

Determining Mass Distributions Considering Natural Isotopes

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Metabolic flux analysis (MFA) has been a powerful tool for the modeling and analysis of intracellular fluxes and the investigation of biochemical network. By use of gas chromatography-mass spectrometry (GC-MS) for fermentation experiments, it is possible to obtain mass distribution data. However, the correction of mass isotopomer distributions is required because of the occurrence of natural isotopes. In this work, we have developed a mass isotope correction tool, which helps avoid errors in the metabolic flux analysis. The result can provide a precise insight into the complex biochemical network.

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