

Poster titles – Retreat 2014

\*The poster presenter is underlined

1. Fast lossless compression via cascading Bloom Filters  
Roye Rozov, Ron Shamir and Eran Halperin
2. Proposing ensemble of conformations for a query protein with known structure using the ConTemplate server  
Aya Narunsky, Haim Ashkenazy, Rachel Kolodny and Nir Ben-Tal
3. Building a BG2 scaffold for next generation sequencing data for analyzing clinical *Candida glabrata* isolates  
Noa Wertheimer, Mor Lurie-Weinberger, Noam Mamet, Darren Abbey, Jane Usher, Ken Haynes, Brendan Cormack, Cecile Fairhead, Ronen Ben-Ami and Judith Berman
4. A new and improved scaffold to use as a *Candida glabrata* reference genome  
Mor Lurie-Weinberger, Toni Gabaldon, Jane Usher, Ken Haynes, Ronen Ben-Ami and Judith Berman
5. New codon model detects novel functional regions within the murine leukemia virus genome  
Alon Rozental, Daniella Bar-Meir, Rachel Zamostiano, Eran Bacharach and Tal Pupko
6. A method for predicting protein-protein interaction types  
Yael Silberberg, Martin Kupiec and Roded Sharan
7. Polyploidy and plant domestication  
Ayelet Salman Minkov, Niv Sabath, Moshe Einhorn, Lior Glick, and Itay Mayrose
8. Nucleotide composition adjacent to intronic splice sites improves retained introns translation costs in fungi  
Zohar Zafrir, Hadas Zur and Tamir Tuller
9. Exploring coding sequence determinants of expression in *S. cerevisiae* via combined synthetic-computational biology approach  
Shimshi Atar, Tuval Ben-Yehzekel, Ehud Shapiro and Tamir Tuller
10. Protein complexes assembly and function revealed by structural motion prediction  
Adva Yeheskel, Rony Seger and Malka Cohen-Armon

---

Edmond J. Safra Center for Bioinformatics at Tel Aviv University

School of Computer Science, Schreiber 223, Tel Aviv University, Tel Aviv 69978, Israel

Tel +972-3-6405391 Fax +972-3-6409373 [safrabio@post.tau.ac.il](mailto:safrabio@post.tau.ac.il) <http://safrabio.cs.tau.ac.il/>

11. Understanding the connection between transcriptome and proteome in non-proliferating tissues through the example of the auditory system  
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
12. Short peptides that stall the ribosome are underrepresented in the proteome  
Renana Sabi and Tamir Tuller
13. Ultra conserved protein elements  
Eyal Cohen and Benny Chor
14. Comprehensive study of gene expression regulating information encoded in viral genomes  
Eli Goz and Tamir Tuller
15. Using state machines to model the ion torrent sequencing process and improve read error-rates  
David Golan and Paul Medvedev
16. Pathway as robust biomarkers for cancer classification: the power of big expression data  
David Amar, Tom Hait and Ron Shamir
17. Network orientation via shortest paths  
Dana Silverbush and Roded Sharan
18. Three dimensional genomic organization of eukaryotic genes is strongly correlated with their codon usage, expression and function  
Alon Diamant, Ron Pinter and Tamir Tuller
19. Beyond sequencing: optical mapping of DNA  
Roei Herzig, Omer Zuqert, Yaron Orenstein, Ron Shamir, Yuval Ebenstein
20. GASP: a greedy alanine scanning peptide design algorithm  
Daniel Zaidman and Haim J. Wolfson
21. eQTL analyses of naïve cc mice  
Aharon Nachshon, Ro'oa Hamed, Hanifa Athamni, Richard Mott, Ron Shamir, Fuad A Iraqi and Irit Gat-Viks
22. Modeling the differentiation and proliferation processes of naïve CD4+T cells into regulatory T cells  
Keren Levinstein Hallak, Irina Zaretsky and Nir Friedman

23. An optimal experimental design scheme for learning Boolean network models  
Nir Atias, Michal Gershenson, Katia Labazin and Roded Sharan
24. A computational study about the effect of oscillations in tRNA pool and translation elongation/initiation factors on translation rate  
Lior Trieman and Tamir Tuller
25. Alignment errors strongly impact likelihood-based tests for comparing topologies  
Eli Levy Karin, Edward Susko and Tal Pupko
26. Accurate detection of unreliable alignment regions: accounting for the uncertainty of multiple parameters  
Haim Ashkenzay, Itamar Sela and Tal Pupko
27. Prediction of *Pantoea Agglomerans* effectors using a machine learning approach  
Michael Gershovits and Tal Pupko
28. Combine genetic polymorphisms with inherited variation in gene expression to explain organismal physiological traits  
Tom Harel, Maya Botzman and Irit Gat-Viks
29. Identification of deafness genes in Middle Eastern families using exome Sequencing  
Fábio Tadeu Arrojo Martins, Zippora Brownstein, Amal Abu-Rayyan, Maria Birkan, Meirav Sokolov, Ofer Isakov, Noam Shomron, Moien Kanaan, and Karen B. Avraham
30. Reconstructing Cancer Karyotypes  
Rami Eitan and Ron Shamir
31. Design, analysis and development of efficient algorithms for finding sequence motifs in HT-SELEX data  
Rotem Katzir
32. Inferring gene-gene interactions from genetic variation utilizing modules of associated traits  
Maya Botzman and Irit Gat-Viks
33. Identification of breast cancer subtypes using RNA-Seq data  
Dvir Netanely and Ron Shamir
34. Inferring binding site motifs from HT-SELEX data  
Yaron Orenstein and Ron Shamir