

You are cordially invited to the next talk in the Edmond J. Safra Bioinformatics Program Distinguished speaker series.

The speaker is Manolis Kellis, Computational Biology Group, Computer Science/Broad Institute, MIT.

Title: "Interpreting the human genome and its regulation using evolutionary, chromatin, and activity signatures"

Time: Wednesday 16th June, at 11:00 (refreshment from 10:50)

Place: Schreiber Building, room 007

Abstract: Our group is focused on the computational underpinning of genomics, developing new algorithms and machine learning techniques for studying complete genomes, understanding their regulatory constructs, and their evolutionary dynamics. We have defined evolutionary signatures in the nucleotide alignments of multiple related species, enabling the systematic discovery and characterization of diverse classes of functional elements, including protein-coding genes, RNA structures, microRNAs, developmental enhancers, regulatory motifs, and biological networks.

We have also defined distinct chromatin signatures from combinations of many histone marks in genome-wide epigenomic datasets, revealing numerous classes of promoter, enhancer, transcribed, and repressed regions, each with distinct functional properties. Lastly, we have defined activity patterns of gene expression, chromatin state, motif enrichment, and positional constraints across multiple cell types to link enhancers to candidate targets, recognize cell-type specific activators and repressors, and evaluate predictive models of gene regulation. These techniques have enabled us to discover many new insights into animal gene regulation, in the context of the ENCODE, modENCODE, and Epigenome Roadmap projects, and in the comparative analysis of many *Drosophila* and mammalian genomes.

BioSketch:

Manolis Kellis is an Associate Professor of Computer Science at MIT, a member of the Computer Science and Artificial Intelligence Laboratory, and of the Broad Institute of MIT and Harvard. He has held the Karl Van Tassel, and the Distinguished Alumnus (1964) chair in EECS, and has received the Ruth and Joel Spira faculty teaching award. He has received the NSF CAREER award, is a Fellow of the Alfred P. Sloan Foundation, and is the PI on several NIH grants for work in regulatory genomics. He was recognized for his research in genomics as a top young innovator by Technology Review Magazine, Genome Technology magazine, and the Boston Museum of Science. He obtained his Ph.D. from MIT, where he received the Sprowls award for the best doctorate thesis in computer science, and the first Paris Kanellakis graduate fellowship. Prior to computational biology, he worked on artificial intelligence, sketch and image recognition, robotics, and computational geometry, at MIT and at the Xerox Palo Alto Research Center. He grew up in Greece and France before moving to the US.