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African Swine Fever Transmission Dynamics: Parameter Estimation and Global Sensitivity Analysis

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Abstract: African swine fever (ASF), a highly contagious and often fatal viral disease caused by the African swine fever virus (ASFV), continues to pose a significant threat to pig production systems in many regions of the world. The disease leads to substantial economic losses and challenges in livestock management. This study presents a comprehensive mathematical analysis of the transmission dynamics of ASF. First, we employ a Least square framework to estimate key epidemiological parameters of the model, allowing for the incorporation of prior knowledge and uncertainty quantification. Second, we conduct a global sensitivity analysis using Latin Hypercube Sampling (LHS) in combination with Partial Rank Correlation Coefficients (PRCC) to systematically identify and rank the parameters that exert the greatest influence on model outcomes. Finally, numerical simulations are performed to complement and validate the analytical findings, providing further insight into the disease's progression under varying parameter scenarios. The results enhance the understanding of ASF transmission mechanisms and highlight critical parameters that could inform targeted control strategies and policy interventions.

Keywords: African swine fever, Mathematical modelling, Sensitivity analysis, Parameter Estimation

1 Introduction

African Swine Fever (ASF) is an acute, viral, hemorrhagic, and highly contagious disease caused by the African swine fever virus (ASFV), a member of the Asfarviridae family and Asfivirus genus [1,2,3]. Highly virulent strains of ASFV can lead to mortality rates approaching 100% in domestic pigs and wild boar of all ages [1,4,5,6]. The disease was first reported in Kenya in 1921 and remains endemic in sub-Saharan Africa, but has spread worldwide, affecting over 50 nations, including major outbreaks in China (starting in 2018) and various European and Asian countries [1,2,7,4,5]. ASF can spread through direct contact with infected animals, their fluids or tissues, or indirectly through contaminated objects (fomites) such as vehicles, clothing, equipment, or feed products. In some regions, the disease involves soft ticks of the Ornithodoros species. ASF represents the main threat to swine production, posing a danger to pork production and commerce due to its high mortality rate and significant socioeconomic impact. For instance, ASF outbreaks in China led to the culling of 1.2 million pigs and resulted in an estimated economic impact of 0.78% of China's 2019 Gross Domestic Product [5,8]. The outbreak in China, the world's largest consumer of pork, caused a huge decrease in breeding volume, a pork shortage, and consequently, a rise in pork prices in 2019 [9,10].

Mathematical modeling is identified as a pivotal tool for studying infectious diseases, offering scientific support for decision-makers and helping to mitigate disease dynamics and limit economic consequences. ASF modeling studies generally focus on understanding viral dynamics to adapt appropriate control measures. Key modeling approaches includes Compartmental Models which are Traditional compartmental disease modeling frameworks, such as the Susceptible-Exposed-Infectious-Removed model, are frequently employed [6,11]. These models are often extended to include specific compartments like presymptomatic infectious, symptomatic infectious, asymptomatic infectious/carrier, detected cases, dead pigs, and the viral load in the environment. Another modeling approach is Fractional Order Models. Several recent studies in modeling ASF have utilized fractional-order differential equations in the Caputo sense, noting their advantage in interpreting the memory

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and genetic characteristics during disease transmission, often offering a better fit to real-world data compared to integer-order models [7,4,10]. These models have been applied to analyze stability, basic reproduction numbers, and optimal control strategies. Another approach in modelling ASF is Wild Boar Ecological Models tailored for wild boar populations incorporate age classes (piglets, yearlings/adults) and track susceptible, infected, survivor, and carcass populations to assess the dynamics of ASF persistence in wildlife [12]. These models also consider seasonal factors in recruitment (births) and their impact on disease dynamics.

A major focus across the literature is the calculation and sensitivity analysis of the basic reproduction number, the average number of secondary cases produced by a single infected individual in an entirely susceptible population [9,7]. Estimates for within-herd transmission parameters vary significantly, with R_0 ranging from 4.4 to 17.3 inferred from mortality data during Russian outbreaks, suggesting that farm-specific characteristics and biosecurity measures play a major role in spread patterns [13]. In a study analyzing ASF in Benin, the researchers found basic reproduction number equal to 2.78 in the absence of control measures, and the control reproduction number was 1.55 when existing controls were factored in [1]. Sensitivity analyses highlight that the dynamics of ASF transmission are significantly impacted by rates of pig recruitment, natural death, disease-induced death, and pig-to-pig transmission. For fractional-order models, the death rate of pigs and the virus clearance rate were found to be sensitive parameters, suggesting that increasing the mortality rate of diseased pigs or disinfection measures could reduce basic reproduction number [7]. For wild boar populations, the pig birth rate, the virus transmission rate, and the rate of virus deposition from infected dead pigs positively influence the control reproduction number. Conversely, the per capita death rate of pigs and the natural decay rate of the virus negatively influence the control reproduction number.

Currently, no effective drugs or commercial vaccines are available for ASF. Therefore, prevention and control measures, particularly strict biosecurity and culling, remain the best means to avoid infection. Effective Control Measures Identified through Modeling includes Culling and Disposal [10,1]. The early detection and culling (stamping out) of infected farms are consistently identified as critical to minimizing spread. In wild boar, the proper disposal, via burial or cremation, of ASFV-infected dead pigs is extremely effective at reducing ASFV transmission dynamics. Modeling wild boar interventions demonstrated that carcass removal is highly effective, although simple homogeneous Ordinary Differential Equation (ODE) models may give unrealistic predictions (like sudden bifurcations), while stochastic models produce more realistic responses to intervention. Biosecurity and Disinfection is also an effective control measure [1,10,14,15]. Modeling results emphasize the need for compliance with external biosecurity and the disinfection of vehicles to limit transmission in the neighborhood of infected farms. Regular disinfection and cleaning of pigstys are essential for preventing further ASF spread. Timely disinfection and sterilization, especially when using optimal control strategies in fractional-order models, can significantly reduce the number of infected pigs. Another effective control measure is media coverage [1,10,14,15]. Introducing media coverage into fractional-order models suggests that real-time media reports about the ASF epidemic are beneficial for breeders to scientifically prevent the spread in a timely manner. Combining media coverage with control measures, such as disinfection, can suppress the spread more effectively.

In essence, the literature underscores that ASF management relies heavily on understanding complex, multi-scale transmission pathways from the microscopic interactions within a herd to the macroscopic movement patterns across a trade network or a wild landscape. However, parameter estimation, a key component in modeling ASF has not been explored enough. Furthermore, studies utilizes local sensitivity analysis approach in understanding sensitive parameters in ASF. The approach is limited due to the fact that this method maintain all other parameters fixed at default levels, they are unable to appropriately measure uncertainty and sensitivity in the system [16]. The study contributes to the understanding of ASF spread by first conducting parameter estimation which is a key component in ASF modeling. Second, the study perform global sensitivity analysis using Latin Hypercube Sampling (LHS) and Partial Rank Correlation Coefficient (PRCC). The paper is organized as follows: The immediate section presents material and methods where a proposed model is extensively explained and formulated. Section 3 presents results and discussions followed by simulations of the model in section in section 4. Section 5 is the conclusion part of the paper.

2 Model formulation

In this part, we develop a mathematical model for the dynamics of African swine fever transmission in a tick-pig cycle, where the host population is domestic pigs. The susceptible S_1 and infectious I_1, subpopulations make up the tick population, and the overall tick population is $N_1 = S_1 + I_1$. In a similar manner, the pig population is separated into two subpopulations: susceptible S_2 and infectious I_2, with $N_2 = S_2 + I_2$ representing the total number of pigs. Let V be the number of infectious units in the environment, and we define the average number of ASFV required for a host to contract ASF as an infectious unit. Infected pigs can discharge ASFV to the environment at the rate ρ. We assume vertical transmission of ASFV in ticks at a rate q and a disease-induced death d in pigs. We also assume that once

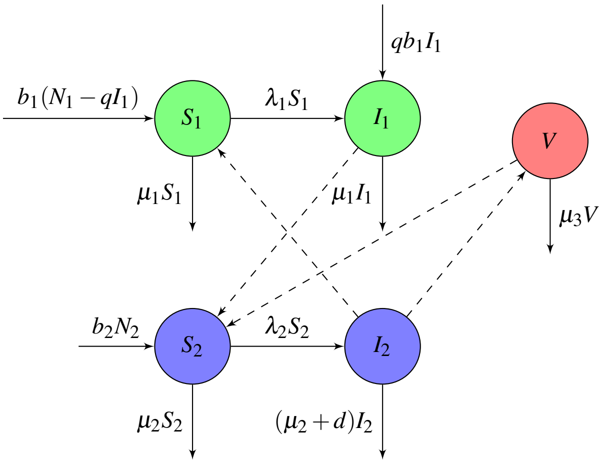


Fig. 1: Flow diagram for the transmission dynamics of African Swine Fever.

Table 1: Parameters and descriptions used in ASF model

Parameter	Description
b_1	Natural growth rate in ticks
b_2	Natural birth rate of pigs
μ_1	Natural death rate of ticks
μ_2	Natural death rate of pigs
μ_3	Removal rate of virus from the environment
β_1	Tick-to-tick transmission rate
β_2	Pig-to-pig transmission rate
β_{12}	Tick-to-pig transmission rate
β_{21}	Pig-to-tick transmission rate
ρ	Disease transmission rate from the environment
η	Deposit rate of virus from infected pigs
q	Vertical transmission rate in ticks
d	Disease-induced death rate of pigs

infected with ASFV ticks and pigs can not recover till death. Figure 1 shows the transmission dynamics of ASF with parameters as described in Table 1.

where $\lambda_1 = \beta_{21}\frac{I_2}{N_2} + \beta_1\frac{I_1}{N_1}$ and $\lambda_2 = \beta_{12}\frac{I_1}{N_1} + \beta_2\frac{I_2}{N_2} + \rho\frac{V}{K}$. First order nonlinear ordinary differential equations are used to derive system 1 using the parameters found in Table 1 and Figure 1.

$$\frac{dS_1}{dt} = b_1(N_1 - qI_1) - (\beta_{21}\frac{I_2}{N_2} + \beta_1\frac{I_1}{N_1})S_1 - \mu_1 S_1, \tag{1a}$$

$$\frac{dI_1}{dt} = \left(\beta_{21}\frac{I_2}{N_2} + \beta_1\frac{I_1}{N_1}\right) S_1 + b_1 q I_1 - \mu_1 I_1, \tag{1b}$$

$$\frac{dS_2}{dt} = b_2 N_2 - \left(\beta_{12}\frac{I_1}{N_1} + \beta_2\frac{I_2}{N_2} + \rho\frac{V}{K}\right) S_2 - \mu_2 S_2, \tag{1c}$$

$$\frac{dI_2}{dt} = \left(\beta_{12}\frac{I_1}{N_1} + \beta_2\frac{I_2}{N_2} + \rho\frac{V}{K}\right) S_2 - (\mu_2 + d) I_2, \tag{1d}$$

$$\frac{dV}{dt} = \eta\frac{I_2}{N_2} - \mu_3 V. \tag{1e}$$

K is the virus carrying capacity of the environment. Rescaling the model gives:

$$\frac{ds_1}{dt} = b_1(1 - qi_1) - (\beta_{21}i_2 + \beta_1 i_1)s_1 - \mu_1 s_1, \tag{2a}$$

$$\frac{di_1}{dt} = (\beta_{21}i_2 + \beta_1 i_1)s_1 + b_1 q i_1 - \mu_1 i_1, \tag{2b}$$

$$\frac{ds_2}{dt} = b_2 - (\beta_{12}i_1 + \beta_2 i_2 + \rho v)s_2 - \mu_2 s_2, \tag{2c}$$

$$\frac{di_2}{dt} = (\beta_{12}i_1 + \beta_2 i_2 + \rho v)s_2 - (\mu_2 + d)i_2, \tag{2d}$$

$$\frac{dv}{dt} = \eta k i_2 - \mu_3 v, \tag{2e}$$

where $k = 1/K$.

3 Analysis of Model

The feasible solution of the model, equilibrium points, the basic reproduction number, local stability of the disease-free equilibrium, global stability of the disease-free equilibrium, and global stability of the endemic equilibrium have been explained in detail in [11]. In this work we concentrate in parameter estimation and sensitivity analysis.

3.1 Parameter Estimation

Parameter estimation is important in all practical situations where a mathematical model is used to describe the behavior of a dynamic system. In this study, parameter estimation was done using the least-squares Method (LSM). Compared to other methods like the Maximum Likelihood Estimation (MLE) method, the least squares method is easy to apply and demands no prior knowledge about the distribution of the parameters [17]. The solutions of the model system (2) using literature values were used as initial values in parameter estimation. To reflect real data, a Gaussian noise with a mean of zero and a standard deviation of one was introduced on the solution. The data set consists of n data points (y_{L_i}, y_{E_i}) of solutions of system (2) where $i = 1, 2 \cdots, n$, y_{L_i} is the solution using literature values and y_{E_i} is the solution using noise data. The model function can be represented by the equation (3) where Π represents m adjustable parameters.

$$y_{L_i} = f(x_i, \Pi) \tag{3}$$

$$y_{E_i} = y_{L_i} + \text{noise} \tag{4}$$

The residual of a model, which is the difference between the observed value and the anticipated value, serves as a gauge of how well the model fits a given data point. The sum of squared residuals in equation (5) is minimized by the least-squares approach to determine the optimal parameter values.

$$\hat{\Pi} = \arg\min_{\Pi} \sum_{i=1}^{n} (y_{E_i} - f(x_i, \Pi))^2 \tag{5}$$

3.2 Global Sensitivity Analysis

The existence of uncertainties in experimental data that are used to determine parameter values frequently makes it difficult to predict results from mathematical and computer models of biological systems [16]. Nowadays, single-parameter or local sensitivity studies are commonly used in mathematical modeling methods. Due to the fact that these methods maintain all other parameters fixed at default levels, they are unable to appropriately measure uncertainty and sensitivity in the system [16]. This study employed Latin Hypercube Sampling (LHS) and Partial Rank Correlation Coefficient (PRCC) to perform global sensitivity analysis.

(i) Latin Hypercube Sampling (LHS)

The LHS method uses Monte Carlo simulations to create random samples of parameter values. LHS has the primary benefit of requiring fewer samples to attain the same accuracy than ordinary random sampling [16]. The work-flow of LHS is shown by Fig. 2 adopted from [16]. Given a system of differential equations, $\dot{\mathbf{X}} = g(\mathbf{X}, \Gamma)$ with $\mathbf{X} \in \mathbb{R}^7$ representing the seven state variables, parameter vector Γ and unidimensional output y as a function of $\mathbf{X}$ and Γ. The probability density functions (pdfs) are assigned to each parameter basing on the underlying distribution. In this study, a uniform distribution was used because there were no prior information on underlying distribution for the parameters used. A total of 1,000 samples (N=1,000) were generated uniformly for each parameter. Seven parameters ($\Gamma \in \mathbb{R}^7$), leaving out mortality and recruitment rates were involved in sensitivity analysis. Thereafter, LHS matrix X is formed by combining samples from each pdf. Then the system $\dot{\mathbf{X}} = g(\mathbf{X}, \Gamma)$ is solved to generate output matrix (Y). The LHS matrix X and output matrix (Y) generated from LHS are used as inputs in computing PRCC.

(ii) Partial Rank Correlation Coefficient (PRCC)

Correlation is the statistic that measure strength of linear association between two variables and it is expressed using correlation coefficient (CC). To compute PRCC, LHS matrix X and output matrix (Y) from Figure 2 are rank transformed to yield matrix $\mathbf{x}$ and y respectively which are used to compute correlation coefficient, r as shown by equation (6).

$$r_{\mathbf{x}_j y} = \frac{Cov(\mathbf{x}_j, y)}{\sqrt{Var(\mathbf{x}_j)Var(y)}} = \frac{\sum_i^N (\mathbf{x}_{ij} - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_{i=1}^N (\mathbf{x}_{ij} - \bar{x})^2 \sum_{i=1}^N (y_i - \bar{y})^2}} \tag{6}$$

The correlation coefficient may have values between -1 and 1. Values approaching 1 and -1 indicate that a parameter has a greater positive and negative association, respectively, while values approaching 0 indicate a weak association. Positive values indicate that as one variable increases, so does the other, and conversely, when one variable decreases, so does the other. A negative correlation means that the variables move in opposite directions.

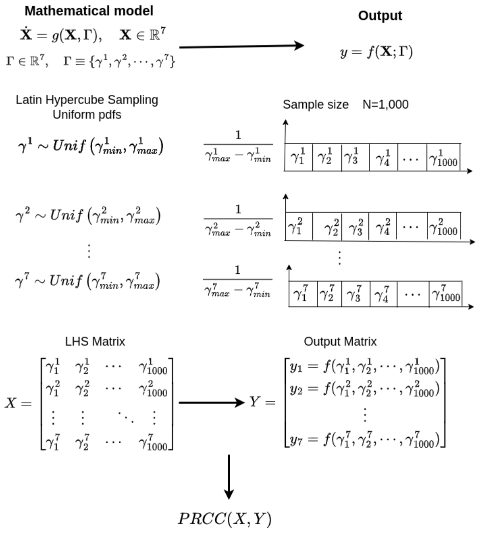


Fig. 2: Scheme of sensitivity analysis performed with LHS and PRCC methods [16]

4 Numerical Results

4.1 Initial Conditions

The ASFV model (2) is numerically simulated in this section. The Euler's formula is implemented to simulate the model in MATLAB software [18,19]. The persistence of ASFV in closed or isolated systems can be studied with the aid of numerical simulations. In simulations, the initial values are $s_1 = 0.8, i_1 = 0.2, s_2 = 0.6, i_2 = 0.4, v = 0.2$. The maximum number of ticks per pig K is taken to be 200 and therefore, $k = 1/200$. Other parameter values are as given in Table 2.

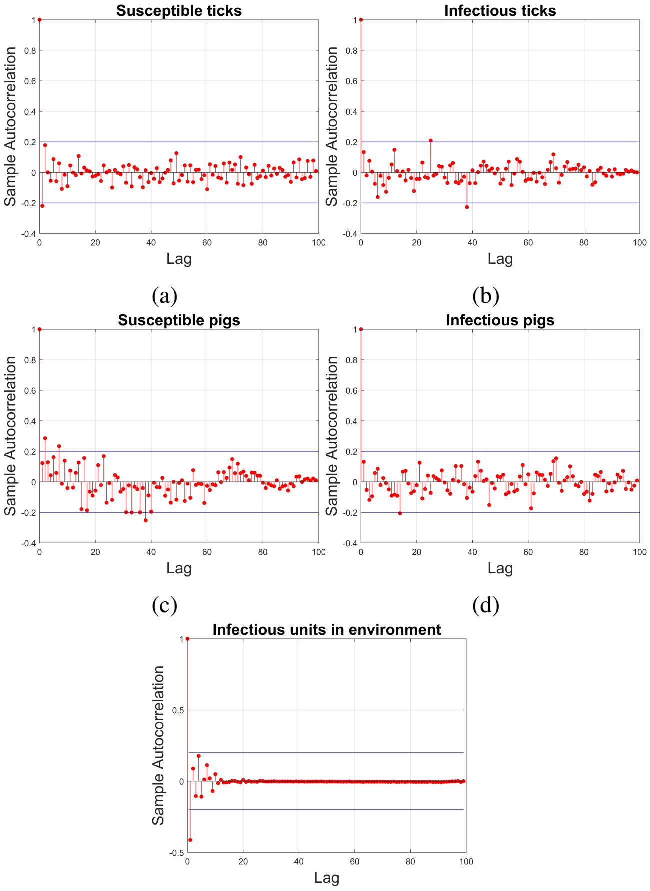
4.2 Parameter Estimation

Implementing the methodology stated in section 3.1, estimated parameters are shown in Table 2.

The autocorrelation was checked using the correlogram in Fig. 3 with 100 lags. It can be seen that, for almost all lags, the autocorrelation values fall within a tolerable range. Since all two assumptions are satisfied,

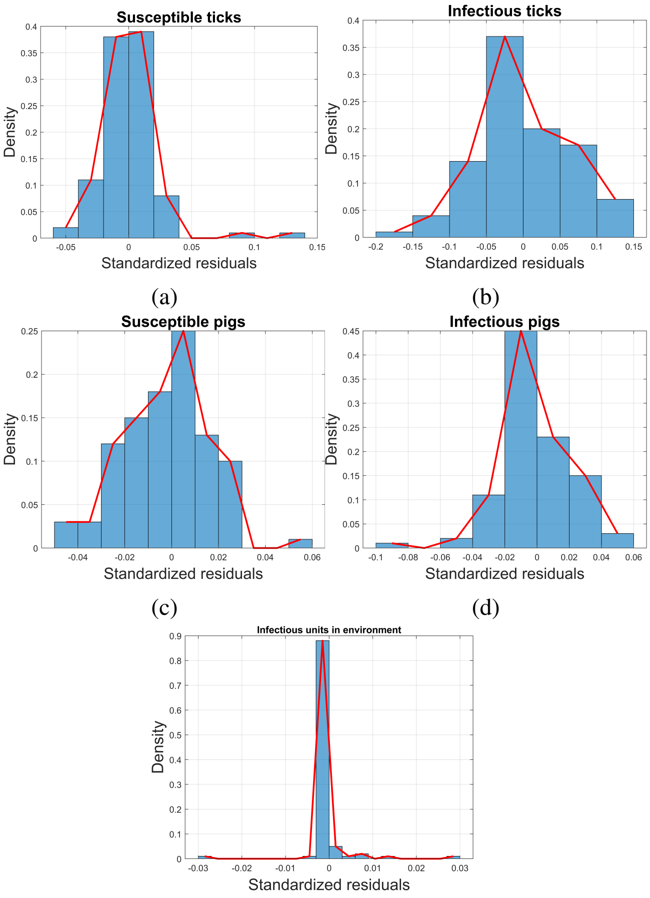
Table 2: Parameters and their values per day

Parameter	Description	Value	Estimated
b_1	Natural growth rate in ticks	0.025	0.0250
b_2	Natural birth rate of pigs	0.05	0.0509
μ_1	Natural death rate of ticks	0.0277	0.0276
μ_2	Natural death rate of pigs	0.0035	0.0031
μ_3	Removal rate of virus from the environment	0.2	0.2031
β_1	Tick-to-tick transmission rate	0.02525	0.0238
β_2	Pig-to-pig transmission rate	0.5	0.4764
β_{12}	Tick-to-pig transmission rate	0.2	0.2095
β_{21}	Pig-to-tick transmission rate	0.2	0.2086
ρ	Disease transmission rate from the environment	0.8	0.8153
η	Deposit rate of virus from the infected pigs	0.07	0.0808
q	Vertical transmission rate in ticks	0.6	0.5816
d	Disease-induced death rate of pigs	0.25	0.2521



(a) (b) (c) (d) (e)

Fig. 3: Correlogram to show autocorrelation



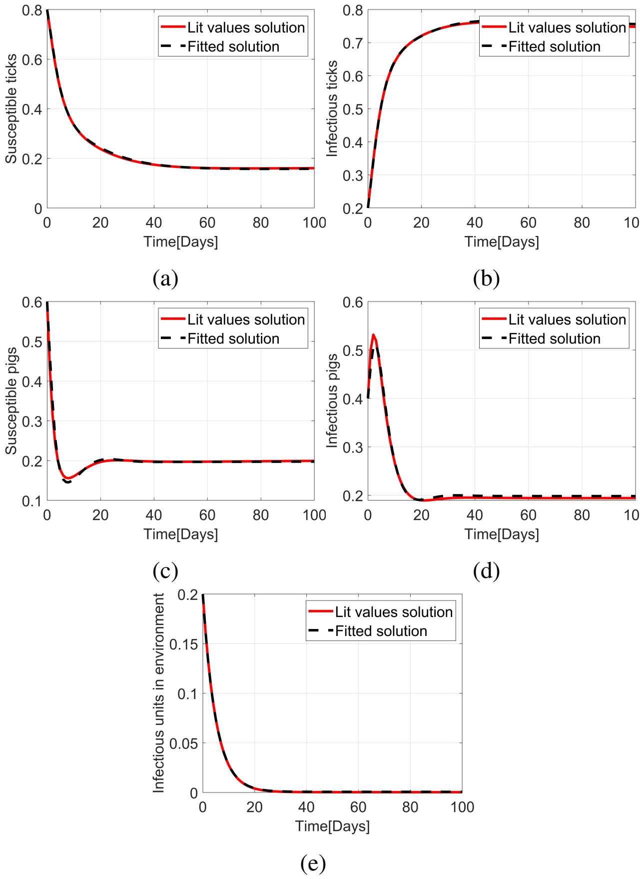
(a) (b) (c) (d) (e)

Fig. 4: Histograms of residuals.

the optimal parameters that minimize the square of residuals were obtained using the least squares method.

The main assumptions of least squares are that residuals should have a normal distribution and that they should not be autocorrelated. The histograms of residuals for all variables in Fig. 4 show that residuals are roughly normally distributed. This satisfies the first assumption of least squares.

Both literature and estimated values are shown in Table 2. For comparison purposes, Fig. 5 shows the solutions from the literature versus estimated parameter values. It can be seen that solutions align to each other.



(a) (b)

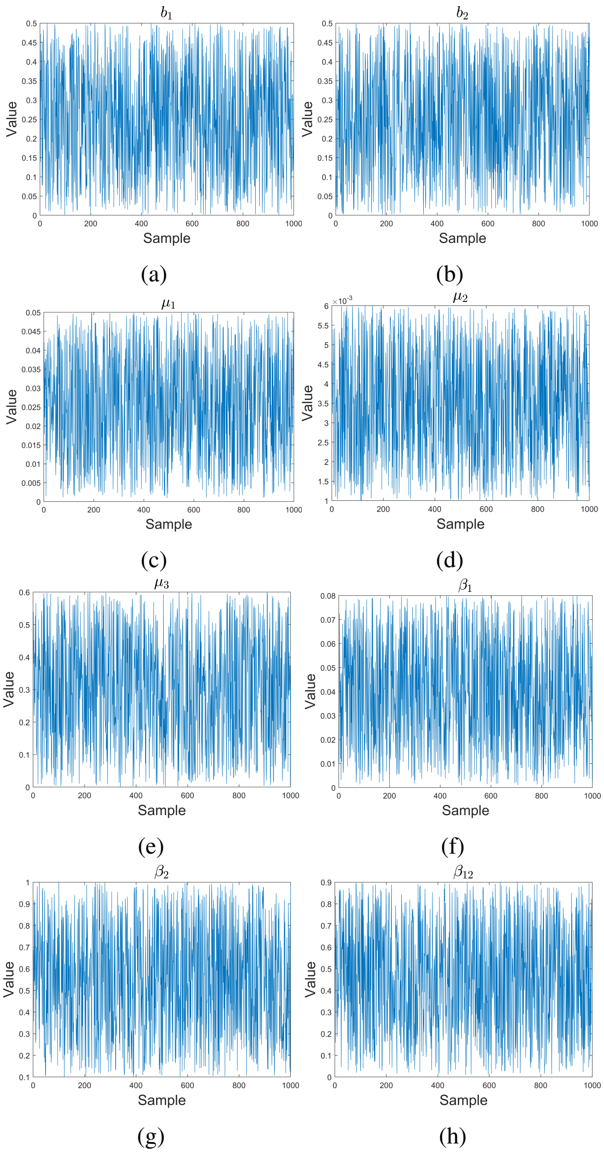
(c) (d)

(e)

Fig. 5: Comparison of Literature-Based Solutions and Estimated Parameters

4.3 Global Sensitivity Analysis

The majority of current mathematical modeling techniques either employ single-parameter or local sensitivity studies. As all other parameters are held fixed at their default values, these methods, however, do not adequately analyze uncertainty and sensitivity in the system. In this study, global sensitivity analysis of parameters with respect to all variables were performed using Latin Hypercube Sampling (LHS) approach as explained by [20]. The partial rank correlation coefficients (PRCCs) of the model parameters with respect to the state variables were also computed to asses weather their uncertainties have significant contribution using the approach described by [16] and [20]. The value of PRCC indicates the influence of a parameter to the state variable. Value approaching 1 or -1 indicates that a parameter have greater influence and vice-versa while values between 0.3 and -0.3 indicate weak influence. The sign of PRCC shows how a parameter influence the state variable with positive values indicating positive influence while negative values indicates negative influence. To asses the significance of PRCC, $p-$values for each parameter were computed and values less than or equal to 0.05 indicates that the corresponding parameter is significant and said to be insignificant otherwise. Since the distributions of parameters is not known, samples were generated using uniform distribution. 1 000 samples were generated for each parameter as shown in Fig. 6.



(a) (b)

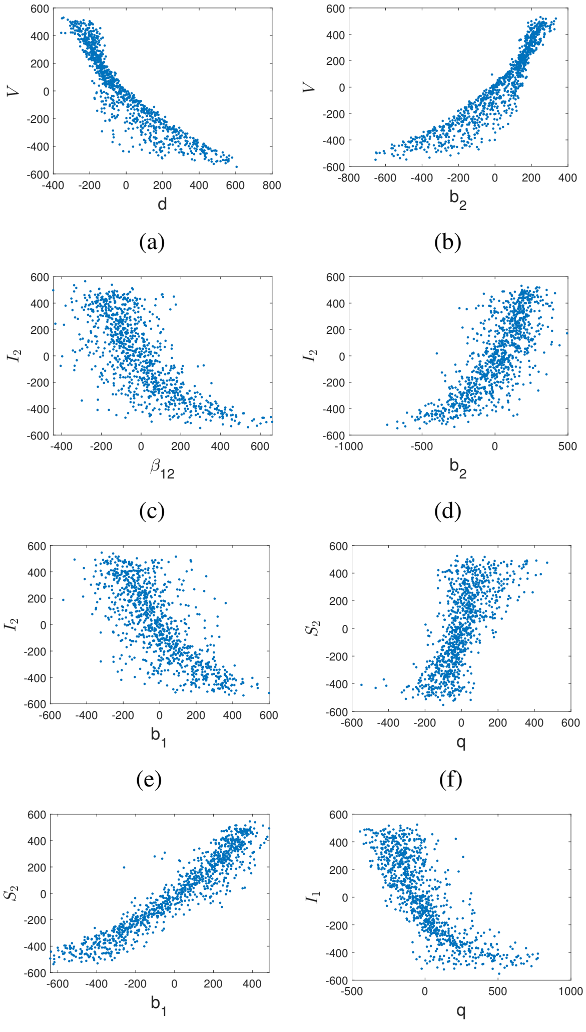
(c) (d)

(e) (f)

(g) (h)

Fig. 6: Probability distribution functions of sampled input parameters values.

The major assumption of PRCC is the monotonic relationship between parameters and state variables. A monotonic relationship is when the value of one variable increases, so does the other variable or when the value of one variable increases, the value of other variable decreases. To show monotonic relation, scatter plots of regression residuals between parameters and state variables were plotted. For each state variables scatter plots of residuals shows a roughly monotonic relationship with parameters as shown by Fig. 7 on some selected graphs.



(a) (b)

(c) (d)

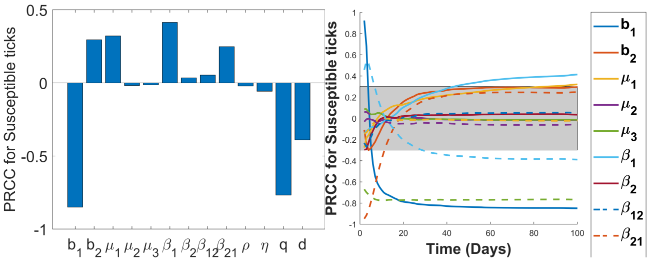
(e) (f)

(g) (h)

Fig. 7: Scatter plots for different parameters

4.3.1 Susceptible ticks

The time variable PRCCs for susceptible ticks are shown in Fig.8a. The PRCCs extracted at time T = 10 years are also shown in Fig. 8b. The most influence parameters are Natural growth rate in ticks (b_1) and Vertical transmission rate in ticks (q). Both of them have negative values meaning that their increase causes decrease in susceptible ticks.

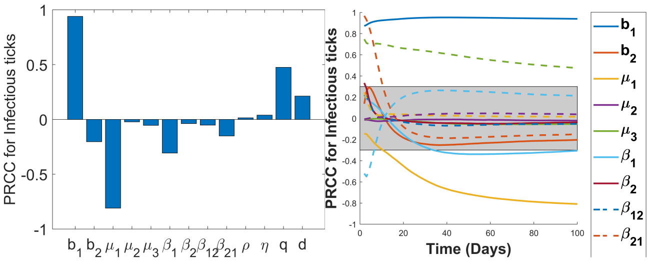


(a) (b)

Fig. 8: Sensitivity analysis PRCCs on susceptible ticks

4.3.2 Infectious ticks

The time variable PRCCs for Infectious ticks are shown in Fig. 9a. The PRCCs extracted at time T = 100 days are also shown in Fig. 9b. The most influence parameters are Natural growth rate in ticks (b_1), Vertical transmission rate in ticks (q) and natural death rate of ticks (μ_1). Natural growth rate in ticks (b_1) and Vertical transmission rate in ticks (q) have positive values meaning that their increase causes increase in infectious ticks. Natural death rate of ticks (μ_1 has negative values meaning that their increase causes decrease in susceptible ticks.

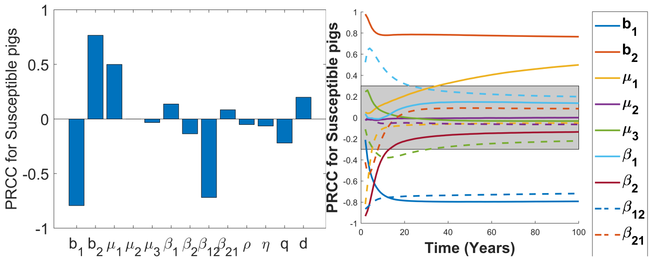


(a) (b)

Fig. 9: Sensitivity analysis PRCCs on Infectious ticks

4.3.3 Susceptible pigs

The time variable PRCCs for Susceptible pigs are shown in Fig. 10a. The PRCCs extracted at time T = 100 days are also shown in Fig. 10b. The most influence parameters are Natural birth rate of pigs (b_2), natural death rate of pigs (μ_1), Natural growth rate in ticks (b_1) and pig-to-tick transmission rate (β_{21}). Natural birth rate of pigs (b_2) and natural death rate of pigs (μ_1) have positive values meaning that their increase causes increase in susceptible ticks. Natural growth rate in ticks (b_1) and pig-to-tick transmission rate (β_{21}) have negative values meaning that their increase causes decrease in susceptible ticks.

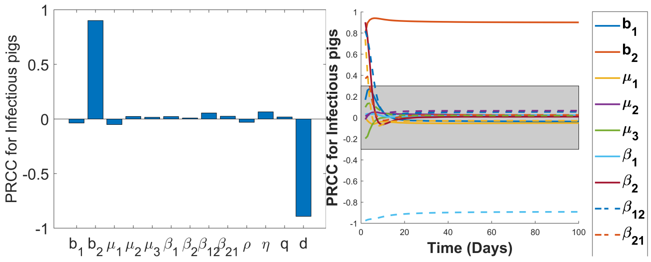


(a) (b)

Fig. 10: Sensitivity analysis PRCCs on Susceptible pigs

4.3.4 Infectious pigs

The time variable PRCCs for Infectious pigs are shown in Fig. 11a. The PRCCs extracted at time T = 100 days are also shown in Fig. 11b. The most influence parameters are Natural birth rate of pigs (b_2) and disease induced death rate of pigs (d). Disease induced death rate of pigs (d) has negative values meaning that its increase causes decrease in susceptible ticks. Natural birth rate of pigs (b_2) has positive values meaning that its increase causes increase in susceptible ticks.

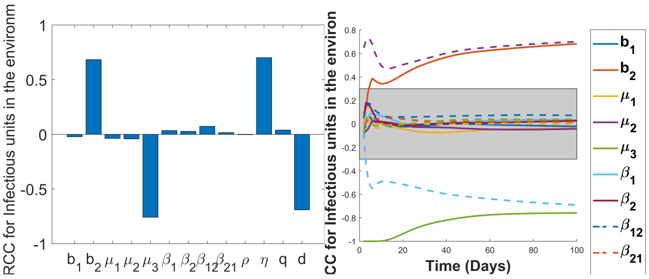


(a) (b)

Fig. 11: Sensitivity analysis PRCCs on Infectious pigs

4.3.5 Infectious units in the Environment

The time variable PRCCs for Infectious units in the Environment are shown in Fig. 12a. The PRCCs extracted at time T = 100 days are also shown in Fig. 12b. The most influence parameters are Natural birth rate of pigs (b_2), Deposit rate of virus from the infected pigs (η), Removal rate of virus from environment (μ_3) and disease induced death rate of pigs (d). Natural birth rate of pigs (b_2) and Deposit rate of virus from the infected pigs (η) have positive values meaning that their increase causes increase in Infectious units in the Environment. Removal rate of virus from environment (μ_3) and disease induced death rate of pigs (d) have negative values meaning that their increase causes decrease in Infectious units in the Environment.



(a) (b)

Fig. 12: Sensitivity analysis PRCCs on Infectious units in the Environment

5 Conclusions

In this work, a mathematical model for the dynamics of African Swine Fever in a tick-to-domestic pig environment was developed and analyzed. Subgroups of the pig and tick populations were identified as vulnerable and infectious. The main aim of this study was to conduct parameter estimation and global sensitivity analysis of estimated parameters. Parameters estimation was done using Least square method while global sensitive analysis of parameters was done using Latin Hypercube Sampling (LHS) and Partial Rank Correlation Coefficients (PRCCs). Results revealed that estimated parameters were aligning with literature parameter values. The study also highlight important parameters in each compartment of African Swine Fever model. For instance, the most influential parameters for infectious pigs are Natural birth rate of pigs (b_2) and disease induced death rate of pigs (d). The study commends that in order to eliminate the disease, controls should focus on sensitive parameters in specific compartment. It also important to consider timing of applying controls as influence of parameters tend change over time.

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Declaration of competing interest

Author do not have any conflict of interest to disclose.

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