

Metabolic flux analysis markup language: Level 2

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The increasing availability of biochemical network models gives the novel approaches for a systematic application to understand the metabolic status. The request for exchange of these models becomes the common process in the biotechnology field. In an attempt to respond to these demands, we have developed an exchange language, the MFAML (metabolic flux analysis markup language). However, significant advances in system-level modeling of cellular behavior require more advanced features to describe more sophisticated metabolic models. Therefore, we are developing MFAML level 2 and report the current progress in this study. MFAML level 2 provides the distinguishing main new features; defining named compartment, pathway, pathway introduction, dynamic representation and mathematical formulae. In MFAML level 1, the static model is mainly expressed but, Level 2 extends the previous model representation and works with the dynamic information. This work is supported by the Korean Systems Biology Research Program (M10309020000-03B5002-00000) of the MOST and by the BK21 project. Further supports by LG Chemical Chair Professorship, Microsoft and IBM-SUR program are greatly appreciated.