Biological networks:
From measurements to modeling

Monday September 10, 2007
Pelton Auditorium, FHCRC

<table>
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<th>Time</th>
<th>Session</th>
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<tr>
<td>9:00 am</td>
<td>Introduction</td>
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| 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 | coffee break |
| 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 | lunch on your own |
| 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 | coffee break |
| 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 | end |

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).