

Poster titles – Retreat 2021

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

1. Estimating the predictive power of silent mutations on cancer classification and prognosis
Tal Gutman, Guy Goren, Omri Efroni and Tamir Tuller
2. Comprehensive transcriptomic analysis of A-T skin fibroblasts reveals unique gene expression and pathway signature of cellular senescence
Majd Haj, Amit Levon, Yann Frey, Judith Campisi, Ran Elkon, Yael Ziv and Yosef Shiloh
3. Type Statistical method for inferring indel dynamics and its application on conserved domains
Elya Wygoda, Gil Loewenthal and Tal Pupko
4. Framework for enriching gene expression data
Daniel Pirak and Roded Sharan
5. How do plasmids overcome the defense systems of recipient bacteria?
Bruria Samuel Hronec, Dov Gertz, Danielle Miller and David Burstein
6. Precision medicine for hearing loss: Gene discovery, gene therapy & CRISPR/Cas9 models
Lara Kamal, Reut Yacobi, Zippora Brownstein, Amal Abu Rayyan, Shahar Taiber, Suleyman Gulsuner, Tal Koffler, Tom Walsh, Jeffrey R. Holt, David Sprinzak, Mary-Claire King, Moien Kanaan and Karen B. Avraham
7. AdaOrder: Tailoring the order of a minimizer scheme to the dataset can improve binning applications
Dan Flomin, David Pellow and Ron Shamir
8. A novel assay illumines new features of chromatin folding state and accessibility
Assaf Grunwald, Gil Nifker, Hagai Hargil, Yael Michaely and Yuval Ebenstein
9. Dissecting the plasma metabolomics of atherosclerosis
Yuval Menaker and Irit Gat-Viks
10. Systematic delineation of interplays between 3D genomic organization and transcriptional regulation
Gony Shanel, Tsung-Han S. Hsieh, Xavier Darzacq and Ran Elkon
11. Integrating random effects into deep learning: Accounting for high-cardinality categorical features and extensions
Giora Simchoni and Saharon Rosset
12. The dog aging project: A microbiome perspective
Efrat Muller*, Yadid Algavi* and Elhanan Borenstein
13. Towards a model for identity choice in planarian stem cell differentiation
Tamar Frankovits and Omri Wurtzel

14. Predicting virus-host association networks from molecular, structural and biological signatures
Keren Halabi and Itay Mayrose
15. Hematopoietic stem cell gene expression in peripheral blood across individuals at single-cell resolution
Nili Saar-Furer*, Nimrod Rappoport*, Amos Tanay, Liran Shlush and Ron Shamir
16. Frequent aneuploidy in primary human T cells following CRISPR-Cas9 cleavage
Alessio D. Nahmad*, Eli Reuveni*, Ella Goldschmidt*, Tamar Tenne, Miriam Horovitz-Fried, Rami Khosravi, Hila Kobo, Eyal Reinstein, Asaf Madi, Uri Ben-David and Adi Barzel
17. FNR regulation and gut dysbiosis in enteroaggregative E. coli (EAEC)
Vanessa Abuhay and Uri Gophna
18. Scalable and integrative predictive machine learning model on FHIR-based EHRs containing clinical and molecular data
Yazeed Zoabi and Noam Shomron
19. Modelling the phenotypic outcomes of CRISPR-Cas genome editing technologies
Shai Cohen, Shaked Bergman and Tamir Tuller
20. Inferring viral mutation rates & fitness effects from long read sequencing data
Itamar Caspi, Moran Meir, Yoav Ram and Adi Stern
21. Single-cell transcriptome analysis of immune cells in murine melanoma model treated with anti-OX40 immunotherapy
Tomer Weiss, Sarah Amar, Keren Reshef, Ayelet Kaminitz and Asaf Madi
22. Genomic analysis of the spatial organization of the genome and its effect on cell type-specific p53 transcriptional responses
Hadar Amira-Haham, Gony Shanel, Tsung-Han S. Hsieh, Xavier Darzacq, Ron Shamir and Ran Elkon
23. Engineering and testing the translation process in prokaryotes via examination of plasmids library, TCP-seq and ribosome profiling
Larissa Fine, Rachel Cohen-Kupiec and Tamir Tuller
24. Gene2Vec – NLP approach for predicting microbial gene function
Danielle Miller, Adi Stern and David Burstein
25. Long reads capture simultaneous enhancer-promoter methylation status for cell-type deconvolution
Sapir Margalit, Yotam Abramson, Hila Sharim, Zohar Manber, Surajit Bhattacharya, Yi-Wen Chen, Eric Vilain, Hayk Barseghyan, Ran Elkon, Roded Sharan and Yuval Ebenstein
26. Predicting personal risk of developing cancer based on routine check-up data: A multi-center study
Dan Coster, Ilan Krause, Liron Sheena, Shani Shenhar-Tsarfaty, Shlomo Berliner, Ben Boursi and Ron Shamir



27. A LASSO-based approach to sample sites for phylogenetic tree search
Noa Ecker, Dana Azouri, Ben Bettisworth, Alexandros Stamatakis, Yishay Mansour, Itay Mayrose and Tal Pupko
28. Detecting and understanding meaningful cancerous mutations based on computational models of mRNA splicing
Nicolas Lynn and Tamir Tuller
29. Shared transcriptional profiles of atypical B cells suggest common drivers of expansion and function in malaria, HIV, and autoimmunity
Prasida Holla, Brian Dizon, Abhijit A. Ambegaonkar, Noga Rogel, Ella Goldschmidt, Arun K. Boddapati, Haewon Sohn, Dan Sturdevant, James W. Austin, Lela Kardava, Li Yuesheng, Poching Liu, Susan Moir, Susan K. Pierce and Asaf Madi
30. BetaAlign: harnessing natural language processing methods for sequence alignment
Edo Dotan, Gil Loewenthal, Oren Avram, Omri Keren, Elya Wygoda, Omer Levi, Adi Stern and Tal Pupko
31. Modelling of translation re-initiation in prokaryotes based on the analysis of heterologous and endogenous operons
Shir Bahiri Elitzur and Tamir Tuller
32. A data-driven approach for predicting the impact of drugs on the human microbiome
Yadid Algavi and Elhanan Borenstein
33. Synthetic design of oncolytic Newcastle disease virus based on computational modeling
Zohar Zafri*, Alon Diamant*, Modi Roopin*, Shimshi Atar* and Tamir Tuller
34. A Machine learning model for predicting deterioration of COVID-19 inpatients
Omer Noy, Dan Coster, Maya Metzger, Itai Attar, Shani Shenhar-Tsafaty, Shlomo Berliner, Galia Rahav, Ori Rogowski and Ron Shamir
35. Evolutionary models of chromosome numbers and ploidy levels
Anat Shafir, Laurent Gueguen and Itay Mayrose
36. Predicting causal genes for ASD and SCZ
Neta Zadok and Roded Sharan
37. Communique – A generic platform for designing genes with selective activity in microbial communities
Rotem Galron, Mai Bonomo, Ido Rippin, Liyam Chitayat Levi, Yarin Udi, Ilya Breslavskiy, Rawan Ibrahim, Noy Meydani, Roni Gattegno, Ronnie Griness, Shir Michael, Moran Kama, Gali Altman, Yoav Navott, Matan Arbel, Adi Yannai and Tamir Tuller
38. Towards understanding protein degradation in bacteria: A combined proteomic-machine-learning approach
Natan Nagar and Tal Pupko
39. Personalized phylogeny-guided detection of cancer driver genes
Naama Kadosh and Ron Shamir

40. m6A is required for resolving progenitor identity during planarian stem cell differentiation
Yarden Yesharim, Yael Dagan and Omri Wurtzel
41. Synonymous mutations in the major coat protein of M13 affect the fitness of both the phage and its host
Rachel Cohen-Kupiec, Shaked Bergman, Sivan Elhanati, Shimshi Atar and Tamir Tuller
42. Measuring the impact of gene knockouts with network propagation
Etay Livne and Roded Sharan
43. Elucidating the principles that underlie the inheritance of non-genetic traits
Prakash V. Cherian, Idit Aviram, Oded Rechavi and Omri Wurtzel
44. Incorporating regulatory interactions into gene-set analyses for GWAS data
David Groenewoud, Avinoam Shye and Ran Elkon
45. Biomarkers for immunotherapy in NSCLC
Yossef Glantzspiegel, Jair Bar and Irit Gat-Viks
46. MHC Class II: A key to understand immune response in Gliomas
Ron Sheinin, Michael Kilian, Lukas Bunse and Asaf Madi
47. Reducing false GO term calls in network-based active module identification: methodology and a new algorithm
Hagai Levi, Ran Elkon and Ron Shamir
48. Interpolation of missing samples in longitudinal microbiome datasets
Omri Peleg and Elhanan Borenstein
49. Identifying gene rewiring in sepsis, using gene expression data
Rachel Brandes Leibovitz and Irit Gat-Viks
50. Characterizing Covid-19 patients using heart echo measurements
Eran Shpigelman, Aviram Hochstadt, Dan Coster, Yan Topilsky and Ron Shamir
51. The effect of genomic 3D structure on CRISPR cleavage efficiency
Shaked Bergman and Tamir Tuller
52. SARS-CoV-2 Intra-host variation for the analyses of transmission, host interaction and surveillance
Guy Shapira, Shir Portugez, Chen Wiener and Noam Shomron
53. Using nanopore sequencing to detect base modifications
Eliran Eitan, Gal Goldner, Brian Yao, Chloe Hsu, Jennifer Listgarten, Yael Michaeli and Yuval Ebenstein