Panelists for Session V: Data Science and Computational Science in Biology

Christoph Börgers, Professor, Department of Mathematics at Tufts University is a Professor of Math and associated faculty of Cognitive Science PhD program at Tufts University. His research focuses on mathematical neuroscience, applied dynamical systems, numerical analysis, scientific computing.

In the past decade, Dr. Börgers'work has been in the area of Computational Neuroscience. Dr. Börgers is the author of "Mathematics of Social Choice: Voting, Compensation and Division."

Diego Martinez is a Senior Informatics Scientist and the Head of Bioinformatics at Veritas Genetics. His experience ranges from DNA sequencing (lab work) and protein structure prediction to high throughput comparative genomics. Dr. Martinez has applied this to evolution of fungi and to lignocellulosic ethanol research. He specializes in Linux, matlab, microsoft, mysql, R, perl, phd, solaris, unix, His past experience includes time as a Senior Analyst at Joint Genome Institute; at Human Genome Project; and as a Postdoctoral Fellow at the Broad Institute of MIT and Harvard.

Grace Peng is the Director of Computational Modeling, Simulation and Analysis at the National Institute of Biomedical Imaging and Bioengineering (NIBIB) within the National Institutes of Health (NIH) in the US Department of Health and Human Services (DHHS). In 2000 she became the Clare Boothe Luce professor of biomedical engineering at the Catholic University of America. Her research focuses on developing computational models of the vestibular system in control of the head and neck, and analytical tools for studying the oculomotor system in patients with vestibular dysfunction. Since 2002, Dr. Peng has been a Program Director in the NIBIB, overseeing various programs promoting the development of mathematical and statistical modeling and analysis methods; medical simulation tools; and next generation engineering systems for rehabilitation, robotics, neuroengineering, and surgical systems. In 2003, Dr. Peng led the creation of the Interagency Modeling and Analysis Group (IMAG), which now consists of program officers from multiple federal agencies of the U.S. government.

Donna Slonim is a Professor of Computer Science at Tufts University with appointments in the Department of Integrative Physiology and Pathobiology at Tufts University School of Medicine. She is also a member of the faculty of the Genetics Program in Tufts' Sackler School of Graduate Biomedical Sciences. Dr. Slonim has worked on the Human Genome Project at the MIT/Whitehead Institute Center for Genome Research, mapping the human, mouse, and rat genomes and designing pioneering computational methods for gene expression data analysis. She conducted pharmacogenomics research at Wyeth Pharmaceuticals, where her work helped identify new drug targets and causes of side effects in clinical trials. Her current research focuses on using genomics to identify new diagnostic and treatment approaches for developmental disorders. Dr. Slonim's researches developing methods for applying genomic data to the diagnosis and treatment of human disease.