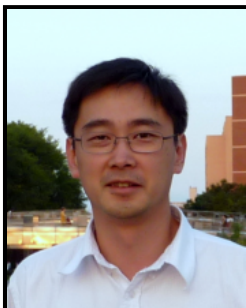




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Special Guest Lectures

Computational Drug Discovery Using Translational Bioinformatics Tools

Jake Chen, Purdue University

Associate Professor

Johnston Hall 338
April 26, 2011 - 02:00 pm**Abstract:**

Today, the default model for small molecule drug discovery is to screen libraries of chemical compounds against a single protein drug target determined to be critical to a disease. The process is long, costly, serendipitous, and infested with failures. New evidence from emerging genome biology studies suggests that complex diseases may never be addressed by simple "one disease one target" or "target-compound docking" models. New translational medicine approaches are needed to save future pharmaceutical industry from crumbling. In this talk, I describe how advances in translational bioinformatics are making it possible to begin approaching such drug discovery challenges with new computational ideas. I will introduce the concept of connectivity maps, and then describe how bioinformatics techniques can be developed to study the complex relationships among diseases, genes, and drugs. I will show how converging techniques, software tools, and databases are being developed in our research program at the Indiana Center for Systems Biology and Personalized Medicine and my lab (<http://bio.informatics.iupui.edu/>) to achieve progress towards a new paradigm of computational drug discovery. This lecture will take place at UNO in SC 002. Access Grid viewing will be in 338 Johnston Hall.

Speaker's Bio:

Dr. Jake Chen is an associate professor with tenure at Indiana University School of Informatics and Purdue University Department of Computer and Information Science in Indianapolis (IUPUI). He is the founding director of the Indiana Center for Systems Biology and Personalized Medicine, a member of the Indiana University Simon Cancer Center, and a member of the Center for Computational Biology and Bioinformatics at Indiana University School of Medicine. He is also an ACM senior member, IEEE senior member, and chair of the IEEE Engineering in Biology and Medicine Society Central Indiana Chapter. He currently serves on the editorial boards of several international bioinformatics journals including BMC Systems Biology, organized over 100 Academic meetings in informatics and computer science, and served on many research panels or committees for NIH, NSF, DOE, and the National Academies. He is the recipient of the Canary Foundation 2008 Bioinformatics Dissemination Award, a Translational Research into Practice (TRIP) scholar at Indiana University, and a 2010 Cambridge Health Institute's Translational Medicine Conference Distinguished Faculty. He holds masters and doctoral degrees in Computer Science & Engineering from the University of Minnesota and a bachelor degree in Biochemistry & Molecular Biology from Peking University of China. His research expertise spans over biological data management, biological data mining, bioinformatics, systems biology, and clinical applications of genomics in predictive and personalized medicine, with more than 90 research publication—including three edited books, Biological Database Modeling, Biological Data Mining, and Translational Bioinformatics (forthcoming)—and more than 100 invited talks worldwide. He also has considerable experience in leading Informatics R&D projects in the biopharmaceutical industry. Prior to joining Academia in 2004, he helped design commercial GeneChip microarray products for human, mouse, and rat at Affymetrix, Inc., San Jose, California and led a team to data mine the world's first comprehensive human protein interactome collected at Myriad Proteomics, Inc., Salt Lake City, Utah. In Indiana, he co-founded the non-profit Indiana Biomedical Entrepreneur's Network (IBEN) to promote biotechnology commercialization efforts and two biotech startup businesses to promote predictive and personalized medicine practices.

