Symposium Key Note Speakers

Dr. Donna L. Mendrick
Director, Division of Systems Biology, NCTR/FDA

Dr. Donna L. Mendrick is the Director of the Division of Systems Biology at the National Center for Toxicology Research (NCTR), a research Center of the FDA. Her division incorporates genomics, proteomics, metabolomics, in silico modeling, stem cells and other innovative approaches to answer the needs of the FDA in terms of medical products and food safety and improving the understanding of human disease. Her FDA committee assignments include the Senior Science Council, Tox21, and the Interagency Coordination Committee on the Validation of Alternative Methods (ICCVAM). Dr. Mendrick is the Chair of the Society of Toxicology's Disease Prevention Task Force, Secretary/Treasurer of the Drug Discovery Toxicology Specialty Section and a member of the Scientific Liaison Coalition's Governance Group.

She was an Assistant Professor of Pathology at Harvard Medical School and Brigham and Women's Hospital. She joined Human Genome Sciences and, as a Group Leader in Pharmacology, oversaw multiple project teams, toxicity studies, pharmacology studies, etc. Prior to joining the FDA, she was a Scientific Fellow and Vice President of Pharmacogenomics at Gene Logic where she oversaw pharmacogenomics and spearheaded its toxicogenomics effort. For the latter, she formed a pharmaceutical consortium to help guide the development of the program. Dr. Mendrick has many years of experience in the fields (in alphabetical order) of immunology, pathology, pharmacogenomics, pharmacology, toxicology and toxicogenomics employing small molecule drugs, recombinant therapeutic proteins and monoclonal antibodies.

Dr. Mendrick has published on the use of pharmacogenomics, metabolomics and proteomics to identify biomarkers. She is past President of the National Capital Area Chapter of the Society of Toxicology. Dr. Mendrick was on the Editorial Board of the Journal of Histochemistry and Cytochemistry for 8 years, a member of the NIH SBIR Immunology Study Section for 8 years and a member of the Board of Directors of the National Kidney Foundation of Massachusetts for 4 years.

Dr. John Quackenbush
Professor of Computational Biology & Bioinformatics, Dana-Farber Cancer Institute

Dr. John Quackenbush received his Ph.D. in 1990 in theoretical physics from UCLA working on string theory models. Following two years as a postdoctoral fellow in physics, Dr. Quackenbush applied for and received a Special Emphasis Research Career Award from the National Center for Human Genome Research to work on the Human Genome Project. He spent two years at the Salk Institute working on developing physical maps of human chromosome 11 and two years at Stanford University working on new laboratory and computational strategies for sequencing the Human Genome. In 1997 he joined the faculty of The Institute for Genomic Research (TIGR) where his focus began to shift to post-genomic applications with an emphasis on microarray analysis. Using a combination of laboratory and computational approaches, Dr. Quackenbush and his group developed analytical methods based on integration of data across domains to learn biological meaning from high-dimensional data.
In 2005, he was appointed Professor of Biostatistics and Computational Biology and Professor of Cancer Biology at the Dana-Farber Cancer Institute (DFCI) and Professor of Computational Biology and Bioinformatics at the Harvard School of Public Health. Since that time, his work has increasingly focused on the analysis of human cancer using systems-based approaches to understanding and modeling biological problems. In 2009 he launched the Center for Cancer Computational Biology (CCCB) at the DFCI which provides broad-based bioinformatics support to the local research community using a collaborative consulting model.

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Dr. Peter Sorger
Professor of Systems Biology, Harvard Medical School (HMS)

Peter Sorger is a Professor of Systems Biology at Harvard Medical School (HMS) and co-chair of the HMS Initiative in Systems Pharmacology (ISP). He received his Ph.D. in 1993 from Trinity College Cambridge under the supervision of Hugh Pelham and trained as a Markey Scholar with Harold Varmus and Andrew Murray at UCSF. As an assistant, associate and then full professor at MIT he studied cell cycle control, chromosome segregation and "systems" approaches to mammalian signaling transduction. Sorger is co-founder of the Open Microscopy Environment (OME), MIT's Computational and Systems Biology Initiative (CSBi) and the Council for Systems Biology in Boston (CSB2; www.csb2.org). Sorger co-founded Merrimack Pharmaceuticals and Glencoe Software and serves on the corporate or scientific advisory boards of several biotech startups. Sorger is Director of the Center for Cell Decision Processes (www.cdpcenter.org), an NIH Center of Excellence in Systems Biology and PI of the HMS LINCS Center (lincs.hms.harvard.edu); he teaches graduate-level biochemistry and pharmacology.

The Sorger laboratory combines computational and experimental approaches to studying signaling pathways that control whether cells live or die. Through a combination of single-cell and intravital imaging, genetic and chemical perturbation and high-throughput biochemistry, the lab collects data necessary to construct and calibrate mathematical models of signal transduction. The lab also develops new algorithms and software for modeling pathways at different levels of detail. Models range from data-driven statistical descriptions of interacting pro-growth and pro-death pathways to detailed physicochemical models of individual steps in ligand-induced apoptosis. The overall aim is to combine detailed molecular descriptions of proteins involved in disease (or targeted by therapeutic drugs) with systems-level understanding of signaling networks.

The laboratory is particularly interested in programmed cell death triggered by extracellular ligands such as TRAIL, Fas and TNF and opposing pro-survival signals emanating from growth factor receptors. Increasingly the laboratory aims to understand why therapeutics targeting disease pathways work in some patients and not others and to explore the use of biomarkers and poly-pharmacology in maximizing therapeutic response. Lab members create pathway-centric pharmacological models based on high-throughput phenotypic and biochemical assays that serve as a complement to prevailing genomic approaches. The laboratory is reducing these ideas to practice in collaboration with several pharmaceutical companies and with academic groups led by Douglas Lauffenburger, Gaudenz Danuser, Ralph Weissleder and Tim Mitchison.

Dr. Birgit Schoeberl
Vice President of Discovery, Merrimack Pharmaceuticals

Dr. Birgit Schoeberl, Vice President of Research at Merrimack Pharmaceuticals: She is responsible for early stage discovery projects. Dr. Schoeberl joined Merrimack in 2004 and has since then spearheaded the formulation of Merrimack's research and development platform, Network Biology. She was also responsible for designing the company's lead Network Biology derived therapeutic, MM-121, and taking it into clinical development. Currently, she also serves on the Board of Directors and Scientific Advisory Board of Silvercreek Pharmaceuticals in San Francisco. Dr. Schoeberl received a M.Sc. degree in chemical engineering from the University of Karlsruhe, Germany, and a Ph.D. degree from the Max-Planck-Institute for Dynamics of Complex Technical Systems, Magdeburg, Germany. She joined Merrimack Pharmaceuticals after being a postdoctoral fellow in the laboratories of Douglas Lauffenburger and Peter Sorger at MIT.