

Virtual BSC RS/Life Session: Probabilistic and algebraic models for mutation data

Objectives

Abstract: Mutational processes shape the genomes of cancer patients, leaving distinct mutational signatures, and their understanding has important applications in diagnosis and treatment. Current approaches for mutational signature discovery and analysis are based to a large extent on non-negative matrix factorization and make multiple assumptions about mutation category repertoire, data richness and independence of mutational processes. In this talk I will challenge each of these assumptions and present alternative probabilistic and algebraic models that can capture spatial dependencies among mutations, handle sparse data as typical in the clinic and derive informative mutation categories.



Short Bio: Roded Sharan is a Professor in the School of Computer Science at

Tel Aviv University. His PhD studies in the School of Computer Science at Tel Aviv University under the guidance of Ron Shamir along with his postdoctoral training at UC Berkeley under the guidance of Richard Karp shaped his interests in bioinformatics and systems biology. At the end of his postdoctoral training, he was offered a Senior Lecturer position at Tel Aviv University to which he returned as an Alon fellow. Additional awards he obtained include the Krill prize of the Wolf Foundation, Best Paper award in the RECOMB'10 conference, Test of time awards in RECOMB'16, RECOMB'17 and RECOMB'20, the Thomson-Reuters highly cited researcher award and the Kadar prize for excellence in research. Currently, Sharan heads a research group that specializes in the analysis of biological networks and mutational signatures and their applications to medicine.

Speakers

Speaker: Roded Sharan, Professor in the School of Computer Science at Tel Aviv University

Host: Natasa Przulj, Integrative Computational Network Biology Leading Researcher, BSC Life Sciences Department

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