

## Poster titles – Retreat 2019

*#The poster presenter is underlined*

*\*Equal contribution*

1. Phylogenetic tree reconstruction using reinforcement learning algorithm  
Dana Azouri, Yishay Mansour, Itay Mayrose and Tal Pupko
2. Dynamic interplay between pathogens and hosts with genetic diversity  
Ofir Cohn, Gal Yankovitz, Naama Peshes-Yaloz, Eran Bacharach and Irit Gat-Viks
3. CT-FOCS: a novel method for genome-wide inference of cell type-specific enhancer-promoter maps  
Tom Aharon Hait, Rani Elkon and Ron Shamir
4. Novel driver synonymous mutations in the coding regions of GCB lymphoma patients improve the transcription levels of BCL2  
Ofek Schnitzer, Zohar Zafir and Tamir Tuller
5. Proteomic analysis of short term versus long term survival in glioblastoma patients  
Gali Yanovich-Arad, Paula Ofek, Eilam Yeini, Artem Danilevsky, Noam Shomron, Ronit Satchi-Fainaro and Tamar Geiger
6. Learning protein constitutive motifs from sequence data  
Jérôme Tubiana, Simona Cocco and Rémi Monasson
7. An entropy-based approach for pattern recognition in viruses using a single sequence  
Danielle Miller and Adi Stern
8. Chromosomal organization in the mouse embryo at single cell resolution  
Nimrod Rappoport, Elad Chomsky, Takashi Nagano, Charlie Seibert, Yaniv Lubling, Aviezer Lifshitz, Zohar Mukamel, Ron Shamir, Peter Fraser and Amos Tanay
9. The interface between atherogenic and immunometabolic heterogeneity in obesity  
Amit Frishberg, Inge Van Den Munckhof, Niels Riksen, Mihai Netea and Irit Gat-Viks
10. Can molecular phylogenies be used to accurately infer alternations in diversification rates?  
Anat Shafir, Dana Azouri, Emma Goldberg and Itay Mayrose
11. Persistence of probiotic strains in the gut microbiomes of patients with inflammatory bowel disease  
Vadim Dubinsky, Leah Reshef, Keren Rabinowitz, Lihi Godny, Karin Yadgar, Hagit Tulchinsky, Iris Dotan and Uri Gophna

12. Noninvasive prenatal diagnosis using deep learning  
Tom Rabinowitz and Noam Shomron
13. A codon model for associating phenotypic traits with altered selective patterns of sequence evolution  
Keren Halabi, Eli Levy Karin and Itay Mayrose
14. Attenuation of RNA Viruses based on a computational rational design  
Zohar Zafrir, Eli Goz, Yoram Zarai, Bunpote Siridechadilok, Modi Ruppim, Roda Dabour, Meital Gal-Tanamy and Tamir Tuller
15. Cell type-specific analysis of alternative polyadenylation using single-cell transcriptomics data  
Eldad Shulman and Rani Elkon
16. Long-read single-molecule maps of the functional methylome  
Sapir Margalit, Hila Sharim , Assaf Grunwald , Tslil Gabrieli , Yael Michaeli , Dmitry Torchinsky, Rani Arielly , Gil Nifker and Yuval Ebenstein
17. Comparing the utility of in vivo transposon mutagenesis approaches in yeast species to identify gene essentiality  
Anton Levitan, Andrew Gale, Kyle Cunningham, Roded Sharan and Judith Berman
18. Exploring the evidences of selection for local intrinsic disorder in proteins across the tree of life  
Arup Panda and Tamir Tuller
19. Inferring rates of insertions and deletions using approximate Bayesian computation  
Dana Rapoport, Dana Azouri, Reed A. Cartwright and Tal Pupko
20. The effect of nucleotide composition at the end of the coding sequence on ribosomal read-through and translation re-initiation of a downstream gene  
Rachel Cohen-Kupiec, Shir Bahiri, Michael Peer and Tamir Tuller
21. Predicting genetic interactions in human cells  
Asia Gervits and Roded Sharan
22. Improving assembly of plasmid sequences in metagenomic samples  
David Pellow, Itzik Mizrahi and Ron Shamir
23. Elevated rates of UA>UG mutations in Picornaviruses suggest ADAR editing  
Oded Kushnir, Maoz Gelbart, Ya'ara Ben-Ari Grosman and Adi Stern
24. Improving the classification of cutaneous melanoma tumors using PROMO  
Dvir Netanely, Neta Stern, Carmit Levy and Ron Shamir
25. Evali - Evaluation of random peptide libraries  
Ora Balber, Anna Roitburd, Oren Avram, Jonathan M. Gershoni and Tal Pupko

26. Enhancing transcriptional network inference by integration of genomic footprinting data  
Naama Messika-Gold and Rani Elkon
27. Full genome sequencing of RNA viruses using MinION: finding associations between mutations  
Noam Harel, Moran Meir, Uri Gophna and Adi Stern
28. Efficient algorithm to design small universal k-mer hitting sets  
Lianrong Pu and Ron Shamir
29. Improving FRET real-time translation monitoring technology signal-to-noise in human based on ribo-seq modeling  
Shimshi Atar and Tamir Tuller
30. ModelTeller: A machine-learning approach for phylogenetic model selection  
Shiran Abadi, Oren Avram, Tal Pupko, and Itay Mayrose
31. Towards efficient algorithms for modulating ribosome traffic jams  
Sophie Vinokour and Tamir Tuller
32. A model for early detection of cancer risk based on routine check-up data using random forest of survival analysis trees for left-truncated and right-censored data  
Dan Coster, Eyal Fisher, Shani Shenhar, Shlomo Berliner, Eran Halperin, Saharon Rosset and Ron Shamir
33. The first iGEM team in Tel Aviv University – a novel method of fighting antibiotic resistance bacteria using genetically engineered Pyocins  
Ofek Schnitzer, Omer Grinboim, Lior Soffer, Dror Hadas and Tamir Tuller
34. Genomic delineation of transcriptional networks that determine auditory hair cells fate  
Michal Sperber, Beatrice Milon, Ronna Hertzano and Rani Elkon
35. Single-molecule optical mapping of 5-hydroxymethylcytosine allows single-cell-like clustering of subpopulations  
Hila Sharim, Yael Michaeli and Yuval Ebenstein
36. Prokaryotic rRNA-mRNA interactions are involved in all translation steps and shape bacterial transcripts  
Shir Bahiri Elitzur, Dana Yacobi, Boaz Apt, Alon Diament and Tamir Tuller
37. Memory efficient de Bruijn graph construction - DOCKS Implementation on MSP  
Yael Ben-Ari and Ron Shamir
38. Characterization of tumor inter and intra- heterogeneity and tumor progression in Ewing Sarcoma using proteomics analysis  
May Arama-Chayoth, Revital Caspi, Benny Dekel and Tamar Geiger
39. Automatic predictions of novel rRNA-mRNA interactions  
Boaz Apt, Shir Bahiri and Tamir Tuller

40. Improving functional characterization of GWAS risk SNPs by utilization of enhancer-promoter maps  
Avinoam Shye, David Groenewoud and Rani Elkon
41. Development of an integrated circuit that performs simulations of mRNA translation dynamics  
Danny Naiger and Tamir Tuller
42. Inferring population genetics parameters of evolving viruses using time-series data  
Tal Zinger, Maoz Gelbart, Danielle Miller, Pleuni S. Pennings and Adi Stern
43. A new computational model for miRNA-mediated repression reveals novel regulatory roles of miRNA bindings inside the coding region  
Shaked Bergman, Alon Diament and Tamir Tuller
44. Towards understanding protein degradation in bacteria: a combined proteomic-machine-learning approach  
Natan Nagar and Tal Pupko
45. Determining eQTLs effects on immune-cells based on the hematopoietic lineage tree  
Gal Yankovitz, Yael Steuerman, Ofir Cohn, Naama Peshes-Yaloz and Irit Gat-Viks
46. Engineering the mRNA-rRNA interaction strength in E. coli based on computational models  
Larissa Fine, Shir Bahiri, Rachel Cohen-Kupiec and Tamir Tuller
47. Engineering patient-specific tissues  
Reuven Edri, Idan Gal, Nadav Noor, Tom Harel, Sharon Fleischer, Nofar Abadi, Shoshy Mizrahy, Lior Heller, Assaf Shapira, Dan Pe'er, Irit Gat-Viks and Tal Dvir
48. Modeling eukaryotic translation initiation based on TCP-seq  
Tamar Shmulevsky and Tamir Tuller
49. Network-based functional analysis: Bias correction and evaluation  
Hagai Levi, Rani Elkon and Ron Shamir
50. Solving the riddle of the evolution of Shine-Dalgarno based translation in chloroplasts  
Iddo Weiner, Noam Shahar, Pini Marco, Iftach Yacoby and Tamir Tuller
51. Methods for multi-omic data visualization  
Nimrod Rappoport, Roy Safra and Ron Shamir
52. M1CR0B1AL1Z3R – a user-friendly web server for the analysis of large-scale microbial genomics data  
Oren Avram, Dana Rapoport, Shir Portugez and Tal Pupko

53. Translation termination in bacteria is regulated by mRNA secondary-structure downstream of the stop codon  
Yonatan Chemla\*, Michael Peeri\*, Mathias Heltberg, Mogens Høgh Jensen, Tamir Tuller and Lital Alfonta
54. Identification of novel type III-secreted effectors of the cucurbit pathogenic bacterium *Acidovorax citrulli* by combination of machine learning and transcriptomics approaches  
Irene Jiménez Guerrero\*, Francisco Pérez-Montañó\*, Gustavo Mateus Da Silva, Naama Wagner, Dafna Shkedy, , Mei Zhao, Ron Walcott, Guido Sessa, Tal Pupko and Saul Burdman
55. Computational analysis of translation elongation in meiosis and cancer  
Renana Sabi and Tamir Tuller
56. Model adequacy for likelihood models of chromosome-number evolution  
Anna Rice and Itay Mayrose
57. The hidden genetic diversity of HIV during acute infection exposed using accurate next generation sequencing  
Maoz Gelbart\*, Sheri Harari\*, Ya'ara Ben-Ari, Talia Kustin, Moran Meir, Danielle Miller, Pleuni Pennings, Orna Mor and Adi Stern