

Department of Mathematics Society for Industrial and Applied Mathematics (SIAM) UH Student Chapter

Integrative Analysis on Pharmacogenomics Data for Biomarker and Drug Discovery

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Abstract

With advances in biomedical technologies, large, complex and diverse pharmacogenomics datasets are being generated, and biomedical research is increasingly becoming data-intensive and data-driven. However, advanced computational/mathematical tools are needed urgently to convert the big data into knowledge(BD2K) for biological and clinical studies. In this study, integrative mathematical/computational analysis algorithms are presented for uncovering clinically relevant cancer subtypes and related driver mutation modules, and for predicting synergistic drug combinations for effective cancer treatment.

Dr. Fuhai Li received his Ph.D in applied mathematics at Peking University, and did his pre-doctoral and postdoctoral training in Bioinformatics at Harvard Medical School and Houston Methodist Research Institute. Dr. Li has more than seven years of training and experience in bioinformatics on several research projects funded by NIH, DoD, CPRIT, and other public and private funding sources. He aims to bring better patient care and drug development through collaborative research in bioinformatics and computational biology in the emerging field of big data to knowledge. In particular, he aims to address technical and computational challenges in solving disease problems, including: precision medicine for biomarker identification, drug repositioning, drug combination discovery, and personalized drug response prediction by integrating and analyzing large-scale genomic, imaging, clinical, and environmental data; and tumor-microenvironment interaction modeling to uncover and model the roles of the tumor-niche interactions in tumor development, metastasis, and drug resistance through the integration of genomics and imaging data.

Pizza will be served 15 minutes prior to the seminar More info at www.math.uh.edu/uhsiam