You are cordially invited to a talk in the Edmond J. Safra Center for Bioinformatics Distinguished Speaker Series.
The speaker is Prof. Alfonso Valencia, Spanish National Cancer Research Centre, CNIO.

Title: "A mESC epigenetics network that combines chromatin localization data and evolutionary information"

Time: Wednesday, November 11 2015, at 11:00 (refreshments from 10:50)

Place: Green building seminar room, ground floor, Biotechnology Department.

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

Abstract: The description of biological systems in terms of networks is by now a well-accepted paradigm. Networks offer the possibility of combining complex information and the system to analyse the properties of individual components in relation to the ones of their interaction partners. In this context, we have analysed the relations between the known components of mouse Embryonic Stem Cells (mESC) epigenome at two orthogonal levels of information, i.e., co-localization in the genome and concerted evolution (co-evolution).

Public repositories contain results of ChIP-Seq experiments for more than 60 Chromatin Related Proteins (CRPs), 14 for Histone modifications, and three different types of DNA methylation, including 5-Hydroxymethylcytosine (5hmc). All this information can be summarized in a network in which the nodes are the CRPs, histone marks and DNA modifications and the arcs connect components that significantly co-localize in the genome. In this network co-localization preferences are specific of chromatin states, such as promoters and enhancers.

A second network was build by connecting proteins that are part of the mESC epigenetic regulatory system and show signals of co-evolution (concerted evolution of the CRPs protein families). The common representation of the two networks reveals a number of interesting patters: i) the co-evolutionary relations are mediated by specific modifications, implying that they do not require a direct physical interaction between the corresponding proteins, ii) most of the co-evolutionary links are mediated by 5hmc, iii) 5hmc is the most crossed node of the network, and iv) 5hmc is one of the nodes with the higher number of input and output connections. Therefore, the analysis of these two very different networks points to the role of 5hmc DNA mark as a key organizational principle of the mESC system, in agreement with previous observations.

Finally, based on the mESC example, I will discuss some of the other projects based on the use of networks to analyse epigenomic data.

The mESC Epigenetic Network was developed in collaboration with Vingron's lab (MPIMG, Berlin) in the context of the BLUEPRINT consortium (Juan et al., in preparation)