You are cordially invited to a talk in the Edmond J. Safra Center for Bioinformatics Distinguished Speaker Series.
The speaker is Prof. Natasa Przulj, Dept. of Computing, Imperial College London

Title: "Revealing Biology from Structure of Molecular Networks"

Time: Thursday, 10 April 2014, at 11:15 (refreshments from 11:00)

Place: School of Computer Science, Schreiber building, third floor, room 309

Abstract: Sequence-based computational approaches have revolutionized biological understanding. However, they can fail to explain some biological phenomena. Since proteins aggregate to perform a function, the connectivity of a protein-protein interaction (PPI) network will provide additional insight into the inner working on the cell. We argue that sequence and network topology (structure) give insights into complementary slices of biological information, which sometimes corroborate each other, but sometimes do not. Hence, the advancement depends on the development of sophisticated graph-theoretic methods for extracting biological knowledge purely from network topology before being integrated with other types of biological data (e.g., sequence).
However, dealing with large networks is non-trivial, since many graph-theoretic problems are computationally intractable, so heuristic algorithms are sought.

We design methods for extraction of biological knowledge from topologies of molecular networks. Our methods show that topology around nodes in PPI networks is a predictor of their function and involvement in disease. Also, we design the GRAAL family of network alignment algorithms that produce the most complete alignments of PPI networks to date, that can be used to transfer annotation and reconstruct phylogeny. In addition, we fuse heterogeneous systems-level molecular network data to discover new disease-disease associations that may help drug repositioning. Finally, we discover that the interaction between a small number of roles, played by nodes in a network, can characterize a network's structure and also provide a clear real-world interpretation.
Given this insight, we develop a framework for analysing and comparing networks, which outperforms all existing ones. We demonstrate its strength by uncovering novel relationships between seemingly unrelated networks, such as Facebook, metabolic, and protein structure networks.
We also use it to track network dynamics. Our approach translates network topology into everyday language, bringing network analysis closer to domain scientists.

Hosts: Prof. Roded Sharan, roded@post.tau.ac.il, Prof. Eytan Ruppin, ruppin@post.tau.ac.il.