The computational simulations for overproduction of biochemical in *Escherichia coli*

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In the industrial biotechnology, there are too many combinatorial gene knock-out targets to achieve the overproduction of desired products. The advent of in silico genome-scale model developed various algorithms for the gene targeting. 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 MOMA and ROOM were developed. However, these algorithms optimize only the limited objective function. 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.]