

COMPUTATION IN BIOLOGY Program

Noon – 12:40 pm	Box Lunch at Grainger Hall, 5120 Capital Conference Room <i>fifth floor</i>
12:40 – 12:50 pm	Welcome by DR. BRAD SCHWARTZ CEO, Morgridge Institute for Research
12:50 – 1:40 pm	TALK 1: MARC A. SUCHARD, M.D., PH.D. Professor, Departments of Biomathematics, Biostatistics, and Human Genetics, David Geffen School of Medicine at UCLA <i>“Big Data Are Ubiquitous in Biomedicine, but Big Tools Remain Spurned”</i> Many large-scale inference problems in biomedicine are unsuitable for current Big Data analytics. Dr. Suchard’s talk explores emerging computational techniques that scale well with exemplars from molecular epidemiology, observational health studies, and the environment.
1:40 – 1:50 pm	Brief Break
1:50 – 2:40 pm	Talk 2: BRIAN SHOICHET, PH.D. Professor, Faculty of Pharmacy, Donnelly Centre, University of Toronto <i>“The Role of Computation in Chemical Biology and Pharmacology”</i> Computation presents great possibilities for the target-based discovery of new reagents, and the discovery of signaling networks using chemical information. Dr. Shoichet will discuss these computational possibilities.
2:40 – 3:00 pm	20-minute Break
3:00 – 3:50 pm	Talk 3: DAVID PAGE, PH.D. Professor, Department of Biostatistics & Medical Informatics, University of Wisconsin-Madison <i>“Predictive Modeling by Machine Learning”</i> Machine learning algorithms are being used increasingly to turn Big Data into models that make predictions about the future. Dr. Page’s talk will try to predict the future of this predictive modeling enterprise.
3:50 – 4:00 pm	Brief Break
4:00 - 4:50 pm	Talk 4: WINSTON HIDE, PH.D. Associate Professor of Bioinformatics and Computational Biology, Department of Biostatistics, Harvard School of Public Health <i>“The New Biology”</i> Biomedical research is more and more a science that performs multi-disciplinary analysis of biological data systems. Dr. Hide will discuss how the current generation of science leaders is transforming to incorporate a new generation of data scientists as the new paradigm.
4:50 – 5:00 pm	Brief Break
5:00 – 5:30 pm	Summary Discussion
5:30 – 7:00 pm	Reception in Grainger Hall, 1266 Executive Dining Room <i>first floor</i>

COMPUTATION IN BIOLOGY SYMPOSIUM

September 24, 2013

Organized by:

Morgridge Institute for Research



Speaker Bios

DAVID PAGE

David Page received his Ph.D. in computer science from the University of Illinois at Urbana-Champaign in 1993. He was a research scientist in the Oxford University Computing Laboratory from 1993 to 1997, where he also served as a visiting member of the Faculty of Mathematics from 1995 to 1997. David is now a professor at the University of Wisconsin-Madison, in the Department of Biostatistics and Medical Informatics within the School of Medicine and Public Health. He directs the Cancer Informatics Shared Resource of the University of Wisconsin's Carbone Cancer Center and is a member of the Genome Center of Wisconsin. Dr. Page served on the NIH's BioData Management and Analysis Study Section when it first became a standing study section, and has previously served on the scientific advisory boards for the Wisconsin Genomics Initiative and the Observational Medical Outcomes Partnership, focused on detecting adverse drug events. He also served on the steering committee for the International Warfarin Pharmacogenetics Consortium. He serves on the editorial boards for Machine Learning and Data Mining and Knowledge Discovery. He currently holds NIH grants on Machine Learning for Adverse Drug Events and Secure Sharing of Clinical and Genetic Data, and participates in grants applying machine learning to mammography and to RNA seq-based prediction of developmental neural toxins.

BRIAN K. SHOICHET

Brian K. Shoichet is a Professor in the Faculty of Pharmacy at the University of Toronto, Donnelly Centre and also Adjunct Professor in the Department of Pharmaceutical Chemistry at the University of California, San Francisco (UCSF). He was previously Director of the California Institute of Quantitative Biology at UCSF, as well as a Professor in the UCSF Department of Pharmaceutical Chemistry for many years. An overarching goal of his lab is bringing chemical reagents to biology, through a combination of computational simulation and experiment. Using a protein-centric approach, his group searches for new ligands that complement protein structures. This effort typically involves molecular docking and the development of model experimental systems to experimentally test new algorithms that are developed. A new research direction adopts a ligand-centric approach that seeks new targets for known drugs. Whereas this lacks the physical foundation of the structure-based docking, it returns to an

older, pharmacological view of biological relationships, bringing to it a quantitative model. A biological focus for both areas is the discovery of reagents to modulate GPCRs. As part of this research, his lab has introduced computational and experimental tools as community resources. Among numerous honors, Dr. Shoichet has been awarded the Society for Biological Screening Accomplishment Award (2011); the Topliss Lectureship, University of Michigan (2011); the Distinguished Scientist Seminar, University of Pittsburgh (2013); and the Bernard Beileau Lectureship, McGill University (2014).

MARC A. SUCHARD

Marc A. Suchard is a Professor in the Departments of Biostatistics, of Biomathematics and of Human Genetics in the UCLA School of Public Health and David Geffen School of Medicine at UCLA. He earned his Ph.D. in biomathematics from UCLA in 2002 and continued for a M.D. degree which he received in 2004. Dr. Suchard is a leading Bayesian statistician who focuses on inference of stochastic processes in genomics and for massive datasets in healthcare. His training in both medicine and applied probability help to bridge the gap of understanding between statistical theory and clinical practicality. Dr. Suchard has been awarded several prestigious statistical awards such as the 2003 Savage Award, the 2006 and 2011 Mitchell Prizes, as well as a 2007 Alfred P. Sloan Research Fellowship in computational and molecular evolutionary biology, and a 2008 Guggenheim Fellowship to further computational statistics. Recently, he received the 2011 Raymond J. Carroll Young Investigator Award and the 2013 Committee of Presidents of Statistical Societies (COPSS) Presidents' Award for outstanding contributions to the statistics profession by a person aged 40 or under.

WINSTON HIDE

Winston Hide is an Associate Professor of Bioinformatics and Computational Biology in the Department of Biostatistics at Harvard School of Public Health (HSPH) where he leads development of bioinformatics addressing the genomic approaches to public health in the developed and developing worlds. His current research addresses integration of 'omics' data to deliver clinical translation. He uses simplifying approaches to discovery in stem cells and cancer stem cells, host response to pathogens, and complex diseases. An associate of the Ludwig Institute for Cancer Research, Dr. Hide has recently been appointed to direct the bioinformatics strategy for the Harvard Stem Cell Institute and is Director of the Center for Stem Cell Bioinformatics at the HSCI. Dr. Hide is a keen contributor to the development of Africa's peoples and is a founder and member of the steering committee of the NIH-Wellcome Trust funded H3 Africa Initiative. His most recent work has established a standard for communication of experimental information across omics technologies (Sansone et al 2012) and has been applied in stem cell systems to integrate data across cancers (Sho Sui et al 2012). Dr. Hide has received the South African National Research Foundation Presidents' award, the Oppenheimer Trust Sabbatical Award, and the First International Society for Computational Biology award for Outstanding Achievement. He graduated in zoology at the University of Wales in 1981, gained a Ph.D. at Temple University in 1992, and was a post-doctoral fellow in molecular evolution under Wen-Hsiung Li at the University of Texas in Houston.