

Strain improvement for biochemical production based on Multi-objective algorithm

박종명, 김현욱, 이상엽*

Dept. of Chemical and Biomolecular Eng., KAIST

(ehukim@kaist.ac.kr*)

The advent of *in silico* genome-scale model developed various algorithms to apply for metabolic engineering. Flux balance analysis (FBA) optimizes a specific objective function by linear programming under pseudo-steady state based on the stoichiometry of metabolic reactions. Previous methods, such as minimization of metabolic adjustment (MOMA) and regulatory on/off minimization (ROOM), optimize only the limited objective function for simulation of knockout condition. To improve a strain for biochemical production, the organism should be investigated from diverse sides simultaneously: for instance, biomass formation, biochemical production, and waste formation. In this respect, we propose a new approach called the Flux Scanning with Compromised Objective Fluxes (FSCOF) that can investigate multi-objective functions such as biomass formation, biochemical production, and waste formation. [This work was supported by Korean Systems Biology Research program (M10309020000-03B5002-00000) of the Ministry of Education, Science and Technology. Further supports by LG Chem Chair Professorship, Microsoft and IBM SUR program are appreciated.]