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Construction of Kinetic Model Library of Metabolic Networks

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Abstract: Kinetic model identification of metabolic networks is important, but still represents a significant challenge. The difficulties faced vary from the vast kinetic parameter search space to the lack of complete parameter identifiability. To meet these challenges, an incremental modeling approach is proposed here, including two key components—dynamic flux calculation and flux-based kinetic parameter estimation. In essence, the identification method relies on time-course concentration data to generate the family of consistent metabolic flux values and by doing so, the parameter estimation step can be done one flux at a time. The key contribution of the method is an efficient generation of a library of kinetic models with similar goodness of fit to the provided data. The performance of this identification method is demonstrated using a generic branched metabolic pathway model and the glycolytic pathway model of *Lactococcus lactis* (*L. lactis*).

Keywords: Library Construction, Dynamic Flux Calculation, Parameter Regression, Metabolic Kinetic Models.

1. INTRODUCTION

The majority of current parameter estimation methods for kinetic modelling of metabolic networks rely on a single step identification, in which parameters are obtained simultaneously by minimizing some functions of model prediction errors using global optimization algorithms (Daisuke and Horton, 2006; Gonzalez et al., 2007; Kikuchi et al., 2003; Kimura et al., 2005; Noman and Iba, 2007). The process of finding a single "best-fit" model or parameter set, however, is typically ill-posed as the inverse problem is usually under-determined. This issue has led to common observations where non-equivalent solutions produce similar simulation error due to error compensation among and within equations and fluxes (Chou and Voit, 2009). In addition, simultaneous identification can suffer from difficulties in high computational requirement, problem initialization and solution convergence.

In order to reduce the estimation time, many estimation algorithms have been created that circumvent the computationally costly integration of kinetic ordinary differential equations (ODEs), such as the decoupling method (Voit and Almeida, 2004), collocation method (Tsai and Wang, 2005) and other decomposition methods (Kimura et al., 2005; Maki et al., 2002; Marino and Voit, 2006). In addition, methods that generate a set or ensemble of models are also available by utilizing not only mass balance equations, but also thermodynamic and steady-state data constraints (Miskovic and Hatzimanikatis, 2011; Tran et al., 2008). Nevertheless, none of these methods has dealt properly with the generation of kinetic models using

metabolic time profiles, which represents the new contribution of this work.

An incremental approach to the identification of kinetic metabolic models has been presented elsewhere (Goel et al., 2008), where dynamic metabolic fluxes are first estimated and the parameter estimation is subsequently done one flux at a time. Such incremental identification approach generally has the advantages of low computational effort, low sub-problem complexity, flexible use of physically motivated equations for each flux, and ease of validation of flux equations (Bardow and Marquardt, 2004). However, as noted above, the lack of full model identifiability means that a unique best-fit model does not exist.

A new incremental identification from time series data is proposed in this work. Like before, the method relies on two-step estimation: dynamic flux estimation and parameter estimation, but in this case, a set of consistent dynamic metabolic fluxes is generated and parameterized. Consequently, the method can efficiently generate a family of "equivalent" kinetic models, instead of a single model (see Method). The proposed method has been applied to two examples taken from power-law kinetic modelling of the branched pathway and the glycolytic pathway of *L. Lactis* in order to demonstrate its efficacy.

2. METHOD

2.1 Problem formulation and solution parameterization

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