

# Curriculum Vitae

Eran Halperin

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## 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:

Computational Biology, Genomics, Epigenomics, Statistical Genetics, Population Genetics, , Algorithms, Machine Learning.

## 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-present **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)

- 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.
- 2015 Invited speaker at the biennial conference of the Cancer Biology Research Center (CBRC) meeting.
- 2015 Invited speaker at the Genetics Society of Israel meeting, Weizmann Institute.
- 2015 Invited speaker at the 'Studying Human Evolution from Ancient DNA' workshop, Hebrew University.
- 2015 Invited speaker at the Bertinoro Computational Biology meeting.

## Students:

### Post-docs

- 2019-now Dr. Misagh Kordi, post-doc, UCLA.
- 2018-now 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

- 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-now Elior Rahmani, PhD candidate, Computer Science, UCLA
- 2016-now 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. 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.
2. 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.
3. 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.
4. 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)
5. 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.
6. 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.
7. 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).
8. 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.
9. Schweiger, Regev, Eyal Fisher, Omer Weissbrod, Elior 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.
10. 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.
11. 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.

12. 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.
13. 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).
14. 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.
15. 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.
16. 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.
17. 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.
18. 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).
19. 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.
20. 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.
21. 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.
22. Rozov, Roye, Gil Goldshlager, Eran Halperin, and Ron Shamir, *Faucet: streaming de novo assembly graph construction*, **Bioinformatics** 34, no. 1 (2017): 147-154.



23. 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.
24. 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.
25. Rhead, Brooke, et al. *Rheumatoid arthritis T cells share hypermethylation sites with synovio-cytes.*, **Arthritis & Rheumatology** (2016).
26. 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
27. 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.
28. Elinor 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.
29. 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.
30. 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).
31. 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
32. 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.
33. 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).

34. 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).
35. 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).
36. 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.
37. 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.
38. 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).
39. 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.
40. Gymrek M, McGuire AL, Golan D, Halperin E, Erlich Y., *Identifying personal genomes by surname inference*, **Science**, Jan 18;339(6117):321-4, 2013.
41. 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.
42. Ronen R, Udpa N, Halperin E, Bafna V, *Learning Natural Selection from the Site Frequency Spectrum*, **Genetics**. 2013 Jun 14.
43. 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.
44. 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
45. 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).

46. Osvaldo Zagordi, Armin Topler, 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).
47. 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.
48. 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).
49. Efros Anatoly, Halperin Eran. *Haplotype reconstruction using perfect phylogeny and sequence data*, **BMC Bioinformatics**. 2012 Apr 19;13 Suppl 6:S3.
50. 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
51. Baran Yael, Halperin Eran, *Joint analysis of multiple metagenomic samples*, **PLoS Computational Biology**, 2012 Feb;8(2):e1002373.
52. Slager SL, et a., *Common variation at 6p21.31 (BAK1) influences the risk of chronic lymphocytic leukemia*, **Blood**, 120(4):843-6, 2012.
53. 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.
54. 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.
55. 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.
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1. United States Patent 6,625,545: Method and apparatus for mRNA assembly (1998).
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