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 Netanely, 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 Diament, Eli Goz and Tamir Tuller

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 Diament 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 Elkon 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 susceptibilty to influenza in mice
    Diana Rosentul, Naama Peshes-Yaloz, Yael Oren, Yael Steuerman, 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