



Poster titles – Retreat 2026

*The presenter is underlined. *indicates equal contribution.*

1. Towards regulatory-confirmed adaptive clinical trials: Machine learning opportunities and solutions
Omer Noy Klein, Alihan Hüyük, Ron Shamir, Uri Shalit, and Mihaela van der Schaar
2. Endotypes of long-term immune dysregulation after sepsis: Impact on clinical outcome
Yoel Tepper, Evangelos J. Giamarellos-Bourboulis, Mihai G. Netea, and Irit Gat-Viks
3. Modeling folding dynamics to understand and improve RNA toehold switches
Daniel Benarroch and Tamir Tuller
4. Pan-cancer analysis reveals genomic fidelity and evolution of patient-derived organoids
Linoy Raz, Tal Ben-Yishay, Amjad Zoabi, Haia Khoury, Giulia Orlandi, Sara Donzelli, Giovanni Blandino, and Uri Ben-David
5. Fast and flexible Bayesian phylogenetic inference with diffusion models
Tal Argov and Regev Schweiger
6. Functional annotation of viral proteins from sequence using protein language models
Bar Jacobi, Ritambhara Singh, and Adi Stern
7. Modeling the evolutionary trajectory of genomes under dynamic rearrangement and fluctuating copy-number
Tal Ben-Yishay and Ron Shamir
8. Likelihood methods for estimating gene family dynamics in plants
Roye Tadmor, Anat Shafir, and Itay Mayrose
9. Decoding transmission success from phylogenetic dead ends: A large-scale analysis of long branches in SARS-CoV-2 evolution
Adi Ben Zvi and Adi Stern
10. Efferocytosis induces pro-angiogenic function and chromatin reprogramming in tumor-associated macrophages
Roi Balaban, Ori Moskowitz, Maiia Levinson, Noam Ofer, Alice Raizman, Gaya Levi Kitron, Eden Aviv, Sandra Camargo, Lihi Goldman, Aviv Leemann, Eden Noachas, Chen Sharon-Yagol, Amir Giladi, and Merav Cohen
11. N-Zinclopedia: Database-scale discovery of candidate transition-metal-binding sites and metalloenzymes across protein fold space
Gilad Mechtering and Nir Ben-Tal
12. Developing an RNA sequence designer for targeted translation
Yehuda Landau, Efi Moree, Matan Arbel, and Tamir Tuller
13. Network-based discovery of exercise-induced inter-tissue signaling
Yael Cohen, Karyn Esser, and David Amar

14. Investigating the role of HNRNPC in neurodevelopment
Ophir Shwarzbard and Miri Danan-Gotthold
15. Identifying predictive markers of response to KIF18A inhibition in chromosomally unstable cancers
Tomer Mashiah, Tiangen Chang, and Uri Ben-David
16. Meta-learning for proteomics-based few-shot disease classification
Roni Meamen Moses and Irit Gat-Viks
17. Data requirements and limitations of deep learning for condition-specific promoter activity prediction in fungi
Moritz Burghardt and Tamir Tuller
18. Integrating common and rare genetic variation: A multi-scale network approach to Systemic Lupus Erythematosus (SLE)
Shachar Bavly and Ran Elkon
19. Short-term success, long-term failure: Strain turnover and virulence re-emergence may drive relapse in pouchitis
Liat Bilinsky, Tzach Shamay, Leah Reshef, Keren Rabinowitz, Iris Dotan, and Uri Gophna
20. Optimal transport for batch effect correction in microbiome data
Amit Shalvi Kali, Tal Bamberger, Omri Peleg, and Elhanan Borenstein
21. Integrating clinical priors into interpretable biomarker trajectory representations
Tammy Wertheimer and Ron Shamir
22. Near-perfect photo-ID of amphibian species with zero-shot deep local-feature matching
Maayan Yesharim, Eli Geffen, Yoav Ram, Uri Roll, and Bina Perl
23. The gut phageome as a window into social structure in rock hyraxes
Tomer Oron, Amiyaal Ilany, and Adi Stern
24. DNA language model embedding geometry reveals epistasis and insight beyond supervised mutation evaluation
Nicolas Lynn and Tamir Tuller
25. Clinically guided autoencoder for identifying multi-disease patterns
Rachel Brandes Leibovitz and Irit Gat-Viks
26. ADP: A deep learning method for adapting polygenic risk scores to diverse ethnic groups
Hagai Levi, Ran Elkon, and Ron Shamir



27. Explainable machine learning model can predict the onset of inflammatory bowel disease using routine clinical data
Eyal Haluts, Emma C. Dyer, Amir Ben Tov, Revital Kariv, Elhanan Borenstein, and Nathaniel Aviv Cohen
28. Biologically informed mendelian randomization methods
Arielle Ruth Arabov and David Amar
29. Deep learning architectures for prediction of future cancer events
Maya Metzger and Ron Shamir
30. Data-driven design for stable RNA delivery
Tal Lilo and Tamir Tuller
31. Genetic innovation in Leviviricetes: Exploring lysis gene evolution and genome plasticity
Arielle Kahn and Adi Stern
32. Plant karyotype evolution: Inferring chromosome number–dependent rate dynamics
Noy Bandel, Tal Pupko, and Itay Mayrose
33. Refining genome-scale metabolic models via genomic data analysis
Din Saadon, Shai Cohen, and Tamir Tuller
34. Uncovering the mechanisms behind exercise response heterogeneity
Lihi Shalmon, Or Zuk, and David Amar
35. TEMPEH: A computational framework for linking gut microbiome composition and function in disease
Alisa Greenberg and Elhanan Borenstein
36. Network propagation-based patient-specific prioritization of cancer driver genes
Shira Einy, Tal Ben-Yishay, Ron Sheinin, Roded Sharan and Ron Shamir
37. Single-cell mapping of extrahepatic cholangiocyte heterogeneity in biliary atresia
Lital Dvora Buchris Barak, Adi Har Zahav, Orith Waisbourd Zinman, and Irit Gat-Viks
38. Antibody language models enable codon engineering for enhanced recombinant expression in CHO cells
Shai Cohen, Nicolas Lynn, and Tamir Tuller
39. Characterization of shared and unique biological processes between the genetics and epigenetics of schizophrenia using integrated network analysis
Daniela Blumrosen and Rani Elkon
40. Two distinct types of immunosuppression in sepsis patients uncovered by splicing-based transcriptomics
Yossef Glantzspiegel, Yoel Tepper, Keren Danan, and Irit Gat-Viks



41. CERNAL: A transcriptome-driven compiler for RNA-based cellular logic circuits
Aviv Hendler, Ziv Bentulila, Jonathan Tirnover, Yair Shoat, Shani Iinzish, Mor Gurwicz, Sivan Ben-Moha, Altar Horowitz, Ella Grisaro, Michal Naor, Liran Raanan Cohen, Daniel Dovrat and Tamir Tuller
42. An annotation-free embedding-based framework for efficient approximation of UniFrac distances among microbiome samples
Mor Tsamir-Rimon and Elhanan Borenstein
43. Construction of programmable RNA-regulated synthetic expression systems
Daniel Dovrat and Tamir Tuller
44. Investigating mitochondrial-gut microbiome associations in canine aging
Danielle Koby, Alisa Greenberg, and Elhanan Borenstein
45. A faster criterion to evaluate a MetaCell's Quality
Omer Shapira and Ron Shamir
46. Closing the gap in fusion protein engineering: Machine learning for linker design
Itamar Menuhin-Gruman and Tamir Tuller
47. Profiling 3'UTR isoform dynamics and polyadenylation site usage in the first-trimester developing human cortex
Shir Adler and Miri Danan-Gotthold
48. Early prediction and biomarkers of rheumatoid arthritis: An AI-driven strategy
Noam Teomim, Efrat Nitay, Tamar Zohar, Sagi Tshori, Shaye Kivity, Carmit Levy, and Ron Shamir
49. A quantitative spatial imaging framework of IL1 β -mediated megakaryocyte-macrophage signaling niches during liver hematopoiesis
Aviv Leemann, Maiia Levinson, Amir Giladi, Lihi Goldman, and Merav Cohen
50. Deep learning-based inference of relevant cellular contexts for complex diseases
Thomy Margalit, Hagai Levi, Ron Shamir, and Ran Elkon
51. BaggingCPP: An inductive PU-learning framework for discovering cell-penetrating peptides
Omri Yakir, Chieh Chang, Maayan Gal, and Jérôme Tubiana
52. A genetic algorithm framework for community detection in complex biological networks
Hillel Charbit, Gal Gilad, and Roded Sharan
53. Multiscale mechanisms of bacterial resistance to the RNA phage MS2
Yuval Resisi, Noam Harel, Moran Meir Oren, and Adi Stern
54. Establishing a high-sensitivity bioinformatics pipeline for viral haplotype reconstruction using nanopore sequencing
Yael Levin and Adi Stern

55. GRANDMA: An iterative phylogenomic framework for inferring nested and multiple allopolyploidization events
Ronen Shtein, Tom Ulanovski, Dorothée Huchon, Tal Pupko, and Itay Mayrose