Simulation of Metabolic Networks Using Carbon Isotope Labeling Experiment

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Metabolic flux analysis (MFA) is a powerful tool for the modeling and simulation of metabolic networks. However, the available extracellular flux data is not always sufficient to determine all intracellular fluxes. Further information or constraints should be acquired for calculation of intracellular fluxes. By use of the carbon isotope labeling experiment for fermentation experiments, it is possible to obtain mass distribution data. Carbon isotope labeled data came from ^{13}C isotope tracer technique with GC-MS (Gas Chromatography-Mass Spectrometry) measurements. In this work, we have developed a metabolic networks simulation tool which can precisely simulate intracellular fluxes using carbon labeled experimental data. The result can provide strict insight into complex biochemical networks.

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