

Biological networks: From measurements to modeling

Monday September 10, 2007
Pelton Auditorium, FHCRC

9:00 am	<i>Introduction</i>
9:15 am	Parts, Modules, and Systems Herbert Sauro, University of Washington
10:00 am	Modularity, feedback and recursion in the EGF receptor system Steven Wiley, Pacific Northwest National Laboratory
10:45 am	<i>coffee break</i>
11:00 am	MicroRNA profiling and discovery through deep sequencing of small RNAs Stacia Wyman, Fred Hutchinson Cancer Research Center
11:30 am	Nucleotide metabolism based systems cancer biology: Identification of reconstituted ligand-induced protein oligomerization systems in equilibrium Tomas Radivoyevitch, Case Western Reserve University
12:15 pm	<i>lunch on your own</i>
1:30 pm	Coarse-grained pathway modeling using phosphoprotein data Armand Bankhead, Rosetta Inpharmatics/Merck & Co., Inc.
2:15 pm	Towards a predictive systems model of cellular responses to environmental perturbations Amy Schmid, Institute for Systems Biology
3:00 pm	<i>coffee break</i>
3:15 pm	A single-cell oxygen consumption measurement platform Sarah McQuaide, University of Washington
4:00 pm	Processing and visualizing biological network models with R, GGobi and Cytoscape Michael Lawrence, Iowa State University
4:45 pm	<i>end</i>

This symposium is an opportunity to hear about some of the *latest tools and applications of systems biology*. We are also featuring presentations on *new laboratory techniques* used to observe or infer the behavior of individual cells.

The talks are open to everyone, and *registration is not necessary*.

Sponsored by the Program in Computational Biology and the Public Health Sciences Division

For additional information, contact Dennis Chao (dchao@fhcrc.org).