

CONTACT INFORMATION

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Stanford University

EDUCATION

University of California Los Angeles, CA, USA

PhD in Computer Science, 2020

- Dissertation: Capturing hidden signals from high-dimensional data and applications to genomics
- Advisor: Prof. Eran Halperin

Tel Aviv University, Israel

MSc in Computer Science, 2016

BSc in Computer Science and Biology, specialization in Bioinformatics, 2013

ACADEMIC APPOINTMENTS

2025–now Assistant Professor, Department of Medicine, Division of Computational Medicine,
Stanford University, CA, USA
2022–2025 Assistant Adjunct Professor, Department of Computational Medicine, University
of California Los Angeles, CA, USA

ACADEMIC TRAINING POSITIONS

2020–2022 Postdoctoral researcher, Department of Electrical Engineering and Computer Sci-
ences, University of California Berkeley, CA, USA
 Advisors: Prof. Nir Yosef and Prof. Michael I. Jordan
2017–2020 Graduate student researcher, Department of Computer Science, University of Cal-
ifornia Los Angeles, CA, USA
 Advisor: Prof. Eran Halperin
7-8/2015 Visiting scholar at the International Computer Science Institute, Berkeley, CA, USA
1-2/2014 Visiting scholar at the International Computer Science Institute, Berkeley, CA, USA
2012-2013 Undergraduate research student, Weizmann Institute of Science, Rehovot, Israel
 Advisor: Prof. Ehud Shapiro
2012-2013 Undergraduate research student, Tel Aviv University, Tel Aviv, Israel
 Advisor: Prof. Eran Halperin

FUNDING

2023 NIH R21, Contrastive machine learning methods for phenotype subtyping, NIH-
NHGRI R21HG013393 (PI). \$428,448.

TEACHING EXPERIENCE

- Winter 2024, Foundations of Data Science (instructor), Department of Computational Medicine,
Fall 2024, University of California Los Angeles, CA, USA
Fall 2025
Spring 2018 Computational Genetics (teaching assistant), Department of Computer Science,
University of California Los Angeles, CA, USA
Spring 2017 Bioinformatics Tools (instructor), Department of Computer Science, Tel Aviv Uni-
versity, Israel
Spring 2016 Bioinformatics Tools (instructor), Department of Computer Science, Tel Aviv Uni-
versity, Israel

HONORS AND AWARDS

- 2022 Travel fellowship award, Research in Computational Molecular Biology (RECOMB)
2021 Charles J. Epstein Trainee Award, The American Society of Human Genetics
(ASHG): semifinalist (among top 16 submissions out of over 2,000)
2021 Life Sciences Research Foundation (LSRF) Fellowship: finalist (~6% of applica-
tions)
2019 Campus-wide nominee for the Schmidt Science Fellows Program, University of Cal-
ifornia Los Angeles (selected among 5 PhD students across the Natural Sciences)
2019 Best poster award, Human Genetics Academic Retreat, University of California Los
Angeles
2019 Travel fellowship award, Research in Computational Molecular Biology (RECOMB)
2019 Dissertation Year Fellowship, University of California Los Angeles
2019 The Google outstanding graduate student research award of the Department of
Computer Science, University of California Los Angeles (a single recipient)
2019 Graduate Student Support Fellowship, University of California Los Angeles
2018 The Northrop-Grumman outstanding graduate student research award of the De-
partment of Computer Science, University of California Los Angeles (a single recip-
ient)
2018 Travel fellowship award, Research in Computational Molecular Biology (RECOMB)
2018 Graduate Student Support Fellowship, University of California Los Angeles (re-
nounced)
2017 Edmond J. Safra excellent research student prize, Tel Aviv University (a single
recipient)
2017 Travel fellowship award, Research in Computational Molecular Biology (RECOMB)
2016–2017 Edmond J. Safra fellowship for graduate students, Tel Aviv University
2016 Celia and Marcos Maus annual prize, Tel Aviv University (selected among 2 Com-
puter Science MSc students)
2014–2015 Edmond J. Safra fellowship for MSc students, Tel Aviv University
2013 The Blavatnik School of Computer Science excellence prize, Tel Aviv University
2013 Maccabim scholarship
2012 The Weizmann Institute of Science scholarship for excellent undergraduate students
2010-2013 Mifal Hapais scholarship

1. Gorla A, Witonsky J, Elhawary J, Chen Z, Mefford J, Perez-Garcia J, Madore AM, Huntsman S, Hu D, Eng C, Bhakta NR, Woodruff P, Laprise C, Sankararaman S, Flint J, Allen CDC, Ziv E, Zaitlen N, Burchard E, **Rahmani E**. *Epigenetic patient stratification reveals a sub-endotype of type 2 asthma with altered B-cell response*. medRxiv.
2. Alvarez M, Li T, Lee SHT, Arasu UT, Selvarajan I, Örd T, **Rahmani E**, Chen ZJ, Avram O, Kar A, Kaminska D, Männistö V, Halperin E, Pihlajamäki J, Luo C, Kaikkonen MU, Zaitlen N, Pajukanta P. *Integrated ambient modeling and genetic demultiplexing of single cell RNA+ATAC Multiome experiments with Ambimux*. bioRxiv.
3. Aw A, McRae J, **Rahmani E***, Song Y*. *Highly parameterized polygenic scores tend to overfit to population stratification via random effects*. bioRxiv. (* - joint senior authorship)
4. **Rahmani E**, Jordan MI, Yosef N. *Identifying systematic variation at the single-cell level by leveraging low-resolution population-level data*. bioRxiv.
5. J Chow, M Tomkova, A Thomas, **E Rahmani**, S Shifman, F Hormozdiari. *Identification of critical cell-types using genetic modules: A case study of neurodevelopmental disorders*. BioRxiv.
6. **Rahmani E**, Jew B, Schweiger R, Rhead B, Criswell L, Barcellos L, Eskin E, Rosset S, Sankararaman S, Halperin E. *Calling differential DNA methylation at cell-type resolution: addressing misconceptions and best practices*. bioRxiv.
7. Gavish M*, Schweiger R*, **Rahmani E**, Halperin E. *ReFACTor: Practical Low-Rank Matrix Estimation Under Column-Sparsity*. arXiv. (* - joint first authorship)

JOURNAL PUBLICATIONS

8. Chen Z*, **Rahmani E***, Halperin E. *Unico: a unified model for cell-type resolution genomics from heterogeneous omics data*. [Genome Biology](#). 2025. (* - joint first authorship)
9. Wells SB, Rainbow DB, Mark M, Szabo PA, Ergen C, Maceiras AR, Caron DP, **Rahmani E**, Benuck E, Amiri VVP, Chen D, Wagner A, Howlett SK, Jarvis LB, Ellis KL, Kubota M, Matsumoto R, Mahbubani K, Saeb-Parsy K, Dominguez-Conde C et al. *Multimodal profiling reveals tissue-directed signatures of human immune cells altered with age*. [Nature Immunology](#). 2025.
10. Chen ZJ, Das SS, Kar A, Lee SHT, Abuhanna KD, Alvarez M, Sukhatme MG, Wang Z, Gelev KZ, Heffel MG, Zhang Y, Avram O, **Rahmani E**, Sankararaman S, Laakso M, Heinonen S, Peltoniemi H, Halperin E, Pietiläinen KH, Luo C, Pajukanta P. *Single-cell DNA methylome and 3D genome atlas of the human subcutaneous adipose tissue*. [Nature Genetics](#). 2025.
11. Di Y, **Rahmani E**, Mefford J, Wang J, Ravi V, Gorla A, Alwan A., Kendler KS, Zhu T, Flint J. *Unraveling the Associations Between Human Pitch and Major Depressive Disorder: A Multisite Genetic Study*. [Molecular Psychiatry](#). 2024.
12. Di Y, Mefford J., **Rahmani E**, Wang J, Ravi V, Gorla A, Alwan A, Zhu T, Flint J. *Genetic association analysis of human voice pitch identifies a common locus for tonal and non-tonal languages*. [Communications Biology](#). 2024.

13. Avram O, Durmus B, Rakocz N, Corradetti G, An U, Nitalla MG, Rudas A, Wakatsuki Y, Hirabayashi K,..., **Rahmani E** et al. *SLiViT: a general AI framework for clinical-feature diagnosis from limited 3D biomedical-imaging data*. [Nature Biomedical Engineering](#). 2024
14. Grunin M, Triffon D, Beykin G, **Rahmani E**, Schweiger R, Tiosano L, Khateb S, Hagbi-Levi S, Rinsky B, Munitz R et al. *Genome-wide association study and genomic risk prediction of age-related macular degeneration in Israel*. [Scientific Reports](#). 2024.
15. **Rahmani E**, Jew B, Halperin E. *The effect of model directionality on cell-type-specific differential DNA methylation analysis*. [Frontiers in Bioinformatics](#). 2022
16. Dominguez Conde C, Xu C, Jarvis LB, Gomes T, Rainbow DB, Wells SB, Howlett SK, Suchanek O, Polanski K, ..., **Rahmani E** et al. *Cross-tissue immune cell analysis reveals clonal and tissue-specific features in humans*. [Science](#). 2022.
17. Alvarez M*, **Rahmani E***, Jew B, Garske KM, Miao Z, Benhammou JN, Ye CJ, Pisegna JR, Pietilainen KH, Halperin E, Pajukanta P. *Enhancing droplet-based single-nucleus RNA-seq resolution using the semi-supervised machine learning classifier DIEM*. [Scientific Reports](#). 2020. (* - joint first authorship)
18. Goodman-Meza D*, Rudas A*, Chiang JN*, Adamson PC, Ebinger J, Sun N, Botting P, Fulcher JA,...,**Elior Rahmani**, Eran Halperin**, and Vladimir Manuel**. *A machine learning algorithm to increase COVID-19 inpatient diagnostic capacity*. [Plos One](#). 2020. (* - joint first authorship; ** - joint senior authorship)
19. Miao Z, Alvarez M, Ko A, Bhagat Y, **Rahmani E**, Jew B, Heinonen S, Munoz-Hernandez LL, Herrera-Hernandez M, Aguilar-Salinas C, Tusie-Luna T. et al. *The causal effect of obesity on prediabetes and insulin resistance reveals the important role of adipose tissue in insulin resistance*. [PLoS Genetics](#). 2020.
20. Grunin M, Beykin G, **Rahmani E**, Schweiger R, Barel G, Hagbi-Levi S, Elbaz-Hayoun S, Rinsky B, Ganiel M, Carmi S, Halperin E. *Association of a variant in VWA3A with response to anti-vascular endothelial growth factor treatment in neovascular AMD*. [Investigative Ophthalmology & Visual Science](#). 2020.
21. Jew B*, Alvarez M*, **Rahmani E**, Miao Z, Ko A, Garske KM, Sul JH, Pietilainen KH, Pajukanta P, Halperin E. *Accurate estimation of cell composition in bulk expression through robust integration of single-cell information*. [Nature Communications](#). 2020. (* - joint first authorship)
22. **Rahmani E**, Schweiger R, Rhead B, Criswell LA, Barcellos LF, Eskin E, Rosset S, Sankararaman S, Halperin E. *Cell-type-specific resolution epigenetics without the need for cell sorting or single-cell biology*. [Nature Communications](#). 2019.
23. Thompson M, Chen ZJ, **Rahmani E**, Halperin E. *CONFINED: distinguishing biological from technical sources of variation by leveraging multiple methylation datasets*. [Genome Biology](#). 2019.
24. **Rahmani E**, Schweiger R, Shenhav L, Wingert T, Hofer I, Gabel E, Eskin E, Halperin E. *BayesCCE: a Bayesian framework for estimating cell-type composition from DNA methylation without the need for methylation reference*. [Genome Biology](#). 2018.
25. Schweiger R, Fisher E, Weissbrod O, **Rahmani E**, Muller-Nurasyid M, Kunze S, Gieger C, Waldenberger M, Rosset S, Halperin E. *Detecting heritable phenotypes without a model using fast permutation testing for heritability and set-tests*. [Nature Communications](#). 2018.

26. Schweiger R, Fisher E, **Rahmani E**, Shenhav L, Rosset S, Halperin E. *Using stochastic approximation techniques to efficiently construct confidence intervals for heritability*. [Journal of Computational Biology](#). 2018.
27. **Rahmani E**, Zaitlen N, Baran Y, Eng C, Hu D, Galanter J, Oh S, Burchard EG, Eskin E, Zou J, Halperin E. *Correcting for cell-type heterogeneity in DNA methylation: a comprehensive evaluation*. [Nature Methods](#). 2017.
28. Schweiger R, Weissbrod O, **Rahmani E**, Muller-Nurasyid M, Kunze S, Gieger C, Waldenberger M, Rosset S, Halperin E. *RL-SKAT: an exact and efficient score test for heritability and set tests*. [Genetics](#). 2017.
29. Weissbrod O, **Rahmani E**, Schweiger R, Rosset S, Halperin E. *Association testing of bisulfite-sequencing methylation data via a Laplace approximation*. [Bioinformatics](#). 2017.
30. **Rahmani E**, Yedidim R, Shenhav L, Schweiger R, Weissbrod O, Zaitlen N, Halperin E. *GLINT: a user-friendly toolset for the analysis of high-throughput DNA-methylation array data*. [Bioinformatics](#). 2017.
31. **Rahmani E**, Shenhav L, Schweiger R, Yousefi P, Huen K, Eskenazi B, Eng C, Huntsman S, Hu D, Galanter J, Oh SS et al. *Genome-wide methylation data mirror ancestry information*. [Epigenetics & Chromatin](#). 2017.
32. Rhead B, Holingue C, Cole M, Shao X, Quach HL, Quach D, Shah K, Sinclair E, Graf J, ..., **Rahmani E** et al. *Rheumatoid arthritis naive T cells share hypermethylation sites with synoviocytes*. [Arthritis & Rheumatology](#). 2017.
33. **Rahmani E**, Zaitlen N, Baran Y, Eng C, Hu D, Galanter J, Oh S, Burchard EG, Eskin E, Zou J, Halperin E. *Sparse PCA corrects for cell type heterogeneity in epigenome-wide association studies*. [Nature Methods](#). 2016.
34. Arkin Y, **Rahmani E**, Kleber ME, Laaksonen R, Marz W, Halperin E. *EPIQ-efficient detection of SNP-SNP epistatic interactions for quantitative traits*. [Bioinformatics](#). 2014.

PEER-REVIEWED CONFERENCE PAPERS

35. Ramteke A, **Rahmani E**. *Disease subtyping using electronic health records via contrastive learning with latent domain generalization*. [ML4H](#). 2024.
36. Gorla A, Sankararaman S, Burchard E, Flint J, Zaitlen N, **Rahmani E**. *Phenotypic subtyping via contrastive learning*. [RECOMB](#). 2023.
37. **Rahmani E**, Halperin E, Jordan MI, Yosef N. *Identifying systematic variation in gene-gene interactions at the single-cell level*. [ICML CompBio workshop](#). 2021.
38. **Rahmani E**, Schweiger R, Rosset S, Sankararaman S, Halperin E. *Tensor Composition Analysis Detects Cell-Type Specific Associations in Epigenetic Studies*. [RECOMB](#). 2018.
39. **Rahmani E**, Schweiger R, Shenhav L, Eskin E, Halperin E. *A Bayesian framework for estimating cell type composition from DNA methylation without the need for methylation reference*. [RECOMB](#). 2017.

40. **Rahmani E**, Schweiger R, Rosset S, Sankararaman S, Halperin E. *Extracting 3D Information from 2D Data and Application for Detecting Cell-Type Specific Associations in Genomic Studies*. [NeurIPS MLCB Workshop](#).2017.

PEER-REVIEWED CONFERENCE PAPERS THAT ALSO APPEARED IN JOURNALS / PREPRINT SERVERS

41. **Rahmani E**, Chen Z, Halperin E. *A unified model for cell-type resolution genomics from heterogeneous omics data*. [RECOMB-Genetics](#). 2023.
42. **Rahmani E**, Jordan MI, Yosef N. *Identifying systematic variation at the single-cell level by leveraging low-resolution population-level data*. [RECOMB](#). 2022.
43. Thompson M, Chen ZJ, **Rahmani E**, Halperin E. *Distinguishing biological from technical sources of variation by leveraging multiple methylation datasets*. [RECOMB](#). 2019.
44. Weissbrod O, **Rahmani E**, Schweiger R, Rosset S, Halperin E. *Association testing of bisulfite-sequencing methylation data via a Laplace approximation*. [ISMB](#). 2017.
45. Schweiger R, Fisher E, **Rahmani E**, Shenhav L, Rosset S, Halperin E. *Using stochastic approximation techniques to efficiently construct confidence intervals for heritability*. [RECOMB](#). 2017.
46. Arkin Y, **Rahmani E**, Kleber ME, Laaksonen R, Marz W, Halperin E. *EPIQ-efficient detection of SNP-SNP epistatic interactions for quantitative traits*. [ISMB](#). 2014.

PATENTS

1. **Rahmani E**, Burchard E, Gorla A, Ziv E, Witonsky J. Use of Epigenetic and Genomic Biomarkers for Assessing Drug Response to Type 2 Inflammatory Diseases. U.S. Patent Application PCT/US2025/010196. 2025.
2. Zaitlen N, Halperin E, **Rahmani E**, Thompson M, Chen Z. Use of Epigenetic and Genomic Biomarkers for Assessing Drug Response to Type 2 Inflammatory Diseases. U.S. Patent Application PCT/US0205/032667. 2025.
3. **Rahmani E**, Ramteke A, Hallaj S, Baxter S. Clinical Score for Predicting Response to Interventions in Glaucoma Patients. U.S. Provisional Application 63/913,631. 2025.