Exploring the gap between dynamic and constraint-based models of metabolism

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Abstract. Systems Biology provides new approaches for metabolic engineering through the development of models and methods for simulation and optimization of the microbial metabolism. Nowadays, two main different modeling frameworks (dynamic and constraint-based models) that have different levels of complexity and scalability coexist. The construction of dynamic models with detailed kinetic rate laws has been limited to central pathways due to the amount of experimental data required for parameter estimation. On the other hand, genome-scale stoichiometric reconstructions have been used in the formulation of constraint-based models that define a space of solutions for the steady-state flux distribution. In this work, we explore the gap between these two kinds of models by comparing and analyzing the dynamic and constraint-based formulations of the same model of the central carbon metabolism of *E. coli*. Our results show that if the kinetic parameters of the dynamic model are unconstrained, the space of solutions described by both kinds of models is the same. However, the imposition of parameter ranges can be mapped into kinetically feasible regions of the solution space. Therefore, if at least a part of the kinetic parameters is known, dynamic models can be used for generating constraints that reduce the solution space of constraint-based models, eliminating infeasible solutions and increasing the accuracy of simulation and optimization methods.