Towards a genome-scale kinetic modeling of *Escherichia coli* metabolism

Rafael S. Costa, Daniel Machado, Isabel Rocha, Eugénio C. Ferreira

IBB-Institute for Biotechnology and Bioengineering, Centre of Biological Engineering, University of Minho, Campus de Gualtar, P-4710-057 Braga, Portugal

Abstract

Understanding the dynamic behavior of living organisms is a great challenge in systems biology. To address this, computational dynamic modeling of metabolic networks is essential to guide experimentation and to explain properties of complex biological systems. Large-scale kinetic models at the reaction network level are usually constructed using mechanistic enzymatic rate equations and a large number of kinetic parameters. However, two of the biggest obstacles to construct accurate dynamic models are model complexity and limited *in vivo* kinetic information. In the present work, we test an alternative strategy with a relatively small number of kinetic parameters composed by the approximated lin-log kinetics, coupled with a constraint-based method and *a priori* model reduction based on time scale analysis and a *conjunctive fusion* approach, for building a genome-scale kinetic model of *Escherichia coli* metabolism. This workflow was evaluated for the condensed version of a genome-scale network of *E. coli* (Orth et al., 2010).

The presented approach appears to be a promising mechanism for detailed kinetic modeling at the genome-scale of the metabolism of other organisms.

Keywords: dynamical modelling, approximate lin-log kinetics, constraint-based modelling, model reduction, model fitting, *E. coli* metabolic network

Reference List

Orth JD, Fleming RMT, Palsson BO (2010) Reconstruction and use of microbial metabolic networks: the core *Escherichia coli* metabolic model as an Educational Guide. In: EcoSal, doi: 10.1128/ecosal.10.2.1.