Simulation environment for the kinetic model reduction of complex biochemical pathways

윤좌문, 이동엽, 오영균, 김상훈, 이상엽, 박선원*
한국과학기술원
(sunwon@kaist.ac.kr*)

A kinetic modeling approach is promising to discover a knowledge map for deciphering the functions and characteristics of living systems in detail. Given the biochemical reaction network, kinetic and regulatory information is incorporated into a kinetic model comprising the continuous differential equations, thereby completely describing the dynamic system and predicting its behavior under any perturbations. The use of this kinetic approach is, however, hampered by the dynamic complexity due to a large number of kinetic parameters and intricate interactions among various reactions. In this study, model simplification methods such as order reduction are considered to relieve the stiffness and to obtain the accurate information on the dominating dynamics. This approach will be especially useful in large networks that are exceedingly intricate to explore their dynamic behaviors.

ACKNOWLEDGMENTS :This work was supported by the Korean Systems Biology Research Program (M10309020000-03B5002-00000) of the Ministry of Science and Technology and by the BK21 project. Further supports from LG Chemicals Chair Professorship and IBM-SUR program are greatly appreciated.