

Poster titles – Retreat 2012

*The poster presenter is underlined

1. Short RNA subtraction and assembly – a method for pathogen detection

Ofer Isakov, Shira Modai and Noam Shomron

2. INDI: A novel framework for inferring drug interactions and their associated recommendations

Assaf Gottlieb, Gideon Y. Stein, Yoram Oron, Eytan Ruppim and Roded Sharan

3. The EXPANDER suite for accessible analysis of microarray data

Hershel Safer, Adi Maron-Katz, David Amar , Ran Elkon , Igor Ulitsky , Chaim Linhart, Amos Tanay, Roded Sharan, Eyal David, Dorit Sagir, Yosef Shiloh and Ron Shamir

4. MGMR: leveraging RNA-Seq population data to optimize expression estimation

Roye Rozov, Eran Halperin and Ron Shamir

5. RAP: accurate prediction of cis regulatory motifs from protein binding microarrays

Yaron Orenstein, Eran Mick and Ron Shamir

6. Efficient manipulations of synonymous mutations for controlling translation rate: an analytical approach

Alexandra Dana and Tamir Tuller

7. Uncovering pre-mRNA splicing regulation code in *s. cerevisiae* using a synthetic intron library

Ido Yofe, Tuval Ben Yehezkel, Zohar Zafrir, Tamir Tuller, Ehud Shapiro and Maya Schuldiner

8. Using computational biology methods to improve post-silicon microprocessor testing

Ron Zeira , Dmitry Korchemny and Ron Shamir

9. Ordered protein sequences: systematics, evolution and function

Erez Persi and David Horn

10. Indel reliability in phylogenetic inference

Haim Ashkenzay, Ofir Cohen, Dorothee Huchon and Tal Pupko

11. FastML: a web server for probabilistic reconstruction of ancestral sequences

Haim Ashkenazy, Osnat Penn, Adi Doron-Faigenboim, Ofir Cohen, Gina Cannarozzi, Oren Zomer and Tal Pupko

12. Ontologies from existence of homologues: human vs. fly viewpoints

Jonathan Witztum, Erez Persi, David Horn, Metsada Pasmanik-Chor and Benny Chor

13. Fishing for virulent factors: machine learning prediction and experimental validation of bacterial effectors

David Burstein, Michael Pe'eri, Tal Zusman, Ziv Lifshitz, Gil Segal and Tal Pupko

14. iPoint: An integer programming based algorithm for inferring protein subnetworks

Nir Atias and Roded Sharan

15. Exclusive row biclustering for gene expression using a combinatorial auction approach

Amichai Painsky and Saharon Rosset

16. Editing of microRNAs in the human brain

Shahar Alon and Eli Eisenberg

17. Modeling and detection of genome plasticity in the pathogenic yeast candida albicans using high-throughput sequencing data

Joshua A. Baller, Darren Abbey and Judith Berman

18. Discovering molecular signals using hidden semi-markov models

Michael Peeri, David Burstein, Gil Segal and Tal Pupko

19. Metabolic phenotypic analysis uncovers reduced proliferation in progressed breast cancer associated with oxidative stress

Livnat Jerby, Lior Wolf, Carsten Denkert, Gideon Y Stein, Mika Hilvo, Matej Oresic, Tamar Geiger and Eytan Ruppin

20. Metabolic homeostasis is disrupted in genetic disorders and is not restored by drugs

Noa Cohen, Allon Wagner and Eytan Ruppin

21. SELERA: a tool to predict antibiotic resistance using genome-scale models

Matthew A. Oberhardt, Raphy Zarecki, Fangfang Xia, Christopher Henry, Uri Gophna and Eytan Ruppin

22. Using Contiguous Bi-Clustering for data driven temporal analysis of fMRIbased functional connectivity

Adi Maron-Katz, Didi Amar, Eti Ben Simon, Yael Jacob, Keren Rosenberg, Richard M. Karp, Talma Hendler and Ron Shamir

23. Local Ancestry Inference in Latinos

Yael Baran, Bogdan Pasaniuc, Sriram Sankararaman and Eran Halperin