From structure to to dynamics of metabolic networks: flux balance analysis

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Biological systems are unimaginably complex, yet also highly robust to genetic perturbations on all levels of organization. For example, the cellular metabolism of the bacterium E. coli maintains its homeostasis, often with little or no effect on the biomass yield under a considerable portion of single gene knockouts. To address the interplay between the robustness of the final biomass yield and the underlying mechanisms in the intracellular metabolism, we first review the structural properties of metabolic networks, and then identify the set of intracellular metabolites of which presences are essential for the cellular-level viability via flux balance analysis. These essential metabolites exhibit the quite different characteristics both in the topological and physiological aspects of the participating reactions, compared with the case for the non-essential ones. Most importantly, it is revealed that in viable case, production and consumption rates of each essential metabolite acquire their robustness responding to the genetic perturbations, by actively reorganizing the reaction fluxes for the ultimate robustness of the biomass yield. We also find that there is strong correlation between essentiality and flux fluctuation of metabolite under the gene deletion purturbations.