

Poster titles – Retreat 2017

*The poster presenter is underlined

1. Multivariate analysis enables personalized prediction of adverse heart and kidney outcomes- lessons from the SPRINT challenge
Gal Dinstag, David Amar and Ron Shamir
2. Significant differences in terms of codon usage bias between early and late bacteriophages gene
Oriah Mioduser, Eli Goz, Alon Diamant and Tamir Tuller
3. Unsupervised approach for inferring biological networks based on the genome alone
Maya Galili, Martin Kupiec and Tamir Tuller
4. Experimental evolution reveals stronger selective constraints at higher temperature for an RNA coliphage MS2
Moran Meir, Danielle Miller, Maoz Gelbart, Adi Stern and Uri Gophna
5. The next generation of ancestral sequence reconstruction- implementation of structural data
Asher Moshe and Tal Pupko
6. PROMO: An interactive tool for analyzing large high-throughput genomic datasets
Dvir Netanely, Neta Stern, Itay Laufer and Ron Shamir
7. Efficient user-friendly toolset for the analysis of high-throughput DNA-methylation data
Reut Yedidim, Elior Rahmani, Liat Shenhav, Regev Schweiger, Omer Weissbrod, Noah Zaitlen and Eran Halperin
8. The pre-initiation complex flow model
Shir Bahiri, Ruth Caspi and Tamir Tuller
9. Non-invasive prenatal diagnosis using massively parallel sequencing of circulating cell-free DNA in maternal blood
Tom Rabinowitz, Avital Polsky, David Golan, Reut Matar and Noam Shomron
10. Compact covering of sequences with universal hitting k-mer sets
David Pellow, Yaron Orenstein, Guillaume Marçais, Daniel Bork, Carl Kingsford and Ron Shamir
11. COP9 signalosome influences the epigenetic landscape of Arabidopsis Thaliana
Shimshi Atar, Avital Yahalom, Alon Diamant, Assaf Zemach, Daniel A. Chamovitz and Tamir Tuller
12. A pipeline for simulation of integrated KEGG pathways
Adam Reiter, Adva Yeheskel, Metsada Pasmanik-Chor and Amir Rubinstein
13. Oscillatory behavior at the translation level induced by transcription periodicity due to finite intracellular

Yoram Zarai and Tamir Tuller

14. Mapping enhancer-promoter interactions using big omic data
Tom Aharon Hait, David Amar, Ran Elkon and Ron Shamir
15. Examining substitution models on phylogenies in mtDNA
Keren Levinstein Hallak and Saharon Rosset
16. Different translation initiation mechanisms among chloroplast genes
Iddo Weiner, Iftach Yacoby and Tamir Tuller
17. Sorting cancer genomes using inversions, tandem duplications and deletions
Ron Zeira and Ron Shamir
18. A code for transcription elongation speed
Eyal Cohen, Zohar Zafir and Tamir Tuller
19. Engineering and optimizing ribosomal traffic jams through whole cell simulations
Rachel Cohen-Kupiec, Hadas Zur and Tamir Tuller
20. Model selection in nucleotide substitutions
Dana Azouri, Shiran Abad and Itay Mayrose
21. Proteomic analysis of breast cancer subtypes
Gali Yanovich, Hadar Agmon, Diana Nemichenitzer, Michal Harel, Amir Sonnenblick and Tamar Geiger
22. The extent of ribosome queuing revealed by disome profiling
Anna Feldman, Alon Diamant, Elisheva Schochet, Yoav Arava, Martin Kupiec and Tamir Tuller
23. Inferring immune cell-type quantities related to disease states
Amit Frishberg, Yael Steuerman, Avital Brodt, Altboum Zeev, Valadarsky Liran, Ido Amit and Irit Gat-Viks
24. TraitRateProp: An integrated model of phenotypic trait changes and site-specific sequence evolution
Eli Levy Karin, Susann Wicke, Tal Pupko and Itay Mayrose
25. Enhancing heterologous expression in *Chlamydomonas reinhardtii* by transcript sequence 6 optimization
Iddo Weiner, Shimshi Atar, Shira Schweitzer, Haviva Eilenberg, Yael Feldman, Meital Avitan, Mor Blau, Avihai Danon, Tamir Tuller and Iftach Yacoby
26. A systematic multi-omics investigation of breast cancer metabolism maps its tiered regulation
Rotem Katzir, Ibrahim H. Polat, Michal Harel, Shir Katz, Carles Foguet, Vitaly A. Selivanov, Philippe Sabatier, Marta Cascante, Tami Geiger and Eytan Ruppim
27. Investigation of the mutation rates of Picornaviruses

Oded Kushnir, Talia Kustin, Maoz Gelbart, Danielle Algranati, Ya'ara Ben-Ari Grosman and Adi Stern

28. Designing genome-wide mutagenesis approaches for non-model organisms by leveraging an artificial transposon, deep sequencing and a stable haploid isolate
Ella Shtifman-Segal, Vladimir Gritsenko, Kevin Mielich, Reinhard Kunze and Judith Berman
29. Widespread selection for complex patterns of synonymous information in viral coding regions
Eli Goz and Tamir Tuller
30. Predicting essential and drug-resistance genes in *Candida albicans* from high-coverage transposition libraries using machine learning
Vladimir Gritsenko, Ella Shtifman-Segal, Alex Rosenberg, Kevin Mielich, Chad Myers, Roded Sharan, Reinhard Kunze and Judith Berman
31. Gut microbiota dynamics in long-term antibiotic pouchitis patients in a time series study
Vadim Dubinsky, Leah Reshef, Nir Bar, Iris Dotan and Uri Gophna
32. Algorithms for gene family silencing using the CRISPR-Cas9 system
Gal Hyams, Shiran Abadi, Adi Avni, Eilon Shani, Eran Halperin and Itay Mayrose
33. Multi-Omics integration
Nimrod Rappoport and Ron Shamir
34. Increase of body mass index predicts development of metabolic syndrome criteria
Eyal Fisher, Shani Shenhar, Shlomo Berliner, Ori Rogowski, Eran Halperin and Saharon Rosset
35. Horizontal gene transfer in the core-genome of the *B. subtilis* group
Shaul Pollak and Avigdor Eldar
36. Discovering disease-relevant cell subsets using single cell-based analysis
Maya Levy, Amit Frishberg and Irit Gat-Viks
37. Examination of sampling input as a way of reducing practical run-time with little damage to the result
Keren Halabi, Eli Levy Karin, Haim Ashkenazy, Nir Ben-Tal, Tal Pupko and Itay Mayrose
38. Modeling the effect of translation factor fluctuations on translation
Doron Levin and Tamir Tuller
39. Disease biomarkers: discovery and analysis tools
Amir VizeI, David Amar and Ron Shamir
40. Nanopore sequencing for pathogen detection: data analysis optimization and applications
Artem Danilevsky, Avital Polsky and Noam Shomron
41. An evolutionary study of inverted repeats – prevalence and conservation

Bar Lavi, Eli Levy Karin, Tal Pupko and Einat Hazkani-Covo

42. Single cell-based deconvolution analysis reveals variation in the quantities of innate immune cells in the lungs of influenza infected mice
Amit Frishberg, Naama Peshes-Yaloz, Ofir Cohn, Yael Steurman, Diana Rosentul, Oded Danziger, Yael Oren, Liran Valadarsky, Eran Bacharach, Ido Amit and Irit Gat-Viks
43. An improved method for constructing large phylogenies
Nomi Hadar, Anna Rice and Itay Mayrose
44. The genetic basis of individual variation in transcriptional responses: a network-based approach
Roni Wilentzik, Chun Jimmie Ye and Irit Gat-Viks
45. Understanding the selection on mRNA folding strength in protein-coding sequences at multiple scales across the tree of life
Michael Peeri and Tamir Tuller
46. Biases in nucleotide substitution rates of viruses as evidence of antiviral activity
Talia Kustin and Adi Stern
47. Population genomics: beyond the consensus
Maoz Gelbart and Adi Stern
48. Understanding molecular mechanisms of heteroresistance
Noa Wertheimer, Noam Shahar, Ronen Ben-Ami and Judith Berman
49. The genetic basis of variation in transcriptional response to invading pathogens
Yael Oren, Naama Peshes-Yaloz, Amit Frishberg, Diana Rosentul, Ofir Cohn, Oded Danziger, Eran Bacharach, Ido Amit and Irit Gat-Viks
50. A machine-learning approach to discover antigen-specific epitopes in polyclonal sera
Haim Ashkenazy, Arie Ryvkin, Yael Weiss-Ottolenghi, Smadar Neeman, Jonathan M. Gershoni and Tal Pupko
51. A Markov chain Monte Carlo (MCMC) framework for predicting and evaluating the effect of sequence context on mutation rates
Guy Ling and Adi Stern
52. What do cancer and development have in common?
Naor Sagy and Iftach Nachman
53. Harnessing genome-scale metabolic modeling for the prediction of novel early-stage drug-targets for Alzheimer's disease
Nir Gonen, Boaz Styr, Irena Vertkin, Ilana Shapira, Ana Rita Pereira, Keren Grinin, Helene Marie, Ami Citri, Inna Slutsky and Eytan Rupp
54. 3-D genomic interactions and their relation to gene expression
Idan Nurick, Ran Elkon and Ron Shamir