



Poster titles – Retreat 2025

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

1. Cross-species translation of immune cellular states
Guy Shani and Asaf Madi
2. Modeling time-varying covariates for prediction of future cancer events
Maya Metzger, Dan Coster and Ron Shamir
3. Harnessing machine learning for development of novel approaches to control the spread of invasive species by marine vessels
Yair Shimony, Noa Lev, Noa Shenkar and Tal Pupko
4. A Snakemake pipeline for SNP calling in ancient DNA: Identifying heterozygous sites for positive selection analysis
Aurora Campo, Pnina Cohen and Viviane Slon
5. Synthetic rational design of live attenuated Zika viruses based on computational model
Modi Roopin*, Zohar Zafrir*, Bunpote Siridechadilok, Amporn Suphatrakul, Justin Julander and Tamir Tuller
6. Cycle-consistent translation for H&E to expression mapping
Ron Sheinin, Asaf Madi and Roded Sharan
7. Strain-level bacterial sharing between rectal and vaginal microbiomes
Mor Tsamir-Rimon, Ilan Youngster, Michal Youngster and Elhanan Borenstein
8. Modulating gene expression within a microbiome by coding sequence modifications
Moran Ben Tulila and Tamir Tuller
9. Evidence for purifying selection of RNA editing
Yuval Birenbaum, Hillel Shallom Roth and Eli Eisenberg
10. Beyond technical noise: Preliminary evidence linking cancer biology to cell-free DNA base quality profiles
Hadas Volkov, Maria Raitses-Gurevich, Dev Leibowitz, Artem Danilevsky, Meitar Grad and Noam Shomron
11. Genetic modifiers of breast cancer risk among Ashkenazi Jewish BRCA1 mutation carriers
Sapir Shemesh, Rinat Bernstein-Molho, Eitan Freidman and Ran Elkon
12. Evolution of SARS-CoV-2 in immunocompromised individuals: Conditions for generation of dramatic novelty
Adi Ben Zvi, Bar Jacobi, Moran Meir, Natalie Rutsinsky and Adi Stern
13. Using time-dependent matching to assess the effect of nephrological intervention on CKD progression
Tammy Wertheimer, Omer Noy Klein, Dana Bielopolski, Benaya Rosen-Zvi and Ron Shamir



14. Self-supervised deep-learning and hyrax vocalizations
Lior Zlotorinsky and Yoav Ram
15. AI-directed gene fusing prolongs the evolutionary half-life of synthetic gene circuits
Itamar Menuhin-Gruman, Matan Arbel, Doron Naki, Shaked Bergman and Tamir Tuller
16. Optimizing antibiotic treatment of bacteraemia using Artificial Intelligence (AI) algorithms: Retrospective study
Sigal Fleishman, Uri Obolski, Leonard Leibovici and Vered Daitch
17. Mapping the human cell-surface interactome
Emilia Fayman and Rotem Rubinstein
18. Robust performance of deep learning in identifying functional non-coding GWAS variants
Thomy Margalit, Hagai Levi, Ran Elkon and Ron Shamir
19. Meta-learning for proteomics-based few-shot classification in sepsis prediction
Roni Meamen and Irit Gat-Viks
20. Multi-omic integration in the Dog Aging Project: Revealing host-phenome-associated multi-omic modules
Tal Bamberger, Yadid Algavi, Efrat Muller, DAP consortium and Elhanan Borenstein
21. Developing an RNA sequence designer for targeted translation
Yehuda Landau, Efi Moree, Matan Arbel and Tamir Tuller
22. The gene behind the mask: Toward better understanding of genomic LLMs
Nadav Shalev, Ella Rannon and David Burstein
23. Clinically guided autoencoder for identifying multi-disease patterns
Rachel Brandes Leibovitz and Irit Gat-Viks
24. Optimizing protein sequence tokenization: Evaluating amino acid representations for efficient and accurate NLP applications
Ella Rannon and David Burstein
25. Interpretable prediction of zinc ion location in proteins with ZincSight
Gilad Mechtinger and Nir Ben-Tal
26. Differential interactomes between conditions
Yael Kupersmidt and Roded Sharan
27. Local protein structure alignment using geometric deep learning
Hagai Ravid, Jérôme Tubiana and Haim Wolfson
28. Modeling RNA structural dynamics to optimize toehold switches for eukaryotic translation
Daniel Benarroch and Tamir Tuller



29. Improve disease classification with a structured time-series model
Keren Rozen and Irit Gat-Viks
30. Investigating phyllosymbiosis in the human gut microbiome through phylogenetic distance comparisons
Aviv Noah, Omri Peleg and Elhanan Borenstein
31. Phylogenomics and trait evolution in kalanchoe (crassulaceae): Insights from whole-genome sequencing and hybridization analyses
Ronen Shtein, Seraina Rodewald, David-Paul Klein, Zhiqing Huang, Claudia Simon, Joan Pere Pascual-Díaz, Gudrun Kadereit, Tal Pupko, Itay Mayrose and Dorothée Huchon
32. Another layer of evolution in SARS-CoV-2: Exploring transcription levels of the virus
Bar Jacobi and Adi Stern
33. Leveraging NLP embedding techniques to explore metagenomic data
Lihi Hacham, Tal Bamberger, Omri Peleg and Elhanan Borenstein
34. The Collective posterior distribution for simulation-based inference from variable experimental replicates
Nadav Ben Nun, David Gresham and Yoav Ram
35. Algorithms for multi-omic integration
Omer Shapira and Ron Shamir
36. Ubinet - A geometric deep learning model for protein-ubiquitin interaction prediction
Omri Yakir, Dori Rimon, Amir Florentin, Gali Prag and Jérôme Tubiana
37. Multimodal deep learning for fetal risk prediction: Latent fusion of cardiotocography and longitudinal electronic health record data
Dev Leibowitz, Omer Dor, Yuval Fouks, Yariv Yogev and Noam Shomron
38. Modeling SARS-CoV-2 cheater-WT dynamics using differential equations
Tomer Oron and Adi Stern
39. The best friend of our best friends – uncovering the microbial diversity and antibiotic resistance genes in the canine microbiome
Yadid Algavi, Tal Bamberger, Efrat Muller, DAP consortium and Elhanan Borenstein
40. Predicting response to immunotherapy: A retrospective, EMR-based, machine learning strategy
Noam Teomim, Carmit Levy and Ron Shamir
41. Amplified induction in programmable RNA-regulated expression systems using engineered genetic circuits
Daniel Dovrat and Tamir Tuller



42. Alternative splicing signatures in sepsis reveal novel regulatory mechanisms and therapeutic targets
Keren Danan, Yossef Glantzspiegel, Yoel Teppper and Irit Gat-Viks
43. Identifying plasmids' origin of transfer (oriT) utilizing a machine learning approach
Ori Ben-Shir, Bruria Samuel and David Burstein
44. Inferring public goods proteins in viruses from deep sequencing data
Yael Maoz, Nadav Bin Nun, Yoav Ram and Adi Stern
45. Enzymatic catalytic site prediction with geometric deep learning
Anna Berdichevskaia and Jérôme Tubiana
46. Uncovering disease similarities through microbiome signatures
Guy Lurie and Elhanan Borenstein
47. Understanding and predicting gene coding sequences with natural language processing
Lorna Bakhit and Tamir Tuller
48. ImmunoSep mediation analysis
Yoel Teppper and Irit Gat-Viks
49. Prioritize functional noncoding genetic variants that affect gene expression using systematic allelic imbalance analyses
Michael Amar and Ran Elkon
50. Modeling and designing promoters for condition-specific gene expression
Moritz Burghardt and Tamir Tuller
51. Improving the accuracy of polygenic risk scores for Non-European populations using deep learning
Hagai Levi, Rani Elkon and Ron Shamir
52. Resistance to an RNA phage: Many enigmas
Noam Harel, Yuval Resisi and Adi Stern
53. Deep cell deconvolution for predicting glioblastoma treatment outcome from bulk gene expression data
Lital Voulichman, Ilan Volovitz and Roded Sharan
54. A novel strategy for the identification of phenotype-associated transcription factors from GWAS data
David Groenewoud and Ran Elkon
55. Understanding and predicting gene coding sequences with natural language processing
Lorna Bakhit and Tamir Tuller



56. KADAIF: An anomaly detection method for complex microbiome data
Omri Peleg, Maya Raytan and Elhanan Borenstein
57. Insights from the analysis of hundreds of gRNAs designed to target genomic locations in thirteen cell types and organisms
Shai Cohen, Shaked Bergman, Mortiz Burghardt, Isana Veksler-Lublinsky, Eran Eyal, Yaron Orenstein, Itay Mayrose, David Burstein and Tamir Tuller
58. PEANUT: Pathway enrichment analysis through network utilization
Yair Pickholz Berliner and Roded Sharan
59. Predicting future patient trajectories using EMR Data from the Sheba IBD cohort
Yael Talmor and Elhanan Borenstein
60. FAMUS: A few-shot learning framework for large-scale protein annotation
Guy Shur and David Burstein
61. Taxonomy-guided feature selection for microbiome cross-sectional data
Shiri Baum, Ido Meshulam, Omri Peleg, Yadid Algavi and Elhanan Borenstein
62. Towards rational toehold switch design: A general model to predict toehold switches performance based on explainable machine learning
Peleg Bazak and Tamir Tuller
63. TEMPEH: A computational framework for linking gut microbiome composition and function in disease
Alisa Greenberg and Elhanan Borenstein
64. A novel HMM-based approach for detecting chromothripsis from copy number data
Tal Ben-Yishay, Gil Leor, Uri Ben-David and Ron Shamir
65. Utilizing developmental single cell/nucleus-RNA seq data for the improved identification of genetic networks implicated in Autism Spectrum Disorder (ASD) pathogenesis
Eleina England, Sapir Shemesh and Ran Elkon
66. Enriched short-range dependencies for improved epistasis detection in genomic language models
Nicolas Lynn, Ron Lavy and Tamir Tuller
67. Personalized cancer treatment using antisense oligonucleotides
Michael Kovaliov, Shir Shance, Idan Eyni, May Lieber, Ariella Nouman, Din Saadon, Niv David, Roni Zarakhovsky, Ester Buderovsky, Oren Haviv, Daniel Dovrat and Tamir Tuller
68. Widespread role of ssDNA promoters in regulating early gene expression in conjugative plasmids
Chen Agassy, Bruria Samuel, Karin Mittelman and David Burstein