Poster titles – Retreat 2011

1. **PREDICT: A method for inferring novel drug indications with application to personalized medicine**
Assaf Gottlieb, Gideon Y. Stein, Eytan Ruppin and Roded Sharan

2. Competitive and cooperative metabolic interactions in bacterial communities
Shiri Freilich, Raphy Zarecki, Omer Eilam, Ella Shtifman Segal, Christopher S. Henry, Martin Kupiec, Uri Gophna, Roded Sharan and Eytan Ruppin

3. **Metabolic model-based feature-selection can enhance expression-based prediction accuracy of normal and disease phenotypes**
Livnat Jerby, Lior Wolf and Eytan Ruppin

4. Towards the computational prediction of drug targets acting to reverse metabolic alterations in ageing
Keren Yizhak and Eytan Ruppin

5. **Selection for Translation Efficiency on Synonymous Polymorphisms in Recent Human Evolution**
Yedael Y. Waldman, Tamir Tuller, Alon Keinan and Eytan Ruppin

6. **Metabolic gene expression in the hippocampus predicts Alzheimer's disease progression**
Shiri Stempler, Yedael Waldman, Lior Wolf and Eytan Ruppin

7. The Operonic Location of Auto-Transcriptional Repressor is Highly Conserved in Bacteria
David Zeevi, Nimrod D. Rubinstein, Yaara Oren, Gil Segal, Tal Pupko

8. **Discovering transcription factor binding site motifs from protein binding microarray data**
Yaron Orenstein, Chaim Linhart and Ron Shamir

9. Pathway Extension: A case study on carotenoid biosynthesis in plants
David Amar, Oren Tzfadia, Elleanore Wurtzel and Ron Shamir

10. SPIKE 2.0: A WEB-BASED database and visualization tool of signaling pathways and protein interactions
Eyal David, Arnon Paz, Dorit Sagir, Ran Elkon, Igor Ulitksy, Yaara Ber, Shani Bialik, Zippora Brownstein, Karen B. Avraham, Adi Kimchi, Yosef Shiloh and Ron Shamir

11. MGMR: Multiple Genome expression estimation incorporating MultiReads
Roye Rozov, Eran Halperin and Ron Shamir

12. Using expression microarray algorithms to improve microprocessor testing
Ron Zeira , Dmitry Korchemny and Ron Shamir

13. Reconstructing logical models for gene regulatory networks : an entropy based approach
Guy Karlebach and Ron Shamir

14. Improving positive selection inference using an alignment confidence score
Osnat Penn, Eyal Privman, Haim Ashkenazy, Giddy Landan, Dan Graur, and Tal Pupko

15. Accurate Estimation of Heritability in Genome Wide Studies using Random Effects Models
David Golan and Saharon Rosset

16. Systematic Detection of Highways of Horizontal Gene Transfer
Guy Banay, Mukul Bansal, Timothy J. Harlow, J. Peter Gogarten and Ron Shamir

17. TAU Bioinformatics Unit: who are we and what do we do ?
Adva Yeheskel and Metsada Pasmanik-Chor

18. A Phylogenetic Approach to Music Performance Analysis
Elad Liebman, Eitan Ornoy, and Benny Chor

19. CRISPR loci reveal networks of gene exchange in archaea
Avital Brodt, Mor N. Lurie-Weinberger and Uri Gophna

20. The EXPANDER suite for accessible analysis of microarray data
Hershel Safer , Adi Maron-Katz , Ran Elkon , Igor Ulitsky, Chaim Linhart , Amos Tanay, Roded Sharan, Eyal David, Dorit Sagir, Yosef Shiloh and Ron Shamir

21. Learning morphological cell fate classifiers from reprogramming live imaging data
Roni Rosner and Iftach Nachman

22. Short RNA Subtraction and Assembly – a method for pathogen detection
Ofer Isakov, Shira Modai and Noam Shomron

23. Whole-Genome Phylogeny of Multi Cellular Eukaryotes: A Saturation of Phylogenetic Signal?
Eyal Cohen and Benny Chor

24. Methods in Metagenomics
Yael Baran and Eran Halperin

25. The complexity hypothesis revisited: connectivity rather than function constitutes a barrier to horizontal gene transfer
Ofir Cohen, Uri Gophna and Tal Pupko