

# BIOENGINEERING

PRESENTS

**Multiscale modeling of stochastic network, chromatin folding, and tissue formation for understanding cellular epigenetic states and tissue patterning**



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2101 ENGINEERING V

**Jie Liang, Ph.D.**

University of Illinois at Chicago

Professor, Department of Bioengineering

#### ABSTRACT:

Genome sequences provide the overall genetic blueprint of cells, but cells possessing the same genome can exhibit diverse phenotypes. There is a multitude of mechanisms controlling cellular epigenetic states and that dictate the behavior of cells. Among these, motifs of networks of interacting molecules, often under stochastic control, can exhibit different landscapes of phenotypic states. In addition, chromosome folding in three-dimensional space provides another important control mechanism for selective activation and repression of gene expression. Fully differentiated cells with different properties grow, divide, and interact through mechanical forces and communicate through signal transduction, resulting in the formation of complex tissue patterns. We discuss recent results of theoretical models, algorithms, and computational tools for studying these multi-scale problems.

#### BIOGRAPHY:

**Dr. Jie Liang** is the Richard and Loan Hill professor in the Richard and Loan Hill Department of Bioengineering at the University of Illinois at Chicago. He joined UIC in 1999 as an assistant professor, and was promoted to associated professor in 2003, and to full professor in 2007. He received his B.S. degree in Biophysics from Fudan University in 1986, MCS and Ph.D. in Biophysics from the University of Illinois at Urbana-Champaign in 1994. He was an NSF CISE postdoctoral research associate (1994-1996) at the Beckman Institute and National Center for Supercomputing and its Applications (NCSA) in Urbana, IL. He spent eight months as a visiting fellow at the NSF Institute of Mathematics and Applications at Minneapolis. From 1997 to 1999, he was an Investigator at SmithKline Beecham Pharmaceuticals in Philadelphia. He was a recipient of the NSF CAREER award in 2003. He was elected as a fellow of the American Institute of Medicine and Biological Engineering in 2007. He is a University Scholar.

Dr. Liang's research interests include systems biology, computational bioengineering, bioinformatics, and computational biophysics, especially the areas of structural bioinformatics, computational proteomics, molecular stochastic networks, and cellular pattern formation. Current projects in his lab include protein function prediction, evolution analysis, membrane protein/nanodevice assembly, stochastic networks, tissue regeneration and wound healing, cell polarity, and cellular pattern formation. His recent work can be accessed at (<http://www.uic.edu/~iliang>).