

Supporting SBML for representation and exchange of biochemical network models in MetaFluxNet

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The systems biology markup language (SBML) has been developed to exchange a common format for different simulation and analysis tools of the biological systems (Hucka et al., 2003). Now, this SBML is supported in MetaFluxNet (Lee et al., 2003) which is a program package for metabolic flux analysis, thereby enabling users to construct computational models easily and to expand research interests. Some examples demonstrate how MetaFluxNet and other tools can complement each other through the exchange format.

Acknowledgements

This work was supported by the Advanced Backbone IT Development project of the MIC and MOST, and by the BK21 project.