

Ilan Gronau, Curriculum Vitae August 7, 2025

CONTACT INFORMATION

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RESEARCH INTERESTS

computational biology, population genetics, ancient DNA, probabilistic modeling, molecular evolution, phylogenetics, algorithms for sequence analysis

EDUCATION

Technion, Israel Institute of Technology, Haifa, Israel
B.S. Computer Science, 2002

Weizmann Institute of Science, Rehovot, Israel
M.S. Computer Science (Bioinformatics track), 2004

Technion, Israel Institute of Technology, Haifa, Israel
Ph.D., Computer Science, 2009

ACADEMIC EMPLOYMENT

Reichman University , Herzliya, Israel <i>Vice Dean, Efi Arazi School of Computer Science</i>	2024–
Reichman University , Herzliya, Israel <i>Associate Professor</i>	2021–
Herzliya Interdisciplinary Center (IDC; now Reichman University) , Herzliya, Israel <i>Senior Lecturer</i>	2014–2021
Cornell University , Ithaca, NY <i>Research Associate at the Siepel Lab</i>	2012–2014
Cornell University , Ithaca, NY <i>Postdoctoral Fellow at the Siepel Lab</i>	2009–2012

ACADEMIC HONORS AND AWARDS

Kavli Fellow of the National Academy of Sciences (NAS) and the Israel Academy of Sciences and Humanities (IAS)	2017
Award for excellence in research from IDC	2017
Kramer award for excellent scientific publication (for fitCons paper)	2015
Semi-finalist, Charles J. Epstein Trainee Award for Excellence in Human Genetics Research	2013
Postdoctoral Fellowship from the Cornell Center for Comparative and Population Genomics (3CPG)	2013
Jacobs-Qualcomm Fellowship for excellent Ph.D. students awarded by the Technion graduate school	2008
Fein Fellowship for excellent first year Ph.D. students awarded by the Technion graduate school	2006
SAMBA Fellowship for excellent undergraduate students in Computer Science awarded by the Technion CS department	2000-2001
The Technion President honor list	1998-2001

RESEARCH GRANTS	ISF	Combined Analysis of ancient DNA and tomb finds to study the movement of Phoenician people and culture in the Mediterraneans	2020-2024	\$ 330,000
	Israel Acad. of Sci. and Hum.	Seed grant for project characterizing the corpora and genetics of the Phoenician and indigenous cemeteries in Sicily	2018	\$ 6,000
	BSF-NSF	Quantifying genomic porosity in non-model radiations	2016-2019	\$ 190,000
	GIF	Inferring the demography of archaic human populations using genomes sequenced from ancient DNA	2016	€20,000

PATENTS	2015	Shapiro, EY, Linshiz, G, Ben-Yehezkel, T, Kaplan, S, Adar, R, Gronau, I., Tuvi, S. Programmable iterated elongation: a method for manufacturing synthetic genes and combinatorial DNA and protein libraries. United States Patent No. 8,962,532.
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PUBLICATION LIST [* – authors contributed equally]

Journal Articles

1. **Gronau I**, Moran S. (2007) Optimal implementations of UPGMA and other common clustering algorithms. *Information Processing Letters*, 104(6):205-210.
2. **Gronau I**, Moran S. (2007) On the hardness of inferring phylogenies from triplet dissimilarities. *Theoretical Computer Science*, 389:44-55.
3. **Gronau I**, Moran S. (2007) Neighbor joining algorithms for inferring phylogenies via LCA-distances. *Journal of Computational Biology*, 14(1):1-15.
4. Linshiz G, Ben-Yehezkel T, Kaplan T, **Gronau I**, Ravid S, Adar A, Shapiro E. (2008) Recursive construction of perfect DNA molecules from imperfect oligonucleotides. *Molecular Systems Biology*, 4:191.
5. **Gronau I**, Moran S, Yavneh I. (2009) Towards optimal distance functions for stochastic substitution models. *Journal of Theoretical Biology*, 260:294-307.
6. **Gronau I**, Moran S, Yavneh I. (2010) Adaptive distance measures for resolving K2P quartets: metric separation versus stochastic noise. *Journal of Computational Biology*, 17(11):1509-1518.

7. Ben-Yehzekel T, Linshiz G, Kaplan T, **Gronau I**, Ravid S, Adar A, and Shapiro E. (2011) Recursive construction and error correction of DNA molecules and libraries from synthetic and natural DNA. *Methods in Enzymology*, 498:207-245.
8. **Gronau I**, Hubisz MJ, Gulko B, Danko CG, Siepel A. (2011) Bayesian inference of ancient human demography from individual genome sequences. *Nature Genetics*, 43:1031-1034.
9. **Gronau I**, Moran S, Snir S. (2012) Fast and reliable reconstruction of phylogenetic trees with indistinguishable edges. *Random Structures and Algorithms*, 40(3):350-384.
* Extended Abstract published in **SODA**, 2008.
10. Choi SC, Rasmussen MD, Hubisz MJ, **Gronau I**, Stanhope, MJ, Siepel A. (2012) Replacing and additive horizontal gene transfer in *Streptococcus*. *Molecular Biology and Evolution*, 29(11):3309-3320.
11. Doerr D, **Gronau I**, Moran S, Yavneh I. (2012) Stochastic errors vs. modeling errors in distance-based phylogenetic reconstruction. *Algorithms in Molecular Biology*, 7(1):22.
* Extended Abstract published in **WABI**, 2011.
12. **Gronau I**, Arbiza L, Mohammed J, Siepel A. (2013) Inference of Natural Selection from Interspersed Genomic Elements Based on Polymorphism and Divergence. *Molecular Biology and Evolution*, 30(5):1159–1171.
13. Arbiza L, **Gronau I**, Aksoy BA, Hubisz MJ, Gulko B, Keinan A, Siepel A. (2013) Genome-wide inference of natural selection on human transcription factor binding sites. *Nature Genetics*, 45:723–729.
14. Freedman A, **Gronau I**, Schweizer RM, Han E, Ortega-Del Vecchyo D, Silva P, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Beale H, Ramirez O, Hormozdiari F, Alkan C, Vila C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadiotola V, Siepel A, Bustamante C, Harkins TT, Nelson SF, Ostrander EA, Marques-Bonet T, Wayne RK, Novembre J. (2014) Genome Sequencing Highlights the Dynamic Early History of Dogs. *PLoS Genetics*, 10(1):e1004016
15. Rasmussen MD, Hubisz MJ, **Gronau I**, Siepel A. (2014) Genome-wide inference of ancestral recombination graphs. *PLoS Genetics*, 10(5):e1004342
16. Mohammed J, Bortolamiol-Becet D, Flynt A, **Gronau I**, Siepel A, Lai E. (2014) Adaptive evolution of testis-specific, recently-evolved, clustered miRNAs in Drosophila. *RNA*, 20(8):1195-1209
17. Gulko B, Hubisz MJ, **Gronau I***, Siepel A*. (2015) Probabilities of fitness consequences for point mutations across the human genome. *Nature Genetics*, 47:276-283
18. Campagna L, **Gronau I**, Silveira LF, Siepel A, Lovette IJ. (2015) Distinguishing noise from signal in patterns of genomic divergence in a highly polymorphic avian radiation. *Molecular Ecology*, 24:4238-4251
19. Fan Z, Silva P, **Gronau I**, Wang S, Armero AS, Schweizer RM, Ramirez O, Pollinger J, Galaverni M, Ortega Del-Vecchyo D, Du L, Zhang W, Zhang Z, Xing J, Vila C, Marques-Bonet T, Godinho R, Yue B, Wayne RK. (2016) Worldwide patterns of genomic variation and admixture in gray wolves. *Genome Research*, 26(2):163-73

20. Kuhlwilm M*, **Gronau I***, Hubisz MJ, de Filippo C, Prado J, Kircher M, Fu Q, Burbano HA, Lalueza-Fox C, de la Rasilla M, Rosas M, Rudan P, Brajkovic D, Kucan Z, Gusic I, Marques-Bonet T, Andres AM, Viola B, Paabo S, Meyer M, Siepe A, Castellano S. (2016) Ancient gene flow from modern humans into Siberian Neanderthals. *Nature*, 530:429-433
21. Freedman A, Schweizer RM, Ortega-Del Vecchyo D, Han E, Davis BW, **Gronau I**, Silva P, Galaverni M, Fan Z, Marx P, Lorente-Galdos B, Ramirez O, Hormozdiari F, Alkan C, Vila C, Squire K, Geffen E, Kusak J, Boyko AR, Parker HG, Lee C, Tadiotla V, Siepel A, Bustamante C, Harkins TT, Nelson SF, Marques-Bonet T, Ostrander EA, Wayne RK, Novembre J. (2016) Demographically-Based Evaluation of Genomic Regions under Selection in Domestic Dogs. *PLoS Genetics*, 23(3):e1005851
22. VonHoldt BM, Cahill JA, Fan Z, **Gronau I**, Robinson J, Pollinger JP, Shapiro B, Wall J, Wayne RK. (2016) Whole-genome sequence analysis shows that two endemic species of North American wolf are admixtures of the coyote and gray wolf. *Science Advances*, 2(7):e1501714
23. VonHoldt BM, Cahill JA, **Gronau I**, Shapiro B, Wall J, Wayne RK. (2017) Response to Hohenlohe et al. *Science Advances*, 3(6):e1701233
24. VonHoldt BM, Cahill JA, **Gronau I**, Shapiro B, Wall J, Wayne RK. (2017) Response to Hohenlohe et al.. *Science Advances*, 3(6):e1701233
(two response letters requested by editorial board)
25. Damty Y, **Gronau I**, Moran S, Yavneh I. (2018) Comparing evolutionary distances via adaptive distance functions. *Journal of Theoretical Biology*, 440:88-99.
26. Chavez DE, **Gronau I**, Hains T, Kliver S, Koepfli KP, Wayne RK. (2019) Comparative genomics provides new insights into the remarkable adaptations of the African wild dog (*Lycaon pictus*). *Scientific Reports*, 9:8329
27. Adrion J, Cole CB, Dukler N, Galloway JG, Gladstein A, Gower G, Kyriazis CC, Ragsdale AP, Tsambos G, Baumdicker F, Carlson J, Cartwright RA, Durvasula A, **Gronau I**, Kim BY, McKenzie P, Messer PW, Noskova E, Del-Vecchio DO, Racimo F, Struck TJ, Gravel S, Gutenkunst RN, Lohmueller KE, Ralph PL, Schrider DR, Siepel A, Kelleher J, Kern AD. (2020) A community-maintained standard library of population genetic models. *eLife* 9:e54967
28. Hejase HA, Salman-Minkov A, Campagna L, Hubisz MJ, Lovette IJ, **Gronau I***, Siepel A* (2020) Genomic islands of differentiation in a rapid avian radiation are driven by recent selective sweeps. *Proceedings of the National Academy of Sciences* 117(48):30554-30565
29. Leibovich Z*+, **Gronau I*** (2022) Optimal design of synthetic DNA sequences without unwanted binding sites. *Journal of Computational Biology* 29(9): 974-986
30. Chavez DE, **Gronau I**, Hains T, Dikow RB, Frandsen PB, Figueiró HV, Garcez FS, Tchaicka L, de Paula RC, Rodrigues FHG, Jorge RSP, Lima ES, Songsasen N, Johnson WE, Eizirik E, Koepfli KP, Wayne RK (2022) Comparative genomics uncovers the evolutionary history, demography, and molecular adaptations of South American canids. *Proceedings of the National Academy of Sciences* 119(34):e2205986119
31. Lauterbur ME, Cavassim MIA*, Gladstein AL*, Gower G*, Pope NS*, Tsambos G*, Adrion J, Belsare S, Biddanda A, Caudill V, Cury J, Echevarria J, Haller BC, Hasan AR, Huang X, Iasi LNM, Noskova E, Obsteter J, Pavinato VAC, Pearson A, Peede D, Perez MF, Rodrigues MF, Smith CCR, Spence JP, Teterina A, Tittes S, Unneberg P, Vazquez JM, Waples RK, Wohns AW, Wong Y, Baumdicker F, Cartwright RA, Gorjanc G, Gutenkunst RN, Kelleher J,

- Kern AD, Ragsdale AP, Ralph PL, Schrider DR, **Gronau I** (2023) Expanding the stdpopsim species catalog, and lessons learned for realistic genome simulations. *eLife* 12:RP84874
32. Ibrahim J, Mintz E, Regev L, Regev D, **Gronau I**, Weiner S, Boaretto E (2024) FIB-SEM Study of Archaeological Human Petrous Bones: 3D Structures and Diagenesis. *Minerals* 14(7):729
 33. Han S*, de Filippo C*, Parra G, Meneu JR, Laurent R, Frandsen P, Hvilsom C, **Gronau I**, Marques-Bonet T, Kuhlwilm M, Andrés AM (2024) Deep genetic divergence within bonobos. *Current Biology* 34(22):5341-5348.e3
 34. Avram O*, Durmus B*, Rakocz N, Corradetti G, An U, Nitalla MG, Terway P, Rudas A, Chen Z, Wakatsuki Y, Hirabayashi K, Velaga S, Tiosano L, Corvi F, Verma A, Karamat A, Lindenberg S, Oncel D, Almidani L, Hull V, Fasih-Ahmad S, Esmaeilkhani H, Cannesson M, Wykoff CC, Rahmani E, Arnold CW, Zhou B, Zaitlen N, **Gronau I**, Sankararaman S, Chiang JN, Sadda SR, Halperin E (2025) SLIViT: a general AI framework for clinical-feature diagnosis from limited 3D biomedical-imaging data. *Nature Biomedical Engineering* 9:507-520
 35. Regev D, Boaretto E, **Gronau I** (2025) Discrepancies between radiocarbon dates and dated finds among Phoenicians tombs in Sicily. *Radiocarbon* 67(3):630-645
 36. Ringbauer H, Salman-Minkov A, Regev D, Olalde I, Peled T, Sineo L, Falsone G, van Dommelen P, Mitnik A, Lazaridis I, Pettener D, Bofill M, Mezquida A, Costa B, Jiménez H, Smith P, Vai S, Modi A, Shaus A, Callan K, Curtis E, Kearns A, Lawson AM, Mah M, Micco A, Oppenheimer J, Qiu L, Stewardson K, Workman JN, Márquez-Grant N, Sáez-Romero AM, Lavado-Flórido ML, Jimenez JM, Moyano IJT, Viguera E, Padilla JS, Marques-Bonet T, Lizano E, Ríaza AR, Olivieri F, Toti P, Giuliana V, Barash A, Carmel L, Boaretto E, Faerman M, Lucci M, La Pastina F, Nava A, Genchi F, Del Vais C, Lauria G, Meli F, Sconzo P, Catalano G, Cilli E, Fariselli AC, Fontani F, Luiselli D, Culleton BJ, Mallick S, Rohland N, Nigro L, Coppa A*, Caramelli D*, Pinhasi R*, Lalueza-Fox C*, **Gronau I**, Reich D (2025) Punic people had exceptionally diverse ancestry with few genetic links to their eastern Phoenician cultural forebears. *Nature* 643:139-147
 37. Gower G, Pope NS, Rodrigues MF, Tittes S, Tran LN, Alam O, Cavassim MIA, Fields PD, Haller BC, Huang X, Jeffrey B, Korfmann K, Kyriazis CC, Min J, Rebollo I, Rehmann CT, Small ST, Smith CCR, Tsambos G, Wong Y, Zhang Y, Huber CD, Gorjanc G, Ragsdale AP, **Gronau I**, Gutenkunst RN, Kelleher J, Lohmueller KE, Schrider DR, Ralph PL, Kern AD (2025) Accessible, realistic genome simulation with selection using stdpopsim *bioRxiv preprint; under revision*

Refereed Conference Papers

38. **Gronau I**, Moran S, Snir S. **Fast and reliable reconstruction of phylogenetic trees with very short edges**. In the proceedings of [the 19th annual ACM-SIAM Symposium on Discrete Algorithms \(SODA '08\)](#).
39. Doerr D, **Gronau I**, Moran S, Yavneh I. **Stochastic errors vs. modeling errors in distance-based phylogenetic reconstruction**. In the proceedings of [the 11th international conference on Algorithms in bioinformatics \(WABI '11\)](#).
40. Ziv R, **Gronau I**, Fire I. **CompanyName2Vec: Company Entity Matching Based on Job Ads**. In the proceedings of [the IEEE 9th International Conference on Data Science and Advanced Analytics \(DSAA '22\)](#).

Unrefereed preprints

41. Ahronoviz S, Gronau I (2024) **Genome-AC-GAN: Enhancing Synthetic Genotype Generation through Auxiliary Classification**. Preprint published in bioRxiv (<https://doi.org/10.1101/2024.02.14.580420>).

Conference Presentations

1. Improving the dates of ancient DNA samples using population-level sequence comparisons. (Feb 2015) The Human Mutation Rate Meeting, Leipzig, Germany, Plenary talk
2. Bayesian hypothesis testing for demographic histories. (Sept 2015) The Probabilistic Modeling in Genomics Meeting, Cold Spring Harbor, NY, Poster
3. Ancient DNA Uncovers a Complex Network of Interbreeding Between Modern and Archaic Humans. (Feb 2016) The 2nd annual Darwin Day Symposium, Haifa, Israel, Plenary talk
4. A New Approach for Bayesian Hypothesis Testing for Population Histories. (Sept 2016) The Probabilistic Modeling in Genomics Meeting, Oxford, UK, Poster
5. Using deep investigation of ancient genomes to uncover complex relations between modern and Neanderthal humans. (Feb 2017) The 3rd Israeli-American Kavli Frontiers of Science Symposium, Irvine, CA, Plenary talk
6. Exploring evolution using genomes and genealogies. (May 2017) The 19th Israeli Bioinformatics Symposium, Rehovot, Israel, Plenary talk
7. Bayesian Model Comparison of Population Histories. (Nov 2018) The Probabilistic Modeling in Genomics Meeting, Cold Spring Harbor, NY, Plenary talk
8. Bayesian model comparison of population histories under the multi-species coalescent. (July 2019) Annual meeting of the Society for Molecular Biology and Evolution (SMBE), Manchester, UK, Poster
9. Inference of complex scenarios of adaptive evolution during rapid species radiation. (July 2019) Annual meeting of the Society for Molecular Biology and Evolution (SMBE), Manchester, UK, Selected talk (given by post doc Sr. Salman-Minkov)
10. The Case for Genetic Genealogies in Population Genomics. (December 2019) 1st meeting of the Israeli Society for Evolutionary Biology (ISEB), Tel Aviv, Israel, Invited talk
11. Studying genetic and cultural admixture of Phoenicians in Sicily. (April 2021) 12th International Congress on the Archaeology of the Ancient Near East (ICAANE), Bologna, Italy, (Joint talk with Dalit Regev)
12. Studying genetic and cultural admixture of Phoenicians in Sicily. (October 2022) 10th International Congress of Phoenician and Punic Studies, Ibiza, Spain, (Joint talk with Dalit Regev)

Other Invited Talks

1. The Neanderthal genome as a window to human pre-history. (April 2016) Technion Innovations in Science Lecture Series.
2. It runs in the family tree – using explicit genealogies to interrogate individual genomes. (July 2016) Tel Aviv University Molecular Evolution Seminar.
3. Surprising relationships between *H. Sapiens* and *H. Neanderthalensis*. (February 2019) Darwin Day event, The Israel Academy of Sciences and Humanities.
4. Investigating Identity and Genealogy through DNA analysis. (March 2019) Innovation in Forensics and the Law, Herzliya, Israel.

STUDENT MENTORSHIP

Boaz Aviv	GPhoCS – Run time optimization by parallelization	M.S. final project	RUNI	2015 – 2016
Yanir Damti	Adaptive methods for computing and comparing evolutionary distances	M.S. thesis	Technion	2014 – 2017
Ron Visbord	A new approach for phylogenetic model comparison using MCMC	M.S. thesis	RUNI	2015 – 2018
Zehavit Leibovitch	Eliminating unwanted patterns with minimal interference	M.S. thesis	RUNI	2018 – 2021
Ayelet S-Minkov	Studying genealogical patterns of divergence during speciation	Postdoc	RUNI	2018 – 2022
	Analyzing ancient DNA samples from Phoenician sites	Postdoc	RUNI	2020 – 2025
Tomer Peled	Analysis of ancient DNA from Phoenician cemeteries in Sicily	M.S. final project	RUNI	2020 – 2023
Shaked Ahronoviz	Synthetic genotype generation through auxiliary classification	M.S. thesis	RUNI	2022 –
Shay Sirek	Methods for optimizing synthetic DNA sequence design	M.S. thesis	RUNI	2023 –
Hadar Pur	Flexible software for design of synthetic DNA sequences	M.S. final project	RUNI	2023 –

OTHER ACADEMIC ACTIVITIES

- Head of the M.Sc program at the Efi Arazi School for Computer Science (2016 – 2024)
- Vice president of the Israeli society for bioinformatics and computational biology (ISBCB) (2023 – present)
- Organizing committee of the Computational genomics summer institute (CGSI) at the University of California, Los Angeles (2023, 2024)
- Sabbatical at the Department of Computational Medicine in University of California, Los Angeles (August 2022 – July 2023)
- Review of grant proposals for the following agencies: Israeli Science Foundation (2015), The U.S-Israel Binational Science Foundation (2016, 2017, 2020), The German-Israeli Foundation for Scientific Research and Development (2019)
- Review of papers for the following journals and conferences: Nature Genetics, Nature Reviews Genetics, Nature Communications, The American Journal of Human Genetics, eLife, PLoS Genetics, PLoS Computational Biology, Molecular Biology and Evolution, Journal of Computational Biology, Journal of Theoretical Biology, Theoretical Population Biology, Molecular Phylogenetics and Evolution, RECOMB, STOC.

COURSES TAUGHT

- Algorithms in Computational Biology (CS3571), Spring 2015 & 2016, Fall 2019, 2021 & 2024
- Probabilistic Models for Data Analysis (CS3575), Spring 2016, Fall 2020, 2022, 2024
- Introduction to Machine Learning (CS3141), Spring 2025
- System programming in C (CS3144), Fall 2016, Spring 2017 – present
- Seminar in algorithms for genome analysis (CS3582), Spring 2017
- Programming Workshop in UNIX and C (CS391), Fall 2014 & 2015