AACR-NCI Conference on Systems Biology

Confronting the Complexity of Cancer

February 27-March 2, 2011
Hyatt Regency La Jolla, San Diego, CA

Sunday, February 27

6:00 p.m. - 7:00 p.m. **Keynote Session**
Aventine Ballroom D,E,F&G

Use of bionetworks to build better maps of disease
Stephen H. Friend, Sage Bionetworks, Seattle, WA

7:00 p.m. - 9:00 p.m. **Session 1: Genomes to Networks: Elucidation of Mutation-related Dysregulated Pathways**
Session Chairperson: Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA
Aventine Ballroom D,E,F&G

Modeling molecular diversity in breast cancer
Joe W. Gray, Lawrence Berkeley National Laboratory, Berkeley, CA

Converging on the Achilles heel of cancer through functional and structural genomics
Louis M. Staudt, National Cancer Institute-Center for Cancer Research, Bethesda, MD

Bringing together host and tumor genetics to identify targetable oncogenic pathways
John M. Maris, Children's Hospital of Philadelphia, Philadelphia, PA

Finding driver genes and pathway in complex cancer genomes
Gad Getz, Broad Institute of MIT and Harvard, Cambridge, MA

9:00 p.m. - 10:00 p.m. **Opening Reception**
Pavilion

Monday, February 28

7:00 a.m. - 8:00 a.m.	**Continental Breakfast** *Aventine Ballroom Foyer I*
8:00 a.m. - 10:30 a.m.	**Session 2: Protein Complexes in Transcription and Signaling** *Session Chairperson: Joe W. Gray, Lawrence Berkeley National Laboratory, Berkeley, CA* *Aventine Ballroom D,E,F&G* **A physicist's view of the complexity of cancer** Jan Liphardt, University of California, Berkeley, CA **DNA repair complexes as keys to cancer initiation and interventions** John A. Tainer, The Scripps Research Institute, La Jolla, CA **Extensive in vivo metabolite-protein interactions revealed by large-scale systematic analysis** Michael Snyder, Stanford University, Stanford, CA **You can't study what you can't measure** Amanda G. Paulovich, Fred Hutchinson Cancer Research Center, Seattle, WA **EMT-mediated rewiring and molecular signature of EGFR-driven cell motility*** Jason R. Neil, Massachusetts Institute of Technology, Cambridge, MA **A systems biology approach to elucidating the consequences of complex ternary interactions of heparin, FGF ligands, and FGF receptor on downstream signaling in NSCLC cells*** Diana H. Chai, Merrimack Pharmaceuticals, Cambridge, MA
10:30 a.m. - 10:45 a.m.	**Break** *Aventine Ballroom Foyer I*
10:45 a.m. - 11:45 a.m.	**TCGA: A Systems Biologist's Resource** *Session Chairperson: Joe W. Gray, Lawrence Berkeley National Laboratory, Berkeley, CA* *Aventine Ballroom D,E,F&G* **Comprehensive characterization of cancer genomes by TCGA** Paul T. Spellman, Lawrence Berkeley National Laboratory, Berkeley, CA **Cancer genomics in the TCGA Project** David Haussler, University of California, Santa Cruz, CA
11:45 a.m. - 2:30 p.m.	**Free time/Lunch on own**

*Short talks from proffered papers

2:30 p.m. - 5:00 p.m.

Session 3: Network Regulation of Cell Function and Dysfunction
Session Chairperson: Andrea Califano, Columbia University, New York, NY
Aventine Ballroom D,E,F&G

Elucidating master integrators of aberrant signals in human malignancies
Andrea Califano

Integrating multiple types of 'omic' data provides a more coherent view of the networks altered in cancer
Ernest Fraenkel, Massachusetts Institute of Technology, Cambridge, MA

Rewiring of genetic networks in response to DNA damage
Trey Ideker, University of California –San Diego, La Jolla, CA

Network transformations during tumorigenesis in hepatocelluar carcinoma are determined by pre-tumor network states
Eric E. Schadt, Pacific Biosciences, Menlo Park, CA

Network medicine and cancer complexity*
Rune Linding, Technical University of Denmark, Lyngby, Denmark

Systems analysis of receptor tyrosine kinase signaling reveals conserved and receptor-specific downstream network topology and dynamics*
Joel P. Wagner, Massachusetts Institute of Technology, Cambridge, MA

5:00 p.m. - 7:00 p.m.

Poster Session
Aventine Ballroom A,B,C& Foyer II

Tuesday, March 1

7:00 a.m. - 8:00 a.m.

Continental Breakfast
Aventine Ballroom Foyer I

8:00 a.m. - 10:30 a.m.

Session 4: Cancer Stem Cells/Developmental Biology
Session Chairperson: Ihor R. Lemischka, Mount Sinai School of Medicine, New York, NY
Aventine Ballroom D,E,F&G

Title to be announced
Ihor R. Lemischka

Title to be announced
Franziska Michor, Memorial Sloan-Kettering Cancer Center, New York, NY

*Short talks from proffered papers

Mechanisms underlying reprogramming to pluripotency
Kathrin Plath, UCLA School of Medicine, Los Angeles, CA

Regulation of pluripotency and lineage differentiation in human male germ cell tumors: A systems biology analysis
Raju S.K. Chaganti, Memorial Sloan-Kettering Cancer Center, New York, NY

Systematic identification of novel markers of differentiation in human bladder cancer that predict survival*
Debashis Sahoo, Stanford University, Stanford, CA

Comparative genomic analysis of human and murine T-ALL to identify critical gene programs of oncogene addiction*
Stacey J. Adam, Stanford University, Stanford, CA

10:30 a.m. - 10:45 a.m. **Break**
Aventine Ballroom Foyer I

10:45 a.m. - 12:15 p.m. **Systems Biology/ICBP - Tools and Resources**
Aventine Ballroom D,E,F&G

R / Bioconductor for exploration, analysis, and comprehension of cancer genomics experiments
Martin Morgan, Fred Hutchinson Cancer Research Center, Seattle, WA

geWorkbench: An integrated analysis platform for cancer systems biology
Aris Floratos, Columbia University, New York, NY

How to use PTMScout to understand the role of post-translational modifications in cell signaling and cancer
Kristen M. Naegle, Massachusetts Institute of Technology, Cambridge, MA

High-throughput quantitative bioimaging tools in cancer biology Stephen T. C. Wong, The Methodist Hospital Research Institute, Houston, TX

12:15 p.m. - 2:30 p.m. **Free time/Lunch on own**

2:30 p.m. - 5:00 p.m. **Session 5: Cell Behavior to Tissue Pathophysiology/Tumor Microenvironment**
Session Chairperson: Jennifer A. Pietenpol, Vanderbilt-Ingram Cancer Center, Nashville, TN
Aventine Ballroom D,E,F&G

Integrative approach to triple negative breast cancer: Subtypes, molecular targets, and therapeutic insights
Jennifer A. Pietenpol

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*Short talks from proffered papers

Responses of the tumor microenvironment to therapeutics: Extrinsic reactions influence cancer cell survival programs
Peter S. Nelson, Fred Hutchinson Cancer Research Center, Seattle, WA

The interplay between intrinsic and extrinsic force and tumor evolution
Valerie M. Weaver, University of California –San Francisco Medical Center, San Francisco, CA

Metagenomic systems biology: A systems biology approach for studying the human microbiome in health and in disease
Elhanan Borenstein, University of Washington, Seattle, WA

Investigating the kinetics of key proteins in the Wnt and MAPK pathways and their roles in cell adhesion utilizing a systems modeling framework*
Michael G. Zager, Pfizer Global Research and Development, San Diego, CA

Tumor dormancy associated microRNAs inhibit tumor growth and induce perturbations in tumor microenvironment*
Nava Almog, Tufts University School of Medicine, Boston, MA

5:00 p.m. - 7:30 p.m. **Free time/Dinner on own**

7:30 p.m. - 9:00 p.m. **Educational Session: Emerging Topics in Systems Biology**
Session Chairperson: Daniel Gallahan, National Cancer Institute, Rockville, MD
Aventine Ballroom D,E,F&G

Integrative analysis of epigenomes in normal and cancer cells
Bing Ren, Ludwig Institute for Cancer Research, La Jolla, CA

Merging systems biology and personalized medicine: What small gadgets can tell us
Andre Levchenko, Johns Hopkins University, Baltimore, MD

A spectrum of cell network modeling: Relations, topology, influence, logic, and mechanism
Douglas A. Lauffenburger, Massachusetts Institute of Technology, Cambridge, MA

*Short talks from proffered papers

Wednesday, March 2

7:30 a.m. - 8:30 a.m.	**Continental Breakfast** *Aventine Ballroom Foyer I*
8:30 a.m. - 11:00 a.m.	**Session 6: System Approaches to Drug Discovery and Development** *Session Chairperson: Douglas A. Lauffenburger, Massachusetts Institute of Technology, Cambridge, MA* *Aventine Ballroom D,E,F&G* **Connectivity map** Todd R. Golub, Broad Institute of MIT and Harvard, Cambridge, MA **Systems design of cancer therapies** Ulrik B. Nielsen, Merrimack Pharmaceuticals, Inc., Cambridge, MA Title to be announced Greg Tucker-Kellogg, Lilly Singapore Centre for Drug Discovery, Singapore **Using RNAi signatures to investigate drug action and resistance mechanisms** Michael T. Hemann, MIT Koch Institute for Integrative Cancer Research, Cambridge, MA **Dynamic re-wiring of apoptotic signaling networks enhances tumor cell killing by DNA damage*** Michael J. Lee, Massachusetts Institute of Technology, Cambridge, MA **Inferring causality to unravel the network intelligence of cancer by employing a novel systems biology drug discovery platform*** Niven Narain, Berg Biosystems, Boston, MA
11:00 a.m.	**Departure**

*Short talks from proffered papers