

# 1 Introduction:

## Outline:

- How dynamic models of metabolism are defined in biology
- How parameter values is important for model-based prediction and design of metabolism
- importance of parameter identifiability, structural and practical identifiability for dynamic models of metabolism
- work done in the are of structural identifiability (numerical and symbolic/computer algebra methods)
  - local vs global identifiability
- work done in the area of practical identifiability (numerical and symbolic/computer algebra methods)
- work done in this paper for practical identifiability
- scalability of computer algebra-based methods for structural identifiability (using CRNT to reduce networks to make structural identifiability scalable)

## 1.1 Identifiability analysis: Definitions and Formulations

Any nonlinear dynamical system can be represented by a set of states  $\mathbf{x}$ , observables  $\mathbf{y}$  that are dependent on the states, parameters  $\mu$ , and inputs  $u$  as in Equation (1).

$$\dot{\mathbf{x}} = g(\mathbf{x}, \mu, u) \tag{1a}$$

$$\mathbf{y} = h(\mathbf{x}, \mu, u) \tag{1b}$$

Identifiability concerns with the ability to determine a unique solution to the problem of estimating parameters  $\mu$  from given data on the system observables  $\mathbf{y}$  for inputs  $u$  (McLean AND McAuley 2012). The identifiability of parameters in nonlinear models of physical processes can be classified into two categories: structural and practical identifiability.

Any system (Equation 1) is said to be structurally or a priori identifiable if, for an input-output mapping defined by  $\mathbf{y} = \Phi(\mu, u)$  for at least one input function  $u$ , any two values of parameters  $\mu_1$  and  $\mu_2$  satisfy the

relationship in Equation (2) below.

$$\Phi(\mu_1, u) = \Phi(\mu_2, u) \iff \mu_1 = \mu_2 \quad (2)$$

Accordingly, any system that has an infinite number of solutions to the parameter estimation problem for all input functions is said to be structurally non-identifiable. The effect of model structure and parameterization on the ability to infer true parameter values from experimental data is determined by the structural identifiability of the parameter.

When parameters are estimated on the basis of noisy data, the ability to estimate unique parameter values to satisfy Equation (2) is referred to as practical identifiability. The effect of the available experimental data on the ability to estimate unique parameter values is determined by the practical identifiability of the parameter. Accordingly, practical identifiability of a parameter is contingent upon the nature, quality and quantity of data available to estimate the parameter as opposed to the structure and parameterization of the model. Thus, on the one hand, establishing the structural identifiability of parameters enables one to propose models that are not only appropriate representations of physical processes, but also are parameterized in such a way that the value of these parameters can be estimated. On the other hand, establishing practical identifiability of parameters in any model helps design experiments that are minimal, informative and useful for parameter estimation.

## 2 Methods:

We use a profile likelihood-based approach (Raue, ET AL. 2009) to establish structural and practical identifiability of parameters in nonlinear kinetic models of metabolism. Briefly, the approach seeks to establish the existence/non-existence of bounds in confidence intervals for the estimates of parameters in nonlinear models. The profile likelihood is calculated based on Equation (3) for each parameter  $\theta_i$  where  $\chi^2(\theta_i)$  is given by Equation (4).

$$\chi_{PL}^2(\theta_i) = \min_{\theta_j \neq i} [\chi^2(\theta)] \quad (3)$$

$$\chi^2(\theta) = \sum_{k=1}^m \sum_{l=1}^d \left( \frac{y_{kl}^* - y_{kl}}{\sigma_{kl}^*} \right)^2 \quad (4)$$

In the minimization objective shown in Equation (4) for parameter estimation,  $y_{kl}^*$  is the available experimental time course data for each observable state  $k$  at each  $l$  time point. The difference between the data and the model estimates at these time points,  $y_{kl}$  is weighted by the variance in the experimental data  $\sigma_{kl}^*$ . An algorithm to calculate the profile likelihood,  $\chi_{PL}^2(\theta_i)$ , based on Equation 3 is given below.

The identifiability of parameters is established through the confidence intervals of their estimates,  $[\sigma_i^-, \sigma_i^+]$ . The likelihood-based confidence interval for any parameter whose profile likelihood is estimated can be written on the basis of a threshold  $\Delta_\alpha$  in the likelihood as in Equation (5).

$$\{\theta | \chi^2(\theta) - \chi^2(\hat{\theta}) < \Delta_\alpha\} \quad (5)$$

The threshold  $\Delta_\alpha$  in the likelihood is the  $1-\alpha$  quantile of the  $\chi^2$  distribution, represented as  $\chi^2(\alpha, df)$ . The confidence intervals obtained hold for  $df$  degrees of freedom. For a choice of  $df=1$  the confidence intervals will hold for each parameter individually, and confidence intervals that hold jointly for all parameters can be obtained by choosing the number of parameters as  $df$ .

The visualization of structurally and practically non-identifiable parameters using the profile likelihood approach is illustrated in Figure 1. The points of intersection between the profile likelihood curves (solid line) with the one parameter likelihood threshold ( $\Delta_\alpha = \chi^2(\alpha, 1)$ , dashed line) provide the confidence intervals of the parameter  $\theta_i$ . The confidence intervals of a structurally non-identifiable parameter are unbounded, i.e.,  $[-\infty, +\infty]$  (Figure 1a), while the confidence intervals of a practically non-identifiable parameter are unbounded in at least one direction, i.e.,  $[\sigma_i^-, \sigma_i^+]$  where either  $\sigma_i^- = -\infty$  or  $\sigma_i^+ = +\infty$  (Figure 1b). If a parameter's estimates have a finite confidence interval then the parameter is said to be identifiable (Figure 1c). Note that the horizontal dotted lines in Figure 1 represent the confidence interval thresholds ( $\Delta_\alpha$ ) that are used to establish identifiability.

Due to the dependence of practical parameter identifiability on the experimental data, the profile likelihood approach can be used to design experiments in such a way that the observables that are derived from these experiments can improve the practical identifiability of the parameters. We show how experimental design can have a meaningful impact on parameter identification and estimation in Figure ???. Assuming a parameter  $\theta_i$  is practically non-identifiable (Figure ??a), performing a profile-likelihood based identifiability analysis using simulated data can help determine the nature of experiments needed to make the parameter

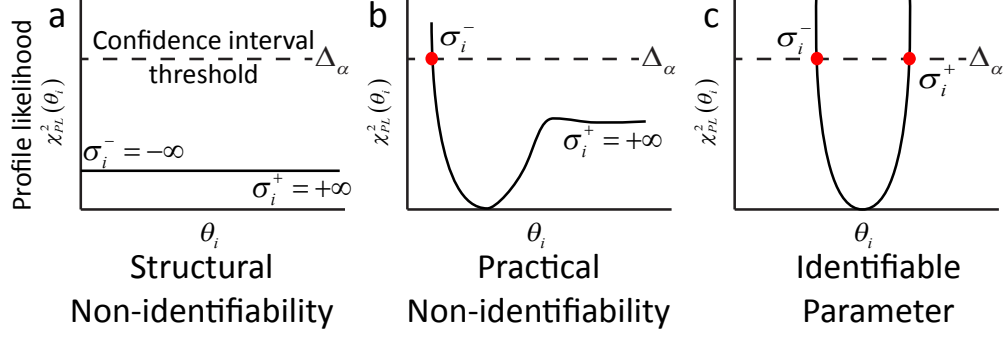


Figure 1: The profile likelihood estimates of a) a structurally non-identifiable, b) a practically non-identifiable and c) an identifiable parameter. The horizontal axis represents the changes in the value of the parameter ( $\theta_i$ ) whose identifiability is being determined and the profile likelihood ( $\chi^2_{PL}(\theta_i)$ ) is shown in the vertical axis. The confidence interval threshold ( $\Delta_\alpha$ ) used to determine the identifiability of the parameter is denoted by the horizontal dotted line. Identifiable parameters are distinguished from non-identifiable parameters by the presence of both upper and lower bounds on their confidence interval estimates  $[\sigma_i^-, \sigma_i^+]$ .

identifiable (Figure ??b). In contrast, performing non-informative experiments without prior knowledge on their ability to change the identifiability of the parameter may provide data that cannot be used to estimate parameter  $\theta_i$  (Figure ??c).

## 2.1 A method to establish posterior identifiability of metabolic network models:

This section 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 6). The fluxes are expressed as a function of the metabolite concentrations  $x$  and the kinetic parameters  $\theta$  in Equation (6).

$$v = f(\mathbf{x}, \theta) \quad (6)$$

Given the nonlinear nature of this model, the function  $f$  in Equation (6) can be expressed, without loss of generality as,

$$v = \frac{N(\mathbf{x}, \theta)}{D(\mathbf{x}, \theta)} \quad (7)$$

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  $\theta$ . 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  $\theta$  can be established to be greater than  $p$ . An example is shown below.

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. The following section demonstrates this methodology for one of the fluxes in the gluconeogenic model of Kotte et al., (**Kotte2014**).

## 2.2 Identifiability analysis of parameters in a kinetic model of gluconeogenesis:

The proposed model for acetate consumption through gluconeogenesis and its corresponding kinetic model is used as a case study to illustrate the utility of identifiability analysis for the design of experiments for estimating parameters in kinetic models of metabolism. The kinetic model is described below.

$$\frac{d}{dt} pep = v_1 - v_2 - v_4 \quad (8)$$

$$\frac{d}{dt} fdp = v_2 - v_3 \quad (9)$$

$$\frac{d}{dt} E = v_{e,max} \left( \frac{1}{1 + \left( \frac{fdp}{K_e^{fdp}} \right)^{n_e}} \right) - dE \quad (10)$$

The kinetic expressions for fluxes  $v_1$  through  $v_4$  are given below. The consumption of acetate through  $v_1$  and conversion of  $pep$  through  $v_2$  are expressed in Equations (11) and (12) respectively using Michaelis-Menten kinetics. The acetate flux through  $v_1$  is also governed by the quantity of available enzyme  $E$ .

$$v_1 = k_1^{cat} E \frac{acetate}{acetate + K_1^{acetate}} \quad (11)$$

$$v_2 = V_2^{max} \frac{pep}{pep + K_2^{pep}} \quad (12)$$

$$v_3 = V_3^{max} \frac{fdp (1 + f\tilde{d}p)^3}{(1 + f\tilde{d}p)^4 + L_3 \left( 1 + \frac{pep}{K_3^{pep}} \right)^{-4}} \quad (13)$$

The allosterically regulated flux  $v_3$  for the consumption of  $fdp$  is expressed in Equation (13) using the Monod-Wyman-Changeux (MWC) model for allosterically regulated enzymes, where  $f\tilde{d}p$  refers to the ratio of  $fdp$

with respect to its allosteric binding constant  $K_3^{fdp}$ . The added flux  $v_4$  for the export of  $pep$  is expressed as a linear equation dependent on  $pep$  in Equation (14).

$$v_4 = k_4^{cat} \cdot pep \quad (14)$$

We use flux  $v_2$  to demonstrate the identifiability analysis method described in the previous section. Flux  $v_2$  has two parameters,  $V_2^{max}$  and  $K_2^{pep}$  that need to be estimated from experimental data. Here, we assume that at least two different sets of experimental data for the concentrations and fluxes are available. Accordingly, we label these dataset as  $pep^1, v_2^1$  and  $pep^2, v_2^2$  respectively. Subsequently, these experimental datasets can be included in the model to form two simultaneous nonlinear algebraic equations in the parameters  $V_2^{max}$  and  $K_2^{pep}$  (Equation 15).

$$V_2^{max} = \frac{v_2^1 v_2^2 (pep^1 - pep^2)}{v_2^2 pep^1 - v_2^1 pep^2} \quad (15a)$$

$$K_2^{pep} = \frac{pep^1 (v_2^1 pep^2 - v_2^2 pep^1)}{v_2^2 pep^1 - v_2^1 pep^2} \quad (15b)$$

Table 1: Table showing the perturbed values of all fluxes used for parameter estimation.

Designation	Perturbed Fluxes	Perturbed Values
P1	$v_1$	2
P2	$v_2$	0.2
P3	$v_3$	0.5

### 3 Results:

## References

- McLean, K. A. P. AND K. B. McAuley (2012) Mathematical modelling of chemical processes-obtaining the best model predictions and parameter estimates using identifiability and estimability procedures, *Can. J. Chem. Eng.* 90.2, 351–366.

Raue, A., ET AL. (2009) Structural and practical identifiability analysis of partially observed dynamical models by exploiting the profile likelihood, *Bioinformatics* 25.15, 1923–1929.