

A two-scale 13C-based method for metabolic flux measurement and prediction

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Project Goals:

To measure and predict intracellular metabolic fluxes by using 13C labeling experiments.

Systems biology aims to provide a predictive and quantitative understanding of cell behaviour as the outcome of the interaction of its comprising parts. Metabolic flux profiles (i.e. the number of molecules traversing each biochemical reaction encoded in its genome per unit time) are not only a key phenotypic characteristic but also embody the essence of this complexity since they represent the final functional output of the interactions of all the molecular machinery studied by all the other “omics” fields. Two of the most popular methods for studying metabolic fluxes are Flux Balance Analysis (FBA) and 13C Metabolic Flux Analysis (13C MFA), each of them displaying its own advantages and disadvantages. Here, we present a new method: Two scale 13C Metabolic Flux Analysis (2S-13CMFA), which combines the advantages of FBA and 13C MFA. We showcase its applications and possibilities with data from the KEIO knockout collection.

This work conducted by the Joint BioEnergy Institute was supported by the Office of Science, Office of Biological and Environmental Research, of the U.S. Department of Energy under Contract No. DE-AC02-05CH11231.