

## **SYMPOSIUM II, June 14, 2017: Data science, connectivity map and drug discovery**



### ***DR. JIE CHENG***

***Associate Director, Data and Statistical Sciences, AbbVie Inc., Worcester, MA, USA***

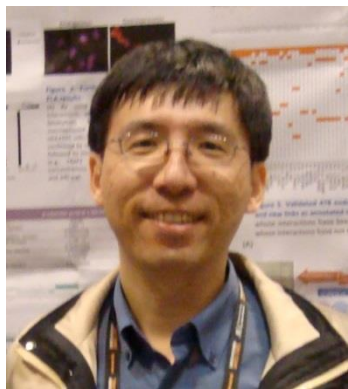
Dr. Jie Cheng is an associate director at the department of exploratory statistics at Abbvie Inc. He received his PhD in computer science in 1998 and has over 15 years of industrial research experience in machine learning and predictive modeling. Dr. Cheng's research interests include biomarker discovery from omics data, patient subgroup identification and Bayesian network/gene association network learning.



### ***DR. BROOKE FRIDLEY***

***Chair, Department Biostatistics and Bioinformatics, Moffitt Cancer Centre, Tampa, Florida USA***

Brooke L. Fridley, PhD joined the Moffitt Cancer Center in January 2017 as the new Chair of the Department of Biostatistics and Bioinformatics. Prior to joining Moffitt Cancer Center, Dr. Fridley was at the University of Kansas Medical Center and the Mayo Clinic. At the University of Kansas, she was Director of the Biostatistics and Informatics Shared Resource for the NCI designated University of Kansas Cancer Center and Site Director for the Kansas-INBRE Bioinformatics Core. Her research focus is in the areas of statistical genomics, molecular epidemiology of cancer, cancer genomics, and pharmacogenomics. She has extensive experience as a collaborating statistician, particularly in the design and analysis of genomic studies involving multiple types of 'omic data (e.g., genotypic, DNA methylation, mRNA expression, copy number). Dr. Fridley has over 200 publications, is on the editorial board for *Journal of the National Cancer Institute*, and has been awarded 3 NIH grants for the development of new statistical methods for genomic studies, which is closely integrated with her collaborations with multidisciplinary scientific teams.



**DR. CHI-YING HUANG**

***Chair, Institute of Biopharmaceutical Sciences, National Yang Ming University, Taipei, Taiwan***

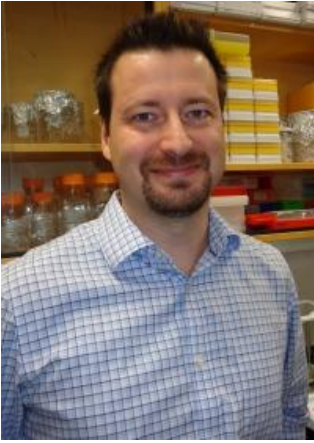
Chi-Ying Huang - Upon completion of his doctorate in Biochemistry and Biophysics at the Iowa State University in 1994, he moved to Stanford University for postdoctoral training where he worked on the signaling pathway of MAPK pathway. Dr. Huang joined the faculty of Division of Molecular and Genomic Medicine at the National Health Research Institutes (NHRI) in Taiwan in 1998 where he was an Assistant Investigator and promoted to Associate Investigator. Currently, Dr. Huang is the Professor and Chairman at the Institute of Biopharmaceutical Sciences at National Yang Ming University. He is using various function genomics techniques to identify treatment strategy for GBM, liver, lung cancer via drug repurposing. Two repurposed drugs are conducting clinical trials for lung adenocarcinoma patients at Taipei-veteran general hospital and National Taiwan University Hospital, Taiwan.



**DR. ARAVIND SUBRAMANIAN**

***Director, Biomedical Science Connectivity Map, LINCS & L1000, Broad Institute of MIT & Harvard, Cambridge, MA, USA***

Aravind Subramanian, Ph.D. Director, Connectivity Map at the Broad Institute of MIT and Harvard. Dr. Subramanian is Director of the Connectivity Map and a Principal Investigator of the NIH Center for Transcriptomics at the Broad that is part of the Library of Integrated Network-based Cellular Signatures (LINCS) and the Big Data to Knowledge (BD2K) initiative. Dr. Subramanian trained as a computational biologist in the laboratories of Dr. Jill Mesirov and Dr. Todd Golub and has contributed to the development of methodological approaches including Gene Set Enrichment Analysis, a popular algorithm for the interpretation of high-dimensionality genomic datasets. Dr. Subramanian leads a group of molecular biologists, software engineers, and computational analysts at the Broad. Their efforts are directed towards inventing technologies for transcriptional profiling and developing machine learning approaches to discover functional relationships between genes, drugs, and diseases. The goals of Connectivity Map include generating a comprehensive reference dataset of perturbational signatures, developing algorithms and software to make these data and results accessible to the biomedical community and to engage in collaborations that leverage these resources for biological and therapeutic discoveries.



***DR. KOLJA EPPERT***

***Leukemia Stem Cells, Cancer, MUHC Pediatric Hematology-Oncology, Glen site, McGill University, Montreal, Canada***

Kolja Eppert PhD is an Assistant Professor, Department of Pediatrics, McGill University and a Medical Scientist, Department of Pediatrics, Division of Hematology- Oncology at the McGill University Health Centre - Montreal Children's Hospital. He holds a Canada Research Chair in Cancer Stem Cell Biology. Since his appointment in January 2013 he established a research program at the Montreal Children's Hospital to study human leukemia stem cell (LSC) biology. He earlier developed LSC and HSC gene expression signatures and demonstrated that they are tightly linked to disease outcome, independently of all other factors. His laboratory is now focused on improving our understanding of LSC development and progression, with the overall goal to improve outcome in patients through better treatment. His program consists of interconnected and complementary areas of interest in drug discovery, LSC-specific cell signaling, and novel epigenetic regulators of LSC function.