

13 December 2012 Research Seminar

Title: **APG: an Active Protein-Gene Network Model to Quantify Regulatory Signals in Complex Biological Systems**

Abstract: Combinatorial interactions among transcription factors (TFs) and their cofactors collectively determine gene expression in complex biological systems. In this work, we develop a novel graphical model, called Active Protein-Gene (APG) network model, to quantify regulatory signals of transcription in complex biomolecular networks through integrating both TF upstream and downstream high-throughput data. Firstly, we theoretically and computationally demonstrate the effectiveness of APG by comparing with the traditional strategy based only on TF downstream information. We then apply this model to study spontaneous type 2 diabetic Goto-Kakizaki (GK) and Wistar control rats. APG model can find hidden TFs with changed activities as well as their network structure in diabetic GK rats. Furthermore, we identify network rewiring of TFs and their regulatory targets. For the first time, we reveal significant correlation of E2F1 and BAHD1 to GSK in Wistar controls, which, however, disappears in GK rats. Finally, our biological experiments validate the theoretical results.

Speaker: **Dr. Luonan Chen** received the M.E. and Ph.D. degrees in the electrical engineering, from Tohoku University, Sendai, Japan, in 1988 and 1991, respectively. From 1997, he was an associate professor of the Osaka Sangyo University, Osaka, Japan, and then a full Professor. Since 2010, he has been an Executive Director and Professor at Key Laboratory of Systems Biology, Chinese Academy of Sciences, and also a research professor at Institute of Industrial Science, The University of Tokyo.

He was the founding director of Institute of Systems Biology, Shanghai University, and serves as Chair of Technical Committee of Systems Biology at IEEE SMC Society, and is also the founding president of Computational Systems Biology Society of ORS China. His fields of interest are systems biology, bioinformatics, and nonlinear dynamics. He serves as editor or editorial board member for many systems biology related journals, e.g. BMC Systems Biology, IEEE/ACM Trans. on Computational Biology and Bioinformatics, J. Royal Society Interface, IET Systems Biology, Journal of Theoretical Biology, Mathematical Biosciences, Int. J. of Systems and Synthetic Biology, Journal of Molecular Cell Biology, and J. of Systems Science and Complexity. In recent five years, he published over 100 journal papers and two monographs (books) in the area of systems biology