Abstract

In this study, we performed local sensitivity analysis on a large-scale kinetic dynamic metabolic network. Time profile for sensitivity indices has been calculated for each kinetic parameters based on highest variance. The dynamic model of E. coli used in this study contain Glycolysis, Pentose Phosphate, TCA cycle, Gluconeogenesis and Glyoxylate pathways in addition to Acetate formation PTS system. The model implicates twenty-four dynamic mass balance for extracellular glucose and intracellular, thirty kinetic rate expressions. We test all the kinetics in
10% and 20% increasing one by one at steady state condition. The former analysis in 20%, has allowed identification of eight kinetic parameters as the most effective on this model.

References

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Index Terms

Computer Science
Control System
Keywords
Metabolic Network  Dynamic Modeling  Sensitivity Analysis.