

Accurate prediction of metabolic fluxes using genomic context and stoichiometric analysis

박종명, 김태용, 이종민, 이상엽*

KAIST

(leejm516@naver.com*)

Flux balance analysis has been applied to predict the physiology of organisms and detect targets for metabolic engineering successfully. However, the Flux balance analysis has problems such the inaccuracy of internal flux distribution and multiple solutions for a same objective value (e.g., growth rate). Herein, we suggest a new method, flux balance analysis with grouping functionally and physically related reactions, considering three types of genomic context analysis across organisms and stoichiometric analysis of carbon fluxes. [This work was supported by Korean Systems Biology Research program (M10309020000-03B5002-00000) of the Ministry of Education, Science and Technology. Further supports by LG Chem Chair Professorship, Microsoft and IBM SUR program are appreciated.]