Elior Rahmani

RESEARCH INTERESTS

Computational biology, statistical and computational genomics, machine learning, AI/ML in healthcare.

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 RESEARCH POSITIONS

2022–now	Assistant Adjunct Professor, Department of Computational Medicine, University of California Los Angeles, CA, USA
2020–2022	Postdoctoral researcher, Department of Electrical Engineering and Computer Sciences, University of California Berkeley, CA ,USA
	Advisors: Prof. Nir Yosef and Prof. Michael I. Jordan
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

TEACHING EXPERIENCE

Spring 2018	Computational Genetics (teaching assistant), Department of Computer Science, University of California Los Angeles, CA, USA
Spring 2017	Bioinformatics Tools (lecturer), Department of Computer Science, Tel Aviv University, Israel
Spring 2016	Bioinformatics Tools (lecturer), Department of Computer Science, Tel Aviv University, Israel

2013-2014	Software Engineer, Advanced Analytics machine learning group, Intel corporation, Israel
2010-2012	Self-employed web developer
2005-2009	Special forces of the Combat Engineering Corps, Israel Defense Forces

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 ($\sim$6% of applications)
2019	Campus-wide nominee for the Schmidt Science Fellows Program, University of California 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 Department of Computer Science, University of California Los Angeles (a single recipient)
2018	Travel fellowship award, Research in Computational Molecular Biology (RECOMB)
2018	Graduate Student Support Fellowship, University of California Los Angeles (renounced)
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 PhD students, Tel Aviv University
2016	Celia and Marcos Maus annual prize, Tel Aviv University (selected among 2 Computer 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

5/2022	Research in Computational Molecular Biology (RECOMB): paper talk, San Diego
10/2021	American Society of Human Genetics (ASHG), platform presentation, Virtual
6/2019	International Conference on Machine Learning (ICML) Workshop on Computational Biology: 2 highlight talks, Long Beach
4/2018	Research in Computational Molecular Biology (RECOMB): paper talk, Paris
12/2017	NIPS Workshop on Machine Learning in Computational Biology (MLCB): spotlight talk, Long Beach
5/2017	Research in Computational Molecular Biology (RECOMB): paper talk and highlight talk, Hong Kong
2/2017	Machine Learning for Healthcare group at IBM Research, Tel Aviv
1/2017	Edmond J. Safra annual fellowship ceremony at Tel Aviv University, Tel Aviv
7/2016	Computational Genomics Summer Institute (CGSI) at UCLA, Los Angeles
5/2016	Edmond J. Safra annual retreat (Tel Aviv University), Ma'agan

Submitted papers / Preprints

1. Gorla A, Sankararaman S, Burchard E, Flint J, Zaitlen N, **Rahmani E**. *Phenotypic subtyping via contrastive learning.* bioRxiv.

2. Di Y, Mefford J, Ravi V, Wang J, Flint J, Alwan A, **Rahmani E**, Zhu T. *Genetic Correlation and Causality between Voice Features and Major Depressive Disorders.* submitted.

3. Gavish M*, Schweiger R*, **Rahmani E**, Halperin E. *ReFACTor: Practical Low-Rank Matrix Estimation Under Column-Sparsity.* arXiv preprint. (* - joint first authorship)

Journal publications

4. **Rahmani E***, Jew B*, Halperin E. *The effect of model directionality on cell-type-specific differential DNA methylation analysis.* Frontiers in Bioinformatics. 2022 (* - joint first authorship)

5. 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.

6. 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)

7. 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)

8. 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. *The causal effect of obesity on predi-*

abetes and insulin resistance reveals the important role of adipose tissue in insulin resistance. PLoS Genetics. 2020.

9. 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.

10. 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)

11. **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.

12. Thompson M, Chen ZJ, **Rahmani E**, Halperin E. *CONFINED: distinguishing biological from technical sources of variation by leveraging multiple methylation datasets.* Genome Biology. 2019.

13. **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.

14. 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.

15. 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.

16. **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.

17. 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.

18. Weissbrod O, **Rahmani E**, Schweiger R, Rosset S, Halperin E. *Association testing of bisulfite-sequencing methylation data via a Laplace approximation.* Bioinformatics. 2017.

19. **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.

20. **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.

21. 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.

22. **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.

23. 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

24. Aditya Gorla, Sriram Sankararaman, Esteban Burchard, Jonathan Flint, Noah Zaitlen,**Rahmani E**, *Phenotypic subtyping via contrastive learning.* RECOMB. 2023.

25. **Rahmani E**, Jordan MI, Yosef N. *Identifying systematic variation at the single-cell level by leveraging low-resolution population-level data.* RECOMB. 2022.

26. **Rahmani E**, Halperin E, Jordan MI, Yosef N. *Identifying systematic variation in gene-gene interactions at the single-cell level.* ICML CompBio workshop. 2021.

27. **Rahmani E**, Schweiger R, Rosset S, Sankararaman S, Halperin E. *Tensor Composition Analysis Detects Cell-Type Specific Associations in Epigenetic Studies.* RECOMB. 2018.

28. **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.

29. **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.* NIPS MLCB Workshop.2017.

PEER-REVIEWED CONFERENCE PAPERS THAT ALSO APPEARED IN JOURNALS

30. Thompson M, Chen ZJ, **Rahmani E**, Halperin E. *Distinguishing biological from technical sources of variation by leveraging multiple methylation datasets.* RECOMB. 2019.

31. Weissbrod O, **Rahmani E**, Schweiger R, Rosset S, Halperin E. *Association testing of bisulfite-sequencing methylation data via a Laplace approximation.* ISMB. 2017.

32. 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.

33. 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.