

Poster titles – Retreat 2015

*The poster presenter is underlined

1. Genetic and non-genetic mechanisms to generate stochastic sub-populations that survive drug stress
Noa Wertheimer, Ronen Ben Ami, Mor Lurie-Weinberger and Judith Berman
2. Identification of breast cancer subtypes using high-throughput genomic data
Dvir Netanel, Ayelet Avraham, Ella Evron and Ron Shamir
3. The correlated evolution of sexual-dimorphism and polyploidy in flowering plants
Lior Glick, Niv Sabath, Emma Goldberg and Itay Mayrose
4. Models for sorting complex genomes with simple operations
Ron Zeira and Ron Shamir
5. A hierarchical Bayesian model for flexible module discovery in three-way time series data
David Amar, Daniel Yekutieli, Adi Maron-Katz, Talma Hendler and Ron Shamir
6. PinaColada – Peptide inhibitor ant colony ad-hoc design algorithm
Daniel Zaidman and Haim Wolfson
7. Poliovirus population mutation patterns suggest involvement of host immune proteins
Eitan Winter and Adi Stern
8. Simulating realistic multiple sequence alignments
Avigayel Rabin, Eli Levy Karin, Haim Ashkenazy, Oren Avram and Tal Pupko
9. Whole genome duplication increased the adaptive potential of crop plants
Niv Sabath, Ayelet Salman and Itay Mayrose
10. Rationally designed, heterologous *S. cerevisiae* transcripts expose novel expression determinants
Shimshi Atar, Tuval Ben-Yehzekel, Alon Diamant, Tzipy Marx, Rafael Cohen, Alexandra Dana, Anna Feldman, Ehud Shapiro and Tamir Tuller
11. Phenotype prediction via multiple kernel learning
Omer Weissbrod and Saharon Rosset



עשור למרכז אדמונד י. ספרא לביואינפורמטיקה

10th anniversary of the Edmond J. Safra Center for Bioinformatics

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12. Functional alignment of metabolic networks
Arnon Mazza, Allon Wagner, Eytan Ruppim and Roded Sharan
13. Understanding Ribo-seq biases towards improving its protocol for large scale in vivo mRNA translation study
Anna Feldman and Tamir Tuller
14. Selection for reduced translation costs at the intronic 5'end in fungi
Zafir Zohar, Zur Hadas and Tuller Tamir
15. Utilizing yeast chemogenomic profiles for the prediction of pharmacogenetic associations in human
Yael Silberberg, Martin Kupiec and Roded Sharan
16. Interaction between the ribosome and the nascent peptides shapes the proteomes of eukaryotes and prokaryotes
Renana Sabi and Tamir Tuller
17. Considering MSA uncertainties in phylogeny inference
Haim Ashkenzay, Itamar Sela and Tal Pupko
18. Widespread signatures of mRNA folding structure selection in four Dengue serotypes
Eli Goz and Tamir Tuller
19. Predicting the evolution of RNA viruses
Tal Zinger and Adi Stern
20. Improving 3D genome reconstructions using orthologous and functional constraints
Alon Diamant and Tamir Tuller
21. Genome wide folding structure selection in Ebola virus
Kiril Lomakin, Eli Goz and Tamir Tuller
22. Discovery of RNA regulatory elements by multiple sequence and structure alignment
Maor Dan, Yaron Orenstein and Ron Shamir



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23. The pre-initiation complex flow model
Ruth Caspi and Tamir Tuller
24. Gene expression shows higher diversity than protein expression in mammalian tissues: observations and hypotheses
Kobi Perl, Yoni Bhonker, Ofer Yizhar-Barnea, Shaked Shivatzki, Kathy Ushakov, Yair Pozniak, Orly Yaron, Noam Shomron, Tamar Geiger, Karen B. Avraham and Ron Shamir
25. Network-level identification of metabolic synthetic dosage lethality is highly predictive of tumor growth and cancer patient survival
Wout Megchelenbrink, Rotem Katzir, Xiaowen Lu, Eytan Ruppim and Richard A. Notebaart.
26. A novel method for selective sweep detection in bacteria.
Oren Avram, Yaara Oren, Eli Levy Karin & Tal Pupko
27. Identifying novel T3SS effectors of the pathogen *Citrobater rodentium* using machine-learning approach
Dafna Shkedy, Michael Gershovits and Tal Pupko
28. A computational study about the effect of oscillations in translation factors on translation rate
Lior Trieman and Tamir Tuller
29. Genome scale metabolic modeling analysis points to a novel protective drug-target against seizures
Nir Gonen, Boaz Styr, Tatiana Fedorova, Keren Yizhak, Inna Slutsky and Eytan Ruppim
30. TemFlexDock: Flexible approach to Template-based docking
Michael Estrin and Haim Wolfson
31. Genetic susceptibility to influenza in mice
Diana Rosentul, Yael Stuerman, Oded Danziger, Fuad Iraqi, Eran Bacharach and Irit Gat-Viks
32. A joint analysis of transcriptomic and metabolomic data uncovers increased metabolic transcriptional regulation in breast cancer



- Keren Yizhak, Adam Weinstock and Eytan Ruppin
33. eQTL analyses of naïve CC mice
Aharon Nachshon, Ro'oa Hamed, Hanifa Athamni, Richard Mott, Ron Shamir, Fuad A Iraqi and Irit Gat-Viks
34. A statistical framework for revealing signaling pathways perturbed by DNA variants
Roni Wilentzik and Irit Gat-Viks
35. Identifying genetic variants that lead to inter-individual variation in immune physiology
Yael Steurman and Irit Gat-Viks
36. Combining genetic polymorphisms with inherited variation in gene expression to explain organismal physiological traits
Tom Harel and Irit Gat-Viks
37. Parameters that affect the fitness of different haploids derived from a highly heterozygous diploid parent
Mor N. Lurie-Weinberger and Judith Berman
38. Harnessing the power of myriad heterogeneous expression profiles to classify diseases and propose drug targets
D. Amar, Tom Hait, Shai Izraeli and Ron Shamir

