

MetaFluxNet for the Metabolic Analysis of *In Silico* Genome-Scale Models

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The *in silico* genome-scale analysis of microbes with myriad of heterologous data generated by x-omics has been applied to improving our understanding of cellular function and physiology and consequently to enhance production of various bioproducts. Development of an upgraded MetaFluxNet allows (1) construction of metabolic models connected to metabolic databases, (2) calculation of fluxes by metabolic flux analysis, (3) comparative flux analysis with flux-profile visualization, (4) the use of metabolic flux analysis markup language to enable models to be exchanged efficiently, and (5) the exporting of data from constraints-based flux analysis into various formats. This integrated software environment promises to enhance our understanding on metabolic network at a whole organism level and to establish novel strategies for improving the properties of organisms for various biotechnological applications. This work was financially supported by the Korean Systems Biology Research program of the Korean Ministry of Science and Technology (MOST), the Brain Korea 21 of the Ministry of Education and LG chemicals Chair Professorship. Hardware for computational analysis supported by the IBM-SUR program.