

## **Identification of metabolic flux distribution in *Escherichia coli* using MetaFluxNet**

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The analysis of structure and flux distribution in metabolic networks has become an important approach for understanding the functionality of metabolic system. For this reason, we developed the analysis software(MetaFluxNet) to facilitate integrated pathway and flux analysis for metabolic networks within a user-friendly graphical user interface. This package provides various desirable features like obtaining maximum theoretical yields, examining and comparing the influences of genetic modification to the flux distributions, classifying the metabolic system with measurements according to the system determinant, and supporting dynamic visualization of calculated fluxes mapped on metabolic pathways. In this study, we applied this MetaFluxNet to identify metabolic flux distribution of *Escherichia coli*. The variation of intracellular metabolic flux distributions of *E. coli* was estimated by MFA under various conditions, and the response of metabolic fluxes were evaluated. As verified in this study, MetaFluxNet could be used for the identification of the pathway function identification of various microorganisms including *E. coli*

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