

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 Zafir, 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 Netanel, 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 Shahrar, 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 Shahaar, 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