

## Poster titles – Retreat 2018

\*The poster presenter is underlined

1. The dynamics of a “cheater” phage detected in experimentally evolved MS2 phage populations  
Moran Meir, Danielle Miller, Maoz Gelbart, Uri Gophna and Adi Stern
2. *Hoobari*: Bayesian-based noninvasive prenatal diagnosis of single-gene disorders  
Tom Rabinowitz, Avital Polsky, David Golan, Guy Shapira, Lina Basel Salmon, Reut Tomashov Matar and Noam Shomron
3. Discrete whole cell model of translation enables connecting the genotype to the phenotype  
Doron Levin and Tamir Tuller
4. FOCS: a new method for enhancer-promoter mapping  
Tom Aharon Hait, David Amar, Ron Shamir and Ran Elkon
5. Epigenetic regulation of pluripotency and neoblast differentiation in planarian regeneration  
Yael Dagan and Omri Wurtzel
6. Non parametric molecular clock dating of species divergences  
Keren Levinstein Hallak and Saharon Rosset
7. "Domain Scan": a tool for the diagnosis of viral infections  
Ora Balber, Smadar Neeman, Oren Avram, Jonathan M. Gershoni and Tal Pupko
8. Computational based design, generation, and tracking of 500 synthetic silent variants of Porcine circovirus reveals the relations between silent genomic information and viral fitness  
Shimshi Atar, Hadas Zur, Eli Goz, Modi Roopin and Tamir Tuller
9. A machine-learning approach for phylogenetic model selection  
Shiran Abadi, Tal Pupko and Itay Mayrose
10. Clinical proteomics of breast cancer unravels a novel layer of breast cancer classification  
Gali Yanovich, Hadar Agmon, Michal Harel, Amir Sonnenblick, Tamar Peretz and Tamar Geiger
11. A deep learning approach for learning intrinsic protein-RNA binding preferences  
Ilan Ben-Bassat, Benny Chor and Yaron Orenstein
12. Histone H1.5 binds over splice sites in chromatin and regulates alternative splicing  
Ohad Glaich and Gil Ast
13. Finding connection between the transcriptomic and phenotypic continuous changes  
Maya Levy and Irit Gat Viks
14. Counting attractors in Boolean networks  
Ariel Bruner and Roded Sharan

15. The NapA antiporter undergoes rocking-bundle alternation between opposite-facing conformations: a simulation study  
Gal Masrati, Amit Kessel, Erik Lindahl and Nir Ben-Tal
16. Novel insights into gene expression regulation during meiosis revealed by translation elongation dynamics  
Renana Sabi and Tamir Tuller
17. PepMatch: knowledge based design of protein binding peptides  
Maria Gorodetski and Haim J. Wolfson
18. Identification of cancer driver mutations in genomic regulatory elements  
Zohar Manber and Ran Elkon
19. Protein-adenine binding: variations on a theme  
Aya Narunsky, Ron Solan, Amit Kessel, Rachel Kolodny and Nir Ben-Tal
20. Attenuation of RNA Viruses based on a computational rational design  
Zohar Zafirir, Eli Goz, Modi Roopin, Yoram Zarai, Bunpote Siridechadilok and Tamir Tuller
21. Distinguishing between acute bacterial and viral infections based on EMR data  
Dan Coster, Shani Shenhar-Tsarfaty, Shlomo Berliner and Ron Shamir
22. Why so many, why so few? A comparative evolutionary analysis of rhinoviruses and polioviruses  
Ella Petter, Oded Kushnir and Adi Stern
23. Multi-omic correlation graph for analyzing cancer genomic data  
Dvir Netanely, Zohar Yakhini and Ron Shamir
24. Engineering and optimizing ribosomal traffic jams through whole cell simulations  
Rachel Cohen-Kupiec, Hadas Zur and Tamir Tuller
25. Dynamics of antibiotic resistance in the human gut microbiome revealed by longitudinal metagenomics of antibiotic-treated patients  
Vadim Dubinsky, Leah Reshef, Nir Bar, Hagit Tulchinsky, Iris Dotan and Uri Gophna
26. Using metabolic gene families for understanding melanoma  
Hagai Levi, Carmit Levy and Ron Shamir
27. cMapApp: unsupervised coding sequence optimization in any given organism  
Alon Diamant, Iddo Weiner, Noam Shahaar, Shira Landman, Yael Feldman, Shimshi Atar, Meital Avitan, Shira Schweitzer, Iftach Yacoby and Tamir Tuller

28. Genetic variation in the pulmonary renin-angiotensin system affects the outcome of influenza infection  
Ofir Cohn, Amit Frishberg, Naama Peshes-Yaloz, Eran Bacharach and Irit Gat-Viks
29. Combining nanopore sequencing with deep learning to perform real-time selective sequencing  
Artem Danilevsky and Noam Shomron
30. Development of an integrated circuit that performs simulations of mRNA translation dynamics  
Yasmin Slonimski and Tamir Tuller
31. Exploring sequence properties in plasmid assemblies  
David Pellow, Itzik Mizrahi and Ron Shamir
32. Examination of current methods for model selection in phylogeny  
Dana Azouri, Shiran Abadi, Tal Pupko and Itay Mayrose
33. Evolutionary selection for short under-represented nucleotide sub-sequences in viruses and related hosts  
Yoram Zarai and Tamir Tuller
34. 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
35. A computational entropy-based approach for decoding new functions in viral genomes  
Danielle Miller and Adi Stern
36. Exploring the evidences of selection for local intrinsic disorder in proteins across the tree of life  
Arup Panda and Tamir Tuller
37. Inference of cell types involved in the pathology of complex diseases using single-cell transcriptomes  
Avinoam Shye, Eldad Shulman and Ran Elkon
38. Comparative genomics analysis of *Mycoplasma bovis* strains isolated from local and imported cattle  
Yael Yair, Inna Mikula, Mor Freed, Rama Falk, Inna Lysnyansky and Uri Gophna
39. Machine learning approach to elucidate *Salmonella* adhesome and its role in host specificity of *Salmonella enterica*  
Dana Rapoport, Ohad Gal-Mor and Tal Pupko
40. Computational modeling of miRNA-mRNA interaction deciphers the biophysics of post-transcriptional regulation and its evolution  
Shaked Bergman, Alon Diamant and Tamir Tuller

41. Genome-scale delineation of cell-type specific transcriptional networks  
Naama Messika-Gold and Ran Elkon
42. MOCCASIN: Cancer subtyping by multi-omics integration  
Nimrod Rappoport and Ron Shamir
43. Determining eQTLs effects on immune-cells based on the hematopoietic lineage tree  
Gal Yankovitz, Yael Steuerman and Irit Gat-Viks
44. High resolution analysis of the selection on local mRNA folding strength in protein-coding sequences across the tree of life  
Michael Peerj and Tamir Tuller
45. ASAP, A webserver for immunoglobulin-sequencing analysis pipeline  
Anna Vaisman-Mentesh, Oren Avram, Dror Yehezkel, Haim Ashkenazy, Tal Pupko and Yariv Wine
46. Computational deciphering and modeling of the regulatory information encoded in the Porcine Circovirus genome  
Lia Baron and Tamir Tuller
47. Exploration of alternative polyadenylation using single-cell RNA-seq  
Eldad Shulman and Ran Elkon
48. Utilizing single cell genomics in deconvolution methods  
Amit Frishberg, Naama Peshes-Yaloz, Ofir Cohn, Yael Steuerman, Diana Rosentul, Yael Oren, Liran Valadarsky, Eran Bacharach, Ido Amit and Irit Gat-Viks
49. PROMO: An interactive tool for integrative analysis of multi-omic cancer data  
Dvir Netanely, Neta Stern, Itay Laufer and Ron Shamir
50. The interaction with the 16S rRNA component of the small ribosomal subunit shapes the transcriptomes of prokaryotes  
Shir Bahirj, Dana Yacobi and Tamir Tuller
51. AccuNGS: Integrative approach for highly accurate next generation sequencing  
Maoz Gelbart, Sheri Harari, Ya'ara Ben Ari, Talia Kustin, Danielle Miller, Orna Mor and Adi Stern
52. Sorting cancer genomes using DCJs, duplications and deletions  
Ron Zeira and Ron Shamir
53. Characterization of the FGF pathway in planarian regeneration  
Ariel Aibester and Omri Wurtzel
54. OneTwoTree: An online tool for phylogeny reconstruction  
Michal Drori\*, Anna Rice\*, Moshe Einhorn, Ofer Chay, Lior Glick and Itay Mayrose

55. Modeling the non-canonical translation initiation regulation in chloroplasts following mutations in the 16S ribosomal RNA  
Iddo Weiner, Noam Shahar, Iftach Yacoby and Tamir Tuller
56. Personalized prioritization of cancer driver genes  
Gal Dinstag and Ron Shamir
57. Chronic Lymphocytic Leukemia (CLL) communication among micro-environmental cells: The role of exosomes  
Asia Gervits, Lian Lipshtein, Einat Beery, Meir Lahav, Uri Rozovski, Roded Sharan and Orit Uziel
58. Dissection of influenza infection *in vivo* by single-cell RNA sequencing  
Yael Steuerman, Merav Cohen, Naama Peshes-Yaloz, Liran Valadarsky, Ofir Cohn, Eyal David, Amit Frishberg, Eran Bacharach, Ido Amit and Irit Gat-Viks