

9:15 - 9:30 Opening Remarks

9:30 - 10:20 Stephen Friend - Sage Bionetworks
The Corruption of Denial

Stephen H. Friend, MD PhD, is the President, Co-founder and Director of Sage Bionetworks. Sage Bionetworks scientists work on comprehensive molecular and clinical datasets to create validated disease models that improve the speed and efficiency of therapeutic drug development. Sage Bionetworks projects span cardiovascular disease, cancer, metabolic disease and neurobiology. At the intersection of 'big data', network modeling and open technologies is a new opportunity (and responsibility) for biomedical discovery.

10:20-11:10 David Hill - Dana-Farber
Interactome networks and genomic analysis of network perturbations in human disease

David E. Hill, PhD, is a Principal Research Scientist at Dana-Farber Cancer Institute's Center for Cancer Systems Biology. The goals of CCSB are to understand how macromolecular networks control biological processes and accordingly how perturbations in such networks can explain human disease. Dr. Hill examines the effects of tumor viral proteins on host cell networks as a complementary approach to identifying and prioritizing cancer-causing driver genes.

11:10-12:00 Tamara Munzner - UBC
Visualization Principles

Tamara Munzner is a Professor at the University of British Columbia Department of Computer Science. Dr. Munzner's research interests include the development, evaluation, and characterization of information visualization systems and techniques from both user-driven and technique-driven perspectives. She has worked on visualization projects in a broad range of application domains, including evolutionary biology, microbiology, topology, and computational linguistics.

12:00-1:00 Lunch break

1:00-1:50 Atul Butte - Stanford
Translational Bioinformatics

Atul Butte, MD PhD, is Chief of the Division of Systems Medicine and Associate Professor of Pediatrics, Medicine, and Computer Science, at Stanford University and Lucile Packard Children's Hospital. The Butte lab builds and applies tools that convert more than 300 billion points of molecular, clinical, and epidemiological data measured by researchers and clinicians over the past decade into diagnostics, therapeutics, and new insights into disease. They have developed bioinformatics methods to take genomic, genetic, and phenotypic data from multiple sources and diseases, and reason over these data to create novel diagnostics, therapeutics, and discover novel molecular mechanisms of disease. Examples of this method includes work on cancer drug discovery, type 2 diabetes, fat cell formation, obesity, and transplantation.

1:50-2:40 Quaid Morris - U Toronto
Networks for Gene Function Prediction

Quaid Morris, PhD, is an Associate Professor at the Donnelly Centre for Cellular and Biomolecular Research. The Morris lab uses machine learning and statistical modeling to help decode the human genome. Currently, the focus is on two core research areas: deciphering the regulatory code for gene expression and predicting the biological function of genes and proteins. They are building a comprehensive atlas of the binding preferences of DNA- and RNA-binding proteins and are using this atlas, along with comparative genomics and RNA expression data, to identify conserved vertebrate enhancer sequences and microRNA targets and other cis-regulatory mRNA elements that influence mRNA expression, localization, stability and splicing.

2:40-3:10 Break

3:10-4:00 Patricia Babbitt - UCSF
Protein Similarity Networks in Functional Inference

Patricia Babbitt, PhD, is a Professor at the Department of Bioengineering and Therapeutic Sciences, UCSF Schools of Pharmacy and Medicine. The Babbitt lab uses both computational and experimental methods to improve our understanding of how protein structures mediate protein function. They develop and use the tools of bioinformatics and computational structural biology to integrate the information coming out of the genome projects with available tertiary structural information. One primary goal of the computational work is to develop a methodology for "rational protein design" that can be used in the laboratory to engineer new functionalities into proteins.

4:00-4:50 James Fowler - UCSD
Friendship and Natural Selection

James Fowler, PhD, is a Professor of Medical Genetics and Political Science at the University of California, San Diego. Dr. Fowler's work lies at the intersection of the natural and social sciences, with a focus on social networks, behavioral science, evolution, politics, genetics, and big data. In particular, Dr. Fowler is a leader in the new field of 'genopolitics' (the study of the genetic basis of political behavior). Together with Dr. Nicholas Christakis, Dr. Fowler has written a book for a general audience called *Connected: The Surprising Power of Our Social Networks and How They Shape Our Lives*.

The National Resource for Network Biology

We are developing freely available, open source software technologies to enable network-based visualization, analysis, and biomedical discovery. We are driving research and development projects, coordinating training opportunities, and actively seeking new collaborations to develop network biology tools and apply them to biomedical research. More at nrnb.org.

