

Development of the Metabolic Flux Analysis Software using Isotope Distributions

오영균, 이동엽, 박선원*
한국과학기술원, 초미세화학공정연구센터
(sunwon@kaist.ac.kr*)

Metabolic flux analysis (MFA) is one of the well-established approaches for rational analysis of a metabolic system. Nevertheless, still several issues remain to be overcome, which is mostly attributable to limited experimental observations. The isotopomer labeling experiments with gas chromatography-mass spectrometry (GC-MS) can be carried out to overcome the lack of such measurable quantities regarding the intracellular fluxes, thus providing additional information to determine the unknown fluxes in MFA. In this study, we have developed MFA tool based on isotopomer analysis (Schmidt et al., 1997). It allows users to formulate isotopomer models for large metabolic networks considering all available labeling information. As a result, the intracellular metabolic fluxes can be estimated by minimizing the deviation from the experimental data.

Acknowledgements: This work was supported by the Korean Systems Biology Research Grant (M10309020000-03B5002-00000) from the Ministry of Science and Technology (MOST) and also was partially supported by IMT2000 project (IMT2000-C3-1) from MOST and the Ministry of Information and Communication (MIC), and BK21 project.