

## MetaFluxNet: Platform for *in silico* metabolic flux analysis

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### Abstract

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. At the heart of this revolution *in silico* genome-scale metabolic model has been reconstructed and a systematic approach employing user-friendly software is required. Metabolic flux analysis of genome-scale metabolic network is becoming widely employed to quantify the flux distribution and validate model-driven hypotheses. Here we describe the development of an upgraded MetaFluxNet<sup>1)</sup> which 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<sup>2)</sup> to enable models to be exchanged efficiently, and (5) the exporting of data from constraints-based flux analysis into various formats. MetaFluxNet also allows cellular physiology to be predicted and strategies for strain improvement to be developed from genome-based information on flux distributions. 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

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#### References

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