ADVANCING SYSTEMS BIOINFORMATICS TO MODELING AND DECIPHERING PLANT GENE REGULATORY NETWORKS

Abstract: Transcriptional regulatory networks, also known as gene regulatory networks (GRNs), regulate gene expression; therefore control the complex development and environmental responses of higher plants. Genome-wide analysis of plant GRNs is the key towards understanding plant’s developmental, stress- and/or disease-resistance mechanisms. My laboratory has been developing systems bioinformatics approaches to modeling and deciphering plant GRNs. In this seminar, I will discuss our recent/ongoing R&D efforts, e.g., developing a series of novel computational methods and algorithms for (1) identification of plant transcription factors (TFs), (2) identification and analysis of plant regulatory small RNAs such as small interfering RNAs (siRNAs), (3) modeling plant sRNA-mRNA interaction and prediction of plant small RNAs’ regulatory target genes, and (4) inference and construction global GRNs from large scale microarray-based and/or RNA-Seq-based gene expression data.

About the speaker: Dr. Patrick X. Zhao is an Associate Professor, Head of Bioinformatics and Computational Biology Lab at the Samuel Roberts Noble Foundation. He also holds an Adjunct Professor appointment in the Department of Computer Science, Oklahoma State University. Dr. Zhao received his Ph.D. degree in Communications and Information Systems from Shanghai Jiao Tong University in 2000. Right after his graduation, he joined the School of Medicine, University of Louisville as a Bioinformatics Research Scientist. In 2004, he joined the Noble Foundation as a faculty member to establish the Laboratory of Bioinformatics and Computational Biology. Dr. Zhao’s current research centers on Machine Learning, Bioinformatics, and Plant and Soil Microbe Functional Genomics. His lab develops innovative computational methods to mine and decipher large-scale plant ‘omics’ data, with focus on: 1) gene function, regulation, and networks, 2) comparative genomics and metabolomics, and 3) biological data integration, mining, and knowledge.