

Publication List

Eran Halperin

Updated to : February 11, 2019.

Journal papers:

1. Fisher, Eyal, et al., *Increase of body mass index and waist circumference predicts development of metabolic syndrome criteria in apparently healthy individuals with 2 and 5 years follow-up.*, **International Journal of Obesity** (2019): 1.
2. Schweiger, Regev, Eyal Fisher, Omer Weissbrod, Elior Rahmani, Martina Mller-Nurasyid, Sonja Kunze, Christian Gieger, Melanie Waldenberger, Saharon Rosset, and Eran Halperin, *Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests.*, **Nature communications** 9, no. 1 (2018): 4919.
3. Rahmani, Elior, Regev Schweiger, Liat Shenhav, Theodora Wingert, Ira Hofer, Eilon Gabel, Eleazar Eskin, and Eran Halperin, *BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference.*, **Genome biology** 19, no. 1 (2018): 141.
4. Schweiger, Regev, Eyal Fisher, Elior Rahmani, Liat Shenhav, Saharon Rosset, and Eran Halperin, *Using Stochastic Approximation Techniques to Efficiently Construct Confidence Intervals for Heritability*, **Journal of Computational Biology** 25, no. 7 (2018): 794-808.
5. Hyams, Gal, Shiran Abadi, Shlomt Zion Lahav, Adi Avni, Eran Halperin, Eilon Shani, and Itay Mayrose, *CRISPyS: Optimal sgRNA design for editing multiple members of a gene family using the CRISPR system.*, **Journal of molecular biology**, (2018).
6. Park, Danny S., Itamar Eskin, Eun Yong Kang, Eric R. Gamazon, Celeste Eng, Christopher R. Gignoux, Joshua M. Galanter, Esteban Burchard Chun J. Ye Hugues Aschard Eleazar Eskin Eran Halperin and Noah Zaitlen *An ancestry-based approach for detecting interactions*, **Genetic epidemiology** 42, no. 1 (2018): 49-63.
7. Galpaz, Navot, Itay Gonda, Doron Shem-Tov, Omer Barad, Galil Tzuri, Shery Lev, Zhangjun Fei et al., *Deciphering genetic factors that determine melon fruit-quality traits using Rna-seq-based high-resolution Qtl and eqtl mapping.*, **The Plant Journal** 94, no. 1 (2018): 169-191.
8. Elior Rahmani, Noah Zaitlen, Yael Baran, Celeste Eng, Donglei Hu, Joshua Galanter, Sam Oh, Esteban G. Burchard, Eleazar Eskin, James Zou, and Eran Halperin, *Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation*, **Nature Methods**, 14(3), pp.218-219, 2017.
9. Schweiger, Regev, Omer Weissbrod, Elior Rahmani, Martina Mller-Nurasyid, Sonja Kunze, Christian Gieger, Melanie Waldenberger, Saharon Rosset, and Eran Halperin, *RL-SKAT: An exact and efficient score test for heritability and set tests*, **Genetics** 207, no. 4 (2017): 1275-1283.

10. Weissbrod, Omer, Elior Rahmani, Regev Schweiger, Saharon Rosset, and Eran Halperin, *Association testing of bisulfite-sequencing methylation data via a Laplace approximation*, **Bioinformatics** 33, no. 14 (2017): i325-i332 (special issue of **ISMB**, 2017).
11. Sasson, Goor, Sheerli Kruger Ben-Shabat, Eyal Seroussi, Adi Doron-Faigenboim, Naama Shterzer, Shamay Yaacoby, Margret E. Berg Miller, Bryan A. White, Eran Halperin, and Itzhak Mizrahi. *Heritable Bovine Rumen Bacteria Are Phylogenetically Related and Correlated with the Cow's Capacity To Harvest Energy from Its Feed*, **mBio** 8, no. 4 (2017): e00703-17
12. Elior Rahmani, Noah Zaitlen, Yael Baran, Celeste Eng, Donglei Hu, Joshua Galanter, Sam Oh, Esteban G. Burchard, Eleazar Eskin, James Zou, and Eran Halperin, *Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation*, **Nature Methods**, 14(3), pp.218-219, 2017.
13. Noah Zaitlen, Scott Huntsman, Donglei Hu, Melissa Spear, Celeste Eng, Sam S. Oh, Marquitta J. White, Angel Mak, Adam Davis, Kelly Meade, Emerita Brigino-Buenaventura, Michael A. LeNoir, Kirsten Bibbins-Domingo, Esteban G. Burchard and Eran Halperin, *The Effects of Migration and Assortative Mating on Admixture Linkage Disequilibrium*, **Genetics**, 205.1 (2017): 375-383.
14. Elior Rahmani, Liat Shenhav, Regev Schweiger, Paul Yousefi, Karen Huen, Brenda Eskenazi, Celeste Eng, Scott Huntsman, Donglei Hu, Joshua Galanter, Sam S. Oh, Melanie Waldenberger, Konstantin Strauch, Harald Grallert, Thomas Meitinger, Christian Gieger, Nina Holland, Esteban G. Burchard, Noah Zaitlen and Eran Halperin, *Genome-wide methylation data mirror ancestry information*, **Epigenetics & Chromatin**, 205.1 (2017): 375-383.
15. Rozov, Roye, Aya Kav Brown, David Bogumil, Eran Halperin, Itzhak Mizrahi, and Ron Shamir, *Recycler: an algorithm for detecting plasmids from de novo assembly graphs*, **Bioinformatics** 33.4 (2017): 475-482.
16. Elior Rahmani Reut Yedidim Liat Shenhav Regev Schweiger Omer Weissbrod Noah Zaitlen and Eran Halperin, *GLINT: a user-friendly toolset for the analysis of high-throughput DNA-methylation array data*, **Bioinformatics** (2017): btx059.
17. Rhead, Brooke, et al. *Rheumatoid arthritis nave T cells share hypermethylation sites with synoviocytes.*, **Arthritis & Rheumatology** (2016).
18. Waldman, Yedaël Y., Arjun Biddanda, Maya Dubrovsky, Christopher L. Campbell, Carole Oddoux, Eitan Friedman, Gil Atzmon, Eran Halperin, Harry Ostrer, and Alon Keinan. *The genetic history of Cochin Jews from India*. **Human Genetics** 135, no. 10 (2016): 1127-1143
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20. Elior Rahmani, Noah Zaitlen, Yael Baran, Celeste Eng, Donglei Hu, Joshua Galanter, Sam Oh, Esteban G. Burchard, Eleazar Eskin, James Zou, and Eran Halperin, *Sparse PCA Corrects for Cell-Type Heterogeneity in Epigenome-Wide Association Studies*, **Nature Methods**, 13.5 (2016): 443-445.

21. Waldman, Yedael Y., et al. *The genetics of Bene Israel from India reveals both substantial Jewish and Indian ancestry*, **PLoS One**, online advanced publication, March 24, 2016.
22. Paula Singmann, Doron Shem-Tov, Simone Wahl, Harald Grallert, Giovanni Fiorito, So-Youn Shin, Katharina Schramm, Petra Wolf, Sonja Kunze, Yael Baran, Simonetta Guarrera, Paolo Vineis, Vittorio Krogh, Salvatore Panico, Rosario Tumino, Anja Kretschmer, Christian Gieger, Annette Peters, Holger Prokisch, Caroline L. Relton, Giuseppe Matullo, Thomas Illig, Melanie Waldenberger, Eran Halperin, *Characterization of whole-genome autosomal differences of DNA methylation between men and women*, **Epigenetics & Chromatin**, 2015, 8:43 (19 October 2015).
23. James Y. Zou, Danny S Park, Esteban G Burchard, Dara G Torgerson, Maria Pino-Yanes, Yun S. Song, Sriram Sankararaman*, Eran Halperin*, Noah Zaitlen*, *A genetic and socio-economic study of mate choice in Latinos reveals novel assortment patterns*, **Proceedings of the National Academy of Science**, 112.44 (2015): 13621-13626.
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24. Baran, Yael, and Eran Halperin, *A Note on the Relations Between Spatio-Genetic Models*, **Journal of Computational Biology**, October 2015, 22(10): 905-917, 2015.
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29. Catherine A Brownstein, . . . , Eran Halperin, . . . , David M Margulies, *An international effort towards developing standards for best practices in analysis, interpretation and reporting of clinical genome sequencing results in the CLARITY Challenge*, **Genome biology**, 15.3: R53, 2014.
30. Itamar Eskin, Farhad Hormozdiari, Lucia Conde, Chris Skibola, Jacques Riby, Eleazar Eskin and Eran Halperin, *eALPS: Estimating Abundance Levels in Pooled Sequencing Using Available Genotyping Data*, **Journal of Computational Biology**, 2013 Nov;20(11):861-77. (Special issue of **RECOMB**, 2013).
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34. Ronen R, Udpa N, Halperin E, Bafna V, *Learning Natural Selection from the Site Frequency Spectrum*, **Genetics**. 2013 Jun 14.
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36. de Boer SP, Cheng JM, Garcia-Garcia HM, Oemrawsingh RM, van Geuns RJ, Regar E, Zijlstra F, Laaksonen R, Halperin E, Kleber ME, Koenig W, Boersma E, Serruys PW, *Relation of genetic profile and novel circulating biomarkers with coronary plaque phenotype as determined by intravascular ultrasound: rationale and design of the ATHEROREMO-IVUS study*, **EuroIntervention**. 2013 Aug 26. doi:pil: 20130113-01
37. Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin, Eleazar Eskin, *CNVeM: Copy Number Variation Detection Using Uncertainty of Read Mapping*, **Journal of Computational Biology**, 2013 Mar; 20(3):224-36. (Special issue of **RECOMB**, 2012).
38. Osvaldo Zagordi, Armin Tpfers, Sandhya Prabhakaran, Volker Roth, Eran Halperin, Niko Beerenwinkel, *Probabilistic Inference of Viral Quasispecies Subject to Recombination*, **Journal of Comput Biology**, 2013 Feb;20(2):113-23. (Special issue of **RECOMB**, 2012).
39. Yang WY, Novembre J, Eskin E, Halperin E, *A model-based approach for analysis of spatial structure in genetic data*, **Nature Genetics**, 20;44(6):725-31, 2012.
40. Baran, Yael and Pasaniuc, Bogdan and Sankararaman, Sriram and Torgerson, Dara G. and Gignoux, Christopher and Eng, Celeste and Rodriguez-Cintron, William and Chapela, Rocio and Ford, Jean G. and Avila, Pedro C. and Rodriguez-Santana, Jose and Burchard, Esteban Gonzalez and Halperin, Eran, *Fast and accurate inference of local ancestry in Latino populations*, **Bioinformatics**, 28 (10), 1359-1367, (2012).
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43. Baran Yael, Halperin Eran, *Joint analysis of multiple metagenomic samples*, **PLoS Computational Biology**, 2012 Feb;8(2):e1002373.
44. Slager SL, et a., *Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia*, **Blood**, 120(4):843-6, 2012.
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52. Amir Kovacs, Noa Ben-Jacob, Hanna Tayem, Eran Halperin, Fuad A. Iraqi and Uri Gophna, *Genotype is a Stronger Determinant than Sex of the Mammalian Gut Microbiota*, **Microbial Ecology**, Feb;61(2):423-428, 2011.
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Papers published as a member of GWAS consortia I contributed to the CARDIOGRAM consortium, the CHARGE consortium, and the 1000 Genomes Project. These are the resulting publications:

99. 1000 Genomes Project *Integrative annotation of variants from 1092 humans: application to cancer genomics*, **Science**. 2013 Oct 4;342(6154)
100. Ho JE, et al., CardioGRAM consortium, *Common genetic variation at the IL1RL1 locus regulates IL-33/ST2 signaling*, **J Clin Invest.**, 2013 Oct 1;123(10):4208-18.
101. Sabater-Lleal M, et al., CardioGRAM consortium, *Multiethnic meta-analysis of genome-wide association studies in ≈ 100 000 subjects identifies 23 fibrinogen-associated Loci but no strong evidence of a causal association between circulating fibrinogen and cardiovascular disease.*, **Circulation**, 2013 Sep 17;128(12):1310-24.
102. Lieb et al., CardioGRAM consortium, *Genetic predisposition to higher blood pressure increases coronary artery disease risk*, **Hypertension**, 2013 May;61(5):995-1001.
103. 1000 Genomes Project *An integrated map of genetic variation from 1,092 human genomes*, **Nature**, 491(7422):56-65, 2012.
104. Demirkan A, et al., (CARDIOGRAM and CHARGE), *Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations*, **PLoS Genetics**, 2012 Feb;8(2):e1002490
105. IBC 50K CAD Consortium (as part of CardioGRAM) *Large-scale gene-centric analysis identifies novel variants for coronary artery disease*, **PLoS Genetics**, 2011 Sep;7(9):e1002260.
106. Suhre K et al., CARDIOGRAM consortium, *Human metabolic individuality in biomedical and pharmaceutical research*, **Nature**, 31;477(7362):54-60, 2011.
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108. Heribert Schunkert, Inke R. Knig, Sekar Kathiresan, . . . , Eran Halperin, . . . , Nilesh J., *Samani for the CARDIOGRAM Consortium, Large-scale association analysis identifies 13 new susceptibility loci for coronary artery disease*, **Nature Genetics**, April ;43(4):333-338, 2011.
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Peer reviewed conference papers:

110. Elinor Rahmani, Regev Schweiger, Saharon Rosset, Sriram Sankararaman and Eran Halperin, *Tensor Composition Analysis Detects Cell-Type Specific Associations in Epigenetic Studies*, **RECOMB**, 2018.
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