Poster titles – Retreat 2023
*The presenter is underlined. * indicates equal contribution.*

1. Unlocking the potential of large-scale biological datasets with NLP tokenization
   Edo Dotan, Gal Jaschek, Tal Pupko and Yonatan Belinkov

2. Engineering and testing the translation re-initiation process of operons in E.coli
   Larissa Fine, Shir Bahiri Elitzur, Rachel Cohen-Kupiec and Tamir Tuller

3. MULTI-KNOCK - Overcoming functional redundancy in plants at targeted genome-scale
   Omer Caldararu, Udi Landau, Anat Shafir, Yangjie Hu, Shir Ben Yaakov, Eilon Shani and Itay Mayrose

4. PPI network signing
   Lorenzo F. Signorini and Roded Sharan

5. Predicting the pathogenic impact of genetic variants in humans using protein 3D-structure information and AI
   Inbar Blech, Juan Fernandez-Recio , Xavier de La Cruz, Fabian Glaser and Karen B. Avraham

6. Correlating methylation patterns at promoters and distal regulatory elements and gene expression of target genes
   Uri Bertocchi and Ran Elkon

7. Advance functional interpretation of noncoding variants that contribute to risk of Autism Spectrum Disease
   Sapir Shemesh and Ran Elkon

8. Analysis of cancer-type specific aneuploidy patterns
   Ron Saad, Uri Ben-David and Ron Shamir

9. Developing an RNA sequence designer for targeted translation
   Yehuda Landau, Efi Moree, Matan Arbel and Tamir Tuller

10. Designing DNT sensing bacteria based on computational models
    Shir Bahiri Elitzur, Etai Shpigel, Shimshon Belkin and Tamir Tuller

11. Large-scale phylogenetic mapping of bacterial secretion systems from genomes and metagenomes
    Yatir Solan and David Burstein

12. Mapping binding sites onto protein structures with interpretable geometric deep learning
    Jérôme Tubiana, Dina Schneidman-Duhovny and Haim J. Wolfson

13. Histone variants H1.2 and H1.5 overexpression as a driver in Autism
    Roni Brudno and Gil Ast

14. Host response heterogeneity of *E. coli* to infection by MS2 bacteriophage
    Noam Harel and Adi Stern

15. Designing a data analysis pipeline for microarray-based cancer diagnosis: Exploring methylation patterns in Acute Myeloid Leukemia
Mika Bell and Yuval Ebenstein

16. Gene expression and epigenetic whole-body state models in Leukemia
Yossef Glantzspiegel and Irit Gat-Viks

17. A multi-view perspective on predicting human diseases based on gut microbiome features
Efrat Muller, Itamar Shiryan and Elhanan Borenstein

18. Advanced computational predictive models of miRNA-mRNA interaction efficiency
Sharon Bader and Tamir Tuller

19. Reconstructing our evolutionary past using sediment DNA: Best practices and applications
Pnina Cohen, Sarah Johnson, Elena I. Zavala, Priya Moorjani and Viviane Slon

20. A novel tool for chromothripsis detection based on copy number data
Tal Ben Yishay, Gil Leor, Yonatan Eliezer, Michal Getz, Eli Reuveni, Linoy Raz, Uri Ben-David and Ron Shamir

21. Automatic deciphering of GWAS based on gene expression models
Noy Meydani and Tamir Tuller

22. Colorectal cancer cells induce a unique transcriptome signature in eosinophils and primes their responses to IL-3-induced activation
Shai Dulberg, Michal Itan, Ayelet Kaminitz, Ariel Munitz and Asaf Madi

23. Revolutionizing CNS tumor classification using Oxford nanopore sequencing and DNA methylation profiling
Assaf grunwald, Galina Deinberg, Shai Izraeli and Yuval Ebenstein

24. Broad analysis of metal utilization in metalloproteins
Gilad Mechtinger and Nir Ben-Tal

25. Dissecting immune-related intercellular crosstalk along mammary gland development and breast cancer
Sandra Camargo, Ori Moskowitz, Roi Balaban, Maiia Levinson and Merav Cohen

26. Codon usage modeling natural language processing
Lorna Bakhit, Rachel Kolodny, Tomer Sidi and Tamir Tuller

27. The characteristics of SARS-CoV-2 evolution and the association with host clinical parameters
Guy Shapira, Chen Weiner, Eden Avnat, Nir Rainy, Reut Sorek-Abramovich, Tal Patalon, Sivan Gazit, Adina Bar Chaim and Noam Shomron

28. Inference of CNV rate and fitness effect from yeast evolutionary experiments using neural networks and evolutionary simulations
Nadav Ben Nun, Julie N Chuong, David Gresham and Yoav Ram

29. Batch correction of single cell sequencing data via an autoencoder architecture
    Reut Danino, Iftach Nachman and Roded Sharan

30. Prediction of novel antimicrobial resistance genes (ARGs) using machine learning methods on metagenomic data
    Ella Rannon, Sagi Shaashua and David Burstein

31. Determinants of translation termination fidelity in eukaryotes
    Noa Gefen and Tamir Tuller

32. Elucidating the molecular biology of age-related hearing impairment using omics analyses of GWAS data
    Mai Eshel, Ronna Hertzano and Ran Elkon

33. covBERTa: A language model for identifying chronic infections in large-scale SARS-CoV-2 sequence dataset
    Danielle Miller, Sheri Harari and Adi Stern

34. long non-coding RNA expression prediction based on the DNA sequence alone
    Yuri Klayman and Tamir Tuller

35. A novel anomaly detection algorithm for microbiome data
    Maya Raytan, Omri Peleg and Elhanan Borenstein

36. A molecular platform for efficient and robust expression of mammalian antibodies
    Rachel Cohen-Kupiec, Zohar Zafrir and Tamir Tuller

37. Prediction of protein-protein interaction networks in different cell-types
    Yael Kupershmidt, Simon Kasif and Roded Sharan

38. Evidence of selection for codon usage in antibodies
    Doron Armon and Tamir Tuller

39. A feature ranking algorithm for clustering medical data
    Eran Shpigelman and Ron Shamir

40. Characterizing changes in lipoprotein levels during aging
    Anton Podobedov and Irit Gat-Viks

41. Revisiting the effects of MDR1 variants using computational approaches
    Tal Gutman and Tamir Tuller

42. Incorporating regulatory interactions into gene-set analyses for genome-wide association study data
    David Groenewoud, Avinoam Shye and Ran Elkon

43. Computational modeling and design of rAAV capsid variants based on brain-wide transgene expression
    Zohar Zafrir and Tamir Tuller

44. Synthetic modification assisted epigenetic sequencing via nanopore
Eliran Eitan and Yuval Ebenstein

45. A robust, reference-free statistical framework for identifying shared copy number alterations across multiple samples in targeted next-generation sequencing data
Hadas Volkov and Noam Shomron

46. The best friends of our best friend: Studying the dog's microbiome and its relation to aging
Tal Bamberger*, Efrat Muller*, Yadid Algavi* and Elhanan Borenstein

47. Inflammatory Bowel Disease - Early detection based on electronic medical records
Gabi Lee and Uri Gophna

48. A non-homogenous model of chromosome-number evolution to reveal shifts in the transition patterns across the phylogeny
Anat Shafir, Keren Halabi, Marcial Escudero and Itay Mayrose

49. The correlation between influenza virus infection and single cell response
Roni Meamen and Irit Gat-Viks

50. Automatic inferring and modeling of viral adaptation to the host gene expression machinery
Alma Davidson and Tamir Tuller

51. Spatial transcriptomic analysis predicts cell type proportions in spots based on gene signatures
Ella Goldschmidt, Asaf Madi and Elhanan Borenstein

52. Mutational signatures analysis
Tal Boazy and Roded Sharan

53. Natural and age-related variation in circulating human hematopoietic stem cells
Nimrod Rappoport*, Nili Saar-Furer*, Naama Zioni, Neville Dusaj, Dan A. Landau, Ron Shamir, Liran Shlush and Amos Tanay

54. Strong association between genomic 3D structure and CRISPR cleavage efficiency
Shaked Bergman and Tamir Tuller

55. The effect of intercellular interactions on cell state in Pulmonary Fibrosis
Victoria Koval, Irit Gat-Viks and Merav Cohen

56. Toehold switch design pipeline for targeted cancer therapy in humans
Peleg Bazak and Tamir Tuller

57. A Manifold-based framework for studying the dynamics of the vaginal microbiome
Mor Tsamir-Rimon and Elhanan Borenstein

58. A tool for CRISPR Cas-9 gRNA evaluation based on computational models of gene expression
Shai Cohen*, Shaked Bergman*, Nicolas Lynn and Tamir Tuller

59. Time-dependent iterative imputation for multivariate longitudinal clinical data
Omer Noy and Ron Shamir

60. Scalable detection and characterization of intra-gene epistatic missplicing mutation sets
Nicolas Lynn and Tamir Tuller

61. Using polygenic prediction models for early breast cancer detection on diverse ethnic groups in Israel
Hagai Levi, Shai Carmi, Saharon Rosset, Rinat Yerushalmi, Aviad Zick, Tamar Yablonski-Peretz, Shay Ben-Sachar, Naama Elefant, Ron Shamir and Ran Elkon

62. Effect of human microbiome supplementation on metabolic disease and other conditions
Shimshi Atar and Tamir Tuller

63. Weaving short term medical records into lifelong trajectories
Matan Levine-Tiefenbrun, Tal Ifargan and Roy Kishony

64. Constructing genomic activation and repression maps at base resolution using deep learning
Tom Aharon Hait, Ran Elkon and Ron Shamir

65. Modulating gene expression within a microbiome by open reading frame sequence modifications
Moran Ben Tulila, Liyam Chitayat Levi and Tamir Tuller

66. Analysis of selection on mRNA secondary structure strength in protein-coding sequences within conserved protein families
Michael Peeri and Tamir Tuller