

You are cordially invited to a talk in the Edmond J. Safra Center for Bioinformatics Distinguished Speaker Series.

The speaker is **Prof. Fabio Vandin**, Department of Information Engineering, University of Padova.

Title: "Algorithms for finding significant combinations of mutations in cancer"

Time: Wednesday, July 27 2016, at 11:00 sharp (refreshments from 10:50)

Place: Schreiber 309, School of Computer Science

Host: Prof. Ron Shamir, rshamir@tau.ac.il, School of Computer Science

Abstract: Cancer is a disease that is driven by somatic mutations accumulating in the genome during an individual's lifetime. Recent advances in DNA sequencing technology have enabled genome-wide measurements of these mutations in large cohorts of cancer patients. A major challenge in analyzing these data is to distinguish functional "driver" mutations responsible for cancer progression from "passenger", random mutations not related to the disease. Recent cancer sequencing studies have shown that somatic mutations are distributed over a large number of genes. This mutational heterogeneity is due in part to the fact that somatic mutations target pathways, or combinations of genes, and that a mutation in any of dozens possible genes might be sufficient to perturb a pathway. While some of the cancer pathways are well characterized, many others are only approximately known.

I will describe algorithms for discovering significant combinations of genes and mutations using DNA mutation data from large cohorts of cancer samples. The first algorithm uses a heat diffusion process on graphs to identify subnetworks of a large gene interaction network that are mutated in a significant number of cancer samples. The second algorithm identifies subnetworks that have mutations associated with survival. I will illustrate applications of these algorithms to data from The Cancer Genome Atlas, a project that has characterized the genomes of thousands of samples from dozens of cancer types.