

Expression levels of flux-coupled genes as additional constraints for flux balance analysis

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

One of the important functions of genome-scale metabolic network modeling is to integrate omics data with the metabolic flux simulation, and several useful algorithms have been reported. To move one step forward, we examined a hypothesis that there might exist metabolic genes, which show correlated changes in their expression levels with their corresponding flux values upon perturbations. We employed expression levels of these so called flux-coupled genes as additional constraints. Most consistent FCGs were identified to be *gnd*, *pfkB*, *rpe*, *sdhB*, *sdhD*, *sucA*, and *zwf* genes based on omics data obtained from its chemostat cultivations at five different dilution rates. This strategy with FCGs is expected to be useful due to the relative easiness of obtaining transcriptional information of only several genes. [This work was supported by the Technology Development Program to Solve Climate Changes on Systems Metabolic Engineering for Biorefineries (NRF-2012-C1AAA001-2012M1A2A2026556) and by the Bio & Medical Technology Development Program (2012048758) from the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea.]