

### Bayesian analysis of modularized metabolic network under perturbation condition

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Intracellular metabolic fluxes are an ultimate phenotype revealed from interplays among various cell components under specific condition. With metabolic flux data, in order to gain more about the effect of various perturbations given to the organism, we developed a framework that reveals the range of effects that the perturbed biochemical reaction exerts on other reactions through constraints-based flux analysis, modularization of metabolic network and Bayesian network analysis in a series. Network modularization clusters biochemical reactions based on their flux values using hierarchical clustering. Finally, Bayesian network analysis infers causal relationships among biochemical reactions in the form of a graphical model. The framework developed herein should serve as a tool complementary to existing omics tools so as to advance our understanding of biological systems. [This work was supported by the Korean Systems Biology Research Project (20100002164) of the Ministry of Education, Science and Technology (MEST) through the National Research Foundation of Korea. Further support by the World Class University Program (R32-2008-000-10142-0) through the National Research Foundation of Korea funded by the MEST is appreciated.]