1 Introduction:

1.1 A method to establish posterior identifiability of metabolic network models:

This document details a method to establish the practical (posterior) identifiability of metabolic network models using the algebraic relationship between fluxes. Every flux, v, in a kinetic model of a metabolic network can be expressed as a nonlinear algebraic equation (Equation 1). The fluxes are expressed as a function of the metabolite concentrations x and the kinetic parameters θ in Equation (1).

$$v = f(\mathbf{x}, \theta) \tag{1}$$

Given the nonlinear nature of this model, the function f in Equation (1) can expressed, without loss of generality as,

$$v = \frac{N(\mathbf{x}, \theta)}{D(\mathbf{x}, \theta)} \tag{2}$$

where $N(\mathbf{x}, \theta)$ is the numerator of f, and $D(\mathbf{x}, \theta)$ is the denominator of f.

If $\theta \in \mathbb{R}^p$, given a set of experimental measurements for the metabolite concentrations $\mathbf{x}$ and the reaction fluxes $\mathbf{v}$, theoretically, it is possible to choose p sets of data from these measurements to solve for the p parameters in θ. However, if any these datasets do not satisfy the condition that $D(\mathbf{x}, \theta) \neq 0$, then the number of experiments required to estimate the p parameters in θ can be established to be greater than p.

This analysis can be performed for each flux in a metabolic network independent of all the other fluxes. This enables this method to be scalable to even genome-scale models.