Parameter estimation in nonlinear mixed effect models based on ordinary differential equations: an optimal control approach

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Summary. We present a parameter estimation method for nonlinear mixed effect models based on ordinary differential equations (NLME-ODEs). The method presented here aims at regularizing the estimation problem in presence of model misspecifications, practical identifiability issues and unknown initial conditions. For doing so, we define our estimator as the minimizer of a cost function which incorporates a possible gap between the assumed model at the population level and the specific individual dynamic. The cost function computation leads to formulate and solve optimal control problems at the subject level. This control theory approach allows to bypass the need to know or estimate initial conditions for each subject and it regularizes the estimation problem in presence of poorly identifiable parameters. Comparing to maximum likelihood, we show on simulation examples that our method improves estimation accuracy in possibly partially observed systems with unknown initial conditions or poorly identifiable parameters with or without model error. We conclude this work with a real application on antibody concentration data after vaccination against Ebola virus coming from phase 1 trials. We use the estimated model discrepancy at the subject level to analyze the presence of model misspecification.

1. Introduction

ODE models are standard in population dynamics, epidemiology, virology, pharmacokinetics, or genetic regulation networks analysis due to their ability to describe the main mechanisms of interaction between different biological components of complex systems, their evolution in time and to provide reasonable approximations of stochastic dynamics (Perelson et al., 1996; Lavielle and Mentre, 2007; Wakefield and Racine-Poon, 1995; Andraud et al., 2012; Pasin et al., 2019; M. Lavielle and Mentre, 2011; Le et al., 2015; Engl et al., 2009; Wu et al., 2014). Evidence of the relevance of ODEs resides for example in their joint use with control theory methods for the purpose of optimal treatment design (Guo and Sun, 2012; Agusto and Adekunle, 2014; Zhang and Xu, 2016; Pasin et al., 2018; Villain et al., 2019). In cases of experimental designs involving a large number of subjects and limited number of individual measurements, non-linear mixed-effect models may be more relevant than subject-by-subject model to gather information from the whole population while allowing between-individual variability. For example, clinical trials and pharmacokinetics/pharmacodynamics studies...
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often fall into this category M. Lavielle and Mentrevé (2011); Guedj et al. (2007); Huang and Lu (2008); Wang et al. (2014); Prague et al. (2013). Formally, we are interested in a population where the dynamics of the compartments of each subject \( i \in [1, n] \) is modeled by the \( d \)-dimensional ODE:

\[
\begin{align*}
\dot{x}_i(t) &= f_{\theta, b_i}(t, x_i(t), z_i(t)) \\
x_i(0) &= x_{i,0}
\end{align*}
\]

(1.1)

where \( f \) is a \( d \)-dimensional vector field, \( \theta \) is a \( p \)-dimensional parameter, \( b_i \sim N(0, \Psi) \) is a \( q \)-dimensional random effect where \( \Psi \) is a variance-covariance matrix, \( x_{i,0} \) is the initial condition for subject \( i \) belonging to \( \mathbb{R}^d \) and \( z_i \) is a covariate function. We denote \( X_{\theta, b_i, x_{i,0}} \) the solution of (1.1) for a given set \( (\theta, b_i, x_{i,0}) \).

Our goal is to estimate the true population parameters \( (\theta^*, \Psi^*) \) as well as the true subject specific realizations \( \{b^*_i\}_{i \in [1, n]} \) from partial and noisy observations coming from \( n \) subjects and described by the following observational model:

\[
y_{ij} = CX_{\theta^*, b^*_i, x^*_{i,0}}(t_{ij}) + \epsilon_{ij}
\]

where \( t_{ij} \) is the \( j \)-th measurement time-point for the \( i \)-th subject on the observation interval \([0, T]\). Here \( C \) is a \( d_o \times d \) sized observation matrix emphasizing the potentially partially observed nature of the process and \( \epsilon_{ij} \sim \sigma^* \times N(0, I_{d_o}) \) is the measurement error. We also assume only a subset of the true initial condition \( x^*_{i,0} \), denoted \( x^{k*}_{i,0} \), is known, the other ones, denoted \( x^{u*}_{i,0} \), being unknown. For the sake of clarity, we order the state variables as follows: \( x_{i,0} = \left( \left( x^{u*}_{i,0} \right)^T, \left( x^{k*}_{i,0} \right)^T \right)^T \). We denote \( n_i \) the number of observations for the \( i \)-th subject, \( y_i = \{y_{ij}\}_{j \in [1, n_i]} \) its corresponding set of observations and \( y = \{y_i\}_{i \in [1, n]} \) the set of all observations in the population.

Our problem belongs to the class parameter estimation problem in nonlinear mixed effect models. In this context, frequentist methods based on likelihood maximization (via different numerical procedures: Laplace approximation Pinheiro and Bates (1994), Gaussian quadrature Pinheiro and Bates (1994); Lindstrom and Bates (1990); Guedj et al. (2007) or SAEM Kuhn and Lavielle (2005); Lavielle and Mentrevé (2007); Comets et al. (2017)) and Bayesian ones aiming to reconstruct the a posteriori distribution or to derive the maximum a posteriori estimator (via MCMC algorithms Lunn et al. (2000);...
Huang and Dagne (2011); Huang et al. (2010), importance sampling Raftery and Bao (2010), approximation of the asymptotic posterior distribution Prague et al. (2013)) have been proposed. In particular, dedicated methods/softwares using the structure of ODE models have been implemented to increase numerical stability and speed up convergence rate Tornoe et al. (2004), to reduce the computational time Donnet and Samson (2006) or to avoid the repeated model integration and estimation of initial conditions Wang et al. (2014). However, all the preceding methods face similar pitfalls due to specific features of population models based on ODEs (with the exception of Wang et al. (2014)):

(a) They do not account for model misspecification presence, a common feature in ODE models used in biology. Indeed, the ODE modeling process suffers from model inadequacy, understood as the discrepancy between the mean model response and real world process, and residual variability issues, that is subject specific stochastic perturbations or missed elements which disappear by averaging over the whole population Kennedy and O’Hagan (2001). As examples of model inadequacy causes, one can think of ODE models used in epidemiology and virology which are derived by approximations where for instance, interactions are modeled by pairwise products while higher order terms and/or the influence of unknown/unmeasured external factors are neglected Stein et al. (2013). Regarding residual variability, let us remind that biological processes are often stochastic Bowsher and Swain (2012); Komorowski et al. (2013) and the justification of deterministic modeling comes from the approximation of stochastic processes Kurtz (1978); Gillespie (2000); Kampen (1992). Moreover, in the context of population models, new sources of model uncertainties emerge. Firstly, error measurement in covariates \( z_i \) which is not often considered leads to use a proxy function \( \hat{z}_i \) instead of \( z_i \) Huang and Dagne (2011). Secondly, the sequential nature of most inference methods leads to estimate \( \{b^*_i\}_{i \in [1,n]} \) based on an approximation \( \hat{\theta} \) instead of the true population parameter value \( \theta^* \). Thus, the structure of mixed-effect models spread measurement uncertainty into the mechanistic model structure during the estimation. It turns classical statistical uncertainties into model error causes. Estimation of \( \theta^* \), \( \Psi^* \) and \( \{b^*_i\}_{i \in [1,n]} \) has to be done with model misspecification presence although
it is known to dramatically impair the accuracy of methods which do not take into
account potential modeling error Brynjarsdottir and O’Hagan (2014); Kirk et al.
(2016).

(b) They have to estimate or make assumptions on $x_{i,0}^u$ values. In ODE models, the
initial conditions are generally nuisance parameters in the sense that knowing their
values does not bring answers to the scientific questions which motivate the model
construction but the estimation of the relevant parameters requires $x_{i,0}^u$ inference as
well. For example partially observed compartmental models used in pharmacoki-
netics/pharmacodynamics often involve unknown initial conditions which needs to
be inferred to estimate the transmission rates between compartments which are the
true parameters of interest. Unknown initial conditions imply either: assumptions
on their values M. Lavielle and Mentre (2011); Guedj et al. (2007); Thiebaut et al.
(2014), another potential cause of model misspecifications, or the need to estimate
them Huang et al. (2006); Huang and Lu (2008) which increases the optimization
problem dimension and degrades estimation accuracy due to covariance effect
between $(\theta^*, \Psi^*)$ and $x_{i,0}^u$ estimate.

(c) They can face accuracy degradation when the inverse problem of parameter esti-
mation is ill-posed Engl et al. (2009); Stuart (2010) due to practical identifiability
issues. Ill-posedness in ODE models is often due to the geometry induced by the
mapping $(\theta, b_i, x_{i,0}) \mapsto CX_{\theta,b_i,x_{i,0}}$, where there can be a small number of relevant
directions of variation skewed from the original parameter axes Gutenkunst et al.
(2007); Transtrum et al. (2011, 2015); Leary et al. (2015). This problem, called
sloppiness, often appears in ODE models used in biology Gutenkunst et al. (2007);
Leary et al. (2015) and leads to an ill-conditioned Fisher Information Matrix. For
maximum likelihood estimators this is a cause for high variance due to the Cramér-
Rao bound. For Bayesian inference, it leads to a nearly singular asymptotic a pos-
teriori distribution because of Bernstein–von Mises theorem (see Campbell (2007)
for the computational induced problems). Despite this problem is in part mitigated
by the population approach which merges different subjects for estimating $(\theta^*, \Psi^*)$
and uses distribution of $b_i | \Psi$ as prior at the subject level Lavielle and Aarons
Mélanie Prague (2015), estimation accuracy can benefit from the use of regularization techniques for the inverse problem.

These specific features of ODE-based population models limit the amount of information classic approaches can extract for estimation purposes from observations no matter their qualities or abundances. This advocates for the development of new estimation procedures. Approximate methods Varah (1982); Ramsay et al. (2007); Clairon and Brunel (2018) have already proven to be useful for ODE models facing these issues with observations coming from one subject. These approaches rely on an approximation of the solution of the original ODE (1.1) which is expected to have a smoother dependence with respect to the parameters and to relax the constraint imposed by the model during the estimation process. The interest of such approximations is twofold. Firstly they produce estimators with a better conditioned variance matrix comparing to classic likelihood based approaches and they reduce the effect of model error on estimator accuracy. Secondly, some of these approximations bypass the need to estimate initial conditions Ramsay et al. (2007); Clairon (2020). In this work, we generalize one of these approaches to population models by developing a new estimation method specific to NLME-ODEs aiming to integrate such approximations to mitigate the effect of model misspecification and poorly identifiable parameter on estimation accuracy, while avoiding the need to estimate $x_{i,0}^*$. We propose here a nested estimation procedure where population parameters $(\theta^*, \Psi^*, \sigma^*)$ are estimated through the maximization of an outer criterion. This requires in turn an estimator for the $\{b^*_i\}_{i\in[1,n]}$ obtained through the repeated optimization of inner criteria. We consider that the actual dynamic for each subject is described by a perturbed version of the ODE (1.1) where the added perturbation captures different sources of errors at the subject level Brynjarsdottir and O’Hagan (2014); Tuo and Wu (2015). We control the magnitude of the acceptable perturbations by defining the inner criteria through a cost function balancing the two contrary objectives of fidelity to the observations and to the original model: to this end, we introduce a model discrepancy penalization term. The practical computation of the $\{b^*_i\}_{i\in[1,n]}$ estimators require to solve optimal control problems Clarke (2013); Kirk (1998); Sontag (1998) known as tracking problems. This is done using a method inspired by Cimen...
and Banks (2004b,a) based on pseudo-linear representation and Linear-Quadratic theory. In addition, our method does not need to estimate $x_{t=0}^{u*}$. Nevertheless, it can provide an estimator of $x_{t=0}^{u*}$ as a direct byproduct of structural parameters estimation with no additional computational costs.

In section 2, we present the estimation method and derive the inner and outer criteria as well as an estimator of the asymptotic Variance-Covariance matrix for the estimators of $(\theta^*, \Psi^*)$. In section 3, we present the optimal control problems related to the different criteria as well as the algorithms used to solve them. In section 4, we compare our approach with classic maximum likelihood in simulations. We then proceed to the real data analysis coming from clinical studies and a model of the antibody concentration dynamics following immunization with an Ebola vaccine in East African participants Pasin et al. (2019). Section 6 concludes and discuss further applications and extensions of the method.

2. Construction of the estimator: definition of the inner and outer criteria

From now on, we use the following Choleski decomposition $\sigma^2\Psi^{-1} = \Delta^T\Delta$ (or equivalently $\Psi = \sigma^2(\Delta^T\Delta)^{-1}$) and the parametrization $(\theta, \Delta, \sigma)$ instead of $(\theta, \Psi, \sigma)$. This parametrization will allow us to enforce positiveness and symmetry of $\Psi$ and to derive an explicit estimator of $\sigma$ given a value for $(\theta, \Delta)$. The norm $\|\cdot\|_2$ will denote the classic Euclidean one defined by $\|b\|_2 = \sqrt{b^Tb}$. Similarly as in the Expectation-Maximization (EM) algorithm, we estimate the population and individual parameters via a nested procedure:

- Estimation of $\hat{b}_i := \hat{b}_i(\theta, \Delta)$ for each subject $i$ by minimization of the inner criterion $g_i$, a modified version of the log joint-likelihood function of the data and the random effects.

- Estimation of $(\theta, \Delta, \sigma)$ via the maximization of an outer criterion defined as an approximation of the profiled joint distribution of $(\theta, \Delta, \sigma, b)$ with respect to $b$ and denoted $G(\theta, \Delta, \sigma)$. 
2.1 Inner criteria

In this section, we describe the procedure used to estimate the $q$-dimensional random effects $\{b_i^s\}_{i\in[1,n]}$ for a given $(\theta, \Delta, \sigma)$ value. A straightforward approach would be to look for the minimum of the log joint-likelihood function of the data and $\{b_i, x_{0,i}^u\}$. However, we want to:

(a) avoid estimation of unknown initial conditions,
(b) allow for each subject an acceptable departure from the assumed model at the population level to take into account possible model misspecifications.

To solve the first point, we define our estimator as the maximizer of the joint conditional likelihood $P(y_1, b_{i} \mid x_{0,i}^u, \theta, \Delta, \sigma)$ profiled on the unknown initial condition. Since

$$P(y_1, b_{i} \mid x_{0,i}^u, \theta, \Delta, \sigma) = \prod_i P(y_{ij} \mid b_{i}, \theta, \Delta, \sigma) = \prod_j (2\pi)^{-d_{x}/2} e^{-0.5\|C X_{\theta,b_i,x_{0,i}}(t_{ij}) - y_{ij}\|^2_{\sigma}^2},$$

by using $P(y_1 \mid b_{i}, \theta, \Delta, \sigma) = (2\pi)^{-q/2} |\Psi|^{-1/2} e^{-0.5\|C X_{\theta,b_i,x_{0,i}}(t_{ij}) - y_{ij}\|^2_{\sigma}^2}$, and $2q |\Psi|^{-1} = |\Delta|^2$, a straightforward mixed-effect estimator would be $\hat{b}_i = \arg\min_{\theta,b_i,x_{0,i}} \left\{ \sum_j \|C X_{\theta,b_i,x_{0,i}}(t_{ij}) - y_{ij}\|^2_{\sigma} + \|\Delta b_i\|^2_{\sigma} \right\}$ that is, the classic maximum likelihood criteria profiled on $x_{0,i}^u$. Concerning the second point, we allow perturbations comparing to the original model, by assuming that the dynamic of each subject $i$ follows a perturbed version of ODE (1.1):

$$\begin{align*}
\dot{x}_i(t) &= f_{\theta,b_i}(t, x_i(t), z_i(t)) + Bu_i(t) \\
x_i(0) &= x_{i,0}
\end{align*}$$

(2.1)

with the addition of the forcing term $t \mapsto Bu_i(t)$ with $B$ a $d \times d_u$ matrix and $u_i$ a function in $L^2([0,T], \mathbb{R}^{d_u})$. We denote $X_{\theta,b_i,x_{i,0},u_i}$ the solution of this new ODE (2.1).

However, to ensure the possible perturbation remains small, we replace the data fitting criterion $\sum_j \|C X_{\theta,b_i,x_{0,i}}(t_{ij}) - y_{ij}\|^2_{\sigma}$ by $\min_{u_i} C_i(b_i, x_{i,0}, u_i \mid \theta, U)$ where $C_i(b_i, x_{i,0}, u_i \mid \theta, U) = \sum_j \|C X_{\theta,b_i,x_{0,i},u_i}(t_{ij}) - y_{ij}\|^2_{\sigma} + \|u_i\|_{L^2}^2$, and $\|u_i\|_{L^2}^2 = \int_0^T u_i(t)^T U u_i(t) dt$ is the weighted Euclidean norm. Therefore the magnitude of the allowed perturbations is controlled by a positive definite and symmetric weighting matrix $U$. Finally, we obtain:

$$\hat{b}_i(\theta, \Delta) := \arg\min_{b_i} g_i(b_i \mid \theta, \Delta, U)$$

(2.2)
where:
\[ g_i(b_i \mid \theta, \Delta, U) = \min_{x_{0,i}} \left\{ \min_{u_i} \mathcal{C}_i(b_i, x_{i,0}, u_i \mid \theta, U) + \| \Delta b_i \|_2^2 \right\}. \]

This requires to solve the infinite dimensional optimization problem \( \min_{u_i} \mathcal{C}_i(b_i, x_{i,0}, u_i \mid \theta, U) \) in \( L^2 ([0, T], \mathbb{R}^{d_u}) \). This problem belongs to the field of optimal control theory for which dedicated approaches have been developed to solve them Sontag (1998); Aliyu (2011); Clarke (2013). Here we use the same method as in Clairon (2020), which ensures the existence and uniqueness of the solution and provides a computationally efficient way to find it for linear ODEs. This method can be extended to non-linear ODEs through an iterative procedure where the original problem is replaced by a sequence of problems involving only linear ODEs. In addition, the methods from Clairon (2020) presents the advantage of formulating \( \min_{u_i} \mathcal{C}_i(b_i, x_{i,0}, u_i \mid \theta, U) \) as a quadratic form (or a sequence of quadratic forms) with respect to \( x_{0,i} \). Thus, the computation of \( \min_{x_{0,i}} \{ \min_{u_i} \mathcal{C}_i(b_i, x_{i,0}, u_i \mid \theta, U) \} \) does not add any computational complexity comparing to \( \min_{u_i} \mathcal{C}_i(b_i, x_{i,0}, u_i \mid \theta, U) \).

The control corresponding to the solution of \( \min_{x_{0,i}} \{ \min_{u_i} \mathcal{C}_i(b_i, x_{i,0}, u_i \mid \theta, U) \} \) is named optimal control and denoted \( u_{i,\theta,b_i} \). The corresponding solution of (2.1) is denoted \( X_{\theta,b_i} \) and named optimal trajectory. In particular, \( X_{\theta,b_i} \) and \( u_{i,\theta,b_i} \) are respectively the subject specific state variable and perturbation such that:

\[ g_i(b_i \mid \theta, \Delta, U) = \sum_j \| C X_{\theta,b_i}(t_{ij}) - y_{ij} \|_2^2 + \| u_{i,\theta,b_i} \|_{U,L^2}^2 + \| \Delta b_i \|_2^2. \]  \tag{2.3} 

To incorporate possible model errors in the estimation process, e.g. due to subject specific exogenous perturbations, \( X_{\theta,b_i} \) is now assumed to be the subject specific regression function, defined as the state-variable which needs the smallest perturbation in order to get close to the observations. The numerical procedure to derive \( X_{\theta,b_i} \) and \( g_i \) is presented in section 3.

**Remark 2.1.** The definition of the optimal control \( u_{i,\theta,b_i} \) has an interpretation in terms of Bayesian inference in an infinite dimensional space. According to Dashti et al. (2013) (theorem 3.5 and Corollary 3.10), \( u_{i,\theta,b_i} \) is a maximum a posteriori estimator where the chosen prior measure is a centered Gaussian random field with the covariance operator determined by \( U \). This link can be fruitful to import tools coming from
deterministic control theory to solve statistical problem formalized in functional spaces.

2.2. Outer criteria definition

We focus in this section on population parameter estimation. Classic approaches rely on maximum a posteriori distribution or the likelihood of the observations in which they get rid of the unknown subject specific parameters by taking the mean value of $P[\theta, \Delta, \sigma, b | y]$ or $P[y | \theta, \Delta, \sigma, b]$, $E_b[P[\theta, \Delta, \sigma, b | y]]$ or $E_b[P[y | \theta, \Delta, \sigma, b]]$ respectively, as outer criteria. This generally requires the numerical approximation of integrals of possibly high dimensions (the same as $b$), a source of approximation and computational issues [Pinheiro and Bates (1994)]. To avoid this, we consider the random effects as nuisance parameters and rely on a classic profiling approach for $(\theta^*, \Delta^*)$ estimation [Murphy and der Vaart (2000)]. Instead of taking the mean, we rely on the maximal value of the joint distribution with respect to $b$. We consider the cost function $\max_b P[\theta, \Delta, \sigma, b | y]$ (or equivalently $\max_b \ln P[\theta, \Delta, \sigma, b | y]$). Bayes formula gives us $P[\theta, \Delta, \sigma, b | y] \propto P[y | \theta, \Delta, \sigma, b] P[\theta, \Delta, \sigma, b]$. Since $P[\theta, \Delta, \sigma, b] = P[b | \theta, \Delta, \sigma] P[\theta, \Delta]$, we get $P[\theta, \Delta, \sigma, b | y] \propto (\prod_i P[y_i | \theta, \Delta, \sigma, b_i] P[b_i | \theta, \Delta, \sigma]) P[\theta, \Delta]$ by conditional independence of subject by subject observations and subject specific parameters. It follows that $\max_b \ln P[\theta, \Delta, \sigma, b | y] \propto \sum_i \max_b (\ln P[y_i | \theta, \Delta, \sigma, b_i] + \ln P[b_i | \theta, \Delta, \sigma]) + \ln P[\theta, \Delta]$. From now on we will use the estimate (2.2) of the previous section to construct a suitable approximation of

$$G^{(1)}(\theta, \Delta, \sigma | y) = \sum_i \max_{b_i} \left(\ln P[y_i | \theta, \Delta, \sigma, b_i] + \ln P[b_i | \theta, \Delta, \sigma]\right) + \ln P[\theta, \Delta]$$

as our criteria to estimate population parameters. As said in the previous section, we define the optimal trajectory $X_{\theta,b}$ as the regression function for each subject. Therefore, we approximate $P[y_i | \theta, \Delta, \sigma, b_i]$ by $\tilde{P}[y_i | \theta, \Delta, \sigma, b_i] \simeq \prod_j (2\pi)^{-d^p/2} \sigma^{-d^p} e^{-0.5\|\mathcal{X}_{\theta,b,(t_i)} - y_i\|^2/\sigma^2}$. By using the previous section computations, we get $\arg \max_{b_i} \left(\ln \tilde{P}[y_i | \theta, \Delta, \sigma, b_i] + \ln P[b_i | \theta, \Delta, \sigma]\right) = \arg \max_{b_i} \left(\sum_j \|C\mathcal{X}_{\theta,b_i} - y_{ij}\|^2_2 + \|\Delta b_i\|^2_2\right)$. We regularize this estimation problem by approximating it via the addition of the Tikhonov penalization term on perturbation magnitude $\|\mathcal{U}_{\theta,b_i}\|^2_{U,L^2}$, thus $\arg \max_{b_i} \left(\ln \tilde{P}[y_i | \theta, \Delta, \sigma, b_i] + \ln P[b_i | \theta, \Delta, \sigma]\right) \simeq \arg \max_{b_i} \left(\ln \tilde{P}[y_i | \theta, \Delta, \sigma, b_i] + \ln P[b_i | \theta, \Delta, \sigma]\right)$.
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arg max_i g_i(b_i | θ, Δ, U) = ̂b_i(θ, Δ) by using definition (2.3). Also, we use

\[ G^{(2)}[θ, Δ, σ | y] = \sum_{i} \left( \ln \tilde{P}\left[y_i | θ, Δ, σ, ̂b_i(θ, Δ)\right] + \ln P\left[ ̂b_i(θ, Δ) | θ, Δ, σ\right] \right) + \ln P[θ, Δ] \]

as an approximation of \( G^{(1)} \). By replacing \( \tilde{P}[y_i | θ, Δ, σ, b_i] \) and \( P[b_i | θ, Δ, σ] \) by their values, we notice that arg max_{(θ, Δ)} \{ G^{(2)}[θ, Δ, σ | y] \} = arg max_{(θ, Δ)} \{ G^{(3)}[θ, Δ, σ | y] \}

for every \( σ > 0 \) where

\[
G^{(3)}[θ, Δ, σ | y] = -\frac{1}{2σ^2} \sum_i \left( \sum_j \left\| C_{X_{θ, ̂b_i(θ, Δ)}(t_{ij})} - y_{ij} \right\|_2^2 + \left\| Δ ̂b_i(θ, Δ) \right\|_2^2 \right) \\
- 0.5 (d^0 \sum_i n_i + qn) \ln (σ^2) + 0.5n \ln (|Δ T Δ|) + \ln P[θ, Δ].
\]

Moreover, for each \( (θ, Δ) \), the maximizer in \( σ^2 \) of \( G^{(3)} \) has a closed form expression:

\[
σ^2(θ, Δ) = \frac{1}{(d^0 \sum_i n_i + qn)} \sum_i \left( \sum_j \left\| C_{X_{θ, ̂b_i(θ, Δ)}(t_{ij})} - y_{ij} \right\|_2^2 + \left\| Δ ̂b_i(θ, Δ) \right\|_2^2 \right) 
\]

(2.4)

By using the expression of \( σ^2(θ, Δ) \) given by equation (2.4), we get that arg max_{(θ, Δ)} max_{σ^2} G^{(3)}(θ, Δ, σ | y) = arg max_{(θ, Δ)} \{ G[θ, Δ | y] \} where:

\[
G[θ, Δ | y] = -0.5 \left( d^0 \sum_i n_i + qn \right) \ln (σ^2(θ, Δ)) + n \ln |Δ| + \ln P[θ, Δ].
\]

Thus we can profile \( G^{(3)} \) on sigma \( σ^2 \) and define our estimator as:

\[
( ̂θ, ̂Δ ) = \arg \max_{(θ, Δ)} \{ G[θ, Δ | y] \}
\]

(2.5)

to reduce the optimization problem dimension and focus on the structural parameters.

An estimator of \( σ^* \) is obtained from there by computing \( σ^2( ̂θ, ̂Δ ) \) given by equation (2.4). The details of the outer criteria derivation are left in appendix A.

2.3. An asymptotic Variance-Covariance matrix estimator of population parameters

In this section, we derive an estimator of the asymptotic variance of \( ( ̂θ, ̂Δ ) \). We highlight that in practice the matrix \( Δ \) is parametrized by a vector \( δ \) of dimension \( q' \), i.e \( Δ := Δ(δ) \).

We give here a variance estimator of \( ( ̂θ, ̂δ ) \). The variance of \( ̂Δ \) can be obtained using
classic delta-methods (see van der Vaart (1998) chapter 3). First of all, we drop the vector field dependence in \( z \) and we introduce the function:

\[
h(b_i, \theta, \Delta, y_1) = \|\Delta b_i\|_2^2 + \sum_j \|C_X\theta, b_i(t_{ij}) - y_{ij}\|_2^2
\]

in order to present sufficient conditions ensuring our estimator is asymptotically normal:

(a) the function \( \tilde{G}[\theta, \Delta(\delta)] = -0.5(d^p \mathbb{E}[n_1] + q) \ln \left( \lim_{n \to \infty} \frac{1}{n} \sum_{i=1}^{n} \mathbb{E}[h(\tilde{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i)] \right) \) + \ln |\Delta(\delta)| has a well separated minimum \( (\bar{\theta}, \bar{\delta}) \) belonging to the interior of a compact \( \Theta \times \Omega \subset \mathbb{R}^{d \times q} \); the true initial conditions \( \{x_{0,i}^*\}_{i \in [1, n]} \in [1, n] \) have finite variance and either

(i) they are i.i.d,

(ii) for \( \nu = 0 \) and \( \nu = 1 \):

\[
\lim_{n \to \infty} \frac{1}{(V^{(\nu)})^2} \mathbb{E} \left[ \sum_{i=1}^{n} \left( \tilde{h}^{(\nu)}(y_1) - \mathbb{E} \left[ \tilde{h}^{(\nu)}(y_1) \right] \right)^2 \right]^{1/2} \left( \mathbb{E}[\tilde{h}(y_1)] - \mathbb{E}[\tilde{h}(y_1)] \right) = 0
\]

where \( \tilde{h}^{(\nu)}(y_1) = \frac{d^{(\nu)}}{d^{(\nu)}(\tilde{\theta}, \tilde{\delta})}(\tilde{b}(\tilde{\theta}, \Delta(\tilde{\delta})), \tilde{\theta}, \Delta(\tilde{\delta}), y_1) \) and \( V^{(\nu)} = \sqrt{\sum_i \text{Var}(\tilde{h}^{(\nu)}(y_1))} \),

(c) the subject specific number of observations \( \{n_i\}_{i \in [1, n]} \) are i.i.d and uniformly bounded,

(d) for all possibles values \( (\theta, b_i) \), the solution \( X_{\theta, b_i, x_{0,i}} \) belongs to a compact \( \chi \) of \( \mathbb{R}^d \), and for all \( (t, \theta, x) \), the mapping \( b_i \mapsto f_{\theta, b_i}(t, x) \) has a compact support \( \Theta_b \),

(e) \( (\theta, b_i, t, x) \mapsto f_{\theta, b_i}(t, x) \) belongs to \( C^1(\Theta \times \Theta_b \times [0, T] \times \chi, \mathbb{R}^d) \),

(f) the matrices \( \frac{\partial^2}{\partial b_i^2} f_{\theta, b_i}(\tilde{b}(\tilde{\theta}, \Delta(\tilde{\delta})), \tilde{\theta}, \Delta(\tilde{\delta}), U) \) and \( \frac{\partial^2}{\partial x_{0,i}^2} f_{\theta, b_i}(\tilde{b}(\tilde{\theta}, \Delta(\tilde{\delta})), \tilde{\theta}, \Delta(\tilde{\delta}), U) \) are of full rank almost surely for every sequence \( y_1 \),

(g) there is a neighborhood \( \Theta_{\tilde{\theta}} \) of \( \tilde{\theta} \) such that \( (\theta, b_i, t, x) \mapsto f_{\theta, b_i}(t, x) \in C^5(\Theta_{\tilde{\theta}} \times \Theta_b \times [0, T] \times \chi, \mathbb{R}^d) \).

Conditions 1-4 are used to derive the consistency of our estimator toward \( (\bar{\theta}, \bar{\delta}) \) by following classic steps for M-estimator by proving 1/the uniform convergence of our stochastic cost function to a deterministic one, 2/the existence of a well-separated minimum for this deterministic function (van der Vaart (1998) chapter 5). Conditions 6-7 ensures that our cost function is asymptotically smooth enough in the vicinity of \( (\bar{\theta}, \bar{\delta}) \) to proceed to a Taylor expansion and transfer the regularity of the cost function to the asymptotic
behavior of $\sqrt{n}(\tilde{\theta} - \bar{\theta}, \tilde{\delta} - \bar{\delta})$. Less restrictive conditions can be established under which our estimator is still asymptotically normal, in particular regarding $f_{\theta,b}$, regularity with respect to $t$. Also, we emphasize that the second assumption does not require to know the distribution of the $x_{0,i}^*$. 

**Theorem 2.1.** Under conditions 1-7, there is a model dependent lower bound $\lambda$ such that if $\|U\|_2 > \lambda$ then the estimator $(\tilde{\theta}, \tilde{\delta})$ is asymptotically normal and:

$$\sqrt{n}(\tilde{\theta} - \bar{\theta}, \tilde{\delta} - \bar{\delta}) \xrightarrow{d} N\left(0, A(\bar{\theta}, \bar{\delta})^{-1}B(\bar{\theta}, \bar{\delta})\left(A(\bar{\theta}, \bar{\delta})^{-1}\right)^T\right)$$

where $A(\bar{\theta}, \bar{\delta}) = \lim_n \frac{1}{n} \sum_{i=1}^n \left[\frac{\partial J(\bar{\theta}, \bar{\delta}, y_i)}{\partial(\theta, \delta)}\right]$, $B(\bar{\theta}, \bar{\delta}) = \lim_n \frac{1}{n} \left[\sum_i J(\bar{\theta}, \bar{\delta}, y_i)J(\bar{\theta}, \bar{\delta}, y_i)^T\right]$ and the vector valued function $\tilde{J}(\theta, \delta, y_i) = \left(\tilde{J}_\theta(\theta, \delta, y_i), \tilde{J}_\delta(\theta, \delta, y_i)\right)$ is given by:

$$\tilde{J}_\theta(\theta, \delta, y_i) = \frac{d}{d\theta} h(\hat{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i)$$

$$\tilde{J}_\delta(\theta, \delta, y_i) = \frac{d}{d\delta} h(\hat{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i) - \frac{2}{d^2 \sum_{i=1}^n \frac{\partial^2 J(\hat{\theta}, \hat{\delta}, y_i)}{\partial\delta^2}} Tr\left(\Delta(\delta)^{-1} \frac{\partial^2 \Delta(\delta)}{\partial\delta^2} \right) h(\hat{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i).$$

The proof is left in appendix C. The practical interest of this theorem is to give an estimator of Variance-Covariance:

$$V(\tilde{\theta}, \tilde{\delta}) \simeq \hat{A}(\tilde{\theta}, \tilde{\delta})^{-1} \hat{B}(\tilde{\theta}, \tilde{\delta}) \left(\hat{A}(\tilde{\theta}, \tilde{\delta})^{-1}\right)^T / n.$$ 

In the last equation the matrices $\hat{A}$ and $\hat{B}$ are defined by:

$$\left\{\begin{array}{c}
\hat{A}(\tilde{\theta}, \tilde{\delta}) = \frac{1}{n} \sum_{i=1}^n \frac{\partial J(\tilde{\theta}, \tilde{\delta}, y_i)}{\partial(\theta, \delta)} \\
\hat{B}(\tilde{\theta}, \tilde{\delta}) = \frac{1}{n} \sum_{i=1}^n J(\tilde{\theta}, \tilde{\delta}, y_i)J(\tilde{\theta}, \tilde{\delta}, y_i)^T
\end{array}\right.$$ 

where the $(p + q)$ components of the vector valued function $J$ for $1 \leq k \leq p$ are given by

$$J_k(\theta, \delta, y_i) = \frac{d}{d\theta_k} h(\hat{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i)$$

and for $p + 1 \leq k \leq p + q$ by

$$J_k(\theta, \delta, y_i) = \frac{d}{d\delta_k} h(\hat{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i) - \frac{2n}{d^2 \sum_{i=1}^n \frac{\partial^2 J(\tilde{\theta}, \tilde{\delta}, y_i)}{\partial\delta^2}} Tr\left(\Delta(\delta)^{-1} \frac{\partial^2 \Delta(\delta)}{\partial\delta^2} \right) h(\hat{b}(\theta, \Delta(\delta)), \theta, \Delta(\delta), y_i).$$

Now that we have proven the existence of the variance matrix $V(\theta^*, \delta^*)$ such that $\tilde{\delta} - \delta^* \xrightarrow{d} N\left(0, V(\theta^*, \delta^*)\right)$, we can use the Delta method to derive the asymptotic normality of the
original matrix $\Psi(\hat{\delta}) = \sigma^2 \left( \Delta(\hat{\delta})^T \Delta(\hat{\delta}) \right)^{-1}$ as well as an estimator of its asymptotic variance. In the case of a diagonal matrix $\Psi$, composed of the elements $(\Psi_1^2, \ldots, \Psi_q^2)$ and of the parametrization $\Delta(\delta) = \begin{pmatrix} e^{\delta_1} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & e^{\delta_q} \end{pmatrix}$ used in section 4, we derive:

$$\begin{pmatrix} \Psi_1(\hat{\delta}) \\ \vdots \\ \Psi_q(\hat{\delta}) \end{pmatrix} - \begin{pmatrix} \Psi_1(\delta^*) \\ \vdots \\ \Psi_q(\delta^*) \end{pmatrix} \rightsquigarrow N \left( \begin{pmatrix} 0 \\ \sigma^2 \begin{pmatrix} e^{-\delta_1} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & e^{-\delta_q} \end{pmatrix} \end{pmatrix} V(\theta^*, \delta^*) \begin{pmatrix} e^{-\delta_1} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & e^{-\delta_q} \end{pmatrix} \right).$$

**Remark 2.2.** The previous theorem 2.1 states that we retrieve a parametric convergence rate despite a number of nuisance parameter increasing with the number of subjects. We avoid the pitfall described in [Sartori (2003)] for profiled methods, thanks to the i.i.d structure of the nuisance parameters. This allows us to prevent bias accumulation for score functions among subjects by using the central limit theorem. Our estimator shares similarities with conditional maximum likelihood ones and our proof for asymptotic normality follows similar steps as in [Andersen (1970)] since the $\{b_i\}_{i \in [1,n]}$ are i.i.d.

### 3. Numerical procedure for $\bar{u}_{i, \theta, b_i}$, $\bar{X}_{\theta, b_i}$ and $g_i$ computation

In this section we explain how to get numerical approximations for $\min_{x_i^0} \{ \min_{u_i} C_i(b_i, x_{i,0}, u_i \mid \theta, U) \}$ and $\bar{u}_{i, \theta, b_i}$, which are then used to evaluate $\bar{X}_{\theta, b_i}$ and $g_i$ defined by equation (2.3). Firstly we approximate $g_i$ with a special type of discrete time optimal control problem, known as ‘tracking problem’. Secondly we adapt the method proposed by [Cimen and Banks (2004a,b)] to solve it.

#### 3.1. $g_i$ expression as an optimal control problem

We introduce a pseudo-linear version of model (2.1):

$$\begin{cases} \dot{x}_i(t) = A_{\theta, b_i}(t, x_i(t), z_i(t)) x_i(t) + r_{\theta, b_i}(t, z_i(t)) + Bu_i(t) \\ x_i(0) = x_{i,0} \end{cases} \quad (3.1)$$
where \(A_{\theta,b_i}(\text{resp. } r_{\theta,b_i})\) is a \(d \times d\) sized matrix (resp. \(d\) dimensional vector) valued function, linked to the original model by the relation
\[
A_{\theta,b_i}(t, x_i(t), z_i(t)) x_i(t) + r_{\theta,b_i}(t, z_i(t)) = f_{\theta,b_i}(t, x_i(t), z_i(t)).
\]
This formulation is crucial for solving the optimal control problem defining our estimators in a computationally efficient way. Linear models already fit in this formalism with \(A_{\theta,b_i}(t,z_i(t)) := A_{\theta,b_i}(t,x_i(t),z_i(t))\).

For nonlinear models, the pseudo-linear representation is not unique but always exists [Cimen and Banks (2004b)](in order to exploit this non-uniqueness as an additional degree of freedom, see [Cimen (2008) section 6]).

We consider a discretized version of the perturbed ODE (2.1) to proceed to parametric estimation:

\[
\begin{cases}
  x_i(t_{k+1}^d) = (I_d + \Delta_k A_{\theta,b_i}(t_k^d, x_i(t_k^d), z_i(t_k^d))) x_i(t_k^d) + \Delta_k r_{\theta,b_i}(t_k^d, z_i(t_k^d)) + B \Delta_k u_i(t_k^d) \\
x_i(0) = x_{i,0}
\end{cases}
\]

(3.2)

where the discretization is made at \(K_i + 1\) time points \(\{t_k^d\}_{0 \leq k \leq K_i}\), with \(t_0^d = 0\) and \(t_{K_i}^d = t_{in_i}\). This set contains the observations time points i.e. \(\{t_{ij}\}_{0 \leq j \leq n_i} \subset \{t_k^d\}_{0 \leq k \leq K_i}\), but can be bigger and patient specific, allowing to accurately approximate \(X_{\theta,b_i,x_{i,0}}\) even when the observations are sparse on \([0, T]\). We define:

- \(\Delta_k = t_{k+1}^d - t_k^d\), the mesh size between two discretization time-points,
- \(u_i^d\) the set of discrete values taken by the control at each time step i.e. \(u_i^d = (u(t_k^d), \ldots, u(t_{K_i-1}^d))\),
- \(w_k = 1_{\exists t_{ij} = t_k^d}/(t_{k+1}^d - t_k^d)\) i.e. \(w_k\) is equal to \(1/(t_{k+1}^d - t_k^d)\) if \(t_k^d\) corresponds to an observation time \(t_{ij}\), otherwise \(w_k = 0\),
- \(y_k^d = y_{ij}\) if \(t_k^d = t_{ij}\), \(0\) otherwise,
- \(X_{\theta,b_i,x_{i,0},u_i^d}\) the solution of (3.2).

The weights \(w_k\) and the set of extended data \(\{y_k^d\}\) are introduced to have a vector of observations with the same length as \(\{t_k^d\}_{0 \leq k \leq K_i}\). We now introduce the discretized
version of the cost $C_i$ to be minimized:

$$C^d_i(b_i, x_{i,0}, u^d_i | \theta, U) = \sum_{j=0}^{n_i} \left\| CX^d_{\theta,b_i,x_{i,0},u^d_i}(t_{ij}) - y_i \right\|_2^2 + \sum_{k=0}^{K_i-1} \Delta_k u_i(t_k)^T U u_i(t_k) + \sum_{k=0}^{K_i-1} \Delta_k \left( \left\| CX^d_{\theta,b_i,x_{i,0},u^d_i}(t_{ik}) - y^d_i \right\|_2^2 w_k + u_i(t_k)^T U u_i(t_k) \right).$$

such that our inner criteria $g_i$ can be approximated by:

$$g_i(b_i | \theta, \Delta, U) \simeq \min_{x_{\theta,b_i}} \min_{u^d_i} C^d_i(b_i, x_{i,0}, u^d_i | \theta, U) + \| \Delta b_i \|_2^2.$$

The solution of this discrete control problem will be denoted $\pi^d_{i,\theta,b_i}$, and the related optimal trajectory $X^d_{\theta,b_i}$: they will be used as numerical approximations of $\pi_{i,\theta,b_i}$ and $X_{\theta,b_i}$ respectively.

### 3.2. Numerical methods for solving the tracking problem

We present how to numerically obtain $\min_{x_{\theta,b_i}} \min_{u^d_i} C^d_i(b_i, x_{i,0}, u^d_i | \theta, U)$ as well as the corresponding minimizer $\pi^d_{i,\theta,b_i}$. We start with linear ODE models (section 3.2.1), then we consider nonlinear models (section 3.2.2).

#### 3.2.1. Linear models

Here, we suppose $A_{\theta,b_i}(t, z_i(t)) := A_{\theta,b_i}(t, x_i(t))$ in model (1.1), for the sake of clarity we drop the dependence of $A_{\theta,b_i}$ and $r_{\theta,b_i}$ in $z_i$. For a given set $(\theta, b_i, x_{i,0})$, Linear-Quadratic theory ensures the existence and uniqueness of the optimal control $\pi^d_{i,\theta,b_i}$ and that $\min_{x_{\theta,b_i}} \min_{u^d_i} C^d_i(b_i, x_{i,0}, u^d_i | \theta, U)$ can be computed by solving a discrete final value problem, called the Riccati equation (e.g. Sontag (1998)).

**Proposition 3.1.** Let us introduce $(R_{\theta,b_i,k}, h_{\theta,b_i,k})$ for $1 \leq k \leq K_i$, the solution of
 Parameter estimation in NLME-ODEs via optimal control theory

the discrete Riccati equation:

\[
R_{\theta,b,k} = R_{\theta,b,k+1} + \Delta_k w_k C^T C + \Delta_k \left( R_{\theta,b,k+1} A_{\theta,b}(t_k^d) + A_{\theta,b}(t_k^d)^T R_{\theta,b,k+1} \right)
+ \Delta^2_k A_{\theta,b}(t_k^d)^T R_{\theta,b,k+1} A_{\theta,b}(t_k^d)
- \Delta_k (I_d + \Delta_k A_{\theta,b}(t_k^d)^T) R_{\theta,b,k+1} B G(\theta_{b,k+1}) B^T R_{\theta,b,k+1} (I_d + \Delta_k A_{\theta,b}(t_k^d))
\]

with final condition \( R_{\theta,b,K} = h_{\theta,b,K} \), (3.3) is unique and equal to:

\[
\frac{\partial}{\partial \theta} (x(t)) = 0,
\]

Remark 3.1. The theoretical basis for replacing \( C_{t_i}^d \) and the perturbed ODE (2.1) by their discretized counterparts can be found in [Cla87] and, under mild regularity...
conditions on $A_{\theta,b_i}$ and $r_{\theta,b_i}$. $X_{\theta,b_i}^d$ and $\pi_{\theta,b_i}^d$ converge to the solution of the continuous optimal control problem.

3.2.2. Non-linear models

We adapt the method proposed by Cimen and Banks (2004b) to solve tracking problem for discrete time models. The outline of the method is the following: we replace the original problem (3.3) by a recursive sequence of problems, where the $l$-th one is defined by:

$$
\min_{u_i^d} C_i^{d,l}(b_i, x_{i,0}, u_i^d | \theta, U) := \left\| CX_{\theta,b_i,x_{i,0},u_i}^{d,l}(t_{im_i}) - y_{im_i} \right\|^2_2 + \sum_{k=0}^{K_i-1} \Delta_k \left( \left\| CX_{\theta,b_i,x_{i,0},u_i}^{d,l}(t_{i,k}) - y_{i,k}^d \right\|^2_2 w_k + u_i(t_k)T U u_i(t_k) \right)
$$

such that

$$
x_i(t_{i,l+1}) = \left( I_d + \Delta_k A_{\theta,b_i}(t_{i,k}, X_{\theta,b_i}^{d,l-1}(t_{i,k}) - z_i(t_{i,k}^d)) \right) x_i(t_{i,k}) + \Delta_k r_{\theta,b_i}(t_{i,k}^d, z_i(t_{i,k}^d)) + B\Delta_k u_i(t_k)
$$

where $X_{\theta,b_i}^{d,l-1}$ is the solution of problem (3.8) at iteration $l - 1$. Thus, for each $l$ the matrix $A_{\theta,b_i}(t_{i,k}, X_{\theta,b_i}^{d,l-1}(t_{i,k}), z_i(t_{i,k}^d))$ does not depend on $x_i$ and the problem (3.8) is a Linear-Quadratic one. We use the results of section 3.2.1 to construct the following algorithm:

(a) Initialization phase: $X_{\theta,b_i}^{u,d,0}(t_{k,0}) = x_{i,0}^{u,r}$ for all $k \in [0, n]$ where $x_{i,0}^{u,r}$ is an arbitrary starting point for the unknown initial condition and $X_{\theta,b_i}^{u,d,0}(t_{k,0}) = x_{i,0}^k$.

(b) At iteration $l$: use proposition 3.1 to obtain $(R_{\theta,b_i}, h_{\theta,b_i}^l, \pi_{\theta,b_i}^{d,l}, X_{\theta,b_i}^{d,l}, g_i^l | \theta, \Delta, U)$.

(c) If $\sum_{k=1}^{K_i} \left\| X_{\theta,b_i}^{d,l}(t_{i,k}) - X_{\theta,b_i}^{d,l-1}(t_{i,k}) \right\|^2_2 < \varepsilon_1$ and $\left| g_i^l(b_i | \theta, \Delta, U) - g_i^{l-1}(b_i | \theta, \Delta, U) \right| < \varepsilon_2$, then step 4; otherwise get back to step 2.

(d) Set $(R_{\theta,b_i}, h_{\theta,b_i}^l) = (R_{\theta,b_i}, h_{\theta,b_i}^l, \pi_{\theta,b_i}^{d,l}, X_{\theta,b_i}^{d,l}, g_i^l(b_i | \theta, \Delta, U) = g_i^l(b_i | \theta, \Delta, U)$.

4. Results on simulated data

We compare the accuracy of our approach with maximum likelihood (ML) in different models and experimental designs reflecting the problems exposed in introduction,
that is estimation in 1/presence of model error, 2/partially observed framework with unknown initial conditions and 3/presence of poorly identifiable parameters. For the fairness of comparison with ML where no prior is specified, we choose a non-informative one i.e. \( \ln P[\theta, \Delta] = 0 \) for our method throughout this section. If the differential equation (1.1) has an analytical solution, the ML estimator is computed via SAEM algorithm (SAEMIX package Comets et al. (2017)). Otherwise it is done via a restricted likelihood method dedicated to ODE models implemented in the nlmeODE package Tornoe et al. (2004). For both our method and the ML, we proceed to Monte-Carlo simulations based on \( N_{MC} = 100 \) runs. At each run, we generate \( n_i \) observations coming from \( n \) subjects on an observation interval \([0, T]\) with Gaussian measurement noise of standard deviation \( \sigma^* \). From these data, we estimate the true population parameters \( \theta^*, \Psi^* \) as well as the subject parameter realizations \( b^*_i \sim N(0, \Psi^*) \) with both estimation methods. We quantify the accuracy of each entry \( \hat{\psi}_p \) of the population parameters estimate \( \hat{\psi} = (\hat{\theta}, \hat{\Psi}) \) via Monte-Carlo computation of the bias \( b(\hat{\psi}_p) = \mathbb{E}[\hat{\psi}_p] - \psi^*_p \), the empirical variance \( V_{emp}(\hat{\psi}_p) = \mathbb{E}[(\mathbb{E}[\hat{\psi}_p] - \psi^*_p)^2] \), the mean square error \( MSE(\hat{\psi}_p) = b(\hat{\psi}_p)^2 + V_{emp}(\hat{\psi}_p) \), the estimated variance \( \hat{V}(\hat{\psi}_p) \) as well as the coverage rate of the 95%-confidence interval derived from it, it corresponds to the frequency at which the interval \( \hat{\psi}_p \pm z_{0.975} \sqrt{\hat{V}(\hat{\psi}_p)} \) contains \( \psi^*_p \) with \( z_{0.975} \) the 0.975-quantile of the centered Gaussian law. We compute the previous quantities for the normalized values \( \hat{\psi}_p^{norm} := \frac{\hat{\psi}_p}{\psi^*_p} \) to make relevant comparisons among parameters with different order of magnitude. For the subject specific parameter, we estimate the mean square error \( MSE(\hat{b}_i) = \mathbb{E}\left[\|b^*_i - \hat{b}_i\|^2\right] \). For each subsequent examples, we give the results for \( n = 50 \) and present in appendix B the case \( n = 20 \) to analyze the evolution of each estimator accuracy with respect to the sparsity of the available observations.

For our method, we need to select \( U \) the matrix appearing in the inner criteria definition (2.3) balancing model and data fidelity. We use for this the forward cross-validation method presented in G. Hooker and Earn (2011). Let us denote \( \hat{\theta}_U, \{\hat{b}_{i,U}\}_{i \in [1, n]} \) the estimators obtained for a given matrix \( U \). For each subject \( i \), we split \([0, T]\) into \( H = 2 \) sub-intervals \([t_h, t_{h+1}]\), such that \( t_1 = 0 \) and \( t_H = T \). We denote \( X_{\hat{\theta}_{b_i}}(\cdot, t_h, x_h) \) the solution of \( \dot{x}(t) = f_{\hat{\theta}_{b_i}}(t, x_i(t), z_i(t)) \) defined on the interval \([t_h, t_{h+1}]\) with initial condition
The forward cross-validation uses the causal relation imposed to the data by the ODE to quantify the prediction error:

\[
EP(i, U) = \sum_{h=1}^{H} \sum_{\{t_{ij} \in [t_h, t_{h+1}]\}} \| y_{ij} - CX_{\hat{\theta}_{\hat{\psi}_{i}}, \hat{b}_{i}, U}(t_{ij}, t_h, \overline{X}_{\hat{\theta}_{\hat{\psi}_{i}}, \hat{b}_{i}, U}(t_h)) \|^2.
\]

The rationale of this selection method is the following: if \( U \) is too small, \( CX_{\hat{\theta}_{\hat{\psi}_{i}}, \hat{b}_{i}, U}(t_h) \) will be close to \( y_h \) but not to the actual ODE solution, and \( t \mapsto CX_{\hat{\theta}_{\hat{\psi}_{i}}, \hat{b}_{i}, U}(t, t_h, \overline{X}_{\hat{\theta}_{\hat{\psi}_{i}}, \hat{b}_{i}, U}(t_h)) \) will diverge from the observations on \([t_h, t_{h+1}]\). If \( U \) is too large, \( \overline{X}_{\hat{\theta}_{\hat{\psi}_{i}}, \hat{b}_{i}, U}(t_h) \) will be close to the ODE solution but far from \( y_h \) and it will lead to a large value for \( EP(i, U) \). Thus, a proper value for \( U \) which minimizes \( EP(i, U) \) will be chosen between these two extreme cases. The global prediction error for the whole population is computed with \( EP(U) = \sum_i EP(i, U) \). We retain the matrix \( U \) which minimizes \( EP \) among a trial of tested values and we denote \( \hat{\theta}, \hat{\psi}, \{ \hat{b}_i \}_{i \in [1, n]} \) the corresponding estimator. In the following, we use the subscript \( ML \) to denote the ML estimator.

For solving the optimization problems required for computing our inner and outer criteria, we use the Nelder-Mead algorithm implemented in the optimr package [Nash (2016)]. All optimization algorithms used by the estimation methods require a starting guess value. We start from the true parameter value for each of them. By doing so, we aim to do not mix two distinct problems: 1) the numerical stability of the estimation procedures, 2) the intrinsic accuracy of the different estimators. These two problems are correlated, but we aim to adress only the latter which corresponds to the issues raised in introduction. Still, we check on preliminary analysis that local minima presence was not an issue in the vicinity of \((\theta^*, \Delta^*)\) by testing different starting points for all methods. No problem appears for our method and SAEMIX. A negligible number of non convergence cases appear for nlmODE which have been discarded thanks to the convergence criteria embedded in the package.
4.1. Partially observed linear model

We consider the population model where each subject $i$ follows the ODE:

$$
\begin{align*}
\dot{X}_{1,i} &= \phi_{2,i}X_{2,i} - \phi_{1,i}X_{1,i} \\
\dot{X}_{2,i} &= -\phi_{2,i}X_{2,i} \\
(X_{1,i}(0), X_{2,i}(0)) &= (x_{1,0}, x_{2,0,i})
\end{align*}
$$

(4.1)

with the following parametrization:

$$
\begin{align*}
\log(\phi_{1,i}) &= \theta_1 + b_i \\
\log(\phi_{2,i}) &= \theta_2
\end{align*}
$$

where $b_i \sim N(0, \Psi)$. The true population parameter values are $\theta^* = (\theta_1^*, \theta_2^*) = (\log(0.5), \log(2))$, and $\Psi^* = 0.5^2$ and we are in a partially observed framework where only $X_{1,i}$ is accessible. The true initial conditions are subject specifics and normally distributed with $x_{1,0,i}^* \sim N(2, 0.5)$ and $x_{2,0,i}^* \sim N(3, 1)$. ODE (4.1) has an analytic solution given by $X_{1,i}(t) = e^{-\phi_{1,i}t}(x_{1,0} + \frac{x_{2,0,i}}{\phi_{1,i} - \phi_{2,i}}(e^{(\phi_{1,i} - \phi_{2,i})t} - 1))$ for its first component which will be used for parameter estimation with the SAEMIX package. We generate $n_i = 11$ observations per subject on $[0, T] = [0, 10]$ with Gaussian measurement noise of standard deviation $\sigma = 0.05$. An example of observations and corresponding solution is plotted in figure 4.1.

We want to investigate the impact of initial condition, especially the unobserved one $x_{2,0,i}^*$, on the ML estimator accuracy. Indeed, our method does not need to estimate $x_{2,0,i}^*$ and thus no additional difficulties appear in this partially observed framework. For the ML, however, it is nuisance subject-specific parameter that should be estimated and for which no observations are available. For this, we compute $\hat{\theta}_{ML,x_{1,0,i},x_{2,0,i}}$, $\hat{\theta}_{ML,x_{1,0,2}}$ and $\hat{\theta}_{ML}$ the ML estimator respectively when: 1) both initial conditions are perfectly known, 2) $x_{1,0,i}^*$ is replaced by the measured value, 3) in addition $x_{2,0,i}^*$ has to be estimated.

4.1.1. Correct model case

We present the estimation results in table 4.1. For ML, the results are goods in terms of accuracy and consistent in terms of asymptotic confidence interval coverage rate when both initial conditions are known: 95% for $\theta_1$ and $\theta_2$ in accordance with theoretical
results. However, there is a significant drop in accuracy when $x_{2,0,i}^*$ has to be estimated, especially for $\theta_2$. In particular, the coverage rate drops to 86% and 80% for $\theta_1$ and $\theta_2$ respectively. Interestingly, ML inaccuracy is driven by bias and under-estimated variance when initial conditions are not known. In this case our method provides a relevant alternative: it gives accurate estimations with a good coverage rate for all parameters while avoiding the estimation of the unobserved initial conditions. Estimation of individual random effects is also more accurate with our method, with a decrease of more than 90% of MSE for $b_i$ comparing to ML.

4.1.2. Estimation in presence of model error at the subject level

To mimic misspecification presence, we now generate the observations from the hypoelliptic stochastic model:

$$
\begin{align*}
\begin{align*}
    dX_{1,i} &= \phi_{2,i}X_{2,i}dt - \phi_{1,i}X_{1,i}dt \\
    dX_{2,i} &= -\phi_{2,i}X_{2,i}dt + \alpha dB_t \\
    (X_{1,i}(0), X_{2,i}(0)) &= (x_{1,0}, x_{2,0,i})
\end{align*}
\end{align*}

(4.2)
Table 4.1. Results of estimation for model (4.1). The different subscripts stand for the following estimation scenarios: 1) \((x_{0,1}, x_{0,2})\) when both initial conditions are set to \((x_{0,1}^*, x_{0,2}^*)\), 2) \(x_{0,2}\) when \(x_{0,i}\) is set to \(y_{i,0}\) and \(x_{0,2}\) to \(x_{0,2}^*\), 3) absence of subscript when \(x_{0,i}\) is set to \(y_{i,0}\) and \(x_{0,2}\) is estimated. Results from our method are in bold.

|                | MSE  | Bias | Emp. Var | Est. Var | Cov. Rate | MSE \(b_i\) |
|----------------|------|------|----------|----------|-----------|-------------|
| \(\theta_1\)   |      |      |          |          |           |             |
| \(\hat{\theta}_{ML, x_{0,1}, x_{0,2}}\) | 0.01 | 0.01 | 0.01     | 0.01     | 0.95      |             |
| \(\hat{\theta}_{ML, x_{0,2}}\) | 0.01 | 0.01 | 0.01     | 0.01     | 0.94      |             |
| \(\hat{\theta}_{ML}\) | 0.04 | -0.04 | 0.04 | 0.01 | 0.86      |             |
| \(\hat{\theta}\) | 5e-3 | 8e-3 | 8e-3     | 1e-2     | 0.97      |             |
| \(\theta_2\)   |      |      |          |          |           |             |
| \(\hat{\theta}_{ML, x_{0,1}, x_{0,2}}\) | 4e-5 | 1e-3 | 4e-5     | 4e-5     | 0.95      |             |
| \(\hat{\theta}_{ML, x_{0,2}}\) | 6e-5 | 1e-3 | 6e-5     | 8e-5     | 0.94      |             |
| \(\hat{\theta}_{ML}\) | 4e-3 | -0.01 | 3e-3 | 1e-4 | 0.80      |             |
| \(\hat{\theta}\) | 5e-5 | 2e-3 | 4e-5     | 4e-5     | 0.93      |             |
| \(\Psi\)       |      |      |          |          |           |             |
| \(\hat{\theta}_{ML, x_{0,1}, x_{0,2}}\) | 0.01 | -0.03 | 0.01     | 7e-3     | 1         | 5e-3        |
| \(\hat{\theta}_{ML, x_{0,2}}\) | 0.02 | -0.03 | 0.01     | 7e-3     | 1         | 5e-3        |
| \(\hat{\theta}_{ML}\) | 0.05 | 0.17 | 0.02     | 0.02     | 1         | 0.10        |
| \(\hat{\theta}\) | 0.01 | -0.01 | 0.01     | 0.01     | 0.92      | 0.01        |

Well-specified model

|                | MSE  | Bias | Emp. Var | Est. Var | Cov. Rate | MSE \(b_i\) |
|----------------|------|------|----------|----------|-----------|-------------|
| \(\hat{\theta}_{ML, x_{0,1}, x_{0,2}}\) | 0.01 | 4e-4 | 0.01     | 0.01     | 0.91      |             |
| \(\hat{\theta}_{ML, x_{0,2}}\) | 0.01 | -3e-4 | 0.01 | 1e-4 | 0.89      |             |
| \(\hat{\theta}_{ML}\) | 0.05 | 0.02 | 0.05     | 0.01     | 0.81      |             |
| \(\hat{\theta}\) | 0.01 | -8e-3 | 7e-3     | 0.05     | 0.97      |             |
| \(\hat{\theta}_{ML, x_{0,1}, x_{0,2}}\) | 1e-4 | -1e-3 | 1e-4     | 1e-4     | 0.83      |             |
| \(\hat{\theta}_{ML, x_{0,2}}\) | 1e-4 | -1e-3 | 2e-4     | 0.01     | 0.82      |             |
| \(\hat{\theta}_{ML}\) | 4e-3 | -2e-3 | 4e-3     | 2e-4     | 0.63      |             |
| \(\hat{\theta}\) | 1e-4 | 2e-5 | 1e-4     | 1e-4     | 0.92      |             |
| \(\hat{\theta}_{ML, x_{0,1}, x_{0,2}}\) | 0.01 | -0.003 | 0.01 | 0.01 | 1         | 0.01        |
| \(\hat{\theta}_{ML, x_{0,2}}\) | 0.01 | -0.005 | 0.01 | 0.01 | 1         | 0.01        |
| \(\hat{\theta}_{ML}\) | 0.09 | 0.21 | 0.04     | 0.03     | 1         | 0.12        |
| \(\hat{\theta}\) | 0.02 | -0.02 | 0.02     | 0.01     | 0.90      | 0.01        |

Misspecified model
with $B_t$ a Wiener process and $\alpha = 0.1$ the diffusion coefficient. For the sake of comparison, a solution of (4.1) and a realization of its perturbed counterpart given by (4.2) are plotted in figure 4.2. This framework where stochasticity only affects the unmeasured compartment is known to be problematic for parameter estimation and inference procedures are yet to be developed for sparse sampling case. From figure 4.2 it is easy to see the diffusion $\alpha$ will be hard to estimate when we only have observations for $X_{1,i}$. Thus, we still estimate the parameters from the model (4.1) which is now seen as a deterministic approximation of the true stochastic process. Still, it is expected that our method will mitigate the effect of stochasticity on the estimation accuracy by taking into account model error presence. Results are presented in table 4.1. The differences between the two methods are similar to the previous well-specified case with an additional loss of accuracy coming from model error for both estimators. However, the misspecification effect for SAEM is more pronounced than for our method which manages to limit the damages done. This confirms the benefits of taking into account model uncertainty for the regularization of the inverse problem, in particular when model error occurs in the unobserved compartment, a situation in which classic statistical criteria for model assessment based on a data fitting criterion are difficult to use.
4.2. Partially observed nonlinear model

We consider a simplified version of the model used in Tornoe et al. (2004) for the analysis of glucose and insulin regulation:

\[
\begin{align*}
\dot{G}_i &= S_G (G_B - G_i) - X_i G_i \\
\dot{I}_i &= \gamma t (G_i - h) - n_i (I_i - I_B) \\
\dot{X}_i &= -p_2 (X_i + S_I (I_i - I_B)).
\end{align*}
\] (4.3)

We are in a partially observed framework where only the glucose \((G_i)\) and insulin \((I_i)\) concentration are measured. The values of parameters \((p_2, \gamma, h, G_B, I_B)\) are fixed to \((-4.93, -6.85, 4.14, 100, 100)\) and we aim to estimate \(\theta = (\theta_{S_G}, \theta_{S_I}, \theta_n)\), linked to the original model via the parametrization:

\[
\begin{align*}
\log(S_G) &= \theta_{S_G} \\
\log(S_I) &= \theta_{S_I} \\
\log(n_i) &= \theta_n + b_i
\end{align*}
\]

where \(b_i \sim N(0, \Psi)\). The true population parameter values are \(\theta^* = (-3.89, -7.09, -1.81)\) and \(\Psi^* = 0.26^2\). The true initial conditions \(x_{i,0}^* = (G_{0,i}^*, I_{0,i}^*, X_{0,i}^*)\) are subject-specific and distributed according to \(\ln(x_{i,0}^*) \sim N(l_{x_i}^*, \Psi_{l_{x_i}^*})\) with \(l_{x_i}^* = (5.52, 4.88, -7)\) and \(\Psi_{l_{x_i}^*} = (0.17^2, 0.1^2, 10^{-4})\). We generate \(n_i = 5\) observations on \([0, T] = [0, 180]\) with Gaussian measurement noise of standard deviation \(\sigma^* = 3\). As in the previous example, we investigate the impact of unknown initial conditions on estimators accuracy. We are particularly interested in the joint estimation of \(\theta_{S_I}\), which appears only in the equation ruling the unobserved state variable \(X_i\), and \(x_{i,0}^*\) required for each subject by the maximum likelihood based method. For this, we distinguish two cases, 1) when \(\theta_{S_I}\) is known, 2) when \(\theta_{S_I}\) has to be estimated here and we respectively denote \(\hat{\theta}_{S_I}\) and \(\hat{\theta}\) the corresponding estimators. Finally, since the model is nonlinear we have to specify a pseudo-linear representation to use the algorithm presented in section 3.2.2:

\[
A_{\theta,b_i}(t, G_i, I_i, X_i) = \begin{pmatrix}
-S_G & 0 & -G_i \\
\gamma t & -n_i & 0 \\
0 & -p_2 S_I & -p_2
\end{pmatrix},
\quad
r_{\theta,b_i}(t) = \begin{pmatrix}
S_G G_B \\
-\gamma h + n_i I_B \\
-p_2 S_I I_B
\end{pmatrix}.
\]
4.2.1. Correct model case

We present the estimation results in table 4.2. Our method obtains smaller MSE than ML and escapes the drop in coverage rate of the confidence interval in the case of $\theta^*_{S_G}$ estimation. The difference between the two estimators behavior is explained by the fact that they are defined through the construction of two different optimization problems. At the population level our approach leads to minimize a cost function depending on a 4-dimensional parameter whereas ML, due to its need to estimate $x_{i,0}^*$, considers a 7-dimensional one. Thus, the topology of the parameter spaces explored by each method to look for the minimum are very different.

4.2.2. Estimation in presence of model error at the subject level

To mimic misspecification presence, we generate the observations from the stochastic model:

$$
\begin{align*}
\text{d}G_i &= (S_G(G_B - G_i) - X_i G_i) \, \text{d}t + \alpha_1 \text{d}B_{1,t} \\
\text{d}I_i &= (\gamma t(G_i - h) - n_i(I_i - I_B)) \, \text{d}t + \alpha_2 \text{d}B_{2,t} \\
\text{d}X_i &= (-p_2(X_i + S_I(I_i - I_B))) \, \text{d}t + \alpha_3 \text{d}B_{3,t}
\end{align*}
$$

(4.4)

where the $B_{i,t}$ are Wiener processes and $(\alpha_1, \alpha_2, \alpha_3) = (2, 2, 2 \times 10^{-4})$ their diffusion coefficients. We present the estimation results in table 4.2. For ML, the drop in coverage rate for $\theta^*_{S_G}$ and $\theta^*_{S_I}$ is even more striking when $\theta^*_{S_I}$ needs to be estimated. This is explained by the effect of model misspecification which increases bias and the fact that ML does not take into account this new source of uncertainty leading here to underestimation of variance and too narrow confidence intervals.

4.3. Antibody concentration evolution model

We consider the model presented in Pasin et al. (2019) to analyze the antibody concentration, denoted $Ab_i$, generated by two populations of antibody secreting cells: the short
Table 4.2. Results of estimation for model (4.3). The different subscripts stand for the following estimation scenarios: 1) $S_i$ when $S_i$ is set to $S_i^*$, 2) absence of subscript when $S_i$ is estimated. Results from our method are in bold.

### Well-specified model

| Parameter    | MSE  | Bias | Emp. Var | Est. Var | Cov. Rate | MSE $b_i$ |
|--------------|------|------|----------|----------|-----------|-----------|
| $\theta_{SG}$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | 4.6e-5 | 2.2e-3 | 4.1e-5 | 8.8e-6 | 0.95      |           |
| $\hat{\theta}_{ML}$ | 2.0e-3 | 0.03  | 1.0e-3 | 7.6e-5 | 0.85      |           |
| $\hat{\theta}_{S_i}$ | 1.0e-5 | 3.8e-4 | 1.0e-5 | 8.2e-6 | 0.95      |           |
| $\hat{\theta}$ | 1.8e-4 | -5.5e-4 | 1.8e-4 | 1.5e-4 | 0.96      |           |
| $\theta_{SI}$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | known |      |      |          |           |           |
| $\hat{\theta}_{ML}$ | 2.2e-3 | 0.03  | 1.2e-3 | 6.4e-5 | 0.90      |           |
| $\hat{\theta}_{S_i}$ | known |      |      |          |           |           |
| $\hat{\theta}$ | 1.3e-4 | -7.1e-4 | 1.3e-4 | 1.1e-4 | 0.96      |           |
| $\theta_n$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | 7.0e-4 | 2.8e-3 | 6.0e-4 | 5.0e-4 | 0.94      |           |
| $\hat{\theta}_{ML}$ | 8.5e-4 | 8.0e-3 | 8.4e-4 | 5.0e-4 | 0.86      |           |
| $\hat{\theta}_{S_i}$ | 5.2e-4 | 5.7e-3 | 5.1e-4 | 5.0e-4 | 0.95      |           |
| $\hat{\theta}$ | 5.6e-4 | 5.6e-3 | 5.2e-4 | 5.1e-4 | 0.95      |           |
| $\Psi$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | 0.02  | 6.5e-4 | 0.02  | 0.02  | 0.95  | 0.02     |
| $\hat{\theta}_{ML}$ | 0.04  | -0.09 | 0.03  | 0.02  | 0.88  | 0.02     |
| $\hat{\theta}_{S_i}$ | 0.01  | -2.0e-3 | 0.01  | 0.01  | 0.95  | 0.01     |
| $\hat{\theta}$ | 0.01  | -2.7e-3 | 0.01  | 0.01  | 0.94  | 0.01     |

### Misspecified model

| Parameter    | MSE  | Bias | Emp. Var | Est. Var | Cov. Rate | MSE $b_i$ |
|--------------|------|------|----------|----------|-----------|-----------|
| $\theta_{SG}$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | 6.4e-5 | 2.6e-3 | 5.7e-5 | 2.2e-5 | 0.85      |           |
| $\hat{\theta}_{ML}$ | 2.3e-3 | 3.1e-3 | 1.4e-3 | 1.9e-4 | 0.54      |           |
| $\hat{\theta}_{S_i}$ | 2.1e-5 | -2.2e-5 | 2.1e-5 | 2.0e-5 | 0.93      |           |
| $\hat{\theta}$ | 3.2e-4 | -1.2e-3 | 3.2e-4 | 4.0e-4 | 0.93      |           |
| $\theta_{SI}$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | known |      |      |          |           |           |
| $\hat{\theta}_{ML}$ | 0.01  | 0.04  | 0.01  | 1.2e-3 | 0.55      |           |
| $\hat{\theta}_{S_i}$ | known |      |      |          |           |           |
| $\hat{\theta}$ | 3.2e-4 | -1.0e-3 | 3.2e-4 | 2.9e-4 | 0.92      |           |
| $\theta_n$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | 7.7e-4 | -3.4e-3 | 7.6e-4 | 5.4e-4 | 0.89      |           |
| $\hat{\theta}_{ML}$ | 4.8e-3 | -4.8e-3 | 4.8e-3 | 5.3e-4 | 0.88      |           |
| $\hat{\theta}_{S_i}$ | 4.2e-4 | 6.9e-4 | 4.2e-4 | 5.1e-4 | 0.95      |           |
| $\hat{\theta}$ | 4.2e-4 | 5.8e-4 | 4.2e-4 | 4.9e-4 | 0.96      |           |
| $\Psi$ |      |      |          |          |           |           |
| $\hat{\theta}_{ML,S_i}$ | 0.03  | -3.4e-3 | 0.03  | 0.02  | 0.93  | 0.03     |
| $\hat{\theta}_{ML}$ | 0.03  | -8.1e-3 | 0.02  | 0.02  | 0.87  | 0.03     |
| $\hat{\theta}_{S_i}$ | 0.01  | -3.9e-3 | 0.01  | 0.02  | 0.94  | 0.01     |
| $\hat{\theta}$ | 0.02  | -7.1e-3 | 0.02  | 0.02  | 0.94  | 0.02     |
Table 4.3. Biological interpretation and parameter values

| Parameters | Biological interpretation | Values |
|------------|---------------------------|--------|
| $\delta_L$ | long-lived cells declining rate | $\log(2)/(364 \times 6)$ |
| $\psi^*_{\delta_S}$ | Mean log-value for $\delta_S$, the short-lived cells declining rate | $\log(\log(2)/1.2) \approx -0.54$ |
| $\psi^*_{\theta_S}$ | Mean log-value for $\theta_S$, the antibodies influx from short-lived cells | $\log(2755) \approx 7.92$ |
| $\psi^*_{\phi_L}$ | Mean log-value for $\phi_L$, the antibodies influx from long-lived cells | $\log(16) \approx 2.78$ |
| $\psi^*_{\delta_{Ab}}$ | Mean log-value for $\delta_{Ab}$, the antibodies declining rate | $\log(\log(2)/24) \approx -3.54$ |
| $\Psi^*_{\phi_S}$ | Inter individual variance for $\log(\phi_{S,i})$ | 0.92² |
| $\Psi^*_{\phi_L}$ | Inter individual variance for $\log(\phi_{L,i})$ | 0.85² |
| $\Psi^*_{\delta_{Ab}}$ | Inter individual variance for $\log(\delta_{Ab,i})$ | 0.3² |

This model is used to quantify the humoral response on different populations after an Ebola vaccine injection with a 2 doses regimen seven days after the second injection when the antibody secreting cells enter in a decreasing phase. These cells being unobserved, the preceding equation can be simplified to focus on antibody concentration evolution:

$$\dot{Ab}_i = \theta_{S,i}S_i + \theta_{L,i}L_i - \delta_{Ab,i}Ab_i$$

(4.6)

This equation has an analytic solution which will be used for maximum likelihood estimation with SAEMIX. We consider the following parametrization:

$$
\begin{align*}
\dot{S}_i &= -\delta_S S_i \\
\dot{L}_i &= -\delta_L L_i \\
\dot{Ab}_i &= \theta_{S,i}S_i + \theta_{L,i}L_i - \delta_{Ab,i}Ab_i
\end{align*}
$$

(4.5)

with $\phi_{S,i} := \theta_{S,i}S_{0,i}$ and $\phi_{L,i} := \theta_{L,i}L_{0,i}$. This equation has an analytic solution which will be used for maximum likelihood estimation with SAEMIX. We consider the following parametrization:

$$
\begin{align*}
\log(\delta_S) &= \psi_{\delta_S} \\
\log(\phi_{S,i}) &= \psi_{\phi_S} + b_{\phi_S,i} \\
\log(\phi_{L,i}) &= \psi_{\phi_L} + b_{\phi_L,i} \\
\log(\delta_{Ab,i}) &= \psi_{\delta_{Ab}} + b_{\delta_{Ab,i}}
\end{align*}
$$

The true parameter values are presented in table 4.3. According to Pasin et al. (2019), the parameter $\delta_L$ was non-identifiable and only a lower bound has been derived for it via
profiled likelihood. So, to make fair comparisons between our approach and maximum likelihood, we do not estimate it. Regarding population parameters, we are particularly interested in the behavior of estimation methods for $\psi_{\delta_S}$ and $\psi_{\phi_S}$. Indeed a parameter sensitivity analysis shows the symmetric role of $\psi_{\delta_S}$ and $\psi_{\phi_S}$ on the ODE solution (see Balelli et al. (2020)). Thus, they are likely to face practical identifiability problems. To investigate this effect, we estimate the parameters when 1) $\psi^*_{\delta_S}$ is known (the corresponding estimators will be denoted with the subscript $\psi_{\delta_S}$), 2) it has to be estimated as well.

4.3.1. Correct model case

We generate $n_i = 11$ observations on the interval $[0, T] = [0, 364]$ with Gaussian measurement noise of standard deviation $\sigma^* = 100$. For each subject $i$, the initial condition has been generated according to $Ab^*_{0,i} \sim N(Ab_0, \sigma^2_{Ab_0})$ with $Ab_0 = 500$ and $\sigma_{Ab_0} = 260$ to reflect the dispersion observed in the data presented in Pasin et al. (2019). We present the estimation results in table 4.4.

Our method improves the estimation of $\psi^*_{\delta_S}$ facing practical identifiability problems comparing to the ML. In particular our method reduces its variance. As advocated in the introduction, our approach provides an improved estimate for the $\{b^*_i\}_{i \in [1,n]}$. We assume that is due to the committed estimation error for $\theta^*$, as it causes model error for $\{b^*_i\}_{i \in [1,n]}$ estimation, which is not taken into account by exact methods. This in turn explains why their variance $\Psi^*$ is better estimated with our approach. In this mixed-effect context, this cause of model error is systematically present and claims for the use of estimation methods taking into account modeling uncertainties when subject specific parameters are critical for the practitioner.

4.3.2. Estimation in presence of model error at the subject level

The data are now generated with a stochastic perturbed version of the original model:

$$dAb_i = \left( \phi_{S,i}e^{-\delta_S t} + \phi_{L,i}e^{-\delta_L t} - \delta_{Ab,i}Ab_i \right) dt + \alpha dB_t \quad (4.7)$$
Table 4.4. Results of estimation for model (4.6). The different subscripts stand for the following estimation scenarios: 1) $\psi_{\delta S}$ when $\psi_{\delta S}$ is set to $\psi^*_{\delta S}$, 2) absence of subscript when $\psi_{\delta S}$ is estimated. Results from our method are in bold.

| Well-specified model | MSE   | Bias  | Emp. Var | Est. Var | Cov. Rate | MSE $b_1$ |
|---------------------|-------|-------|----------|----------|-----------|-----------|
| $\psi_{\delta S}$   | $\hat{\theta}_{ML,\psi_{\delta S}}$ | known |          |          |           |           |
|                     | $\hat{\theta}_{ML}$ | 2.13  | 0.78     | 1.51     | 70.64     | 0.92      |
|                     | $\hat{\theta}_{\psi_{\delta S}}$ | known |          |          |           |           |
|                     | $\tilde{\theta}$ | 0.62  | -0.34    | 0.50     | 0.66      | 0.92      |
| $\psi_{\phi S}$     | $\hat{\theta}_{ML,\psi_{\phi S}}$ | 4e-4  | 0.01     | 3e-4     | 3e-4      | 0.94      |
|                     | $\hat{\theta}_{ML}$ | 0.01  | -0.05    | 7e-3     | 0.40      | 0.92      |
|                     | $\hat{\theta}_{\psi_{\phi S}}$ | 2e-3  | -0.05    | 2e-4     | 1e-3      | 0.94      |
|                     | $\tilde{\theta}$ | 2e-3  | 1e-3     | 2e-3     | 2e-3      | 0.93      |
| $\psi_{\phi L}$     | $\hat{\theta}_{ML,\psi_{\phi L}}$ | 3e-3  | 0.02     | 3e-3     | 2e-3      | 0.95      |
|                     | $\hat{\theta}_{ML}$ | 4e-3  | 0.03     | 4e-3     | 3e-3      | 0.90      |
|                     | $\hat{\theta}_{\psi_{\phi L}}$ | 7e-4  | -0.01    | 5e-4     | 3e-3      | 0.95      |
|                     | $\tilde{\theta}$ | 3e-3  | -3e-3    | 3e-3     | 2e-3      | 0.91      |
| $\psi_{\delta A_b}$ | $\hat{\theta}_{ML,\psi_{\delta A_b}}$ | 7e-4  | -0.02    | 5e-4     | 3e-4      | 0.93      |
|                     | $\hat{\theta}_{ML}$ | 2e-3  | -0.02    | 1e-3     | 4e-4      | 0.88      |
|                     | $\hat{\theta}_{\psi_{\delta A_b}}$ | 2e-4  | 0.01     | 1e-4     | 3e-4      | 0.95      |
|                     | $\tilde{\theta}$ | 4e-4  | 0.01     | 3e-4     | 2e-4      | 0.90      |
| $\Psi_{\phi S}$     | $\hat{\theta}_{ML,\Psi_{\phi S}}$ | 0.04  | -1e-3    | 0.04     | 0.07      | 1         | 0.15      |
|                     | $\hat{\theta}_{ML}$ | 0.11  | 0.01     | 0.11     | 0.05      | 1         | 0.17      |
|                     | $\hat{\theta}_{\psi_{\phi S}}$ | 0.02  | 8e-3     | 0.02     | 0.01      | 0.94      | 0.06      |
|                     | $\tilde{\theta}$ | 0.02  | -0.03    | 0.02     | 0.02      | 0.94      | 0.07      |
| $\Psi_{\phi L}$     | $\hat{\theta}_{ML,\Psi_{\phi L}}$ | 0.03  | 0.04     | 0.02     | 0.04      | 1         | 0.30      |
|                     | $\hat{\theta}_{ML}$ | 0.03  | 0.05     | 0.02     | 0.04      | 1         | 0.60      |
|                     | $\hat{\theta}_{\psi_{\phi L}}$ | 0.02  | -0.1     | 5e-3     | 8e-3      | 0.93      | 0.07      |
|                     | $\tilde{\theta}$ | 0.03  | -0.06    | 0.02     | 0.01      | 0.92      | 0.08      |
| $\Psi_{\delta A_b}$ | $\hat{\theta}_{ML,\Psi_{\delta A_b}}$ | 0.11  | 0.18     | 0.08     | 0.02      | 1         | 0.10      |
|                     | $\hat{\theta}_{ML}$ | 0.20  | 0.29     | 0.11     | 0.02      | 1         | 0.50      |
|                     | $\hat{\theta}_{\psi_{\delta A_b}}$ | 0.10  | -0.30    | 0.01     | 0.01      | 0.95      | 0.03      |
|                     | $\tilde{\theta}$ | 0.11  | -0.27    | 0.04     | 0.04      | 0.95      | 0.04      |
where $B_t$ is a Wiener process and $\alpha = 10$ its diffusion coefficient. The value for $\alpha$ has been chosen big enough to produce significantly perturbed trajectories but small enough to ensure that ODE (4.6) is still a relevant approximation for estimation purpose. We keep the same parameter values and measurement noise level as in the previous section. The results are presented in table 4.5.

Our method still outperforms the maximum likelihood for $\psi_{\delta_S}^*$ as well as the $\{b_i^*\}_{i \in [1, n]}$ estimation and their variances. In addition, we mitigate the effect of model error on estimation accuracy.

5. Real data analysis

We now proceed to the estimation using real data presented in Pasin et al. (2019) from which the parameter values given in table 4.3 come from. In Pasin et al. (2019), the estimation is made from cohorts coming from three phase I trials performed in African and European countries. Each subject was vaccinated with two doses, Ad26.ZEBOV (Janssen Vaccines and Prevention) and MVA-BN-Filo (Bavarian Nordic). In these cohorts, both the effect of injection order, either Ad26.ZEBOV first and MVA-BN-Filo second, or MVA-BN-Filo first and Ad26.ZEBOV second, and the delay between, 28 or 56 days, were evaluated. In this study, we focus on an east African subpopulation where Ad26.ZEBOV was injected first and then MVA-BN-Filo with a delay of 28 days between the two doses. As in Pasin et al. (2019) and the simulation section, to stay in the temporal domain of validity of the model we use measurements made seven days after the second dose injection. It leaves us with 5 measurements of antibody concentration between days 7 up to days 330 per subject. The estimation in the original work has been done using the NIMROD software Prague et al. (2013) and log-transformed antibody concentration measurement. We now estimate the parameters with our method with the aim to compare our results with the existing one. We used the same prior distribution $\pi(\theta) \sim N \left( \begin{pmatrix} -1 \\ 0 \\ 0 \end{pmatrix}, \begin{pmatrix} 25 & 0 & 0 \\ 0 & 100 & 0 \\ 0 & 0 & 100 \end{pmatrix} \right)$ for $\theta = (\psi_{\delta_S}, \psi_{\phi_S}, \psi_{\phi_L}, \psi_{\delta_{ab}})$ as
Table 4.5. Results of estimation in presence of model error when data are generated from (4.7). The different subscripts stand for the same estimation scenario as in table 4.4. Results from our method are in bold.

| Misspecified model | MSE | Bias | Emp. Var | Est. Var | Cov. Rate | MSE \(b_i\) |
|-------------------|-----|------|----------|----------|-----------|-------------|
| \(\psi_{gS}\)     | \(\hat{\theta}_{ML,\psi_{gS}}\) | known       | 3.88 1.48 1.68 4.10 0.80 |
|                   | \(\hat{\theta}_{ML}\)          | known       | 0.93 -0.40 0.77 0.62 0.90 |
|                   | \(\hat{\psi}_{gS}\)           | known       | 0.93 -0.40 0.77 0.62 0.90 |
| \(\psi_{gL}\)     | \(\hat{\theta}_{ML,\psi_{gL}}\) | 1e-3 0.02 1e-3 5e-4 0.91 |
|                   | \(\hat{\theta}_{ML}\)          | 0.02 -0.10 0.01 0.02 0.88 |
|                   | \(\hat{\theta}_{\psi_{gL}}\)   | 7e-4 -0.02 3e-4 1e-3 0.92 |
|                   | \(\hat{\theta}\)               | 4e-3 -6e-3 3e-3 0.01 0.90 |
| \(\psi_{gA}\)     | \(\hat{\theta}_{ML,\psi_{gA}}\) | 5e-3 0.03 4e-3 3e-3 0.93 |
|                   | \(\hat{\theta}_{ML}\)          | 9e-3 0.05 7e-3 4e-3 0.90 |
|                   | \(\hat{\theta}_{\psi_{gA}}\)   | 2e-3 -0.02 3e-3 2e-3 0.97 |
|                   | \(\hat{\theta}\)               | 6e-3 -8e-3 6e-3 7e-3 0.90 |
| \(\Psi_{gS}\)     | \(\hat{\theta}_{ML,\Psi_{gS}}\) | 0.05 0.03 0.05 0.08 1.08 |
|                   | \(\hat{\theta}_{ML}\)          | 0.13 0.01 0.13 0.25 1.01 |
|                   | \(\hat{\theta}_{\Psi_{gS}}\)   | 0.02 2e-3 0.02 0.02 0.94 |
|                   | \(\hat{\theta}\)               | 0.02 -0.05 0.02 0.03 0.92 |
| \(\Psi_{gL}\)     | \(\hat{\theta}_{ML,\Psi_{gL}}\) | 0.05 0.03 0.05 0.06 1.06 |
|                   | \(\hat{\theta}_{ML}\)          | 0.03 0.05 0.02 0.07 1.07 |
|                   | \(\hat{\theta}_{\Psi_{gL}}\)   | 0.02 -0.10 0.01 0.02 0.91 |
|                   | \(\hat{\theta}\)               | 0.03 -0.06 0.02 0.03 0.87 |
| \(\Psi_{gA}\)     | \(\hat{\theta}_{ML,\Psi_{gA}}\) | 0.33 0.41 0.17 0.05 1.05 |
|                   | \(\hat{\theta}_{ML}\)          | 0.30 0.34 0.19 0.05 1.05 |
|                   | \(\hat{\theta}_{\Psi_{gA}}\)   | 0.10 -0.16 0.08 0.06 0.91 |
|                   | \(\hat{\theta}\)               | 0.15 -0.29 0.06 0.10 0.88 |
the one defined in the NIMROD software. We choose our mesh-size such that we get 200 discretization points for each subject on the observation interval and we use $U = 10$ i.e. a value lower than in the simulated data case because of the model error presence. We also proceed to the log-transformation of the data to stabilize the measurement noise variance. This drives us to use the nonlinear model:

$$\hat{A}_b_i(t) = \frac{1}{\ln(10)} \left( \phi_{S,i} e^{-\delta_S t} + \phi_{L,i} e^{-\delta_L t} \right) 10^{-\hat{A}_b_i(t)} - \frac{\delta_{A_b,i}}{\ln(10)} \tag{5.1}$$

describing the dynamic of $\hat{A}_b_i(t) := \log_{10} A_b_i(t)$ for parameter estimation purpose. We use $A_{\hat{\theta},b_i}(t, x, z_i(t)) = \frac{1}{\ln(10)} \left( \phi_{S,i} e^{-\delta_S t} + \phi_{L,i} e^{-\delta_L t} \right) \ln x$ and $r_{\theta,b_i}(t, z_i(t)) = -\frac{\delta_{A_b,i}}{\ln(10)}$ for the pseudo-linear formulation of the model. Our estimations and the ones from the original paper Pasin et al. (2019) are presented in Table 5.1 for the sake of comparison. In the following, we denote $\left( \hat{\theta}^P, \hat{b}_i^P \right)$ (respectively $\left( \hat{\theta}, \hat{b}_i \right)$) the estimation obtained by Pasin et al. (2019) (respectively our approach) for the mean population parameter and subject specific ones. Both methods produce estimations with overlapping confidence intervals for $\theta$. Still, significant differences appear for $(\Psi_{\phi_S}, \Psi_{\phi_L}, \Psi_{\delta_{A_b}})$ estimation which quantifies the dispersion of random effects. This is explained by the fact that we only consider a subset of the subjects used in Pasin et al. (2019) for estimation. This has an effect on the observed diversity within the cohort of patients and thus on $(\Psi_{\phi_S}, \Psi_{\phi_L}, \Psi_{\delta_{A_b}})$ estimation. Regarding the predictions, we present in figure 5.1 examples of estimated trajectories. The confidence intervals are computed via Monte-Carlo sampling from the approximated

### Table 5.1. Estimation presented in Pasin et al. (2019) (left) and via our approach (right)

| Parameter | Pasin et al. | CI (95%) | OCA | CI (95%) |
|-----------|--------------|----------|-----|----------|
| $\psi_{\delta_S}$ | -0.57 | [-1.02, -0.02] | -0.18 | [-0.58, 0.22] |
| $\psi_{\phi_S}$ | 7.92 | [7.52, 8.30] | 7.45 | [6.85, 7.96] |
| $\psi_{\phi_L}$ | 2.78 | [2.62, 3.01] | 2.58 | [2.15, 3.01] |
| $\psi_{\delta_{A_b}}$ | -3.54 | [-3.62, -3.45] | -3.48 | [-3.95, -3.01] |
| $\Psi_{\phi_S}$ | 0.92 | [0.83, 1.01] | 0.64 | [0.60, 0.70] |
| $\Psi_{\phi_L}$ | 0.85 | [0.78, 0.92] | 0.70 | [0.55, 0.90] |
| $\Psi_{\delta_{A_b}}$ | 0.3 | [0.24, 0.36] | 0.25 | [0.19, 0.31] |
Fig. 5.1. Examples of fitted trajectories for both methods for different subjects. Here Time=0 is the 7th day post-second dose. Dashed lines: fitted ODE solutions \( \hat{\theta}^P, \hat{b}_i^P \). Solid line: optimal trajectories \( X_{\hat{\theta}, \hat{b}_i} \). Shaded area are the 95% confidence intervals.
normal laws $N(\hat{\theta}, V(\hat{\theta}))$ and $N(\hat{\theta}^P, V(\hat{\theta}^P))$ to quantify the effect of estimation uncertainty on $\theta$ on the predicted trajectories. For NIMROD estimation, for a given sampled value $\hat{\theta}^P \sim N(\hat{\theta}^P, V(\hat{\theta}^P))$ and subject $i$, the sampled regression function $X_{\hat{\theta}^P, \hat{b}_i, x_{0,i}}$ is obtained by solving ODE (5.1) for parameter values $(\theta, b_i, x_{0,i}) = (\hat{\theta}^P, \hat{b}_i, y_{0,i})$. Regarding our approach we recall the regression functions are now defined as optimal trajectories. So, for $\tilde{\theta} \sim N(\tilde{\theta}, V(\tilde{\theta}))$ the sampled regression function for subject $i$ is the optimal trajectory $X_{\tilde{\theta}, \hat{b}_i}$ obtained via the minimization of the cost function $C_i(\hat{b}_i, x_{i,0}, u_i | \tilde{\theta}, U)$. This explain the differences between the two confidence intervals in terms of shape and width. Our method gives narrower intervals because for each sampled value an optimal control problem is solved to obtain the related optimal trajectory. This imposes a common goal of data fidelity to each sampled $X_{\tilde{\theta}, \hat{b}_i}$ which limits their inter-variability. Still, despite these differences in shapes, both prediction intervals cover the same points. Moreover, on the long-term our intervals are nearly always contained in the ones given by NIMROD.

Our estimation of $\theta$ supports the parameter inference obtained in [Pasin et al. (2019)] via another method and the subsequent analysis made on the antibody concentration dynamics. In addition to this parametric comparison, we want to assess the model adequacy via the temporal evolution analysis of the optimal controls $\pi_{i, \tilde{\theta}, b_i(\hat{\theta})}$ estimated as byproducts of our method. Indeed, they quantify the exogenous perturbations $u_i$ we need to add to model (5.1) so that the solution of its perturbed counterpart,

$$\tilde{Ab}_{i,u}(t) = \frac{1}{\ln(10)} \left( \phi_{S,i} e^{-\delta_S t} + \phi_{L,i} e^{-\delta_L t} \right) \frac{10 - \tilde{Ab}_{i,u}(t)}{\ln(10)} + u_i$$

(5.2)

reproduce the observations. This approach is similar to the one developed in [Hooker et al. (2015)] where control theory replaces non-parametric procedures to estimate $u_i$. Still, their approach relies on a finite basis approximation of $\tilde{Ab}_{i,u}$ which requires to specify a basis function family, its dimension as well as a penalization parameter similar to $U$. At the contrary, our method avoids this complex step of hyper-parameter selection and only needs $U$. For comparison, we also quantify the committed model error for $(\hat{\theta}^P, \hat{b}_i^P)$. To do so we compute $\pi_{i}^P$, the solution of the optimal control problem: $\pi_{i}^P = \arg \min_{u_i} \left\{ \sum_j \left\| \tilde{Ab}_{i, \hat{\theta}^P, \hat{b}_i^P, y_{0,i}, u_i} (t_{ij}) - y_{ij} \right\|^2_2 + \| u_i \|_{U,L}^2 \right\}$ by using the procedure described
in section 3 for non-linear models. In the last expression, \( \tilde{A}_{t_i, \hat{\theta}, \hat{b}_i, y_{i0}, U_i} \) is the solution of the perturbed ODE (5.2) for \((\theta, b_i) = (\hat{\theta}_P, \hat{b}_i)\) and \(y_{i0}\) is the measured concentration at \(t = 0\) used as a surrogate value for the initial condition (as they did in Pasin et al. (2019)). We still use \(U = 10\) for this optimal control problem to allow for the same level of perturbation magnitude for both methods. In figure 5.2, we plot \( u_{t_i, \hat{\theta}, \hat{b}_i(\hat{\theta})} \) and \( u_P \) as well as their mean values and confidence intervals. Our method leads to residual perturbations of smaller magnitudes and narrower confidence intervals. This means our approach produces an estimation which minimizes the committed model error for each subject comparing to a method based only on a data fitting criteria. This is particularly clear at the beginning of the observation interval when the influence of the initial conditions is the highest. In this case our narrower confidence interval clearly excludes a null perturbation and advocates for an over-estimation of the predicted antibody concentration by the model. This makes sense because model (4.5) assumes that both populations of antibody secreting cells decrease with time, and that is probably not completely true at the beginning of the dynamic. Thus, despite similar results regarding parameter values between our estimation and Pasin et al. (2019), the insight given by our method at the dynamic scale leads us to the additional conclusion of model misspecification presence at the beginning of the observation interval.

6. Conclusion

In this work, we propose an estimation method addressing issues encountered by classic approaches for the problem of parameter estimation in NLME-ODEs. We identify three potential sources of problems for exact methods such as likelihood based inference: their difficulties in presence of model error, their need to estimate initial conditions and their dramatic performance degradation when facing poorly identifiable parameters. We propose here a method based on control theory accounting for the presence of potential model uncertainty at the subject level and which can be easily profiled on the initial conditions. Simulations with both presence and absence of model errors illustrate the benefits of regularization techniques for estimating poorly identifiable parameters, subject specific parameters as well as their variances in NLME-ODEs. In addition, bypass-
Fig. 5.2. 1) Up: Estimated residual controls for each subject, 2) bottom: mean optimal control and 95% confidence interval for the optimal controls a) left: \( \bar{\pi}^P_i \) obtained from parameter estimation in Pasin et al. [2019], b) right: \( \bar{\pi}_{\mu, \beta_i(\tilde{\theta})} \) obtained from our estimation.
ing estimation of initial conditions represents a clear advantage for partially observed systems comparing to likelihood based approaches, as emphasized in simulations.

Still, this benefit in term of estimation accuracy comes with a computational price. On a server with the parallelization package Snow in R language, it takes approximately 10-15 minutes to obtain an estimation for the two-dimensional linear model, 30 minutes for the insulin model and 3-4 hour for the antibody concentration evolution one, whereas it was a matter of minutes for the other approaches. Nevertheless, the use of compiled languages and proper parallelization could reduce the computation time. Moreover, we have willingly separated the formal definition of the optimal control problem required by our method and the numerical procedure used to solve it, in case it may exist better suited approaches for this specific control problem. Right now, our current strategy allows us to profile on initial conditions, so looking for another numerical procedure is beyond the scope of this paper.

An under-exploited feature of the method so far is the obtained optimal controls. The qualitative based analysis exposed in section 5 can be made more rigorous. For example, to stay in a Bayesian setting, we can specify a prior distribution for the controls and then compare it with the obtained posterior once the inference is made. This would lead to a semi-parametric inference problem for which an optimal control based approach has already been proven useful (see Clairon and Brunel (2018); Clairon (2020)). This is a subject for further work.

Software

Our estimation method is implemented in R and a code reproducing the examples of Section 4 is available on a GitHub repository located here.

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