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A review of Large- Scale Kinetic Parameters in Metabolic Network Model of *Escherichia Coli*

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Metabolic engineering is attentive about the alteration properties of metabolic pathways with the point of improving the generation of a few metabolics of intrigue. An essential range of metabolic engineering, the development is quite useful in the parameter identification/estimation of kinetic parameters in the metabolic pathway. The development of metabolic kinetic model requires a detailed information of the initial concentration of enzymes, metabolites, co-metabolites, kinetic parameters and the cell condition. However, kinetic parameters play a significant role in building dynamic model. Kinetic parameters identification is usually used to reduce the errors in the simulation of the model or in the estimation of the model's enzymes and metabolites. Moreover, the inverse problem, irreversible problem and the large scale attributes are the main issues to be considered for optimizing and estimating large scale kinetic parameters. This paper highlights the challenges inherent in the identification/estimation of kinetic parameters and the methods applied in solving the problems in the kinetic metabolic model of *E. Coli* following comprehensive analyses and discussions.

Keywords: Metabolic Engineering, dynamic model, metabolic network, kinetic parameters, optimization

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A Hybrid ACO-Graph Entropy for Functional Modules Detection From Protein-Protein Interaction Network

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Recent high-throughput experiments have generated protein-protein interaction data on a genomic scale, yielding the complete protein-protein interaction network for several organisms. Various graph clustering algorithms have been applied to protein interaction networks for detecting protein functional modules. Although the previous algorithms are scalable and robust, their accuracy is still limited because of the complex connectivity found in protein interaction networks. The Ant Colony Optimization (ACO) Algorithm has been adapted for the protein functional module detection by modeling the problem as an optimization problem. The adapted ACO (ACO-PFMDA) has obtained feasible solution but not as magnificent as those reported in the literature. Some shortcomings were identified and addressed by proposing a Modified Ant Colony Optimization Algorithm (ACO-PFMDM), which introduces two new scheme for controlling the two main parameters of ACO to solve PFMDP. Experiments on one popular benchmark dataset namely "Saccharomyces cerevisiae" which taken from two popular databases DIP and MIPS has been performed. The experimental result have proved that ACO-PFMDM have improved the overall performance of protein functional module detection. The search process of ACO-PFMDM has converged effectively compared to some state-of-art algorithms. Moreover, the proposed dynamic update of the heuristic parameters based on entropy has generated high quality tours and it can guide ants toward the effective solutions space in the initial search stages.

Keywords: Ant Colony Optimization Algorithm; Graph Entropy, Protein Functional Module, Protein Interaction Network