

ICB'07 Special session: Pharmacogenomics

Brief Description of technical session:

In 2000, scientists triumphantly announced they had deciphered the human genome, the blueprint for human life; and then in 2001, almost the entire human genome sequence became principally known. In 2003, the Human Genome Project was completed. By laying out in order the 3.2 billion units of our DNA, researchers sparked a firestorm of discovery and an explosion of genomic knowledge. Accompanied with them are the rapidly emerging novel genomic technologies including microarrays, whole-genome single nucleotide polymorphism [SNP] chips, RNA interference high-throughput screening etc. All these launch a new era, the genomic revolution era. Genomic revolution offers us boundless potential and great promise. Foremost are prospects in our health, ranging from discovering cures for cancer to developing personalized medical products for each individual. The application of “genomic revolution” in the discovery and development of new medical products nurtures a new subject of science, pharmacogenomics. Pharmacogenomics may enable pharmaceutical companies to create drugs based on the proteins, enzymes, and RNA molecules associated with genes and diseases, enable doctors to analyze a patient's genetic profile and prescribe the best available drug therapy from the beginning, and enable drug dosages to be determined based on a person's genetics. Pharmacogenomics will also improve the drug discovery and approval process and decrease the overall cost of health care.

Despite of the great promise of pharmacogenomics, we have to face a tough reality: significantly declining applications and approvals of new drug and biological products in FDA while soaring cost of medical product development. According to FDA's 2004 white paper on pharmacogenomics, the pharmaceutical industry submitted almost 50% fewer applications of major drug and biological products to the FDA while investment in biomedical research spending for the private and public sectors was about twice in 2002–2003 than it did in 1996–1997. Apparently, pharmacogenomics is a developing research field that is still in its infancy. It requires biomedical scientists, physicians, computer scientists and statisticians to work closely together. In this session, we aim to organize researchers in biomedical science, computer science and statistics to share their existing research and experience, to elaborate new opportunities of research and publication, and to address the benefits and challenges in this new interdisciplinary research area.

Topics of interest include, but are not limited to:

- RNA interference
- microarrays
- SNP and genomics association
- genetic markers
- data analysis
- statistical computing
- gene regulation and networks
- drug discovery and development

- theory and application in high-throughput screening assays
- regulatory and ethic considerations in pharmacogenomics

Special session chair:

Dr. Xiaohua (Douglas) Zhang

Senior biometrician, Merck Research Laboratories, West Point, PA, USA

Xiaohua Douglas Zhang is currently a senior biometrician, an expert in analyzing data from high-throughput biotechnologies and other genomic technologies, in Merck Research Laboratories, West Point, PA, USA. He obtained his Ph.D. in statistics from Carnegie Mellon University. He has been making contributions in methodology development and application in RNA interference high-throughput screening assays, genomic association studies and microarrays. He is active in publishing papers in peer-reviewed journals and conference proceedings and in giving presentations at professional conferences. He has membership in professional competition committee and has served as a referee in multiple peer-reviewed journals. He also has rich experience in organizing/chairing professional meetings as shown in the following professional meeting services that he has had.

- 2007, is selected to organize and chair workshop “Informatics and Statistics in Biopharmaceutical Research” at the International Conference on Bioinformatics & Computational Biology in Las Vegas, NV, USA
- June 2006, chaired “Session 8-BIOCOMP: Intelligent Drug Design” at the International Conference on Bioinformatics & Computational Biology in Las Vegas, NV, USA
- August 2005, organized and chaired invited session “Pharmacogenomics” at the Joint Statistical Meetings in Minneapolis, MN, USA
- August 2005, organized and chaired roundtable “Pharmacogenomics: the Critical path to Personalized Medical Products” at the Joint Statistical Meetings in Minneapolis, MN, USA
- August 2004, organized contributed session “Microarray” for the Joint Statistical Meetings in Toronto, Ontario, Canada. (Could not attend meeting.)

August 2003, organized and chaired contributed session “Genetics Data Analysis I” at the Joint Statistical Meetings in San Francisco, CA, USA