

Identifying gene knockout strategies using a hybrid of bees algorithm and flux balance analysis for in silico optimization of microbial strains

Abstract

Genome-scale metabolic networks reconstructions from different organisms have become popular in recent years. Genetic engineering is proven to be able to obtain the desirable phenotypes. Optimization algorithms are implemented in previous works to identify the effects of gene knockout on the results. However, the previous works face the problem of falling into local minima. Thus, a hybrid of Bees Algorithm and Flux Balance Analysis (BAFBA) is proposed in this paper to solve the local minima problem and to predict optimal sets of gene deletion for maximizing the growth rate of certain metabolite. This paper involves two case studies that consider the production of succinate and lactate as targets, by using *E.coli* as model organism. The results from this experiment are the list of knockout genes and the growth rate after the deletion. BAFBA shows better results compared to the other methods. The identified list suggests gene modifications over several pathways and may be useful in solving challenging genetic engineering problems.