Application of flux-coupled genes in flux balance analysis

유재용, 김현욱, 김원준, 이상엽*
한국과학기술원
(leesy@kaist.ac.kr*)

Genome-scale metabolic network modeling and simulation have contributed to systematic analyses of organisms of interest. One of the important features of the genome-scale metabolic network modeling is to simulate genome-wide intracellular metabolic fluxes under the given genetic and environmental conditions. For this, integration of experimental data, especially omics data, are critical for better accuracy. To this end, we looked for so called flux-coupled genes (FCGs) as additional constraints in flux balance analysis (FBA), which show consistent changes in their expression levels with their respective flux values upon perturbations. Most consistent FCGs (i.e. gnd, pfkB, rpe, sdhB, sdhD, sucA, and zwf) were identified using transcriptome and 13C-flux data of Escherichia coli at five different dilution rates during its chemostat cultivations. FBA with FCGs was later compared with conventional simulation approaches. This strategy with FCGs will be useful due to the relative easiness of obtaining transcriptional information of only several genes.