Flux balance analysis of metabolic network using flux coupled-genes as constraints

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Genome-scale metabolic network modeling and flux balance analysis have played important roles in metabolic engineering. Its major role is to integrate omics data with metabolic network for more accurate prediction. We hypothesized that there might be genes which change in their expression correlated with their corresponding flux values after perturbations. These flux-coupled genes (FCGs) were investigated using transcriptome and 13C-flux data of Escherichia coli, and most consistent FCGs were identified as gnd, pfkB, rpe, sdhB, sdhD, sucA, and zwf. The corresponding reactions were then given as additional constraints in flux balance analysis (FBA). The results were also compared with conventional simulation methods. This strategy has usefulness due to its relative easiness of obtaining a few genes' transcriptional information. [This work was supported by the Technology Development Program to Solve Climate Changes (systems metabolic engineering for biorefineries) from the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea (NRF-2012-C1AAA001-2012M1A2A2026556)]