Poster titles – Retreat 2014
*The poster presenter is underlined

1. Fast lossless compression via cascading Bloom Filters
   <u>Roye Rozov</u>, Ron Shamir and Eran Halperin

2. Proposing ensemble of conformations for a query protein with known structure using the ConTemplate server
   <u>Aya Narunsky</u>, Haim Ashkenazy, Rachel Kolodny and Nir Ben-Tal

3. Building a BG2 scaffold for next generation sequencing data for analyzing clinical Candida glabrata isolates
   <u>Noa Wertheimer</u>, 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
   <u>Mor Lurie-Weinberger</u>, 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
   <u>Alon Rozental</u>, Daniella Bar-Meir, Rachel Zamostiano, Eran Bacharach and Tal Pupko

6. A method for predicting protein-protein interaction types
   <u>Yael Silberberg</u>, Martin Kupiec and Roded Sharan

7. Polyploidy and plant domestication
   <u>Ayelet Salman Minkov</u>, Niv Sabath, Moshe Einhorn, Lior Glick, and Itay Mayrose

8. Nucleotide composition adjacent to intronic splice sites improves retained introns translation costs in fungi
   <u>Zohar Zafrir</u>, Hadas Zur and Tamir Tuller

9. Exploring coding sequence determinants of expression in *s. cerevisiae* via combined synthetic-computational biology approach
   <u>Shimshi Atar</u>, Tuval Ben-Yehezkel, Ehud Shapiro and Tamir Tuller

10. Protein complexes assembly and function revealed by structural motion prediction
    <u>Adva Yeheskel</u>, Rony Seger and Malka Cohen-Armon

11. Understanding the connection between transcriptome and proteome in non-proliferating tissues through the example of the auditory system
<u>Kobi Perl</u>, 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
<u>Renana Sabi</u> and Tamir Tuller

13. Ultra conserved protein elements
<u>Eyal Cohen</u> and Benny Chor

14. Comperhensive study of gene expression regulating information encoded in viral genomes
<u>Eli Goz</u> and Tamir Tuller

15. Using state machines to model the ion torrent sequencing process and improve read error-rates
<u>David Golan</u> and Paul Medvedev

16. Pathway as robust biomarkers for cancer classification: the power of big expression data
<u>David Amar</u>, <u>Tom Hait</u> and Ron Shamir

17. Network orientation via shortest paths
<u>Dana Silverbush</u> and Roded Sharan

18. Three dimensional genomic organization of eukaryotic genes is strongly correlated with their codon usage, expression and function
<u>Alon Diament</u>, Ron Pinter and Tamir Tuller

19. Beyond sequencing: optical mapping of DNA
<u>Roei Herzig</u>, Omer Zuqert, Yaron Orenstein, Ron Shamir, Yuval Ebenstein

20. GASP: a greedy alanine scanning peptide design algorithm
<u>Daniel Zaidman</u> and Haim J. Wolfson

21. eQTL analyses of naïve cc mice
<u>Aharon Nachshon</u>, 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
<u>Keren Levinstein Hallak</u>, Irina Zaretsky and Nir Friedman

23. An optimal experimental design scheme for learning Boolean network models
    Nir Atias, Michal Gershenzon, 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