

Poster titles – Retreat 2016

*The poster presenter is underlined

1. Mapping of environmental effects on the human immune system
Maya Botzman, Yael Steuerman and Irit Gat-Viks
2. Cancer subtype classification using somatic mutation data alone and its applications
David Amar, Shai Izraeli and Ron Shamir
3. PROMO: A new tool for analyzing large high-throughput genomic datasets
Dvir Netanel, Itay Laufer and Ron Shamir
4. 3-D chromosomal domains and their relation to genomic function
Idan Nurick, Michal Ozery-Flato, Liat Ein-Dor and Ron Shamir
5. On copy number transformation problems
Ron Zeira, Meirav Zehavi and Ron Shamir
6. Extending partial haplotypes to full genome haplotypes using chromosomal conformation capture data
Shay Ben-Elazar, Benny Chor and Zohar Yakhini
7. The worldwide distribution of polyploid plants
Anna Rice, Petr Šmarda, Niv Sabath, Maria Novosolov, Lior Glick, Michal Drori, Shai Meiri and Itay Mayrose
8. Algorithms for gene family silencing using the CRISPR-Cas9 system
Gal Hyams, Shiran Abadi, Adi Avni, Eilon Shani, Eran Halperin and Itay Mayrose
9. COP9 signalosome influences the epigenetic landscape of Arabidopsis Thaliana
Shimshi Atar, Avital Yahalom, Daniel A. Chamovitz and Tamir Tuller
10. High-resolution view of bacteriophage lambda translation regulation and evolution by ribosome profiling
Oriah Mioduser, Alon Diamant, Eli Goz and Tamir Tuller



עשור למרכז אדמונד י. ספרא לביואינפורמטיקה

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

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11. Integrated live imaging and molecular profiling of embryoid bodies reveals a synchronized progression of early differentiation
Naor Sagy, Jonathan Boxman, Sirisha Achanta, Rajanikanth Vadigepalli and Iftach Nachman
12. A computational algorithm for estimating cleavage probability of the CRISPR-Cas9 system
Shiran Abadi, Winston Yan, David Amar, Feng Zhang and Itay Mayrose
13. Changes in transcription levels across non-proliferating tissues are buffered on the protein level
Kobi Perl, Kathy Ushakov, Yair Pozniak, Ofer Yizhar-Barnea, Yoni Bhonker, Shaked Shivatzki, Tamar Geiger, Karen B. Avraham and Ron Shamir
14. Tracking the evolution of 3D gene organization
Alon Diamant and Tamir Tuller
15. Evidence that the interaction of short peptide with the ribosomal exit tunnel shapes the proteome
Renana Sabi and Tamir Tuller
16. Universal selection for high dimensional signatures of viral coding regions adaptation to hosts
Eli Goz and Tamir Tuller
17. Unsupervised detection of regulatory gene expression information in various genomic regions enables gene expression prediction
Zohar Zafrir and Tamir Tuller
18. Towards improved ribosomal profiling protocol for large scale in vivo mRNA translation study
Anna Feldman and Tamir Tuller
19. Recycler: an algorithm for detecting plasmids from de novo assembly graphs
Roye Rozov, Aya Brown Kav, David Bogumil, Eran Halperin, Itzhak Mizrahi and Ron Shamir
20. Enhancer RNAs as markers of active enhancers
Tom Aharon Hait, Rani Elkouf and Ron Shamir
21. Averaging over alternative multiple sequence alignments increases the accuracy of phylogenetic tree reconstruction
Haim Ashkenazy, Itamar Sela, Giddy Landan and Tal Pupko



22. The genetic basis of individual variation in transcriptional responses: a network-based approach
Roni Wilentzik and Irit Gat-Viks
23. PloiDB: A ploidy-level database of angiosperm genera
Niv Sabath, Michal Drori, Moshe Einhorn, Lior Glick, Anna Rice, Shiran Abadi, Ofer Chai, Ayelet Salman Minkov and Itay Mayrose.
24. Modeling translation initiation in the chloroplast genome
Iddo Weiner, Iftach Yacoby and Tamir Tuller
25. Whole genome duplication as a key factor in crop domestication
Ayelet Salman Minkov, Niv Sabath and Itay Mayrose
26. Genetic susceptibility to influenza in mice
Diana Rosentul, Naama Peshes-Yaloz, Yael Oren, Yael Steerman, Fuad Iraqi, Eran Bacharach and Irit Gat-Viks
27. A novel phylogeny-based algorithm for selective sweeps detection in bacteria
Oren Avram, Yaara Oren, Eli Levy Karin and Tal Pupko
28. Clustering optical map intensity profiles for metagenomics applications
David Pellow and Ron Shamir
29. Improved unsupervised approach for ranking the gene expression optimality of genomic sequences
Maya Galili, Martin Kupiec and Tamir Tuller
30. SPARTA-ABC - Inferring indel parameters using approximate Bayesian computation
 Eli Levy Karin, Dafna Shkedy, Haim Ashkenazi and Tal Pupko
31. An improved method for constructing large phylogenies
Nomi Hadar and Itay Mayrose
32. Modeling the impact of context dependent mutations in RNA viruses
Guy Ling and Adi Stern
33. Inferring HIV-1 variability and fitness from high throughput sequencing data
Maoz Gelbart, Roy Moscona, Orna Mor and Adi Stern
34. Data-driven metabolic pathway compositions enhance cancer survival prediction
Noam Auslander, Allon Wagner, Matthew Oberhardt and Eytan Ruppin



35. Biases in nucleotide substitution rates of RNA viruses as evidence of antiviral activity
Talia Kustin and Adi Stern
36. Detection of positively selected genes involved in human neurodegenerative diseases
Nareman Abd El Hade, Eli Levy Karin and Tal Pupko



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