Dr. Marc Vidal

Director, Center for Cancer Systems Biology (CCSB)
Dana-Farber Cancer Institute

Associate Professor of Genetics, Harvard Medical School

Interactome Networks and Human Disease

Friday, April 11, 2008
MIT Building 3, Room 270
Light Refreshments served at 2:45 p.m.

For over half a century it has been conjectured that macromolecules form complex networks of functionally interacting components, and that the molecular mechanisms underlying most biological processes correspond to particular steady states adopted by such cellular networks. However, until recently, systems-level theoretical conjectures remained largely unappreciated, mainly because of lack of supporting experimental data.

To generate the information necessary to eventually address how complex cellular networks relate to biology, we initiated, at the scale of the whole proteome, an integrated approach for modeling protein-protein interaction or “interactome” networks. Our main questions are: How are interactome networks organized at the scale of the whole cell? How can we uncover local and global features underlying this organization, and how are interactome networks modified in human disease, such as cancer?

Host: Alexander van Oudenaarden
avano@MIT.EDU

http://csbi.mit.edu

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