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Estimation of the Lubuma-Gumel Buffalo-only Model with Incomplete Data

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Abstract

In this work, a reduced model proposed by Lubuma and Gumel for transmission dynamics of Mycobacterium tuberculosis and Bovine tuberculosis in a community consisting of humans and African buffaloes is considered. The buffalo-only component of the model is however, examined for parameter estimation. The problem is to propose an analytical approach for restoring the state variables, E_{B1} and E_{B2} which are the early and advanced-exposed buffaloes to Bovine tuberculosis respectively. These model variables are the assumed missing information about the population of susceptible Buffaloes. The discussed method is then used to restore this missing information in the susceptibles. The approach uses differential equations that are linearized through new parameters to form an objective function that is minimized using the least-squares methods in order to compute the required model coefficients. The Results show that the approach is efficient given the relatively small absolute errors of order 10^{-3} and 10^{-4} also the estimated trends that closely mimic the simulated (observed) data of the state variables.

AMS subject classification:
Keywords: Parameter estimation, Nonlinear models, Ecological models, Incomplete data

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1. Introduction

Ecologists and environmentalist rely on mathematical models, both to understand ecological systems and to predict future system behavior. For the last several decades mathematical modeling has become an important part of ecological research [3, 6, 8]. Mathematical models make assessments and predictions in ecology more objective and reliable [5]. In turn, models rely on suitable estimates of their parameters [10] for reliability of any inferences they make. Parameter estimation of dynamical models is of an important concern in numerical ecology. A mathematical model of a real object is a totality of logical connections, formalized dependencies, and formulas, which enables the studying of a real object without its experimental analysis [5, 2, 1]. The objects of ecological research are populations, communities, and ecosystems. Mathematical modeling is important in ecological studies, as it is known that conducting experiments on such objects is not possible and always restricted in cases were it could be possible, because it can lead to changes or even destruction of the ecological objects [5].

The non-linearity of the models and data scarcity are all major issues that contribute to the complexity of the problem, whose solutions are usually obtained by numerical methods [9]. Incomplete data presents a problem in both inferential and predictive modeling applications. Other statistical traditional methods such as complete case analysis and simple imputation tend to produce results that inadequately estimate standard errors and parameter estimates, particularly where missingness is not purely at random [4, 13]. This paper presents an analytical method that can be used to estimate all parameters and restore missing data of an ecological model. The problem of the identifiability of mathematical models in ecology and epidemiology is considered.

2. Problem

Incomplete data are a rule rather than an exception in both qualitative and quantitative research [4]. In this study, the model that is analyzed is based on the transmission dynamics of *Mycobacterium tuberculosis* (MTB) and *Bovine tuberculosis* (BTB) in a population consisting of humans and African buffaloes [7]. However, in this case, the buffalo-only component is studied assuming that the human component is set to zero [7]. BTB remains a serious problem for animals and human health in many developing countries [12]. The total buffalo population (in the herd) at time *t*, denoted by $N_B(t)$, is subdivided into five mutually exclusive compartments which are

$$\begin{aligned}
S_B(t) &= \text{susceptible;}\\
E_{B1}(t) &= \text{early exposed with BTB;}\\
E_{B2}(t) &= \text{advanced exposed with BTB;}\\
I_{BB}(t) &= \text{infected with clinical symptoms of BTB;}\\
R_{BB}(t) &= \text{recovered from BTB.}
\end{aligned}$$

2.1. The *Lubuma-Gumel* reduced Model

Considering the reduced buffalo-only [7] model

$$\frac{dS_B}{dt} = \pi_B - (\lambda_B + \mu_B)\, S_B, \tag{2.1}$$

$$\frac{dE_{B1}}{dt} = \lambda_B S_B - (\theta_{EB}\lambda_B + \kappa_1 + \mu_B)\, E_{B1}, \tag{2.2}$$

$$\frac{dE_{B2}}{dt} = \kappa_1 E_{B1} - (\theta_{EB}\lambda_B + \sigma_{B2} + \mu_B)\, E_{B2}, \tag{2.3}$$

$$\begin{aligned}\frac{dI_{BB}}{dt} &= \sigma_{B2}E_{B2} - (E_{B1} + E_2)\,\theta_{EB}\lambda_B + \\ &\quad \theta_{RB}\lambda_B R_{BB} - \left(\gamma_{B1} + \mu_B + \delta_B\right) I_{BB},\end{aligned} \tag{2.4}$$

$$\frac{dR_{BB}}{dt} = \gamma_{B1} I_{BB} - (\theta_{RB}\lambda_B + \mu_B)\, R_{BB}. \tag{2.5}$$

The system or model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), has nine unknowns which are

$$\Pi_B, \lambda_B, \mu_B;\ \theta_{EB}, \theta_{RB};\ \kappa_1, \sigma_{B2}, \gamma_{B2}, \delta_B.$$

It is also known that

$$\begin{aligned} S_B &= S_B(t);\ I_{BB} = I_{BB}(t);\ R_{BB} = R_{BB}(t) \text{ and} \\ N_B &= S_B + (E_{B1} + E_{B2}) + I_{BB} + R_{BB} = N_B(t), \end{aligned}$$

are observable.

However, in this research, it is assumed that the individual compartments of the early exposed, E_{B1} and advanced exposed with BTB, E_{B2} are missing, and only their sum $(E_{B1} + E_{B2})$ is known. The problem is to propose an analytical method that will restore the individual compartments at a time t. That is, this study shows that it is possible to calculate all coefficients of the system, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), and find the required compartments. In other words, we wish to determine $E_{B1} = E_{B1}(t)$ and $E_{B2} = E_{B2}(t)$. For a full description of the model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), parameters see Table 1.

Table 2 contains selected parameter values of the buffalo-only model on which the assumptions in Section 3 are based. The derived assumption enable the enhance the computation approaches of the proposed method.

3. Methodological Assumptions

In modeling, the actual assumptions used to decide on a given course of action are rarely laid out explicitly, however. Instead, they are only implied by the nature of the action itself. In our methodological development the implicit assumptions are regarded inherent to the proposed process modeling steps, just as they are to most other types of action

Table 1: Parameter description of BTB model

Parameter	Interpretation
Π_B	Recruitment rate of buffaloes
μ_B	Natural death rate of buffaloes
γ_{B1}	Recovery rate of buffaloes
κ_1	Progression rate from E_{B1} to E_{B2} class
σ_{B2}	Progression rate from E_{B2} to I_{BB} class
θ_{RB}	Exogenous reinfection rate for recovered buffaloes
θ_{EB}	Exogenous reinfection rate for buffaloes in the exposed and recovered classes, respectively
δ_B	Disease induced death rate for buffaloes

Table 2: Baseline values for selected parameters of the BTB model [7]

Parameter	Baseline value (day^{-1})
μ_B	0.0001053
η_{B1}	0.45
η_{B2}	0.55
κ_1	0.5
σ_{B2}	0.3
θ_{EB}	0.00271

[11]. Some assumptions with reference to the model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), are

Assumption 3.1. $\eta_{B1} = \eta_{B2} = \eta_B$, from Table 2 the baseline values for η_{B1} and η_{B2} are 0.5 and 0.53, with a difference of 0.05 which is assumed to be small. Hence the equality of the parameters.

Assumption 3.2. From Equation (2.2), $(\theta_{EB}\lambda_B + \kappa_1 + \mu_B) \cong \kappa_1$, it is noted from Table 2 that the values of θ_{EB} and μ_B are 0.00271 and 0.0001053 respectively. Hence substantially small relative to the value of κ_1 =0.5 and can be ignored.

Assumption 3.3. From Equation (2.3), $(\theta_{EB}\lambda_B + \sigma_{B2} + \mu_B) \cong \sigma_{B2}$, Table 2 indicates that the values of μ_B and θ_{EB} are respectively 0.0001053 and 0.00271, significantly small compared to $\sigma_{B2} = 0.3$ and thus can be ignored in the computation.

4. Analysis of the model

Consider the buffalo-only model presented by the system of Equations (2.1), (2.2), (2.3), (2.4) and (2.5) at steady state [7]. Summing the system, Equations (2.1), (2.2), (2.3), (2.4) and (2.5) we obtain

$$\frac{dN_B(t)}{dt} = \Pi_B - \mu_B N_B(t) - \delta_B I_{BB}, \tag{4.1}$$

from which parameter coefficients μ_B and δ_B can be observed. By summing Equations (2.2), (2.3) and (2.4) of the system, Equations (2.1), (2.2), (2.3), (2.4) and (2.5) the result is

$$\frac{d(E_{B1} + E_{B2} + I_{BB})}{dt} = \frac{d(N_B - S_{B2} - R_{BB})}{dt}. \tag{4.2}$$

Equation 4.2 can be represented as

$$\begin{aligned}\frac{dY}{dt} &= \lambda_B S_B + \theta_{RB}\lambda_B R_{BB} - \mu_B(E_{B1} + E_{B2} + I_{BB}) \\ &\quad - (\gamma_{B1} + \delta_B)I_{BB} + \theta_{RB}\lambda_B R_{BB},\end{aligned} \tag{4.3}$$

which does not present us with any new additional information.

5. Method of solution

Our ultimate goal is to obtain estimates for the individual compartments E_{B1} and E_{B2} such that the solutions are close to the observed data.

Using assumption 3.1 and Equation (23) of [7], we obtain,

$$\begin{aligned}\lambda_B &= \frac{\beta_B}{N_B}[(E_{B1} + E_{B2})\eta_B + I_{BB}] \\ &= (\beta_B)\frac{I_{BB}}{N_B} + (\beta_B\eta_B)\frac{E_{B1} + E_{B2}}{N_B} \\ &= (\beta_B)\frac{I_{BB}}{N_B} + (\beta_B\eta_B)\frac{Z}{N_B},\end{aligned} \tag{5.1}$$

where

$$Z = E_{B1} + E_{B2} = N_B - I_{BB} - S_B - R_{BB}$$

all are known model compartments, Z is a new representation of the compartments. Considering Equation (2.1) of model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), parameters Π_B, μ_B and S_B are known or can be obtained since

$$\frac{dS_B}{d_t} = (\Pi_B - \mu_B S_B) - \lambda_B S_B,$$

where, $\dfrac{dS_B}{dt}$ is also known.

Then,

$$\lambda_B = \frac{\Pi_B}{S_B} - \mu_B - \frac{\dot{S_B}}{S_B}, \tag{5.2}$$

where, $\dot{S_B} = \dfrac{dS_B}{d_t}$.
Therefore,

$$\begin{aligned}\lambda_B &= \frac{I_{BB}}{N_B}(\beta_B) + (\beta_B\eta_B)\frac{Z}{N_B},\\ &= \frac{\Pi_B}{S_B} - \mu_B - \frac{\dot{S_B}}{S_B}.\end{aligned} \tag{5.3}$$

It can therefore, be observed that λ_B is estimated from Equation (5.3) by applying numerical integration,

$$\begin{aligned}\lambda_B &= \beta_B \int_0^t \frac{I_{BB}(\tau)}{N_B(\tau)}d\tau + (\beta_B\eta_B)\int_0^t \frac{Z(\tau)}{N_B(\tau)}d\tau,\\ &= \Pi_B \int_0^t \frac{d\tau}{S_B(\tau)} - \mu_B t - \ln\left[\frac{S_B(t)}{S_B(t)}\right].\end{aligned} \tag{5.4}$$

It can then be concluded that

$$\lambda_B = \lambda_B(t) = \frac{I_{BB}}{N_B}(\beta_B) + (\beta_B\eta_B)\frac{Z}{N_B},$$

is a known function of t in τ Equation (5.3).

Considering assumptions 3.2 and 3.3, Then Equations (2.2 & 2.3) of model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), can be rewritten as

$$\frac{dE_{B1}}{dt} \cong \lambda_B S_B - \kappa_1 E_{B1}; \tag{5.5}$$

$$\frac{dE_{B2}}{dt} \cong \kappa_1 E_{B1} - \sigma_{B2} E_{B2}. \tag{5.6}$$

Equations (5.5 and 5.6) present an under-determined system, from which only $(E_{B1} + E_{B2})$, λ_B and S_B are known, we therefore need to find E_{B1}, E_{B2}, κ_1 and σ_{B2}. From

$$E_{B1} + E_{B2} = Z = Z(t),$$

and adding Equations (5.5 & 5.6), we obtain

$$\frac{dZ}{dt} = \lambda_B S_B - \sigma_{B2} E_{B2}, \tag{5.7}$$

From Equation (5.7), it implies that

$$\sigma_{B2} E_{B2} = \lambda_B(t) S_B(t) - \frac{dZ(t)}{dt} = V(t), \tag{5.8}$$

It can be noted that all terms on the right hand side of Equation (5.8) are known. Hence we can estimate compartment E_{B2} as

$$E_{B2}(t) = \frac{1}{\sigma_{B2}} V(t), \tag{5.9}$$

and compartment E_{B1} can be estimated as

$$\begin{aligned} E_{B1}(t) &= Z(t) - E_{B2} \\ &= Z(t) - \frac{1}{\sigma_{B2}} V(t). \end{aligned} \tag{5.10}$$

However, it has to be noted that coefficients σ_{B2} and κ_1 are also unknown ad have to be estimated.

Substituting Equation (5.10) into Equation (5.5)

$$\frac{d[Z - \frac{1}{\sigma_{B2}} V]}{dt} + \kappa_1 [Z - \frac{1}{\sigma_{B2}} V] - \lambda_B S_B \cong 0. \tag{5.11}$$

Equation (5.11) can be written as

$$\frac{dZ}{dt} + C_1 (-\frac{dV}{dt}) + C_2 Z + C_3 (-V) - \lambda_B S_B = 0, \tag{5.12}$$

where,

$$C_1 = \frac{1}{\sigma_{B2}};\ C_2 = \kappa_1;\ C_3 = \frac{\kappa_1}{\sigma_{B2}}$$

Constraining Equation (5.12), as

$$C_1 C_2 - C_3 = 0,$$

and integrating, we obtain

$$\begin{aligned} & C_1 [V(0) - V(t)] + C_2 \int_0^t Z(\tau) d\tau + C_3 - \\ & \left[- \int_0^t V(\tau) d\tau \right] - W(t) = 0. \end{aligned} \tag{5.13}$$

where,

$$W(t) = \int_0^t \lambda_B(\tau) S_B(\tau) d\tau + Z(0) - Z(t). \tag{5.14}$$

The optimal values for $C_1,\ C_2$ and C_3 can then be computed using the least squares method by minimizing the objective function

$$G(\Omega) = \sum_{k=1}^{N} \{C_1 F + C_2 G + C_3 H - W(t)\}^2 + \\ \lambda(C_1 C_2 - C_3) \to min \tag{5.15}$$

where,

$$\Omega = C_1, C_2, C_3, \lambda_B,\ F = V(0) - V(t_k), \\ G = \int_0^{t_k} Z(\tau)d\tau,\ H = -\int_0^{t} V(\tau)d\tau.$$

6. Numerical Simulation

From [7], the buffalo-only model was fitted using data obtained from South Africa's Kruger National Park, Table 4 of [7]. In this study, a simulation of system, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), is done. It is assumed that on the first instance all the model parameters and the initial conditions of the state variables are known. Hence the system, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), can numerically be identified. Using initial values provided by [7] we have

$$\mu_B = 0.02,\ \delta_B = 0.9,\ \gamma_B = 0.06,\ \Pi_B = 10, \\ b = 0.8,\ \xi = 0.04,\ \alpha_B = 0.04,\ \eta = 0.03, \\ \lambda = 0.01,\ \beta_1 = 0.006,\ \beta_2 = 0.012,\ \sigma_B = 0.6$$

The solution of the buffalo-only model, system [2.1-2.5] is obtained using Adam's method in Mathcad® software. Also parameter values and initial conditions from [7] are used.

Figure 1 presents simulations of the buffalo-only model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), indicating the population of susceptible buffaloes ($S_B = Z^{\langle 1 \rangle}$), population of buffaloes ($I_{BB} = Z^{\langle 2 \rangle}$) with clinical symptoms of BTB, population of buffaloes ($R_{BB} = Z^{\langle 3 \rangle}$) which recovered from BTB, population of buffaloes ($E_{B1} = Z^{\langle 4 \rangle}$) early exposed to BTB and population of buffaloes ($E_{B2} = Z^{\langle 5 \rangle}$) at advanced-exposed BTB stage. In this study, the trends shown in Figure 1 are assumed to be from observed data and we wish to restore the data (compartments) which are regarded as missing using parameter coefficients given in Table 3.

The proposed method is firstly used to compute the model, , Equations (2.1), (2.2), (2.3), (2.4) and (2.5), coefficients and the coefficients subsequently used to estimated the required state variables or compartments. Table 3, shows the estimated parameter coefficients and their corresponding absolute percentage error relative to the "'true"' or observed coefficients.

Table 3: Parameter comparison for the observed and estimated values using the absolute % error

Parameter	Observed	Estimated	Abs % Error
Π_B	10	10.148	1.477
μ_B	0.02	0.016	19.63
δ_B	0.9	0.934	3.797
γ_B	0.06	0.055	8.893
β_B	0.8	0.826	3.258

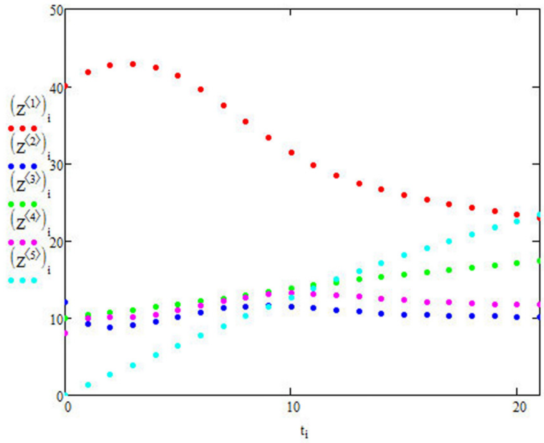

Figure 1: Compartmental trends for the buffalo-only model [2.1-2.5], using simulations based on data from South Africa's Kruger National Park (Table 4) [7].

7. Results and Discussion

In this section, results of the estimated and simulated state variable are presented. The estimates are a result of using parameter coefficients computed using the proposed approach in Section 5. In this case the approach presented is able to restore and reconstruct the original state variable trends. The observed data (no missing compartments) is used to construct the trends as shown in Figure 1; which are ideally the simulations of the observed data.

From Figure 2, it is observed that the trend obtained from the estimated values clearly mimics that of the simulated observed population of the susceptible buffaloes. This is further justified by Figure 3 which shows the absolute percentage error. It indicates how far off the estimated values are from the simulated values. It is also observed that minimum error is approximately of order 10^{-4} at 0.01 just where the graph starts to raise. Considering Figure 4, it is also observed that the estimated trend for the buffaloes $RR(t_i)$ which recovered from BTB is coherent with the simulated $Z^{\langle 3\rangle}$ trend (considered as the observed trend). An error analysis is performed to obtain the absolute percentage error that is due to the simulated values of $Z^{\langle 3\rangle}$ in comparison with the estimated $RR(t_i)$

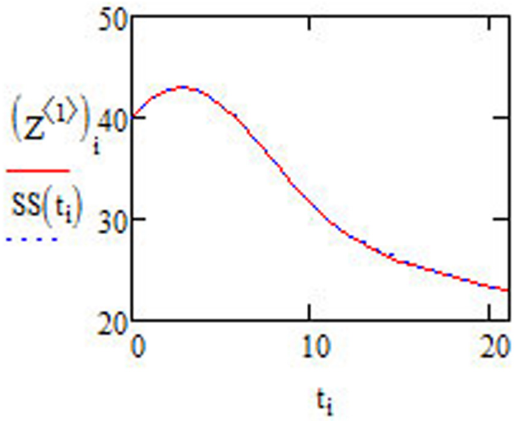

Figure 2: Data fit of the estimated $SS_{(ti)}$ and simulated $Z^{\langle 1 \rangle}$ total number of susceptible buffaloes over time t_i.

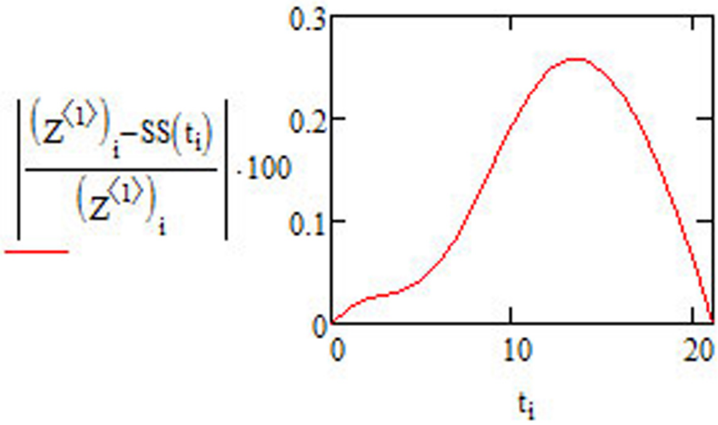

Figure 3: Absolute percentage error for the estimated and the simulated values for the population of susceptible buffaloes.

data of the population of buffaloes which recovered from BTB, Figure 5. From the error analysis graph, Figure 5, it can be observed that the best estimated results occur when the error is of order 10^{-3} at 0.1.

The trends of the population of buffaloes that are early exposed to BTB over time, (t_i), E_{B1} are shown in Figure 6. It is observed that, the estimated trend $DD(t_i)$ mimics the trend of the simulated $Z^{\langle 4 \rangle}$ quite well over the entire period of time considered.

The minimum error between the estimated $DD(t_i)$ and the simulated (observed) $Z^{\langle 4 \rangle}$ (E_{B1}) population of buffaloes which are early exposed to BTB over time is of order 2.5×10^{-3} at 0.25, Figure 7. It is at this error point that "good" estimates from the proposed method best fit the simulated observations.

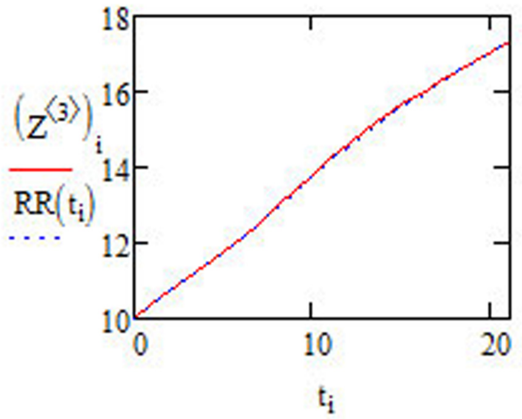

Figure 4: Trends of the fitted $RR(ti)$ and simulated $Z^{\langle 3\rangle}$ population of buffaloes which recovered from BTB.

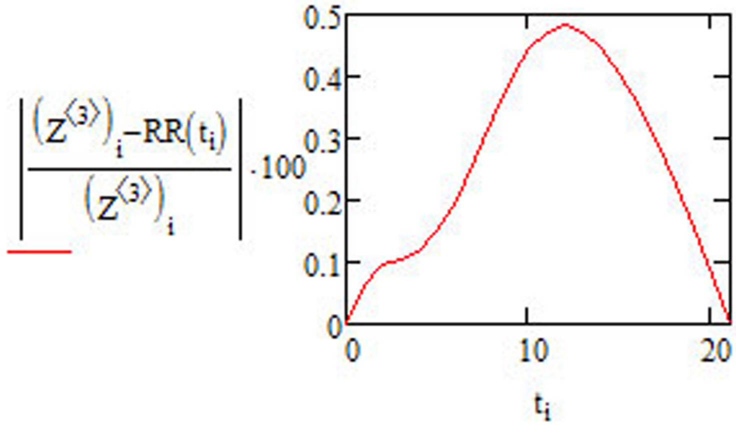

Figure 5: Error analysis for the estimated $RR(t_i)$ and the simulated $Z^{\langle 3\rangle}$ values for the population of buffaloes which recovered from BTB.

8. Conclusion

An analytical method for estimating the parameters of a reduced deterministic model, for the transmission dynamics of BTB and MTB in a community consisting of humans and buffaloes is discussed. The method is formulated to estimate the missing state variables for the buffalo-only component, model, Equations (2.1), (2.2), (2.3), (2.4) and (2.5), proposed by [7]. From Figure 1, simulated trends of the state variables are firstly presented, then from Figures 2, 4 & 6, using the estimated model coefficients in Table 3, the estimated and simulated state variables are plotted on the same axes. It is observed that the estimated and the simulated profiles of the model variables mimic each other

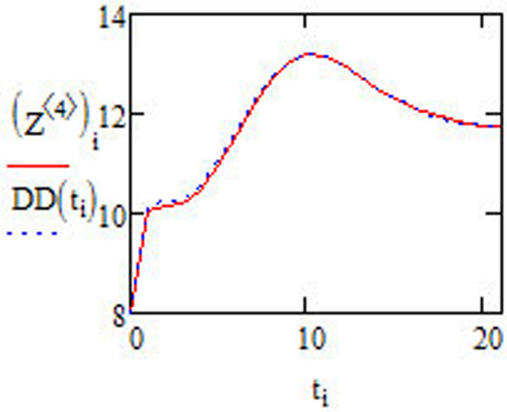

Figure 6: Trends of the fitted $DD(t_i)$ and observed $Z^{\langle 4\rangle}$ population of buffaloes early-exposed to BTB.

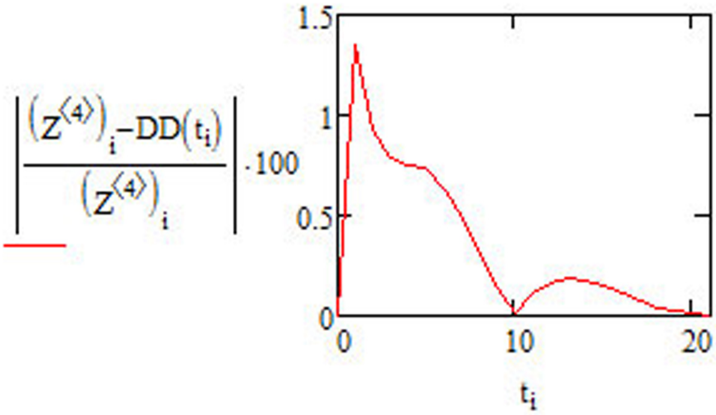

Figure 7: Absolute % error between the estimated $DD(t_i)$ and the simulated $Z^{\langle 4\rangle}$ values for the population of buffaloes early exposed to BTB.

quite well over a period of time, Figures 2, 4 & 6. This is also supported by the small estimation orders of 10^{-3} and 10^{-4} in the errors, Figures 3, 5 & 7.

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References

[1] Abanda, F., Tah, J., and Cheung, F. Mathematical modelling of embodied energy, greenhouse gases, waste, time–cost parameters of building projects: A review. *Building and environment 59* (2013), 23–37.

[2] Bender, E. A. *An introduction to mathematical modeling*. Courier Corporation, 2012.

[3] Ciarletta, P., Hillen, T., Othmer, H., and Trucu, D. *Mathematical Models and Methods for Living Systems: Levico Terme, Italy 2014*, vol. 2167. Springer, 2016.

[4] Dong, Y., and Peng, C.-Y. J. Principled missing data methods for researchers. *SpringerPlus 2*, 1 (2013), 222.

[5] Gertsev, V., and Gertseva, V. Classification of mathematical models in ecology. *Ecological Modelling 178*, 3 (2004), 329–334.

[6] Goel, N. S., and Richter-Dyn, N. *Stochastic models in biology*. Elsevier, 2016.

[7] Hassan, A. S., Garba, S. M., Gumel, A. B., and Lubuma, J.-S. Dynamics of mycobacterium and bovine tuberculosis in a human-buffalo population. *Computational and mathematical methods in medicine 2014* (2014).

[8] Kabanikhin, S., Voronov, D., Grodz, A., and Krivorotko, O. Identifiability of mathematical models in medical biology. *Russian Journal of Genetics: Applied Research 6*, 8 (2016), 838–844.

[9] Marsili-Libelli, S., Guerrizio, S., and Checchi, N. Confidence regions of estimated parameters for ecological systems. *Ecological Modelling 165*, 2 (2003), 127–146.

[10] McCallum, H. *Population Parameters: Estimation for Ecological Models*. Wiley-Blackwell, 1999.

[11] NIST/SEMATECH. *e-Handbook of Statistical Methods*. US Department of Commerce, 2013.

[12] Palmer, M. V., Waters, W. R., and Whipple, D. L. Investigation of the transmission of mycobacterium bovis from deer to cattle through indirect contact. *American Journal of Veterinary Research 65*, 11 (2004), 1483–1489.

[13] Truxillo, C. Maximum likelihood parameter estimation with incomplete data.