Data Reconciliation of GC/MS based Flux Distribution in Large-scale Metabolic Flux Analysis

김태용, 홍순호, 이상엽*

한국과학기술원 생명화학공학과, 대사 및 생물분자공학 연구실

(leesy@kaist.ac.kr*)

Various techniques and strategies were developed for the identification of intracellular metabolic conditions, and the gas chromatography/mass spectrometry (GC/MS) based flux analysis has been highlighted in these days. In this study, the combination of isotope based flux data with MFA analysis was examined as a new strategy allowing more accurate quantification of intracellular flux distribution in large metabolic system. To impose GC/MS based data into large metabolic network and obtain optimum flux distribution profile, data reconciliation procedure was applied. As a result, reconciliation of isotopic flux data in large scale MFA is introduced for studying whether experimental isotopic flux data are consistent with optimized flux data based on linear programming.