Bayesian Analysis of Perturbed Metabolism from the Perspective of Metabolic Fluxes

김현욱, 김태용, 윤홍석, 의종민, 이상엽*

KAIST

(joungmin@kaist.ac.kr*)

Metabolic flux is an ultimate cellular phenotype as an outcome of interplays among various cell components under specific conditions. In this study, we developed a framework that analyzes the effect of genetic/environmental perturbation using constraints-based flux analysis and Bayesian network analysis. A genome-scale stoichiometric model of Escherichia coli was employed for this work as an example. Metabolic fluxes calculated from constraints-based flux analysis were subsequently subjected to data preprocessing, clustering and finally Bayesian network analysis. As a result, a Bayesian network was predicted, showing causal relationships among metabolic fluxes that play critical roles in response to a specific perturbation. This framework enables systematic organization of metabolic fluxes in terms of causal relationships, which might serve as a useful supplemental tool in metabolic flux analysis. [This work was supported by the Korean Systems Biology Program from the Ministry of Education, Science and Technology through the Korea Science and Engineering Foundation (No. M10309020000-03B5002-00000). Further support by LG Chem Chair Professorship is appreciated.]