





An Approach for Identifiability of Population Pharmacokinetic-Pharmacodynamic Models

<u>Vittal Shivva^{1*}</u>, Julia Korell^{1,2}, Ian Tucker¹, Stephen Duffull¹

¹School of Pharmacy, University of Otago, Dunedin, New Zealand ²Department of Pharmaceutical Biosciences, Uppsala University, Sweden

*Recipient of University of Otago Postgraduate Scholarship

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Example PK model

- Combined parent-metabolite PK model of ivabradine^{1,2}
- Bradycardiac agent for prevention of myocardial ischemia



• Issues with this model - difficulties in estimating the parameters

¹Duffull et al. (2000). Eur. J. Pharm. Sci. 10(4):285-294; ²Evans et al. (2001). J. Pharmacokin. Pharmacodyn. 28(1):93-105

Identifiability

- <u>Structural identifiability</u>: Whether the parameters in a model have unique solutions given a perfect input-output data³
 - Structurally globally identifiable: All parameters have unique solutions
 - Structurally locally identifiable: One or more parameters have a finite number of alternate solutions
 - Structurally unidentifiable: One or more parameters have an infinite number of alternate solutions
- <u>Deterministic identifiability</u>: Whether the parameters in a model can be estimated precisely given data that contains random noise⁴

³Godfrey *et al.* (1980). *J. Pharmacokin. Biopharm.* 8(6):633-648 ⁴Foo LK and Duffull SB (2011). *Optimal design of PK-PD studies.* Springer US. 175-193

Available approaches

- Structural identifiability analysis:
 - Mathematical approaches
 - Laplace transformation approach
 - Similarity transformation approach
 - Differential algebra
 - Software
 - DAISY⁵
 - GenSSI⁶
- Deterministic identifiability analysis: No special software is available, any optimal design software can be used

⁵Bellu *et al.* (2007). *Comput. Methods Programs Biomed.* 88(1):52-61; ⁶Chis *et al.* (2011). *Bioinformatics.* 27(18):2610-2611

Motivating context

- Structural and deterministic identifiability are not simultaneously assessed
- Formal methods for assessing identifiability of random effects parameters in population models do not exist in the literature

Aim & Objectives

<u>Aim</u>: To develop an informal approach that can serve as a unified method for assessing structural and deterministic identifiability of population PKPD models based on an information theoretic framework

<u>Objectives:</u>

- 1. To develop a criterion for identifiability analysis of models
- 2. To evaluate the criterion for testing identifiability
- 3. To explore the criterion for testing identifiability of random effects parameters in population PK models
- 4. To apply the criterion for identifiability analysis of the practical example PK model

Objective 1 Criterion for identifiability analysis

Fisher Information Matrix

• Structure of a PK model

$$\mathbf{y} = f(D, \boldsymbol{\xi}, \boldsymbol{\theta}) + \boldsymbol{\varepsilon}; \ \boldsymbol{\varepsilon} \sim N(0, \sigma^2)$$

• Sensitivity matrix (Jacobian matrix \mathbf{J}) with first partial derivatives

	$\int \partial f(D,\xi_1,\mathbf{\theta})$		$\underline{\partial f(D,\xi_1,\boldsymbol{\theta})}$
T	$\partial heta_1$	•	$\partial \theta_p$
J =	$\partial f(D,\xi_n,\mathbf{\theta})$	•••	$\partial f(D, \xi_n, \mathbf{\theta})$
	$\partial \theta_1$		$\partial \theta_p$

Variance-covariance matrix

$$\boldsymbol{\Sigma} = \boldsymbol{\sigma}^2 \cdot \mathbf{I}_n \rightarrow \begin{bmatrix} \sigma_1^2 & \cdots & 0 \\ \vdots & \ddots & \vdots \\ 0 & \cdots & \sigma_n^2 \end{bmatrix}$$

• Fisher Information Matrix $(\mathbf{M}_{\mathbf{F}})$ for the fixed effects model $\mathbf{M}_{\mathbf{F}}(D,\xi,\theta,\Sigma) = \mathbf{J}^{\mathrm{T}} \cdot \Sigma^{-1} \cdot \mathbf{J}$

Criterion for identifiability analysis

- Mathematical basis of the criterion determinant of $M_F(|M_F|)$
- Criterion for fixed effects models

$$\forall \boldsymbol{\xi} : |\mathbf{M}_{\mathbf{F}}(D, \boldsymbol{\xi}, \boldsymbol{\theta}, \boldsymbol{\Sigma})| = \infty$$
, where $n > p, \ \boldsymbol{\xi}_i \neq \boldsymbol{\xi}_j$; for all $i \neq j$

• Criterion for mixed effects models

 $\forall \boldsymbol{\xi} : \left| \mathbf{M}_{\mathbf{F}}(D, \boldsymbol{\xi}, \boldsymbol{\theta}, \boldsymbol{\Omega}, \boldsymbol{\Sigma}) \right|_{\lim \sigma^2 \to 0} = \boldsymbol{\Psi}, \text{ where } n > p, \ \boldsymbol{\xi}_i \neq \boldsymbol{\xi}_j \text{ ; for all } i \neq j$ here $0 < \boldsymbol{\Psi} < \infty, \ \boldsymbol{\Psi} = f(\mathbf{V}); \ \mathbf{V} \approx \mathbf{J}^{\mathrm{T}} \cdot \boldsymbol{\Omega} \cdot \mathbf{J} + \boldsymbol{\Sigma}$

Identifiable PK model

Two conditions are needed for identifiability

- log $|\mathbf{M}_{\mathbf{F}}|$ should have continuous relationship with log random noise
- $|\mathbf{M}_{\mathbf{F}}|$ should approach infinity (or non-infinite asymptote for mixed effects models) as noise approaches zero



Objective 2

Evaluation of the criterion for testing identifiability

Methods

- Models tested: One compartment first order input PK models (fixed effects)
 - Bateman model

$$f(D,\xi_j,\mathbf{\theta}) = \frac{D \cdot F \cdot k_a}{V \cdot (k_a - k)} \left(\exp\left(-k \cdot t_j\right) - \exp\left(-k_a \cdot t_j\right) \right)$$
$$k = \frac{CL}{V}$$

Parameters in the model: V, CL, k_a and F

- Dost model

$$f(D,\xi_j,\mathbf{\theta}) = \frac{D \cdot F \cdot k^* \cdot t_j}{V} \left(\exp\left(-k^* \cdot t_j\right) \right)$$

Parameters in the model: V, k^* and F

Methods

- Study design: Generic study design with sampling times 0, 0.25, 0.5, 0.75, 1, 2, 4, 8, 12, 18 and 24 h post dose
- Dose and parameter values:
 - Dose = 100 mg (for all models)
 - V = 20 L, CL = 4 L.h⁻¹, $k_a = 1$ h⁻¹ and F = 1 (Bateman)
 - V = 20 L, $k^* = 0.5$ h⁻¹ and F = 1 (Dost)
- Random noise assumed in the observed data - $\sigma^2 = 0.00001$ to 0.1
- Software: MatlabR2011a

Results



- Full models unidentifiable (discontinuous relationship)
- *F* fixed in the models identifiable (continuous relationship)

Objective 3

Exploration of the criterion for population PK model

Methods

- Structure of the population PK model (mixed effects model)
 Two stage hierarchical models
 - Model for the data (structural model)

$$y_{ij} = f(D_i, \xi_{ij}, \mathbf{\theta_i}) + \varepsilon_{ij} ; \ \varepsilon_{ij} \stackrel{iid}{\sim} N(0, \sigma^2)$$

- Model for heterogeneity (covariate model) $\theta_i = g(\mathbf{Z}_i, \theta_{pop}) \exp(\eta_i); \ \eta_i \stackrel{iid}{\sim} N(0, \Omega)$
- Models tested
 - Bateman & Dost

Methods

- Study design, dose & random noise in the data: as in the fixed effects model
- Parameters & size of the population:
 - Fixed effects: as in the fixed effects models
 - Random effects: log normal variance of 0.1 was assumed for all parameters (only diagonal elements of Ω were considered)
 - Population size: 100 subjects
- Software: Population OPTimal design (POPT)

Bateman model



- Full population model unidentifiable
- Fixed effects *F* was unidentifiable

N.B. Random effects - all parameters were identifiable

Dost model



- Full population model unidentifiable
- Fixed effects F was unidentifiable
- Random effects ω_F^2 was unidentifiable

Objective 4

Application of the criterion for the practical example PK model

Example PK model

Combined parent-metabolite PK model of ivabradine



Oral PK model

- Two linked two compartment parent-metabolite PK model
- Parameters:
 - $CL_{_p}, V_{1_p}, Q_{_p}, V_{2_p}, CL_{_pm}, F_{_pm}, k_{a_p}, F_{_p}, CL_{_m}, V_{1_m}, Q_{_m}, V_{2_m}, k_{a_m}, F_{_m}$
 - Population parameter values for the assessment are from the literature¹
- Study design, dose, random noise and population size

- As described in the simple example models

¹Duffull et al. (2000). Eur. J. Pharm. Sci. 10(4):285-294

Oral PK model



- Full population model unidentifiable
- Fixed effects V_{1_m} and F_p were unidentifiable (comparable to the literature data²)
- N.B. Random effects all parameters were identifiable

²Evans et al. (2001). J. Pharmacokin. Pharmacodyn. 28(1):93-105

Discussion

- The approach was able to assess the identifiability of the simple and practical example PK models
- The approach provides an informal way of assessing the identifiability of random effects parameters in population models
- Random effects parameters may or may not follow the same rule as fixed effects parameters for identifiability
- Assessment of deterministic identifiability is straight forward given the diagonal elements of inverse of $\mathbf{M}_{\mathbf{F}}$

Discussion

- A range of the random noise needs to be tested in assessing identifiability
 - Current assessment used 5 different values for the variance of random noise ranging from 10⁻⁵ to 10⁻¹
- Simple, practical approach and any optimal design software (PFIM, PopED & PopDes) can be used
- This informal approach can serve as a unified method for assessing structural and deterministic identifiability of population PKPD models

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Coagulation Network Model

