

Curriculum Vitae

Eran Halperin

Updated to : September 29, 2020.

Affiliation:

Professor, Department of Computer Science, University of California, Los Angeles (UCLA)
Professor, Department of Human Genetics, University of California, Los Angeles (UCLA)
Professor, Department of Anesthesiology, University of California, Los Angeles (UCLA)
Professor, Department of Computational Medicine, University of California, Los Angeles (UCLA)
Associate Director of Informatics, Institute of Precision Health, UCLA
Co-Director, Computational Genomics Summer Institute, UCLA
Director, AI in Medicine Program, UCLA

Research areas:

Statistical Genomics (microbiome, epigenomics, genetics, single-cell techniques), Algorithms (graphs, approximation, combinatorial), Machine Learning (applied to genomics and medicine), Computational Medicine.

Education:

- 1997-01 **Ph.D. in Computer Science**, Tel-Aviv University.
Thesis: *Approximation algorithms for optimization problems*.
Advisor: Prof. Uri Zwick.
- 1993-96 **M.Sc. in Computer Science**, Tel-Aviv University (Summa Cum Laude).
Thesis: *Bipartite subgraphs of integer weighted graphs*.
Advisor: Prof. Noga Alon.
- 1990-93 **B.Sc. in Mathematics and Computer Science**, Tel-Aviv University (Summa Cum Laude),

Experience

Academic Research Positions:

- 2018-now **Professor**, Department of Biomathematics, University of California, Los Angeles (**UCLA**)
- 2017-now **Professor**, Department of Human Genetics, University of California, Los Angeles (**UCLA**)
- 2017-now **Associate Director, Informatics**, The Institute of Precision Health, **UCLA**.
- 2016-now **Professor**, Departments of Computer Science , University of California, Los Angeles (**UCLA**)
- 2016-now **Professor**, Departments of Anesthesiology, University of California, Los Angeles (**UCLA**)
- 2011-2016 **Associate Professor**, Blavatnik School of Computer Science, and the Department of Molecular Microbiology and Biotechnology, **Tel-Aviv University**.
- 2004-2016 **Senior Research Scientist** at the International Computer Science Institute (**ICSI, Berkeley**).

2008-2011 **Senior Lecturer**, Blavatnik School of Computer Science, and the Department of Molecular Microbiology and Biotechnology, **Tel-Aviv University**.

2003-2004 **Research Associate** at the Computer Science department of **Princeton University**.

2001-03 **Post doc** at the Computer Science department of the University of California in **Berkeley**, and at the International Computer Science Institute (**ICSI**).

Hosts: Richard Karp, Christos Papadimitriou, Satish Rao, Alistair Sinclair.

July-August 2000 **Summer intern** in **AT&T research labs**, Florham Park, New Jersey.

Mentor: Edith Cohen.

Positions in the industry:

05/12-05/2020 **Computational Advisory Board** in **DNA Nexus**

07/11-12/2016 **Scientific Advisory Board** in **Genia Technologies** (nanopores sequencing technologies)

10/12-10/13 **Scientific Advisory Board** in **Gene by Gene**

07/07-12/08 **Director of Bioinformatics** in **Navigenics, Inc.** (genetic testing)

06/97-02/00 **Bioinformatics Scientist** at the **Algorithms group** in **Compugen LTD.**

1993-96 Programmer in the Israeli Defense Forces.

Consulting in the past for: **Intel**, **Invitae**, **Occam Law** , **Evogene**, **Micromedic**, **KHealth**, stealth start-ups.

Funding

1. Methods for Genomic Analysis in Heterogeneous Tissues, **NIH-NHGRI** HG010505 (PI), \$2,613,950, 9/2019-6/2023.
2. Replication studies for high dimensional data: Insights into confounding and heterogeneity, **NSF** 1705197 (co-PI), Eleazar Eskin (PI), \$499,995, 8/2019-7/2022.
3. Epigenetics of Socio-Environmental Effects on Asthma in Minorities, **NIH** 1R56MD013312-01 (co-I), Esteban Burchard (PI), Noah Zaitlen (PI). \$458,438.
4. Machine Learning Models for the Prediction of Adverse Outcomes after Surgery using EMR and Genetic Data, David Geffen School of Medicine Seed Grant, \$250,000, 9/1/2018-9/30/19.
5. Developing a pathway from genetic locus to gene for complex traits in rodents, **NIH-NIMH** 1R01MH115979 (co-I), Jonathan Flint (PI), 6/2018-2/2023.
6. III: Medium: Detecting Low Dimensional Structures in Genomic Data, **NSF** award number 1705197 (PI) , Eleazar Eskin (co-PI), and Jae-Hoon Sul (co-PI). Total award: \$1,199,663, 08/15/2017-8/15/2021.
7. Computational Methods for the Analysis of Methylation Data, **Blavatnik Research Fund**, \$50,000, period: 10/2015-10/2016.
8. Analytical method development for investigating the role of the X chromosome in population genetics and disease, **NIH** (Subcontract from Alon Keinan, Cornell). Total award: \$63,358, 2014-2016.

9. Methods for the Analysis of Rare Variants in Disease DNA-Sequencing Studies, **ISF** (Leading PI). Total award: \$264,000, 2013-2017.
10. Methods for preprocessing population sequence data, Binational Science Foundation, **BSF** and the **Gilbert Foundation** (Leading PI with Eleazar Eskin). Total award: \$197,600, 2013-2017.
11. Requequencing and Functional Studies, **NIH** (subcontract). Total subcontract award: \$303,780, period: 10/2011-9/2015.
12. Combinatorial Optimization Methods for Problems in Molecular Biology and Genetics, **NSF**: Award no. 1217615, \$497,380, period: 9/1/2012 - 8/31/2014.
13. Integrated Analysis of Novel Molecular Diagnostic Markers for Type 2 Diabetes, German Israeli Foundation, **GIF** (leading PI with Thomas Illig). Total award: 199,800 Euros, period: 1/2012-12/2014.
14. Open Collaborative Research. **IBM** (PI, together with Ron Shamir and Saharon Rosset). Total award: \$132,000, period: 10/2010-10/2012.
15. Efficient Design and Analysis of Disease Association Studies, Israeli Science Foundation, **ISF**. Total award: \$223,640, period: 10/2008-10/2012.
16. Genome-wide Association Study of Non-Hodgkin's Lymphoma, **NIH**: R01 (subcontract). Leading PI: Christine Skibola (UC Berkeley). Total subcontract award: \$127,704., period: 08/01/2006-07/31/2011
17. Estimating Haplotype Frequencies, **NSF**: IIS-0513599 (leading PI). Total award: \$603,773, period: 09/15/2005-08/31/2008.
18. Population Stratification Methods, **NSF**: IIS-0713254 (leading PI). Total award: \$449,962, period: 08/15/2007-07/31/2009.

Awards and Honors:

- 2014 The **Juludan Research Fund Prize**
- 2012 Chosen by The Marker Magazine (Israeli business magazine) as one of the **40 promising Israelis younger than 40**.
- 2010 The Raymond and Beverly Sackler **Career Development Chair**.
- 2010 The **Krill** prize for excellence in scientific research.
- 2001 The **Rothschild** fellowship (for post-doc).
- 2000 The **Intel** prize (for Ph.D.), Tel-Aviv University.
- 2000 The **Checkpoint** prize (for Ph.D.), Tel-Aviv University.
- 1999 The **Maus** prize (for Ph.D.), Tel-Aviv University.
- 1993 24th in the **Putnum** mathematics competition.
- 1991-92 Prize of excellence in the 32nd and in the 33rd Grossman mathematics Olympics of the Israel Institute of Technology, the Technion.

Academic Activities:

1. Scientific committees (Past 5 years):

- Co-director and organizer, Computational Genomics Summer Institute (CGSI), 2016-now
- Organizer: Bertinoro Computational Biology, 2014,2018.
- Steering Committee, RECOMB-SEQ, 2013-now.
- Program Committee, RECOMB, 2016
- Program Committee, RECOMB-Genetics, 2016
- Steering Committee, RECOMB-SEQ, 2015.
- Program Committee: RECOMB, 2015

2. Invited speaker (selected from past 5 years)

- 2020 Invited speaker, AI for COVID-19 in LA Symposium, University of Southern California (virtual)
- 2020 Invited speaker, The Doheny-UCLA International Retina Symposium, Pasadena, CA
- 2019 Invited speaker, Annual meeting of the American Society of Anesthesiology, Orlando.
- 2019 Invited speaker and panelist, UC-wide AI in Biomedicine.
- 2019 Invited speaker, Bioinformatics seminar series, UCSD.
- 2018 Invited speaker, IPM Seminar series, Mount Sinai.
- 2018 Invited speaker, CS Colloquium Series, University of Indiana
- 2017 Invited speaker, Banff International Research Station, Oaxaca, Mexico.
- 2017 Keynote speaker, NIPS workshop on Machine Learning in Computational Biology.
- 2017 Keynote speaker, 2nd QCB Symposium, UCLA.
- 2017 Invited speaker, department of Electrical Engineering, UCLA.
- 2016 Invited speaker, Computer Science colloquium, The Hebrew University.
- 2016 Invited speaker, The Technion Machine Learning seminar.
- 2016 Invited speaker, Computer Science colloquium, Ben-Gurion University.
- 2016 Invited speaker, Life Sciences colloquium, Ben-Gurion University.
- 2016 Invited speaker at the biostatistics seminar, Stanford University.
- 2016 Invited speaker at the Annual meeting of the Israeli Statistical Association
- 2016 Invited speaker at the Waterman Symposium, Los Angeles.

Students:

Post-docs

- 2019-2020 Dr. Misagh Kordi, post-doc, UCLA.
- 2018-2020 Dr. Igor Mandric, post-doc, UCLA.
- 2014-2016 Dr. Yedael Waldman, Post-doc, Tel-Aviv University,
- 2009-2009 Dr. Noah Zaitlen, Post-doc, Tel-Aviv University. (currently an associate professor at UCLA).

- 2008-2009 Dr. Bogdan Pasaniuc, Post-doc, International Computer Science Institute, Berkeley (currently an associate professor at UCLA).
- 2007-2008 Dr. Lucia Conde, Post-doc, International Computer Science Institute, Berkeley (currently at University College London)
- 2006-2008 Dr. Gad Kimmel, Post-doc, International Computer Science Institute, Berkeley.

PhD

- 2020-now Nadav Rakocz, PhD candidate, Computer Science, UCLA.
- 2019-now Ulzee An, PhD candidate, Computer Science, UCLA.
- 2019-now Zeuyan Chen, PhD candidate, Computer Science, UCLA
- 2018-now Leah Briscoe, PhD candidate, Bioinformatics, UCLA
- 2018-now Mike Thompson PhD candidate, Bioinformatics, UCLA
- 2018-now Brandon Jew, PhD candidate, Bioinformatics, UCLA
- 2018-now Brian Hill, PhD candidate, Computer Science, UCLA
- 2016-2020 Elior Rahmani, PhD candidate, Computer Science, UCLA
- 2016-2020 Liat Shenhav, PhD candidate, Computer Science, UCLA
- 2013-2018 Regev Schweiger, PhD candidate, Computer Science, Tel-Aviv University (currently at MyHeritage).
- 2011-2018 Roye Rozov Ph.D, Computer Science, Tel-Aviv University (joint supervision with Prof. Ron Shamir).
- 2012-2016 Yael Baran, PhD , Computer Science, Tel-Aviv University (currently post-doc at Weizmann Institute)

MSC

- 2015-2017 Gal Hayms (joint supervision with Dr. Itay Mayrose), MSc candidate, Life Sciences, Tel-Aviv University.
- 2013-2016 Goor Sasson, (joint supervision with Prof. Itzhak Mizrahi, Volcani), MSc candidate, Life Sciences, Tel-Aviv University
- 2013-2016 Elior Rahmani, MSc candidate, Computer Science, Tel-Aviv University.
- 2012-2014 Doron Shem-Tov, MSc, Computer Science, Tel-Aviv University.
- 2011-2013 Itamar Eskin , (joint supervision with Dr. Yoel Shkolnisky), M.Sc., Applied Math, Tel-Aviv University
- 2011-2014 Yaara Arkin, M.Sc., Bioinformatics track, Computer Science, Tel-Aviv University
- 2011-2015 Yaron Margalit, M.Sc. , Computer Science, Tel-Aviv University
- 2010-2013 Noam Mamet (joint supervision with Prof. Uri Gophna), M.Sc., Mathematical Biology track, Life Sciences, Tel-Aviv University
- 2009-2012 Tal Efros, M.Sc., Computer Science, Tel-Aviv University
- 2009-2012 Oron Navon, M.Sc., Bioinformatics track, Life Sciences, Tel-Aviv University
- 2009-2012 Yael Baran, MSc., Bioinformatics track, Computer Science, Tel-Aviv University

Teaching (last five years):

- 2020 Machine Learning in Genetics (CM124), UCLA.
- 2019 Computational Genetics (CM124), UCLA.
- 2018 Computational Genetics (CM124), UCLA.
- 2017 Computational Genetics (CM124), UCLA.
- 2015-16 Advanced seminar in Bioinformatics, Tel-Aviv University.
- 2015-16 Introduction to Machine Learning, Tel-Aviv University.
- 2015-16 Introduction to Data Structure, Tel-Aviv University.
- 2015-16 Introduction to Bioinformatics, Tel-Aviv University.

Publication List

Journal papers:

1. Goodman-Meza D, Rudas A, Chiang JN, Adamson PC, Ebinger J, Sun N, Botting P, Fulcher JA, Saab FG, Brook R, Eskin E, An U, Kordi M, Jew B, Balliu B, Chen Z, Hill BL, Rahmani E, Halperin E, Manuel V. *A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity.* **PLoS One.** 2020 Sep 22;15(9):e0239474. doi: 10.1371/journal.pone.0239474. PMID: 32960917.
2. Miao Z, Alvarez M, Ko A, Bhagat Y, Rahmani E, Jew B, Heinonen S, Muñoz-Hernandez LL, Herrera-Hernandez M, Aguilar-Salinas C, Tusie-Luna T, Mohlke KL, Laakso M, Pietiläinen KH, Halperin E, Pajukanta P. *The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance.* **PLoS Genetics** 2020 Sep 14;16(9):e1009018. doi: 10.1371/journal.pgen.1009018. PMID: 32925908.
3. Martino C, Shenhav L, Marotz CA, Armstrong G, McDonald D, Vázquez-Baeza Y, Morton JT, Jiang L, Dominguez-Bello MG, Swafford AD, Halperin E, Knight R. *Context-aware dimensionality reduction deconvolutes gut microbial community dynamics.* **Nature Biotechnology.** 2020 Aug 31. doi: 10.1038/s41587-020-0660-7. Epub ahead of print. PMID: 32868914.
4. Alvarez M, Rahmani E, Jew B, Garske KM, Miao Z, Benhammou JN, Ye CJ, Pisegna JR, Pietiläinen KH, Halperin E, Pajukanta P. *Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM.* **Scientific reports.** 2020 Jul 3;10(1):11019. doi: 10.1038/s41598-020-67513-5. PMID: 32620816; PMCID: PMC7335186.
5. Mandric I, Hill BL, Freund MK, Thompson M, Halperin E. *BATMAN: Fast and Accurate Integration of Single-Cell RNA-Seq Datasets via Minimum-Weight Matching.* **iScience.** 2020 Jun 26;23(6):101185. doi: 10.1016/j.isci.2020.101185. Epub 2020 May 20. PMID: 32504875; PMCID: PMC7276436.
6. Agrawal A, Chiu AM, Le M, Halperin E, Sankararaman S. *Scalable probabilistic PCA for large-scale genetic variation data.* **PLoS Genetics** 2020 May 29;16(5):e1008773. doi: 10.1371/journal.pgen.1008773. PMID: 32469896; PMCID: PMC7286535.
7. Joseph TA, Shenhav L, Xavier JB, Halperin E, Pe'er I. *Compositional Lotka-Volterra describes microbial dynamics in the simplex.* **PLoS Computational Biology** 2020 May 29;16(5):e1007917. doi: 10.1371/journal.pcbi.1007917. PMID: 32469867; PMCID: PMC7325845.
8. Jew B, Alvarez M, Rahmani E, Miao Z, Ko A, Garske KM, Sul JH, Pietiläinen KH, Pajukanta P, Halperin E. *Accurate estimation of cell composition in bulk expression through robust integration of single-cell information.* **Nature Communications** 2020 Apr 24;11(1):1971. doi: 10.1038/s41467-020-15816-6. Erratum in: Nat Commun. 2020 Jun 3;11(1):2891. PMID: 32332754; PMCID: PMC7181686.
9. Furman O, Shenhav L, Sasson G, Kokou F, Honig H, Jacoby S, Hertz T, Cordero OX, Halperin E, Mizrahi I. *Stochasticity constrained by deterministic effects of diet and age drive rumen microbiome assembly dynamics.* **Nature Communications.** 2020 Apr 20;11(1):1904. doi: 10.1038/s41467-020-15652-8. PMID: 32312972; PMCID: PMC7170844.

10. Grunin M, Beykin G, Rahmani E, Schweiger R, Barel G, Hagbi-Levi S, Elbaz-Hayoun S, Rinsky B, Ganiel M, Carmi S, Halperin E, Chowers I. *Association of a Variant in VWA3A with Response to Anti-Vascular Endothelial Growth Factor Treatment in Neovascular AMD*. **investigative ophthalmology & visual science** 2020 Feb 7;61(2):48. doi: 10.1167/iovs.61.2.48. PMID: 32106291; PMCID: PMC7329947.
11. Brown Kav A, Rozov R, Bogumil D, Sørensen SJ, Hansen LH, Benhar I, Halperin E, Shamir R, Mizrahi I. *Unravelling plasmidome distribution and interaction with its hosting microbiome*. **Environmental microbiology** 2020 Jan;22(1):32-44. doi: 10.1111/1462-2920.14813. Epub 2019 Dec 15. PMID: 31602783.
12. Shenhav, Liat, Mike Thompson, Tyler A. Joseph, Leah Briscoe, Ori Furman, David Bogumil, Itzhak Mizrahi, Itsik Pe'er, and Eran Halperin. *FEAST: fast expectation-maximization for microbial source tracking.*, **Nature methods** (2019): 1.
13. Rahmani, E., Schweiger, R., Rhead, B., Criswell, L.A., Barcellos, L.F., Eskin, E., Rosset, S., Sankararaman, S. and Halperin, E. , *Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology*, **Nature Communications**, Jul 31;10(1):3417, 2019.
14. Thompson, M., Chen, Z.J., Rahmani, E. and Halperin, E., *CONFINED: distinguishing biological from technical sources of variation by leveraging multiple methylation datasets*. **Genome biology**, 20(1), p.138, 2019.
15. Hill, B.L., Brown, R., Gabel, E., Rakocz, N., Lee, C., Cannesson, M., Baldi, P., Loohuis, L.O., Johnson, R., Jew, B. and Maoz, U., *An automated machine learning-based model predicts postoperative mortality using readily-extractable preoperative electronic health record data*. **British Journal of Anaesthesia**, 123(6), pp.877-886 (2019)
16. Fisher, Eyal, Rafael Y. Brzezinski, Michal Ehrenwald, Itzhak Shapira, David Zeltser, Shlomo Berliner, Yonit Marcus 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** 43, no. 4 (2019): 800.
17. Shenhav, Liat, Ori Furman, Leah Briscoe, Mike Thompson, Justin D. Silverman, Itzhak Mizrahi, and Eran Halperin. *Modeling the temporal dynamics of the gut microbial community in adults and infants*. **PLOS Computational Biology** 15, no. 6 (2019): e1006960.
18. Kav, A.B., Rozov, R., Bogumil, D., Sørensen, S.J., Hansen, L.H., Benhar, I., Halperin, E., Shamir, R. and Mizrahi, I., *Unravelling plasmidome distribution and interaction with its hosting microbiome*, **Environmental microbiology**. (2019).
19. Wallace, R. John, Goor Sasson, Philip C. Garnsworthy, Ilma Tapio, Emma Gregson, Paolo Bani, Pekka Huhtanen et al. *A heritable subset of the core rumen microbiome dictates dairy cow productivity and emissions.*, **Science advances** 5, no. 7 (2019): eaav8391.
20. Schweiger, Regev, Eyal Fisher, Omer Weissbrod, Elinor Rahmani, Martina Müller-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.

21. 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.
22. Hofer, Ira S., Eran Halperin, and Maxime Cannesson. *Opening the Black Box: Understanding the Science Behind Big Data and Predictive Analytics.*, **Anesthesia & Analgesia** 127, no. 5 (2018): 1139-1143.
23. 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.
24. 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).
25. 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.
26. 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.
27. 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.
28. Schweiger, Regev, Omer Weissbrod, Elior Rahmani, Martina Müller-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.
29. 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**).
30. 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.
31. 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.

32. Elijor 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.
33. Rozov, Roye, Gil Goldshlager, Eran Halperin, and Ron Shamir, *Faucet: streaming de novo assembly graph construction*, **Bioinformatics** 34, no. 1 (2017): 147-154.
34. 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.
35. 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.
36. Rhead, Brooke, et al. *Rheumatoid arthritis T cells share hypermethylation sites with synovio-cytes.*, **Arthritis & Rheumatology** (2016).
37. 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
38. Schweiger, Regev, Shachar Kaufman, Reijo Laaksonen, Marcus E. Kleber, Winfried März, Eleazar Eskin, Saharon Rosset, and Eran Halperin. *Fast and accurate construction of confidence intervals for heritability.*, **The American Journal of Human Genetics**, 98.6 (2016): 1181-1192.
39. Elijor 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.
40. Waldman, Yedaël 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.
41. 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).
42. 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.

* Equal contribution

43. 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.
44. Zou, J. Y., Eran Halperin, Burchard, E., and Sankararaman, S., *Inferring parental genomic ancestries using pooled semi-Markov processes*, **Bioinformatics**, 31 (12) : i190-i196, 2015 (Special issue of **ISMB**, 2015).
45. Rozov, Roye, Ron Shamir, and Eran Halperin, *Fast lossless compression via cascading Bloom filters* **BMC bioinformatics** 15.Suppl 9 (2014): S7. (Special issue of **RECOMB-SEQ**, 2014).
46. Yaara Arkin, Elior Rahmani, Marcus E. Kleber, Reijo Laaksonen, Winfried Marz and Eran Halperin, *EPIQ efficient detection of SNP SNP epistatic interactions for quantitative traits*, **Bioinformatics**, 30 (12): i19-i25, 2014. (Special issue of **ISMB**, 2014).
47. Doron Shem-Tov and Eran Halperin, *Historical Pedigree Reconstruction from Extant Populations Using PArtitioning of RElatives (PREPARE)*. **PLoS Comput Bio**, 10(6): e1003610. doi:10.1371/journal.pcbi.1003610, 2014.
48. 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.
49. 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).
50. Baran Y, Quintela I, Carracedo A, Pasaniuc B, Halperin E. *Enhanced Localization of Genetic Samples through Linkage-Disequilibrium Correction.*, **American Journal of Human Genetics**, 2013.
51. Gymrek M, McGuire AL, Golan D, Halperin E, Erlich Y., *Identifying personal genomes by surname inference*, **Science**, Jan 18;339(6117):321-4, 2013.
52. Navon O, Sul JH, Han B, Conde L, Bracci P, Riby J, Skibola CF, Eskin E, *Halperin E. Rare Variant Association Testing Under Low-Coverage Sequencing*, **Genetics**, 2013.
53. Ronen R, Udpa N, Halperin E, Bafna V, *Learning Natural Selection from the Site Frequency Spectrum*, **Genetics**. 2013 Jun 14.
54. Pasaniuc B, Sankararaman S, Torgerson DG, Gignoux C, Zaitlen N, Eng C, Rodriguez-Cintron W, Chapela R, Ford JG, Avila PC, Rodriguez-Santana J, Chen GK, Le Marchand L, Henderson B, Reich D, Haiman CA, Gonzalez Burchard E, Halperin E., *Analysis of Latino populations from GALA and MEC studies reveals genomic loci with biased local ancestry estimation*, **Bioinformatics**,. 2013 Jun 1;29(11):1407-1415.
55. 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:p11: 20130113-01

56. 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).
57. Osvaldo Zagordi, Armin Topler, Sandhya Prabhakaran, Volker Roth, Eran Halperin, Niko Beerenwinkel, *Probabilistic Inference of Viral Quasispecies Subject to Recombination*, **Journal of Comput Biol**, 2013 Feb;20(2):113-23. (Special issue of **RECOMB**, 2012).
58. 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.
59. 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).
60. Efron Anatoly, Halperin Eran. *Haplotype reconstruction using perfect phylogeny and sequence data*, **BMC Bioinformatics**. 2012 Apr 19;13 Suppl 6:S3.
61. Rozov Roye, Halperin Eran, Shamir Ron., *MGMR: leveraging RNA-Seq population data to optimize expression estimation*, **BMC Bioinformatics**. 2012 Apr 19;13 Suppl 6:S2
62. Baran Yael, Halperin Eran, *Joint analysis of multiple metagenomic samples*, **PLoS Computational Biology**, 2012 Feb;8(2):e1002373.
63. Slager SL, et a., *Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia*, **Blood**, 120(4):843-6, 2012.
64. Bonnie Kirkpatrick, Shuai Cheng Li, Richard M. Karp and Eran Halperin, *Pedigree Reconstruction Using Identity by Descent*, **Journal of Computational Biology**, 18.11 (2011): 1481-1493.
65. Conde L, Bevan S, Sitzler M, Klopp N, Illig T, Thiery J, Seissler J, Baumert J, Raitakari O. Khnen M, Lytikinen LP, Laaksonen R, Viikari J, Lehtimki T, Koernig W, Halperin E, Markus HS, *Novel associations for coronary artery disease derived from genome wide association studies are not associated with increased carotid intima-media thickness, suggesting they do not act via early atherosclerosis or vessel remodeling*, **Atherosclerosis**, 2011 Dec;219(2):684-9.
66. Salton M, Elkon R, Borodina T, Davydov A, Yaspo ML, Halperin E, Shiloh Y, *Matrin 3 binds and stabilizes mRNA*, **PLoS One**, 6(8), pages 1-7, 2011.
67. Wang J, Geesman GJ, Hostikka SL, Atallah M, Blackwell B, Lee E, Cook PJ, Pasaniuc B, Shariat G, Halperin E, Dobke M, Rosenfeld MG, Jordan IK, Lunyak VV, *Inhibition of activated pericentromeric SINE/Alu repeat transcription in senescent human adult stem cells reinstates self-renewal*, **Cell Cycle**. Sep 1;10(17), 3016-3030, 2011.
68. Lucia Conde, Paige Bracci, Eran Halperin, and Christine F. Skibola, *A search for overlapping susceptibility loci between non-Hodgkin lymphoma and autoimmune diseases*, **Genomics**, Jul;98(1):9-14, 2011.

69. Dan He, Noah Zaitlen, Bogdan Pasaniuc, Eleazar Eskin, and Eran Halperin, *Genotyping common and rare variation using overlapping pool sequencing*, **BMC Bioinformatics**, 12(Suppl 6):S2, 1-8, 2011.
70. Bogdan Pasaniuc, Noah Zaitlen and Eran Halperin, *Accurate estimation of expression levels of homologous genes in RNA-seq experiments*, **Journal of Computational Biology**, Mar; 18(3):459-68, 2011. (Special issue of **RECOMB**).
71. 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.
72. Badri Padhukashashasram, Eran Halperin, Jennifer Wessel, Daryl Thomas, Elana Silver, Heather Trumbower, Michelle Cargill, Dietrich Stephan, *Presymptomatic risk assessment for chronic non-communicable diseases*, **Plos One**, Dec 31;5(12):e14338, pages 1-15, 2010.
73. Bogdan Pasaniuc, Ram Avinery, Tom Gur, Christine F. Skibola, Paige M. Bracci, and Eran Halperin, *A Generic Coalescent-based Method for the Selection of a Reference Panel for Imputation*, **Genetic Epidemiology**, 34(8):773-82, 2010.
74. Roy Ronen, Ido Gan, Shira Modai, Alona Sukacheov, Gideon Dror, Eran Halperin and Noam Shomron, *miRNAkey: a software for microRNA deep sequencing analysis*, **Bioinformatics**, 26 (20), 2615-2616, 2010.
75. Lucia Conde, Eran Halprein, et al., *Genome-wide association study of follicular lymphoma identifies a risk locus at 6p21.32*, **Nature Genetics**, 42(8), 661-664, 2010.
76. Bonnie Kirkpatrick, Eran Halperin, and Richard Karp, *Haplotype inference in complex pedigrees*, **Journal of Computational Biology**, Mar;17(3):269-80, 2010. (special issue of **RECOMB**).
77. O. Davidovich, G. Kimmel, E. Halperin, R. Shamir, *Increasing the Power of Association Studies by Imputation-based Sparse Tag SNP Selection*, **Communications in Information and Systems**, 9 (3) 269-282 (2009).
78. Noah Zaitlen, Bogdan Pasaniuc, Tom Gur, Elad Ziv, Eran Halperin, *Leveraging genetic variability across populations for the identification of causal variants*, **The American Journal of Human Genetics**, 2010 Jan; 86(1):23-33.
79. Bracci PM, Skibola CF, Conde L, Halperin E, Lightfoot T, Smith A, Paynter RA, Skibola DR, Agana L, Roman E, Kane E, Wiencke JK, *Chemokine polymorphisms and lymphoma: a pooled analysis*, **Leuk Lymphoma**, 2010 Mar;51(3):497-506.
80. Lindfors E, Gopalacharyulu PV, Halperin E, Oresic M., *Detection of molecular paths associated with insulinitis and type 1 diabetes in non-obese diabetic mouse*, **Plos One**, 2009 Oct 2;4(10).
81. Sriram Sankararaman, Guillaume Obozinski, Michael I. Jordan, and Eran Halperin, *Genomic Privacy and Limits of Individual Detection in a Pool*, **Nature Genetics**, 41, 965 - 967 (2009).

82. Christine F Skibola, Paige M Bracci, Eran Halperin, Lucia Conde, David W Craig, Luz Agana, Kelly Iyadurai, Nikolaus Becker, Angela Brooks-Wilson, John D Curry, John J Spinelli, Elizabeth A Holly, Jacques Riby, Luoping Zhang, Alexandra Nieters, Martyn T Smith and Kevin M Brown, *Genetic variants at 6p21.33 are associated with susceptibility to follicular lymphoma*, **Nature Genetics**, 41, 873 - 875 (2009)
83. Bogdan Pasaniuc, Sriram Sankararaman, Gad Kimmel and Eran Halperin, *Inference of Locus-Specific Ancestry in Closely Related Populations*, **Bioinformatics**, 2009 Jun 15;25(12):i213-21.
84. Eran Halperin and Dietrich A. Stephan, *Maximizing power in association studies*, **Nature Biotechnology**, 27(3), 255-6, 2009.
85. Eran Halperin and Dietrich A. Stephan *SNP imputation in association studies*, **Nature Biotechnology**, 27(4), 349-51, 2009.
86. Peddinti V. Gopalacharyulu, Vidya R. Velagapudi, Erno Lindfors, Eran Halperin and Matej Oresic, *Dynamic network topology changes in functional modules predict responses to oxidative stress in yeast*, **Molecular BioSystems**, 2009, DOI: 10.1039/b815347g.
87. Gad Kimmel, Richard M. Karp, Michael I. Jordan, and Eran Halperin, *Association Mapping and Significance Estimation via the Coalescent*, **The American Journal of Human Genetics**, 83(6) pp. 675-683, 2008.
88. Skibola CF, Bracci PM, Halperin E, Nieters A, Hubbard A, Paynter RA, Skibola DR, Agana L, Becker N, Tressler P, Forrest MS, Sankararaman S, Conde L, Holly EA, Smith MT, *Poly-morphisms in the estrogen receptor 1 and vitamin C and matrix metalloproteinase gene families are associated with susceptibility to lymphoma*, **PLoS ONE**, 3(7), 2008.
89. Sriram Sankararaman, Gad Kimmel, Eran Halperin, and Michael I. Jordan, *On the inference of ancestries in admixed populations*, **Genome Research**, 18:668-675, 2008. (special issue of RECOMB, 2008).
90. Sriram Sankararaman, Srinath Sridhar, Gad Kimmel, and Eran Halperin, *LAMP: Local Ancestry in adMixed Populations*, **The American Journal of Human Genetics**, Volume 82, Issue 2, 290-303, 2008.
91. Bonnie Kirkpatrick, Carlos Santos Armendariz, Richard M Karp, and Eran Halperin, *HAP-LOPOOL: Improving Haplotype Frequency Estimation through DNA Pools and Phylogenetic Modeling*, **Bioinformatics**, 23(22): 3048-3055 (2007).
92. Gad Kimmel, Michael I. Jordan, Eran Halperin, Ron Shamir and Richard M. Karp, *randomization test for controlling population stratification in whole-genome association studies*, **The American Journal of Human Genetics**, 81:895-905, 2007.
93. Noah Zaitlen, Hyun Min Kang, Eleazar Eskin, and Eran Halperin, *Leveraging the HapMap Correlation Structure in Association Studies*, **The American Journal of Human Genetics**, 80:683-691, 2007.
94. Srinath Sridhar, Kedar Dhamdhare, Guy E. Blleloch, Eran Halperin, R. Ravi, and Russell Schwartz, *Algorithms for Efficient Near-Perfect Phylogenetic Tree Reconstruction in Theory*

- and Practice*, **IEEE/ACM Trans. Comput. Biology Bioinform.** (TCBB) 4(4):561-571 (2007).
95. Kenneth B. Beckman, Kenneth A. Abel, Andreas Braun and Eran Halperin *Using DNA Pools for Genotyping Trios*, **Nucleic Acids Research**, 2006; doi: 10.1093/nar/gkl700.
 96. Jonathan Marchini, David Cutler, Nick Patterson, Matthew Stephens, Eleazar Eskin, Eran Halperin, Shin Lin, Steve Qin, Goncalo Abecassis, Heather Munro and Peter Donnelly, *A comparison of phasing algorithms for trios and unrelated individuals*, **American Journal of Human Genetics**, 78 437-450, 2006.
 97. Eleazar Eskin, Roded Sharan and Eran Halperin, *Optimally Phasing Long Genomic Regions using Local Haplotype Predictions*, *Journal of Bioinformatics and Computational Biology (JBCB)*, 4, pp. 639-647, 2006.
 98. Rajiv Gandhi, Eran Halperin, Samir Khuller, Guy Kortsarz and Aravind Srinivasan, *Improved bounds for vertex cover with hard capacities*, *Journal of Computer Systems Sciences (JCSS)*, 72(1):16–33 (2006).
 99. Eran Halperin and Elad Hazan, *HAPLOFREQ - Estimating Haplotype Frequencies Efficiently*, special issue of *Journal of Computational Biology (JCB)*, March 2006, Vol. 13, No. 2: 481-500. Also appeared in the proceedings of the 9th conference on Research in Computational Biology (**RECOMB**), 2005, 553–568.
 100. Noah A. Zaitlen, Hyun Min Kang, Michael L. Feolo, Stephen T. Sherry, Eran Halperin, and Eleazar Eskin, *Inference and analysis of haplotypes from combined genotyping studies deposited in dbSNP*, **Genome Research**, 2005, 15:1594-1600.
 101. 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 2005: 1072-1079.
 102. Eran Halperin, Gad Kimmel, Ron Shamir, *Tag SNP Selection in Genotype Data for Maximizing SNP Prediction Accuracy*, proceedings of the international conference on Intelligent Systems for Molecular Biology (**ISMB**, 2005). Also as **Bioinformatics**, Vol. 21 Suppl. 1 pp. i195-i203 (2005).
 103. Julia Chuzoy, Sudipto Guha, Eran Halperin, Sanjeev Khanna, Guy Kortsarz and Seffi Naor, *Tight lower bounds for the asymmetric k-center problem*, *Journal of the ACM (JACM)*, 52(4):538-551, 2005.
 104. Edith Cohen, Eran Halperin and Haim Kaplan, *Performance aspects of distributed caches using TTL-based consistency*, a special issue of *Theoretical Computer Science (TCS)*, 331(1): 73-96 (2005).
 105. Eran Halperin and Richard Karp, *The Minimum-Entropy Set Cover Problem*, a special issue of *Theoretical Computer Science (TCS)*, 348: 240-250 (2005).
 106. Eran Halperin and Eleazar Eskin, *Haplotype Reconstruction from Genotype Data using Imperfect Phylogeny*, **Bioinformatics** 20(12): 1842-1849 (2004).

107. Eran Halperin, Jeremy Buhler, Richard M. Karp, Robert Krauthgamer and Ben Westover, *Detecting protein sequence conservation via metric embedding*, proceedings of the eleventh international conference on Intelligent Systems for Molecular Biology (**ISMB**, 2003). Also, as a **Bioinformatics** supplement, 2003;19 Suppl 1:i122-9.
108. Eleazar Eskin, Eran Halperin and Richard M. Karp, *Efficient Reconstruction of Haplotype Structure via Perfect Phylogeny*, a special issue of Journal of Bioinformatics and Computational Biology (**JBCB**), 1 (1), 1-20, (2003).
109. Eran Halperin, Guy Kortsarz, Robert Krauthgamer, Aravind Srinivasan and Nan Wang. *Integrality ratio for Group Steiner Trees and Directed Steiner Trees*, proceedings of the 12th Symposium on Discrete Algorithms (**SODA**), 2003, 275–284. Accepted to Siam Journal on Computing (**SICOMP**).
110. Edith Cohen, Eran Halperin, Haim Kaplan and Uri Zwick, *Reachability and Distance Queries via 2-Hop Labels*, Siam Journal on Computing (**SICOMP**), 32 (5):1338-1355 (2003).
111. Eran Halperin, Shay Halperin, Tzvika Hartman and Ron Shamir, *Handling long targets and errors in sequencing by hybridization*, a special issue of the Journal of Computational Biology (**JCB**), 10 (3-4), 483-497, (2003). Also appeared in the proceedings of the 6th conference on Research in Computational Biology (**RECOMB**), 2002.
112. Eran Halperin, *Improved approximation algorithms for the vertex cover problem in graphs and hypergraphs*, Siam Journal on Computing (**SICOMP**), 31, 1608-1623, (2002).
113. Eran Halperin and Uri Zwick, *A unified framework for obtaining improved approximation algorithms for maximum graph bisection problems*, a special issue of **Random Structures and Algorithms**, 20(3):382-402 (2002).
114. Eran Halperin, Ram Nathaniel and Uri Zwick, *Coloring k -colorable graphs using smaller palettes*, **Journal of Algorithms**, 45(1): 72-90 (2002).
115. Eran Halperin and Uri Zwick, *Approximation algorithms for MAX 4-SAT and rounding procedures for semidefinite programs*, **Journal of Algorithms**, 40, 184-211 (2001).
116. Eran Halperin, Simchon Faigler and Raveh Gill-More, *FramePlus: A sensitive algorithm for aligning DNA to protein sequences*, a special issue of **Bioinformatics** 15 (11):867-873 1999.
117. Noga Alon and Eran Halperin, *Bipartite subgraphs of integer weighted graphs*, **Discrete Mathematics** 181, 1998, 19-29.

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:

118. 1000 Genomes Project *Integrative annotation of variants from 1092 humans: application to cancer genomics*, **Science**. 2013 Oct 4;342(6154)
119. 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.

120. 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.
121. Lieb et al., CardioGRAM consortium, *Genetic predisposition to higher blood pressure increases coronary artery disease risk*, **Hypertension**, 2013 May;61(5):995-1001.
122. 1000 Genomes Project *An integrated map of genetic variation from 1,092 human genomes*, **Nature**, 491(7422):56-65, 2012.
123. Demirkan A, et el., (CARDIOGRAM and CHARGE), *Genome-wide association study identifies novel loci associated with circulating phospho- and sphingolipid concentrations*, **PLoS Genetics**, 2012 Feb;8(2):e1002490
124. 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.
125. Suhre K et al., CARDIOGRAM consortium, *Human metabolic individuality in biomedical and pharmaceutical research*, **Nature**, 31;477(7362):54-60, 2011.
126. Bis JC, . . . , Halperin E, et al., *Meta-analysis of genome-wide association studies from the CHARGE consortium identifies common variants associated with carotid intima media thickness and plaque*, **Nature Genetics**, 2011, Sep 11;43(10):940-7.
127. 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.
128. Preuss, M., . . . , Halperin E., et al., *Design of the Coronary Artery Disease Genome-Wide Replication and Meta-Analysis (CARDIoGRAM) Study: A Genome-Wide Association Meta-Analysis Involving More than 22,000 Cases and 60,000 Controls*, **Circulation: Cardiovascular Genetics** , 3(5):475-483, 2010.

Peer reviewed conference papers:

129. Yaron Margalit, Yael Baran and Eran Halperin, *Multiple-Ancestor Localization for Recently Admixed Individuals*, **WABI**, 2015
130. Srinath Sridhar, Satish Rao, and Eran Halperin, *A Discrete Algorithm Approach to Detect Population Substructure*, the proceedings of the 11th conference on Research in Computational **RECOMB**, 2007.
131. Kamalika Chaudhuri, Eran Halperin, Satish Rao and Shuheng Zhou, *A Rigorous Analysis of Population Stratification with Limited Data*, proceedings of the 16th Symposium on Discrete Algorithms (**SODA**), 2007.
132. Guy E. Blelloch, Kedar Dhamdhere, Eran Halperin, R. Ravi, Russell Schwartz, and Srinath Sridhar, *Fixed Parameter tractability of Binary Near-Perfect Phylogenetic Tree Reconstructions*, proceedings of the International Colloquium on Automata, Languages and Programming (**ICALP**), 2006.

133. Srinath Sridhar, Kedar Dhamdhere, Guy E. Blleloch, Eran Halperin, R. Ravi and Russell Schwartz, *Simple Reconstruction of Binary Near-Perfect Phylogenetics Trees*, **PICCS**, 2006.
134. Eran Halperin and Richard Karp, *Perfect Phylogeny and Haplotype Assignment*, proceedings of the 7th conference on Research in Computational Biology (**RECOMB**), 2004, 10-19.
135. Eran Halperin, Robert Krauthgamer, *Polylogarithmic Inapproximability*, proceedings of the 35th Annual ACM Symposium on Theory of Computing (**STOC**), 2003, 585–594.
136. Eleazar Eskin, Eran Halperin and Richard M. Karp. *Large Scale Reconstruction of Haplotypes from Genotype Data*, proceedings of the 7th conference on Research in Computational Biology (**RECOMB**), 2003, 104–113.
137. Micah Adler, Eran Halperin, Richard M. Karp and Vijay V. Vazirani, *A stochastic process on the hypercube with applications to peer-to-peer networks*, proceedings of the 35th Annual ACM Symposium on Theory of Computing (**STOC**), 2003, 575–584.
138. Eran Halperin and Aravind Srinivasan, *Improved approximation algorithms for the partial vertex cover problem*, proceedings of the 5th International Workshop on Approximation Algorithms for Combinatorial Optimization (**APPROX**), 2002, 161-175.
139. Eran Halperin and Uri Zwick, *Combinatorial approximation algorithms for the maximum directed cut problem*, proceedings of the 12th Symposium on Discrete Algorithms (**SODA**) 2001, 1-7.

Peer reviewed conference papers that also appeared as a journal publication:

1. Mike Thompson, Zeyuan Johnson Chen, Elinor Rahmani, Eran Halperin: *Distinguishing Biological from Technical Sources of Variation Using a Combination of Methylation Datasets*. **RECOMB** 2019.
2. Elinor Rahmani, Regev Schweiger, Saharon Rosset, Sriram Sankararaman and Eran Halperin, *Tensor Composition Analysis Detects Cell-Type Specific Associations in Epigenetic Studies*, **RECOMB**, 2018.
3. Liat Shenhav, Mike Thompson, Tyler Joseph, Ori Furman, David Bogumil, Itzik Mizrahi and Eran Halperin, *Fast expectation maximization source tracking*, **RECOMB-SEQ**, 2018.
4. Schweiger, Regev, Eyal Fisher, Elinor Rahmani, Liat Shenhav, Saharon Rosset, and Eran Halperin, *Using Stochastic Approximation Techniques to Efficiently Construct Confidence Intervals for Heritability*, **RECOMB**, 2017.
5. Rahmani, Elinor, Regev Schweiger, Liat Shenhav, Eleazar Eskin, and Eran Halperin, *A Bayesian Framework for Estimating Cell Type Composition from DNA Methylation Without the Need for Methylation Reference.*, **RECOMB**, 2017.
6. Royce Rozov, Gil Goldshlager, Eran Halperin, Ron Shamir, *Faucet: streaming de novo assembly graph construction*, **RECOMB-SEQ**, 2017.
7. Weissbrod, Omer, Elinor Rahmani, Regev Schweiger, Saharon Rosset, and Eran Halperin, *Association testing of bisulfite-sequencing methylation data via a Laplace approximation*, **ISMB**, 2017.

8. Zou, J. Y., Eran Halperin, Burchard, E., and Sankararaman, S., *Inferring parental genomic ancestries using pooled semi-Markov processes*, **ISMB**, 2015
9. Arkin, Yaara, Elior Rahmani, Marcus E. Kleber, Reijo Laaksonen, Winfried Marz, and Eran Halperin, *EPIQ - efficient detection of SNP-SNP epistatic interactions for quantitative traits*, **ISMB**, 2014
10. Rozov, Roye, Ron Shamir, and Eran Halperin, *Fast lossless compression via cascading Bloom filters*, **RECOMB-SEQ**, 2014
11. Roy Ronen, Nitin Udpa, Eran Halperin and Vineet Bafna, *Learning Natural Selection from the Site Frequency Spectrum*, **RECOMB** 2013.
12. 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*, **RECOMB**, 2013.
13. Osvaldo Zagordi, Armin Tpfers, Sandhya Prabhakaran, Volker Roth, Eran Halperin, Niko Beerenwinkel, *Probabilistic Inference of Viral Quasispecies Subject to Recombination*, **RECOMB**, 2012.
14. Zhanyong Wang, Farhad Hormozdiari, Wen-Yun Yang, Eran Halperin, Eleazar Eskin, *CN-*VeM*: Copy Number Variation Detection Using Uncertainty of Read Mapping*, **RECOMB**, 2012.
15. Anatoly Efros, Eran Halperin, *Haplotype reconstruction using perfect phylogeny and sequence data*, **RECOMB-SEQ**, 2012
16. Rozov Roye, Eran Halperin, Shamir Ron, *MGMR: leveraging RNA-Seq population data to optimize expression estimation*, **RECOMB-SEQ**, 2012
17. Bonnie Kirkpatrick, Shuai Cheng Li, Richard M. Karp, and Eran Halperin, *Pedigree Reconstruction using Identity by Descent*, **RECOMB**, 2011.
18. Dan He, Noah Zaitlen, Bogdan Pasaniuc, Eleazar Eskin, and Eran Halperin, *Genotyping common and rare variation using overlapping pool sequencing*, **RECOMB**, 2011.
19. Bogdan Pasaniuc, Noah Zaitlen, and Eran Halperin, *Accurate Estimation of Expression Levels of Homologous Genes in RNA-seq Experiments*, **RECOMB**, 2011.
20. Bonnie Kirkpatrick, Eran Halperin, and Richard Karp, *Haplotype inference in complex pedigrees*, **RECOMB**, 2009.
21. Bogdan Pasaniuc, Sriram Sankararaman, Gad Kimmel and Eran Halperin, *Inference of Locus-Specific Ancestry in Closely Related Populations*, **ISMB**, 2009
22. Sriram Sankararaman, Gad Kimmel, Eran Halperin and Michael I. Jordan, *On the inference of ancestries in admixed populations*, **RECOMB**, 2008.
23. Eran Halperin and Elad Hazan, *HAPLOFREQ - Estimating Haplotype Frequencies Efficiently*, **RECOMB**, 2005.

24. Eran Halperin, Gad Kimmel, Ron Shamir, *Tag SNP Selection in Genotype Data for Maximizing SNP Prediction Accuracy*, **ISMB**, 2005.
25. Eran Halperin and Richard Karp, *The Minimum-Entropy Set Cover Problem*, **ICALP**, 2004
26. Julia Chuzoy, Sudipto Guha, Eran Halperin, Sanjeev Khanna, Guy Kortsarz and Seffi Naor, *Asymmetric k -center is \log^*n -hard to approximate*, **STOC**, 2004
27. Eran Halperin and Richard Karp, *Perfect Phylogeny and Haplotype Assignment*, **RECOMB**, 2004.
28. Eran Halperin, Guy Kortsarz, Robert Krauthgamer, Aravind Srinivasan and Nan-Wang, *Integrality ratio for Group Steiner Trees and Directed Steiner Trees*, **SODA**, 2003.
29. Rajiv Gandhi, Eran Halperin, Samir Khuller, Guy Kortsarz and Aravind Srinivasan, *An Improved approximation algorithm for vertex cover with hard capacities*, **ICALP**, 2003.
30. Eran Halperin, Jeremy Buhler, Richard M. Karp, Robert Krauthgamer and Ben Westover, *Detecting protein sequence conservation via metric embedding*, **ISMB**, 2003.
31. Eran Halperin, Shay Halperin, Tzvika Hartman and Ron Shamir, *Handling long targets and errors in sequencing by hybridization*, **RECOMB**, 2002.
32. Edith Cohen, Eran Halperin, Haim Kaplan and Uri Zwick, *Reachability and Distance Queries via 2-Hop Labels*, **SODA**, 2002.
33. Eran Halperin, Dror Livnat and Uri Zwick. *Max Cut in cubic graphs*, proceeding of the 13th Symposium on Discrete Algorithms (**SODA**) 2002, 506-513.
34. Edith Cohen, Eran Halperin and Haim Kaplan, *Performance aspects of distributed caches using TTL-based consistency*, **ICALP**, 2001.
35. Eran Halperin, Ram Nathaniel and Uri Zwick, *Coloring k -colorable graphs using smaller palettes*, **SODA**, 2001.
36. Eran Halperin and Uri Zwick, *A unified framework for obtaining improved approximation algorithms for maximum graph bisection problems*, **IPCO**, 2001.
37. Eran Halperin, *Improved approximation algorithms for the vertex cover problem in graphs and hypergraphs*, **SODA**, 2000.
38. Eran Halperin and Uri Zwick, *Approximation algorithms for MAX 4-SAT and rounding procedures for semidefinite programs*, **IPCO**, 1999.

Patents:

1. United States Patent 6,625,545: Method and apparatus for mRNA assembly (1998).
2. United Kingdom Patent GB2444410: Genetic Analysis and systems and methods (2007).