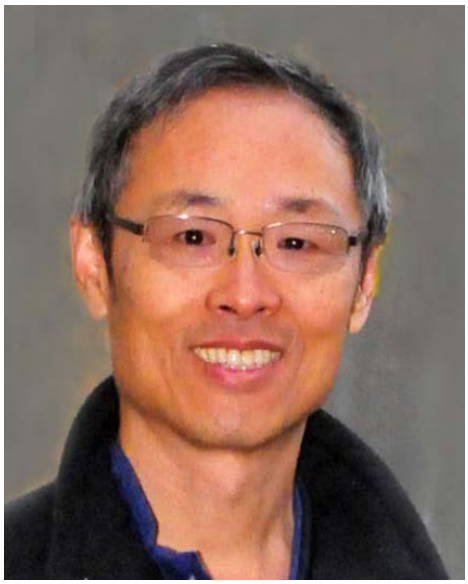
UNIVERSITY OF DELAWARE

CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY



CBCB
SEMINAR
09/23/2019

3:30 PM
DELAWARE BIOTECHNOLOGY INSTITUTE
Room 102

bioinformatics.udel.edu

BIOINFORMATICS SEMINAR

KEJI ZHAO

Senior Investigator

SYSTEMS BIOLOGY CENTER, NATIONAL HEART, LUNG AND BLOOD INSTITUTE, NATIONAL INSTITUTES OF HEALTH

EPIGENETIC MECHANISMS OF CELLULAR HETEROGENEITY IN GENE EXPRESSION

Recent studies have revealed a substantial variation in gene expression across different single cells, even within a homogeneous population of cells. In order to understand the underlying mechanisms of the cellular variation, we have developed single-cell techniques, including scDNase-seq and scMNase-seq, to analyze the epigenomic profiles at a single-cell level. Application of these techniques to various cell types revealed unexpected rules of chromatin organization and provided insights into the epigenetic basis of cellular heterogeneity in gene expression.

BIOGRAPHY

Keji Zhao, Ph.D., is director of the Systems Biology Center at the NHLBI, as well as a senior investigator in the Laboratory of Epigenome Biology. Dr. Zhao joined the NHLBI in 1999 and has been a senior investigator since 2007. He was elected to the rank of AAAS Fellow in 2012.

Dr. Zhao received his undergraduate degree from Changwei Normal College in Weifang, China in 1980 and his Doctor of Philosophy from the University of Geneva, Switzerland in 1996. Prior to joining the NHLBI, Dr. Zhao was a Damon Runyon-Walter Winchel Cancer Research Postdoctoral Fellow at Stanford University, Calif.

Dr. Zhao's research focuses on the epigenetic regulation of chromatin. Understanding how epigenetic patterns are established during development and how improper epigenetic signals contribute to disease is the long-term goal for his lab. His lab developed the ChIP-SAGE, ChIP-Seq, MNase-Seq, and scDNase-seq techniques and also developed corresponding algorithms to analyze these data. Using these approaches, Dr. Zhao's lab has been pioneering whole-genome analyses of chromatin modifications in higher eukaryotic systems. By identifying these genome-wide epigenetic patterns, Dr. Zhao's research has revealed numerous insights into the relationship between the epigenome, chromatin-modifying enzymes, and gene expression.

College of Engineering
CENTER FOR BIOINFORMATICS & COMPUTATIONAL BIOLOGY