. David Goodman-Meza, Akos Rudas, Jeffrey N Chiang, Paul C Adamson, Joseph Ebinger, Nancy Sun, Patrick Botting, Jennifer A Fulcher, Faysal G Saab, Rachel Brook, Eleazar Eskin, Ulzee An, Misagh Kordi, Brandon Jew, Brunilda Balliu, Zeyuan Chen, Brian L Hill, Elinor Rahmani, Eran Halperin, Vladimir Manuel. “A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity.” *PLoS One*. **15(9):e0239474.**, 2020.
13. Lihua Jiang, Meng Wang, Shin Lin, Ruiqi Jian, Xiao Li, Joanne Chan, Guanlan Dong, Huaying Fang, Aaron E Robinson, GTEx Consortium; Michael P Snyder. “A Quantitative Proteome Map of the Human Body.” *Cell*. **183(1):269-283.e19.**, 2020.
14. Meritxell Oliva, Manuel Muoz-Aguirre, Sarah Kim-Hellmuth, Valentin Wucher, Ariel D H Gewirtz, Daniel J Cotter, Princy Parsana, Silva Kasela, Brunilda Balliu, Ana Viuela, Stephane E Caste, Pejman Mohammadi, Francois Aguet, Yuxin Zou, Ekaterina A Khrantsova, Andrew D Skol , Diego Garrido-Martn, Ferran Reverter, Andrew Brown, Patrick Evans, Eric R Gamazon, Anthony Payne, Rodrigo Bonazzola, Alvaro N Barbeira, Andrew R Hamel, Angel Martinez-Perez, Jos Manuel Soria, GTEx Consortium; Brando, Hae Kyung Im, Barbara E Engelhardt, Kristin G Ardlie, Stephen B Montgomery, Alexis J Battle, Tuuli Lappalainen, Roderic Guig, Barbara

- E Stranger. "The impact of sex on gene expression across human tissues." **Science**. **369(6509):eaba3066.**, 2020.
15. Stephane E Castel, Francois Aguet, Pejman Mohammadi, GTEx Consortium; Kristin G Ardlie, Tuuli Lappalainen. "A vast resource of allelic expression data spanning human tissues." **Genome Biol.** **21(1):234.**, 2020.
 16. Nathan LaPierre, Mohammed Alser, Eleazar Eskin, David Koslicki, Serghei Mangul. "Metalign: efficient alignment-based metagenomic profiling via containment min hash." **Genome Biol.** **21(1):242.**, 2020.
 17. Joshua S Bloom, Eric M Jones, Molly Gasperini, Nathan B Lubock, Laila Sathe, Chetan Munugala, A Sina Boeshaghi, Oliver F Brandenburg, Longhua Guo, James Boocock, Scott W Simpkins, Isabella Lin, Nathan LaPierre, Duke Hong, Yi Zhang, Gabriel Oland, Bianca Judy Choe, Sukantha Chandrasekaran, Evann E Hilt, Manish J Butte, Robert Damoiseaux, Aaron R Cooper, Yi Yin, Lior Pachter, Omai B Garner, Jonathan Flint, Eleazar Eskin, Chongyuan Luo, Sriram Kosuri, Leonid Kruglyak, Valerie A Arboleda. "Swab-Seq: A high-throughput platform for massively scaled up SARS-CoV-2 testing." **MedRxiv.** **2020.08.04.20167874.**, 2020.
 18. Igor Mandric, Jeremy Rotman, Harry Taegyun Yang, Nicolas Strauli, Dennis J Montoya, William Van Der Wey, Jiem R Ronas, Benjamin Statz, Douglas Ya, Velislava Petrova, Alex Zelikovsky, Roberto Spreafico, Sagiv Shifman, Noah Zaitlen, Maura Rossetti, K Mark Ansel, Eleazar Eskin, Serghei Mangul. "Author Correction: Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing." **Nat Commun.** **11(1):4499**, 2020.
 19. Caitlin Loeffler, Aaron Karlsberg, Lana S Martin, Eleazar Eskin, David Koslicki, Serghei Mangul. "Correction to: Improving the usability and comprehensiveness of microbial databases." **BMC Biol.** **18(1):92**, 2020.
 20. Igor Mandric, Jeremy Rotman, Harry Taegyun Yang, Nicolas Strauli, Dennis J Montoya, William Van Der Wey, Jiem R Ronas, Benjamin Statz, Douglas Yao, Velislava Petrova, Alex Zelikovsky, Roberto Spreafico, Sagiv Shifman, Noah Zaitlen, Maura Rossetti, K Mark Ansel, Eleazar Eskin, Serghei Mangul. "Profiling immunoglobulin repertoires across multiple human tissues using RNA sequencing." **Nat Commun.** **11(1):3126.**, 2020.
 21. Yi Han, Qiong Jia, Pedram Shafiei Jahani, Benjamin P Hurrell, Calvin Pan, Pin Huang, Janet Gukasyan, Nicholas C Woodward, Eleazar Eskin, Frank D Gilliland, Omid Akbari, Jaana A Hartiala, Hooman Allayee. "Genome-wide analysis highlights contribution of immune system pathways to the genetic architecture of asthma." **Nat Commun.** **11(1):1776.**, 2020.
 22. Caitlin Loeffler, Aaron Karlsberg, Lana S Martin, Eleazar Eskin, David Koslicki, Serghei Mangul. "Improving the usability and comprehensiveness of microbial databases." **BMC Biol.** **18(1):37.**, 2020.
 23. Keith Mitchell, Jaqueline J Brito, Igor Mandric, Qiaozhen Wu, Sergey Knyazev, Sei Chang, Lana S Martin, Aaron Karlsberg, Ekaterina Gerasimov, Russell Littman, Brian L Hill, Nicholas C Wu, Harry Taegyun Yang, Kevin Hsieh, Linus Chen, Eli Littman, Taylor Shabani, German Enik, Douglas Yao, Ren Sun, Jan Schroeder, Eleazar Eskin, Alex Zelikovsky, Pavel Skums, Mihai Pop, Serghei Mangul. "Benchmarking of computational error-correction methods for next-generation sequencing data." **Genome Biol.** **21(1):71.**, 2020.

24. Yue Wu, Eleazar Eskin, Sriram Sankararaman. "A Unifying Framework for Imputing Summary Statistics in Genome-Wide Association Studies." **Comput Biol.** **27(3):418-428.**, 2020.
25. Hadi Maazi, Jaana A Hartiala, Yuzo Suzuki, Amanda L Crow, Pedram Shafiei Jahani, Jonathan Lam, Nisheel Patel, Diamanda Rigas, Yi Han, Pin Huang, Eleazar Eskin, Aldons J Lulus, Frank D Gilliland, Omid Akbari, Hooman Allayee. "A GWAS approach identifies Dapp1 as a determinant of air pollution-induced airway hyperreactivity." **PLoS Genet.** **15(12):e1008528.**, 2019.
26. Jennifer Zou, Farhad Hormozdiari, Brandon Jew, Stephane E Castel, Tuuli Lapalainen, Jason Ernst, Jae Hoon Sul, Eleazar Eskin. "Leveraging allelic imbalance to refine fine-mapping for eQTL studies." **PLoS Genet.** **15(12):e1008481.**, 2019.
27. Changhoon Lee, Eun Yong Kang, Michael J Gandal, Eleazar Eskin, Daniel H Geschwind. "Profiling allele-specific gene expression in brains from individuals with autism spectrum disorder reveals preferential minor allele usage." **Nat Neurosci.** **22(9):1521-1532.**, 2019.
28. Kunhee Kim, Hyungryul Baik, Chloe Soohyun Jang, Jin Kyung Roh, Eleazar Eskin, Buhm Han. "Genomic GPS: using genetic distance from individuals to public data for genomic analysis without disclosing personal genomes." **Genome Biol.** **20(1):175.**, 2019.
29. Douglas W Yao, Nikolas G Balanis, Eleazar Eskin, Thomas G Graeber. "A linear mixed model approach to gene expression-tumor aneuploidy association studies." **Sci Rep.** **9(1):11944.**, 2019.
30. Elinor Rahmani, Regev Schweiger, Brooke Rhead, Lindsey A Criswell, Lisa F Barcellos, Eleazar Eskin, Saharon Rosset, Sriram Sankararaman, Eran Halperin. "Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology." **Nat Commun.** **10(1):3417.**, 2019.
31. Serghei Mangul, Thiago Mosqueiro, Richard J Abdill, Dat Duong, Keith Mitchell, Varuni Sarwal, Brian Hill, Jaqueline Brito, Russell Jared Littman, Benjamin Statz, Angela Ka-Mei Lam, Gargi Dayama, Laura Grieneisen, Lana S Martin, Jonathan Flint, Eleazar Eskin, Ran Blekhman. "Challenges and recommendations to improve the installability and archival stability of omics computational tools." **PLoS Biol.** **20;17(6):e3000333**, 2019.
32. Nathan LaPierre, Serghei Mangul, Mohammed Alser, Igor Mandric, Nicholas C. Wu, David Koslicki, Eleazar Eskin. "MiCoP: microbial community profiling method for detecting viral and fungal organisms in metagenomic samples." **BMC Genomics.** **20(Suppl 5):423**, 2019.
33. Serghei Mangul, Lana S. Martin, Brian L. Hill, Angela Ka-Mei Lam, Margaret G. Distler, Alex Zelikovsky, Eleazar Eskin, Jonathan Flint. "Systematic benchmarking of omics computational tools." **Nature Communications** **10. 1393** 2019.
34. Serghei Mangul, Lana S. Martin, Ben Langmead, Javier E. Sanchez-Galan, Ian Toma, Fereydoun Hormozdiari, Pavel Pevzner, Eleazar Eskin. "How bioinformatics and open data can boost basic science in countries and universities with limited resources." **Nature Biotechnology** **37.324326**, 2019.
35. Serghei Mangul, Lana S. Martin, Eleazar Eskin, Ran Blekhman. "Improving the usability and archival stability of bioinformatics software." **Genome Biology.** **20:47**, 2019.

36. Jae Hoon Sul, Lana S. Martin, Eleazar Eskin. "Population structure in genetic studies: Confounding factors and mixed models." **PLoS Genetics**. **14(12):e1007309**, 2019
37. Dat Duong, Wasi Uddin Ahmad, Eleazar Eskin, Kai-Wei Chang, Jingyi Jessica Li. "Word and Sentence Embedding Tools to Measure Semantic Similarity of Gene Ontology Terms by Their Definitions." **Journal of Computational Biology**. **26(1):38-52**, 2019.
38. Yue Wu, Farhad Hormozdiari, Jong Wha Joanne Joo, Eleazar Eskin. "Improving Imputation Accuracy by Inferring Causal Variants in Genetic Studies." **Journal of Computational Biology**, (In Press) 2018.
39. Elinor Rahmani, Regev Schweiger, Liat Shenhav, Theodora Wingert, Ira Hofer, Eilon Gabel, Eleazar Eskin, Eran Halperin. "BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference" **Genome Biology**. **19:141**, 2018.
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201. Eleazar Eskin, William Stafford Noble, and Yoram Singer. "Protein Family Classification using Sparse Markov Transducers." **Journal of Computational Biology**. **10(2):187-213**. 2003.
202. 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.
203. 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.
204. 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

200. Nathan LaPierre, Kodi Taraszka, Helen Huang, Rosemary He, Farhad Hormozdiari, Eleazar Eskin. "Identifying causal variants by fine mapping across multiple studies." *In Proceedings of the Twenty Fourth Annual Conference on Research in Computational Biology (RECOMB-2020)*. Virtual: June 22nd-25th, 2020.
201. Yue Wu, Sriram Sankararaman and Eleazar Eskin. "A unifying framework for summary statistics imputation." *In Proceedings of the Twenty Second Annual Conference on Research in Computational Biology (RECOMB-2018)*. Paris, France: April 20th-24th. 2018.
202. Elinor 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.
203. 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.
204. 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.
205. 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.
206. Jong Wha J. Joo, Eun Yong Kang, Elin Org, Nick Furlotte, Brian Parks, Aldons J. Lulis, 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.
207. 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.
208. 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.
209. 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.

210. 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.
211. 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.
212. 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.
213. 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.
214. 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.
215. 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.
216. 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.
217. 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.
218. 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.
219. 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.
220. 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.

221. 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.
222. 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.
223. 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
224. 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.
225. 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.
226. 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.
227. 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.
228. 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.
229. 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.
230. 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.
231. 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.
232. 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.

233. 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.
234. 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.
235. 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.
236. 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.
237. 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.
238. 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.
239. 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)**
240. 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.
241. 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.
242. 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.
243. 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.

244. 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.
245. 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.
246. 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

247. Robert Brown, Jong Wha J. Joo, Robert L. Smith, Bogdan Pasaniuc, Eleazar Eskin. "GGmend: A Mendelian randomization method for finding gene-on-gene regulatory effects in the presence of unobserved confounders." *In Proceedings of the Fifth RECOMB Satellites Workshop on Computational Methods in Genetics (RECOMB-Genetics)* Los Angeles, CA: July 27th-28th, 2017.
248. Jennifer Zou, Farhad Hormozdiari, Jason Ernst, Jae-Hoon Sul, Eleazar Eskin. "Leveraging allele-specific expression to refine fine-mapping for eQTL studies." *In Proceedings of the Fifth RECOMB Satellites Workshop on Computational Methods in Genetics (RECOMB-Genetics)* Los Angeles, CA: July 27th-28th, 2017.
249. 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.
250. 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.
251. 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.
252. 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.
253. 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.

254. 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.
255. 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.
256. 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.
257. 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.
258. 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.
259. 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.
260. 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.
261. 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.
262. 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.
263. 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.
264. 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.
265. 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

266. Serghei Mangul, Harry Taegyun Yang, Eleazar Eskin, Noah Zaitlen. "Hidden Treasures in Contemporary RNA Sequencing." Springer. Briefs in Computer Science. 2019.
267. Can Alkan, Emidio Capriotti, Eleazar Eskin, Fereydoun Hormozdiari, Maricel G. Kann. "PERSONAL GENOMICS - Session Introduction." Pacific Symposium in Biocomputing. 2011:229-30.
268. Buhm Han, Eleazar Eskin. "Multiple Testing in Genetic Epidemiology." Encyclopedia of Life Sciences, 2010.
269. 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.
270. 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.
271. 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.
272. 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.
273. 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.
274. 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

International Society for Computational Biology Fellow 2019.

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 Computational Systems Biology Field Chair 2016-present.

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:

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

Nathan LaPierre UCLA Computer Science Ph.D. Program. 2015-
Kodi Collins UCLA Computer Science Ph.D. Program. 2016-

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, Los Angeles.

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 Faculty at Dongguk University.

Farhad Hormozdiari UCLA Computer Science Ph.D. Program. 2010-2016. Now Scientist at Google Health.

Dat Duong UCLA Computer Science Ph.D. Program. 2014-2020. Now Scientist at NIH

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 benefited 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.

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