MetaFluxNet 2: The integrated modeling and simulation environment for the genome-scale metabolic network

박종명, 윤홍석, 윤좌문, 김현욱, 이상엽*
한국과학기술원 생명화학공학과
(leesy@kaist.ac.kr*)

The genome-scale metabolic network models combined with metabolic flux analysis become the effective methodology to explain the vast quantities of complex experimental data. To respond to the research needs, we have developed the MetaFluxNet. However, significant advances require more advanced features to describe more sophisticated metabolic models. Therefore, we develop the MetaFluxNet2. It has some new features include modeling method which provides a network editor using graphical representation and an information retrieval method using database search. In addition, MetaFluxNet2 integrates several analysis methods such as metabolic flux analysis, multi-objective linear programming, and minimization of metabolic adjustment. MetaFluxNet2 provides a more systematic approach in design of the model and metabolic engineering strategies for strain improvements. [This work was supported by the Korea Science and Engineering Foundation (KOSEF) grant funded by the Korea government (MOST) (No. M10309020000-03B5002-00000). Further supports by LG Chem Chair Professorship, Microsoft and IBM SUR program are appreciated.]