

Multi-objective computational simulation to improve the strain for overproduction of
biochemical in
Escherichia coli

박종명, 김태용, 이상엽*
한국과학기술원
(leesy@kaist.ac.kr*)

There are too many combinatorial gene knock-out targets to achieve the overproduction of desired biochemicals in *Escherichia coli*. However, researchers cannot perform every experiment to identify the best combination of gene knock-out targets. Flux balance analysis (FBA) optimizes a specific objective function under pseudo-steady state based on the stoichiometry of metabolic reactions. In order to incorporate the physiological characteristics of the organisms under gene knock-out conditions, various methods such as minimization of metabolic adjustment (MOMA) and regulatory on/off minimization (ROOM) were developed. However, to improve a strain for biochemical production, the organism should be investigated from diverse sides simultaneously. In this respect, we propose a new approach called the flux scanning with compromised objective fluxes (FSCOF) that optimizes multi-objective functions. [This work was supported by the Korea Science and Engineering Foundation (KOSEF) grant funded by the Korea government (MOST) (No. M10309020000-03B5002-00000). Further supports by LG Chem Chair Professorship, Microsoft and IBM SUR program are appreciated.]