Ru-Dong Li, J Comput Sci Syst Biol, 5:1
doi: http://dx.doi.org/10.4172/0974-7230.S1.09

OMICS Group Conferences
Accelerating Scientific Discovery

International Conference and Exhibition on
Metabolomics & Systems Biology

20-22 February 2012 San Francisco Airport Marriott Waterfront, USA

Improved methods for metabolic kinetic modeling and complex bio-system analysis

Ru-Dong Li

Key Laboratory of Systems Biology, Chinese Academy of Sciences, China

Comprehensive kinetic models on metabolic systems facilitate understanding the dynamics, functional behavior, and mechanisms of living organisms at the system level. It is critical in revealing interplays of molecules and between molecules and conditional factors. In the present work, we attempted towards developing better modeling and analysis method for investigating complex metabolic systems, using organisms *Clostridium acetobutylicum* and *Escherichia coli* as working examples. Firstly, we extended the traditional biochemical system theory (BST) by integrating genetic regulations, forming a new strategy and formulism of kinetic modeling (Li *et al*., *BMC Syst Biol*, 2011). It is exemplified that our new modeling method generates results that are more consistent with experimental ones and superior to those produced by previous methods. Secondly, we developed a new method for characterizing system-level properties of components in a metabolic system. This new method not only differs from traditional topology-based ones but also improves the conventional metabolic control analysis (MCA). Our method turns the framework of individual sensitivity analysis in MCA into systemic criticality analysis, which is exemplified to be advantageous over previous methods by its results. Moreover, the theoretical basis of the method is not confined to metabolism, but can be applied to other molecular interaction systems including transcriptional networks and signaling networks. Prospective researches based on these methodological advancements are underway to study systems biology properties of molecules, as well as complex biological systems themselves.

Biography

Ru-Dong Li received both his B.S degree in bioinformatics and B.S. degree in mathematics & applied mathematics from Shanghai Jiaotong University in 2008. After that, he did doctoral studies on computational systems biology in the Key Laboratory of Systems Biology, Chinese Academy of Sciences. His recent research is focused on mathematical modeling of molecular interaction systems, and application of mathematical methods and theories in computational studies of complex biological systems.