Poster titles – Retreat 2019

#The poster presenter is underlined
*Equal contribution

1. Phylogenetic tree reconstruction using reinforcement learning algorithm
   Dana Azouri, Yishay Mansour, Itay Mayrose and Tal Pupko

2. Dynamic interplay between pathogens and hosts with genetic diversity
   Ofir Cohn, Gal Yankovitz, Naama Peshes-Yaloz, Eran Bacharach and Irit Gat-Viks

3. CT-FOCS: a novel method for genome-wide inference of cell type-specific enhancer-promoter maps
   Tom Aharon Hait, Rani Elkon and Ron Shamir

4. Novel driver synonymous mutations in the coding regions of GCB lymphoma patients improve the transcription levels of BCL2
   Ofek Schnitzer, Zohar Zafir and Tamir Tuller

5. Proteomic analysis of short term versus long term survival in glioblastoma patients
   Gali Yanovich-Arad, Paula Ofek, Eilam Yeini, Artem Danilevsky, Noam Shomron, Ronit Satchi-Fainaro and Tamar Geiger

6. Learning protein constitutive motifs from sequence data
   Jérôme Tubiana, Simona Cocco and Rémi Monasson

7. An entropy-based approach for pattern recognition in viruses using a single sequence
   Danielle Miller and Adi Stern

8. Chromosomal organization in the mouse embryo at single cell resolution
   Nimrod Rappoport, Elad Chomsky, Takashi Nagano, Charlie Seibert, Yaniv Lubling, Aviezer Lifshitz, Zohar Mukamel, Ron Shamir, Peter Fraser and Amos Tanay

9. The interface between atherogenic and immunometabolic heterogeneity in obesity
   Amit Frishberg, Inge Van Den Munckhof, Niels Riksen, Mihai Netea and Irit Gat-Viks

10. Can molecular phylogenies be used to accurately infer alternations in diversification rates?
    Anat Shafir, Dana Azouri, Emma Goldberg and Itay Mayrose

11. Persistence of probiotic strains in the gut microbiomes of patients with inflammatory bowel disease
    Vadim Dubinsky, Leah Reshef, Keren Rabinowitz, Lihi Godny, Karin Yadgar, Hagit Tulchinsky, Iris Dotan and Uri Gophna

12. Noninvasive prenatal diagnosis using deep learning
    Tom Rabinowitz and Noam Shomron

13. A codon model for associating phenotypic traits with altered selective patterns of sequence evolution
    Keren Halabi, Eli Levy Karin and Itay Mayrose

14. Attenuation of RNA Viruses based on a computational rational design
    Zohar Zafrir, Eli Goz, Yoram Zarai, Bunpote Siridechadilok, Modi Ruppin, Roda Dabour, Meital Gal-Tanamy and Tamir Tuller

15. Cell type-specific analysis of alternative polyadenylation using single-cell transcriptomics data
    Eldad Shulman and Rani Elkon

16. Long-read single-molecule maps of the functional methylome
    Sapir Margalit, Hila Sharim , Assaf Grunwald , Tslil Gabrieli , Yael Michaeli , Dmitry Torchinsky, Rani Arielly , Gil Nifker and Yuval Ebenstein

17. Comparing the utility of in vivo transposon mutagenesis approaches in yeast species to identify gene essentiality
    Anton Levitan, Andrew Gale, Kyle Cunningham, Roded Sharan and Judith Berman

18. Exploring the evidences of selection for local intrinsic disorder in proteins across the tree of life
    Arup Panda and Tamir Tuller

19. Inferring rates of insertions and deletions using approximate Bayesian computation
    Dana Rapoport, Dana Azouri, Reed A. Cartwright and Tal Pupko

20. The effect of nucleotide composition at the end of the coding sequence on ribosomal read-through and translation re-initiation of a downstream gene
    Rachel Cohen-Kupiec, Shir Bahiri, Michael Peer and Tamir Tuller

21. Predicting genetic interactions in human cells
    Asia Gervits and Roded Sharan

22. Improving assembly of plasmid sequences in metagenomic samples
    David Pellow, Itzik Mizrahi and Ron Shamir

23. Elevated rates of UA>UG mutations in Picornaviruses suggest ADAR editing
    Oded Kushnir, Maoz Gelbart, Ya'ara Ben-Ari Grosman and Adi Stern

24. Improving the classification of cutaneous melanoma tumors using PROMO
    Dvir Netanely, Neta Stern, Carmit Levy and Ron Shamir

25. EvaLi - Evaluation of random peptide libraries
    Ora Balber, Anna Roitburd, Oren Avram, Jonathan M. Gershoni and Tal Pupko

26. Enhancing transcriptional network inference by integration of genomic footprinting data
Naama Messika-Gold and Rani Elkon

27. Full genome sequencing of RNA viruses using MinION: finding associations between mutations
Noam Harel, Moran Meir, Uri Gophna and Adi Stern

28. Efficient algorithm to design small universal k-mer hitting sets
Lianrong Pu and Ron Shamir

29. Improving FRET real-time translation monitoring technology signal-to-noise in human based on ribo-seq modeling
Shimshi Atar and Tamir Tuller

30. ModelTeller: A machine-learning approach for phylogenetic model selection
Shiran Abadi, Oren Avram, Tal Pupko, and Itay Mayrose

31. Towards efficient algorithms for modulating ribosome traffic jams
Sophie Vinokour and Tamir Tuller

32. A model for early detection of cancer risk based on routine check-up data using random forest of survival analysis trees for left-truncated and right-censored data
Dan Coster, Eyal Fisher, Shani Shenhar, Shlomo Berliner, Eran Halperin, Saharon Rosset and Ron Shamir

33. The first iGEM team in Tel Aviv University – a novel method of fighting antibiotic resistance bacteria using genetically engineered Pyocins
Ofek Schnitzer, Omer Grinboim, Lior Soffer, Dror Hadas and Tamir Tuller

34. Genomic delineation of transcriptional networks that determine auditory hair cells fate
Michal Sperber, Beatrice Milon, Ronna Hertzano and Rani Elkon

35. Single-molecule optical mapping of 5-hydroxymethylcytosine allows single-cell-like clustering of subpopulations
Hila Sharim, Yael Michaeli and Yuval Ebenstein

36. Prokaryotic rRNA-mRNA interactions are involved in all translation steps and shape bacterial transcripts
Shir Bahiri Elitzur, Dana Yacobi, Boaz Apt, Alon Diament and Tamir Tuller

37. Memory efficient de Bruijn graph construction - DOCKS Implementation on MSP
Yael Ben-Ari and Ron Shamir

38. Characterization of tumor inter and intra- heterogeneity and tumor progression in Ewing Sarcoma using proteomics analysis
May Arama-Chayoth, Revital Caspi, Benny Dekel and Tamar Geiger

39. Automatic predictions of novel rRNA-mRNA interactions
Boaz Apt, Shir Bahiri and Tamir Tuller

40. Improving functional characterization of GWAS risk SNPs by utilization of enhancer-promoter maps
Avinoam Shye, David Groenewoud and Rani Elkon

41. Development of an integrated circuit that performs simulations of mRNA translation dynamics
Danny Naiger and Tamir Tuller

42. Inferring population genetics parameters of evolving viruses using time-series data
Tal Zinger, Maoz Gelbart, Danielle Miller, Pleuni S. Pennings and Adi Stern

43. A new computational model for miRNA-mediated repression reveals novel regulatory roles of miRNA bindings inside the coding region
Shaked Bergman, Alon Diament and Tamir Tuller

44. Towards understanding protein degradation in bacteria: a combined proteomic-machine-learning approach
Natan Nagar and Tal Pupko

45. Determining eQTLs effects on immune-cells based on the hematopoietic lineage tree
Gal Yankovitz, Yael Steuerman, Ofir Cohn, Naama Peshes-Yaloz and Irit Gat-Viks

46. Engineering the mRNA-rRNA interaction strength in E. coli based on computational models
Larissa Fine, Shir Bahiri, Rachel Cohen-Kupiec and Tamir Tuller

47. Engineering patient-specific tissues
Reuven Edri, Idan Gal, Nadav Noor, Tom Harel, Sharon Fleischer, Nofar Abadi, Shoshy Mizrahy, Lior Heller, Assaf Shapira, Dan Pe'er, Irit Gat-Viks and Tal Dvir

48. Modeling eukaryotic translation initiation based on TCP-seq
Tamar Shmulevsky and Tamir Tuller

49. Network-based functional analysis: Bias correction and evaluation
Hagai Levi, Rani Elkon and Ron Shamir

50. Solving the riddle of the evolution of Shine-Dalgarno based translation in chloroplasts
Iddo Weiner, Noam Shahar, Pini Marco, Iftach Yacoby and Tamir Tuller

51. Methods for multi-omic data visualization
Nimrod Rappoport, Roy Safra and Ron Shamir

52. M1CR0B1AL1Z3R – a user-friendly web server for the analysis of large-scale microbial genomics data
Oren Avram, Dana Rapoport, Shir Portugez and Tal Pupko

53. Translation termination in bacteria is regulated by mRNA secondary-structure downstream of the stop codon
Yonatan Chemla*, Michael Peeri*, Mathias Heltberg, Mogens HØgh Jensen, Tamir Tuller and Lital Alfonta

54. Identification of novel type III-secreted effectors of the cucurbit pathogenic bacterium Acidovorax citrulli by combination of machine learning and transcriptomics approaches
Irene Jiménez Guerrero*, Francisco Pérez-Montaño*, Gustavo Mateus Da Silva, Naama Wagner, Dafna Shkedy, , Mei Zhao, Ron Walcott, Guido Sessa, Tal Pupko and Saul Burdman

55. Computational analysis of translation elongation in meiosis and cancer
Renana Sabi and Tamir Tuller

56. Model adequacy for likelihood models of chromosome-number evolution
Anna Rice and Itay Mayrose

57. The hidden genetic diversity of HIV during acute infection exposed using accurate next generation sequencing
Maoz Gelbart*, Sheri Harari*, Ya'ara Ben-Ari, Talia Kustin, Moran Meir, Danielle Miller, Pleuni Pennings, Orna Mor and Adi Stern