Metaheuristic optimization in the mathematical model development for in vivo analysis of dynamic biochemical systems

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The goal of our research is to develop a speedy modeling technique to be used for in vivo analysis. This paper investigated the problem of parameter estimation in nonlinear dynamic models of biological systems by taking advantages of metaheuristic optimization methods. HIV proteinase prohibition and glycolysis in Saccharomyces cerevisiae were used to compare the performance of the proposed method against competing methods. The problem of HIV proteinase consists a number of rate constants of a model for the reaction mechanism of irreversible inhibition, including 20 adjustable parameters to be estimated. In the Saccharomyces cerevisiae analysis, the model structure and experiments are related to the aerobic growth of the yeast and based on material balance equations. The kinetic analysis focuses on a time scale of seconds and the experiment is estimated simultaneously based on the mathemetical model. For the robust and efficient parameter estimation, we implemented a hybrid system based on the Particle Swarm Optimization. The proposed method shows satisfied results in fast convergence speed, accurate estimations and easy implementations.