

**Poster titles – Retreat 2024**

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

1. Leveraging deep learning for the early detection of multiple cancers through minimal cfDNA quantities  
Artem Danilevsky, Ilya Margolin, Benjamin Braun, Sarel Ben Asher, Hadas Volkov, Neta Moskovit, Salomon M. Stemmer and Noam Shomron
2. Unraveling destiny - Unraveling fate priming mechanisms in cancer cells  
Itai Fabian and Yaara Oren
3. A novel HMM-based approach for detecting chromothripsis from copy number data  
Tal Ben-Yishay, Gil Leor, Uri Ben-David and Ron Shamir
4. Developing an RNA sequence designer for targeted translation  
Yehuda Landau, Efi Moree, Matan Arbel and Tamir Tuller
5. Exploring cheater virus dynamics in a long-term evolution experiment of MS2 bacteriophage  
Arielle Kahn, Moran Meir, Noam Harel and Adi Stern
6. BLINCHES - A novel league-based approach for studying differential abundance in microbiome data  
Maya Metzger, Omri Peleg, and Elhanan Borenstein
7. NLP-Based detection of genetic editing in bacteria  
Edan Gabay and David Burstein
8. Unraveling microbial dynamics in inflammatory bowel diseases  
Liat Bilinsky, Tzach Shamay, Leah Reshef, Iris Dotan and Uri Gophna
9. Exploring RNA velocity patterns in tumor-infiltrating regulatory T cells  
Michael Monsonogo, Keren Reshef, Shai Dulberg, Ron Sheinin, Ella Goldshmidt, Ayelet Kaminitz and Asaf Madi
10. Human lung adenocarcinoma microenvironment displays cell population dynamics and cell-cell crosstalk changes across disease stage  
Ori Moskowitz\*, Roi Balaban\*, Maiia Levinson, Firas Darawsha, Sandra Camargo, Alice Tamar Raizman, Ran Kremer and Merav Cohen
11. Gatsbi-Net: Constructing cell-type-specific protein-protein interaction networks  
Yael Kupersmidt and Roded Sharan
12. GenomeFLTR: Filtering reads made easy  
Edo Dotan\*, Michael Albuquerque\*, Elya Wygoda\*, Dorothée Huchon and Tal Pupko
13. A rapid and precise tool for large-scale zinc ion location prediction in proteins  
Gilad Mechtinger and Nir Ben-Tal

14. CRISP: A novel adaptation of isolation forest for microbiome anomaly detection  
Omri Peleg, Maya Raytan and Elhanan Borenstein
15. Insights from phylogenetic analysis: Rapid recombination and modular dynamics of the Arbitrium system  
Tom Borenstein and Avigdor Eldar
16. Characterizing lipoprotein changes in aging and cardiovascular disease  
Anton Podobedov and Irit Gat-Viks
17. Enhancing evolutionary stability of synthetic gene circuits through AI-directed gene fusion  
Itamar Menuhin-Gruman\*, Matan Arble-Groissman\*, Shaked Bergman, Doron Naki, Yariv Udi and Tamir Tuller
18. Integrating sequence and structural embeddings for Gene Ontology term prediction  
Daniel Brotzky, Jérôme Tubiana and Haim J. Wolfson
19. Predicting the pathogenicity of genetic variants in humans using protein 3D-structure and AI  
Inbar Blech, Zippora Brownstein, Juan Fernandez-Recio, Xavier de La Cruz, Fabian Glaser and Karen B. Avraham
20. Analysis of cancer-type specific aneuploidy patterns  
Ron Saad, Uri Ben-David and Ron Shamir
21. ProTech - RNA toehold switch for targeting specific RNA in cancerous cell  
Daniel Benarroch, Netanel Erlich, Shani Elimelech, Gal Shwartz, Tal Shemesh, Itamar Eilstein, Rotem Gal, Neve Tzvi, Itamar Menuhin-Gruman, Yonatan Mimran, Oren Ben Moshe, Peleg Bazak, Shaked Nizan, Jonathan Yoni Klein, Matan Arbela and Tamir Tuller
22. Phenotype-driven embedding of microbiome multi-omic data for characterizing disease progression  
Tal Bamberger and Elhanan Borenstein
23. Detecting novel pathogenic variation in the autism genome using developmental timepoint RNA sequencing data  
Eleina England and Ran Elkon
24. Using electronic health records to understand, predict, and manage kidney disease  
Tammy Wertheimer, Omer Noy, Dana Beilopolsky, Bnaia Rosen-Zvi and Ron Shamir
25. Understanding and predicting gene coding sequences with natural language processing  
Lorna Bakhit and Tamir Tuller
26. Exploring the unique interactions of monocyte-derived dendritic cells in activating CD8+ T cells within the tumor microenvironment  
Kfir Inbal, Aseel Khateeb, Nadine Santana Magal, Ayelet Kaminitz, Asaf Madi and Yaron Carmi

27. The predictive capacity of polygenic risk scores for disease risk is only moderately influenced by imputation panels tailored to the target population  
Hagai Levi, Ran Elkon and Ron Shamir
28. A novel strategy for the identification of phenotype-associated transcription factors from GWAS data  
David Groenewoud and Ran Elkon
29. Neutrophils physically interact with cancer cells induce the expression of a molecular program correlated with breast cancer aggressiveness  
Sandra Camargo\*, Ori Moskowitz\*, Shani Gola, Amir Giladi, Maiia Levinson, Roi Balaban, Alice Raizman, Alon Richter, Noa Keren-Khadmy, Oren Barboy, Yael Dugach, Yaron Carmi, Amir Sonnenblick and Merav Cohen
30. Fungi populations differ across races in many tumor types  
Dan Coster, Thomy Margalit, Ben Boursi and Ron Shamir
31. Comparative analysis of genes across endemic human viruses  
Shir T. Segev and Adi Stern
32. rRNA-mRNA interaction subsequence optimization model  
Shir Bahiri Elitzur\*, Larissa Fine\* and Tamir Tuller
33. Taxonomy-guided feature selection for microbiome cross-sectional data  
Shiri Baum, Ido Meshulam, Omri Peleg, Yadid Algavi and Elhanan Borenstein
34. Advance functional interpretation of noncoding variants that contribute to risk of Autism Spectrum Disease  
Sapir Shemesh and Ran Elkon
35. Insights from the analysis of hundreds of gRNAs designed to target genomic locations in eight cell types and organisms  
Shaked Bergman\*, Shai Cohen\*, Isana Veksler-Lublinsky, Eran Eyal, Yaron Orenstein, Itay Mayrose, David Burstein and Tamir Tuller
36. Development of dual taxonomic-functional annotation pipeline for metagenomic microbiome analysis  
Alisa Greenberg and Elhanan Borenstein
37. Substrate selectivity determinants of small multidrug resistance transporters  
David Bern and Nir Ben-Tal
38. Enhanced PPI reliability prediction for ANAT networks  
Lital Voulichman and Roded Sharan
39. Deciphering microbial decision-making mechanisms  
Yadid Algavi and Elhanan Borenstein

40. Evidence of selection for codon usage bias in antibodies  
Doron Armon, Rachel Cohen-Kupiec, Zohar Zafrir and Tamir Tuller
41. Digging in big sequencing data of SARS-CoV-2: Identifying infection patterns  
Adi Ben Zvi\*, Yael Maoz\*, Sheri Harari, Danielle Miller and Adi Stern
42. Algorithms for multi-omic integration  
Omer Shapira and Ron Shamir
43. Revisiting the effects of MDR1 variants using computational approaches  
Tal Gutman and Tamir Tuller
44. Investigating the role of mitochondria in cancer persistence and drug resistance  
Marina Khachatryan and Yaara Oren
45. Immune cell crosstalk disrupted: Effects of eosinophil absence in the tumor microenvironment  
Shai Dulberg, Ofri Kestin, Ayelet Kaminitz, Ariel Munitz and Asaf Madi
46. Modeling coding sequence design for transient expression in tobacco  
Moritz Burghardt and Tamir Tuller
47. Tracking genetic diversity across time during chronic SARS-CoV-2 infections  
Natalie Rutsinsky, Shir T. Segev, Ido Fabian, Sheri Harari, Suzy Meijer, Ora Halutz, Amos Adler, Yael Paran and Adi Stern
48. DNA methylation: A novel role in metabolic syndrome and immune responses  
Yossef Glantzspiegel and Irit Gat-Viks
49. Characterizing the general impact and reach of intra-gene epistasis in cancer and in the general population  
Nicolas Lynn and Tamir Tuller
50. M1CROB1AL1Z3R – a user-friendly web server for the analysis of large-scale microbial genomics data  
Yair Shimony, Oren Avram, Edo Dotan, Elya Wygoda, Noa Ecker, Naama Wagner, Gianna Durante, Jeff Chang and Tal Pupko