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BAYESIAN REASONING AND SIR MALARIA MODELS

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Abstract. Various sources of uncertainty are involved in malaria modelling, arising from intricate interplay between parasite biology, vector ecology, human factors and environmental variables. These uncertainties are magnified by data constraints, the spread of drug and insecticide resistance and the difficulties associated with reliably accounting for intervention effects and long-term climate impacts. It is imperative to employ complicated statistical techniques, ensemble modelling approaches and consistently improve models as new information becomes available for purposes of offering strong guidance to public health decision-making about the inherent complexity and fluctuation in transmission dynamics of malaria. To assess the impact of intervention measures put in place, it is important to quantify the uncertainty and take it into account when making decisions. Bayesian inference makes this possible in the sense that the posterior parameter inference can characterize uncertainty in the estimates of unknown parameter values and indeed the uncertainty over a set of candidate models.

In this work, we apply Bayesian inference based on Markov chain Monte Carlo (MCMC) sampling to a compartmental models (SIR) Ross' original model. We define a ground truth, subject it to actual data and infer the posterior distribution of the initial state and the parameters of the model. We investigate several scenarios for the

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observations generated corresponding to realistic situations. This way, we can contrast the inferred posterior to the ground truth and the amount of uncertainty injected in the observations.

Keywords: Bayesian inference; SIR models; malaria transmission; parameter estimation; Markov Chain Monte Carlo.

2020 AMS Subject Classification: 92C60, 62F15.

1. INTRODUCTION

Malaria remains a significant public health challenge in Kenya. The World Health Organization [1] reports that approximately 3.5 million new clinical cases and 10,700 deaths are reported annually. The disease primarily affects children under five years and pregnant women. This disease is endemic in certain regions, particularly along the coastal areas and around Lake Victoria, [2] while other areas experience seasonal transmission or are largely malaria-free.

Several measures have been introduced to tackle the diseases by various stakeholders including the Kenyan government, international organizations, NGOs, and other stakeholders. Some key strategies put in place include indoor residual spraying, distribution of insecticide-treated bed nets, and the use of rapid diagnostic tests. Despite these efforts, the effectiveness of these interventions and their influence on malaria transmission patterns remain uncertain. This uncertainty highlights the need for mathematical models to forecast outcomes and evaluate the impact of these interventions.

One commonly used model to study infectious diseases such as malaria is the Susceptible-Infected-Recovered (SIR) model. This compartmental model divides the population into distinct groups (susceptible, infected, and recovered) and describe the transitions between these states using differential equations [3]. However, applying the SIR model to malaria in Kenya presents several challenges, particularly due to limited data on prevalence in humans and even less data on mosquito populations [4].

In addition, heterogeneity of malaria transmission across different Kenyan regions complicates model design. Transmission patterns can be extremely varied from one coastal, lake, or highland area to another, as well as between rural and urban settings [5]. This space heterogeneity combined with temporal heterogeneity due to seasonal fluctuations and long-term patterns in climate enhances parameter uncertainty and prediction uncertainty within models.

In order to address such uncertainties, researchers employ Bayesian inference methods. Unlike frequentist methods based on point estimates from information at hand, Bayesian inference allows for incorporation of prior beliefs and provides a probability distribution for all parameters considered [6]. The method is most applicable in the scenario of malaria modelling in Kenya, where parameter uncertainties and data limitations are significant. The Bayesian framework enables researchers to quantify uncertainties in model parameters and predictions, providing a more comprehensive understanding of the range of possible outcomes. This is crucial for informing policy decisions and designing effective intervention strategies, as it allows decision-makers to consider the full spectrum of potential scenarios rather than relying on potentially misleading point estimates.

In this paper, we aim to demonstrate how Bayesian inference can be performed on the Ross model. First, we will introduce the Ross model and its relevance to malaria transmission in Kenya. Next, we will explain the principles of Bayesian inference and how it can be applied to estimate the posterior distribution of the parameters of the Ross model. We will then describe the implementation of the Bayesian inference procedure. We will specify prior distributions, define a likelihood function, and the setup the Markov Chain Monte Carlo (MCMC) sampler to estimate the posterior distributions of the model parameters. After obtaining the posterior samples, we will analyze the results and compare them with the ground truth values. We will assess the convergence of the MCMC sampler using diagnostic plots. We will display the uncertainties associated with the parameter estimates and their implications for understanding malaria transmission dynamics.

The rest of the paper is structured as follows: Section 2 introduces the Ross-Macdonald model and its mathematical formulation. Section 3 explains the principles of Bayesian inference and its application to the Ross model. Section 4 describes the implementation of the Bayesian inference procedure and presents the results of the analysis and discusses the implications for malaria transmission dynamics in Kenya. Finally, we conclude the paper and outlines future research directions.

2. SIR Models for Malaria

WHO [7], describes malaria as a disease caused by *plasmodium parasites* and transmitted to humans through the bites of infected female *Anopheles mosquitoes*. The spread of malaria involves a complex interaction between the mosquito vectors, parasites and the human hosts, making it a challenge to accurately model the disease. To solve this problem SIR models have been widely used to capture the essential dynamics of malaria transmission [3].

The basic malaria transmission cycle can be summarized as follows:

- An infected mosquito (parasite) bites a susceptible human, potentially transmitting the parasite.
- If transmission from the parasite occurs, the human host goes through an incubation period before becoming infectious.
- An uninfected mosquito may bite an infectious human, potentially becoming infected itself.
- The infected mosquito goes through a sporogonic cycle (parasite multiplication in malaria), after which it can transmit the parasite to other humans.

To model this process, researchers have adapted the classic SIR model to include both human and mosquito populations [8]. A basic SIR malaria model includes the following compartments:

For humans:

- S_h: Susceptible humans.
- I_h: Infected (and infectious) humans.
- R_h: Recovered humans with temporary immunity.

For mosquitoes:

- S_m: Susceptible mosquitoes.
- I_m: Infected (and infectious) mosquitoes.

These models help researchers and public health officials to understand the dynamics of malaria transmission in different settings, forecast the effect of interventions like bed nets, indoor residual spraying, and drug therapy, examine malaria control and elimination strategy scenarios as

well as study how climate change is expected to affect malaria transmission. However, it's important to note that while these models provide valuable insights, they also come with limitations and uncertainties, particularly due to the complexity of malaria transmission and the variability in human and mosquito populations across different regions [9].

2.1. SIR Malaria Models. We focus on the original Ross model. We call it $\mathscr{M}_0$. The Ross-model, $\mathscr{M}_0$, is historically the first and also the simplest malaria model [10]. It only considers infections in the human (I_h) and mosquito population (I_m). The change in these infections is given by ODEs cf. Eq. (1).

$\mathscr{M}_0$ model considers two interacting populations: humans and mosquitoes. The model describes the dynamics of malaria transmission by considering factors such as the biting rate of mosquitoes, the duration of the infectious period, the probability of transmission from infected mosquitoes to humans and vice versa, and the mortality rates of both humans and mosquitoes. SIR models, such as the $\mathscr{M}_0$ model, are typically formulated as a system ODEs that describe the flow of individuals between the different compartments over time [11]. The ODEs capture the key processes of disease transmission, including the rate at which susceptible individuals become infected, the rate at which infected individuals recover, and the rate at which recovered individuals lose immunity (if applicable) [12].

A key property of ODE models is that, given a set of initial conditions for each compartment $(S(0), I(0), R(0))$ and fixed parameter values, there exists a unique solution to the system of ODEs. This means that the model can predict the trajectory of the disease over time, starting from the specified initial state. The unique solution property is important for understanding the deterministic behaviour of the model and for comparing the model's predictions with observed data.

The $\mathscr{M}_0$ model, as a specific instance of an SIR model, also possesses this unique solution property. The model's ODEs describe the dynamics of malaria transmission between humans and mosquitoes, and the solution to these equations provides insights into the progression of the disease over time [8] . By specifying the initial conditions for the human and mosquito populations and the relevant parameters, such as biting rates and transmission probabilities,

[13], the Ross-Macdonald model can be used to simulate the spread of malaria and to evaluate the impact of different control strategies.

However, it is important to note that the unique solution property of SIR models, including the $\mathscr{M}_0$ model, relies on the assumption of fixed parameter values. In reality, the parameters governing disease transmission may vary over time or across different populations [14]. To account for this variability, researchers often use statistical methods, such as Bayesian inference, to estimate the parameters from observed data and to quantify the uncertainty associated with these estimates as shown by [3].

2.2. Basic Ross Model. The foundation of mathematical modelling in malaria epidemiology was laid by Ronald Ross in the early 20th century. Ross introduced the term "pathometry" to describe the "quantitative study of a disease either in the individual or in the community" [10]. His groundbreaking work demonstrated that reducing mosquito populations below a critical threshold could effectively control malaria transmission [15]. This concept, known as the transmission threshold, was revolutionary for its time and set the stage for future developments in malaria control strategies.

$\mathscr{M}_0$, while simplistic by modern standards, captured the essential dynamics of malaria transmission between humans and mosquitoes. It laid the groundwork for understanding the basic reproductive number (R_0) in vector-borne diseases, a concept that would later be formalized and expanded upon [16]. The $\mathscr{M}_0$ only considers infections in humans and mosquito population. The change in these infections is given by the ODEs [3]

$$\begin{aligned} \dot{I_h} &= abmI_m(1-I_h) - rI_h \\ \dot{I_m} &= acI_h(1-I_m) - \mu_m I_m \end{aligned} \tag{1}$$

There are two compartments; (I_h) for the human population and (I_m) for the mosquito population. a, b, c, m, r, μ are parameters of $\mathscr{M}_0$ in Eq. (1) with plausible ranges shown in Table 1.

TABLE 1. Table showing typical parameter ranges of $\mathscr{M}_0$ model, [3].

Parameter	**Description**	**Typical Range**	Value
a	Man biting rate/day	$[0.01, 0.5]$	0.2
b	Proportion of bites that produces an infection in humans	$[0.2, 0.5]$	0.5
c	Proportion of bites by which one susceptible mosquito becomes infected	$[0.5]$	0.5
m	Female mosquito-human ratio	$[0.5, 40]$	2.0
r	Average recovery rate/day of humans	$[0.005, 0.05day]$	0.05
μ	Per capita rate/day of mosquito mortality	$[0.05, 0.5]$	0.05

In this model the *basic reproductive number* is given by $R_0 = ma^2bc/r\mu$. R_0 is an important parameter to make predictions. If $R_0 > 1$ we get exponential growth of the diseases in the population and if $R_0 < 1$ we experience exponential decay.

3. BAYESIAN INFERENCE

Bayesian inference is a statistical approach that combines prior knowledge with observed data to update our understanding of model parameters and make probabilistic predictions. This method is particularly useful in the context of complex systems like malaria transmission, where uncertainty is inherent and data may be limited [6].

3.1. Bayesian Inference in SIR Malaria Models. In the context of SIR malaria models, Bayesian inference can be applied to estimate model parameters, quantify uncertainties, and make predictions about disease spread [17]. The process typically involves:

(1) **Prior Specification:** Defining prior distributions for parameters such as transmission rates, recovery rates, and mosquito lifespan based on existing literature or expert knowledge. For example:

$$\beta \sim \text{Gamma}(\alpha, \beta) \quad \text{// transmission rate}$$

$$\gamma \sim \text{Uniform}(a, b) \quad \text{// recovery rate}$$

(2) **Likelihood Function:** Defining a likelihood function that quantifies the probability of observing the malaria incidence data given the SIR model parameters. This often involves solving the SIR differential equations and comparing the model output to the observed data.

(3) **Posterior Computation:** Using MCMC methods or other sampling techniques to approximate the posterior distribution of the parameters [6]. This step often requires sophisticated computational tools due to the complexity of SIR models.

(4) **Inference and Prediction:** Analyzing the posterior distributions to make inferences about parameter values, assess the effectiveness of interventions, and make probabilistic predictions about future malaria spread.

In $\mathscr{M}_0$, the parameters of interest may include the biting rate of mosquitoes (a), the probability of transmission from infected mosquitoes to humans (b), the probability of transmission from infected humans to mosquitoes (c), the recovery rate of humans (r), and the mortality rate of mosquitoes (μ). Prior distributions for these parameters can be specified based on existing knowledge from literature, expert opinion, or previous studies.

The likelihood function, which quantifies the probability of observing the data given the model parameters, plays a central role in Bayesian inference [6]. In the case of the $\mathscr{M}_0$, the likelihood function describes the probability of observing the reported malaria cases or other relevant data, such as mosquito infection rates, given the model parameters and the assumed observation process.

3.2. Markov Chain Monte Carlo (MCMC). MCMC methods are crucial for sampling from complex, high-dimensional probability distributions, such as the posterior distributions in Bayesian inference for SIR malaria models [6]. The fundamental principle of MCMC is to construct a Markov chain that converges to a stationary distribution, which in our case is the desired posterior distribution.

In the context of the $\mathscr{M}_0$ for malaria transmission, MCMC is employed to generate a large number of samples from the posterior distribution of the model parameters. These samples can then be used to estimate the parameters and quantify their uncertainties [3]. The process involves:

(1) Defining a Markov chain whose stationary distribution is the posterior distribution of interest.

(2) Running the chain for a sufficient number of iterations to ensure convergence.

(3) Using the generated samples to approximate the posterior distribution and derive parameter estimates.

3.3. Bayesian Inference for Malaria models. Once convergence and adequate mixing have been established, the samples from the MCMC algorithm can be used to estimate the posterior distributions of the $\mathscr{M}_0$ model parameters, along with their uncertainties. These posterior distributions can then be used to make inferences about the malaria transmission dynamics, to compare different intervention strategies, and to guide public health decision-making.

The key distinction in Bayesian inference is between the unknown quantities, $\boldsymbol{\theta}$, which follow a probability distribution (the prior), and the observed data D, which are used to update the prior and obtain the posterior distribution. One challenge in Bayesian inference for SIR models lies in defining a suitable likelihood function. The likelihood quantifies the probability of observing the data given the model parameters and plays a crucial role in updating the prior beliefs to obtain the posterior distribution [6]. In the context of SIR models, the likelihood function should capture the stochastic nature of the disease transmission process and the observational noise in the data, [18].

3.3.1. *Bayesian Inference for $\mathscr{M}_0$.* To apply Bayesian inference to $\mathscr{M}_0$ we have to define a prior and a generative model. From those we derive the posterior. It is conditioned on synthetic observations D.

A clear distinction between parameters of the ODEs and those in Bayesian inference is made. In Bayesian inference, the parameters are what we are uncertain about, and we express that uncertainty as a probability distribution, i.e. degree belief in their values. This is the case for the parameters of $\mathscr{M}_0$ when we do not know their values exactly. (Part of) the initial state is also a Bayesian parameter if we lack complete information. Unknowns are represented as $\Theta = (\theta_1, \cdots, \theta_d)$ when there are d unknowns, e.g. $\Theta = (a, b, c, m, r, \mu, I_h(0), I_m(0))$ in case of $\mathscr{M}_0$.

Unknowns refers to Bayesian inference parameters while the mathematical models under consideration also has parameters which will be referred to as *parameters* cf. Section 3.3.1. In the case of SIR model the unknowns are usually the parameters of the ODEs, the basic reproductive number, the initial state or variance of Gaussian noise. One approach is to estimate the

unknowns using the data and use this values in the ODEs (The frequentist approach). Another approach, is to use Bayesian inference. These unknowns are estimated using the available data on the prevalence of malaria in some region. Often, they are few and biased. Hence, we are uncertain about the values of the unknowns and the reliability of our models' predictions.

We incorporate domain knowledge into the *prior* cf. Section 2.2. e.g. the proportion of bites that infect humans ,b, is within the range $[0.2, 0.5]$. We can choose a uniform prior over this range if we believe that any b is equally likely or we can use a lognormal prior to express that $b > 0$.

The synthetic observations are derived from the *ground truths* for each model. The ground truths are true values of all the unknowns used to generate synthetic data. In experiments, we want to see how well Bayesian inference recovers the ground truth. We know that with each combination of values of the parameters and the initial state, there corresponds a unique solution $\mathbf{S}(t)$ defined over the time interval $\left[0, t_f\right]$ such that $\mathbf{S}(0)$ is the initial state. Numerical integration from $t_i = 0$ to t_f gives that solution. For example, the ground truth for $\mathscr{M}_0$, cf. eq. (1), is given by $a = 0.2, b = 0.5, c = 0.5, m = 20, r = 0.01$ and $\mu = 0.12$ and the initial state is $(I_h(0), I_m(0)) = (x, y)$. For each state variable $S_i, i = 1, \cdots, d$, we want to observe, we specify n_i observation times $t_1, \cdots, t_j, \cdots, t_{n_i}$ in $\left[0, t_f\right]$. This way, we obtain the values $S_i(t_1), \cdots, S_i(t_j), \cdots, S_i(t_{n_i})$ of state variable S_i. Next, we add some *noise* ε_j to $x_i(t_j)$ to obtain the simulated observations $o_{t_j} = S_i(t_j) + \varepsilon_j$ for $j = 1, \cdots, n_i$. Note that the number of observations and the noise can differ between state variables. We consider several scenarios: 1) Number of observations are the same for all components and are equally spaced in the time interval $\left[0, t_f\right]$. The noise introduced is Gaussian and its variance is the same everywhere. And 2), Same as before but the noise variance per state variable differs.

4. Results and Experiments

We have set up experiments to test the methodology described in Section 3 on the models described in Section 2.1. For the first experiment, we formulate a ground truth by specifying the initial state and the parameter values of the model. They determine the unique solution of the system of ODEs. Next, we generate synthetic observations. At specified time steps we determine the state of the solution and add Gaussian noise. These are the observations/data

used by Bayesian inference. Inference returns an average solution with associated uncertainty. We contrast this to the ground truth. Synthetic observations makes this possible while this is out of question for real-world data. We use synthetic observation to allow us compare the final predictive posterior with the ground truth that was used to generate the synthetic observations.

In this experiment, the ground truth is the solution to $\mathscr{M}_0$, cf. Eq. (1). with parameters $a = 0.2, b = 0.5, c = 0.5, m = 20, r = 0.01$, and $\mu_m = 0.12$ corresponding to the initial state $(I_h(0), I_m(0)) = (0.001, 0.001)$. We use data which shows observed malaria cases and infected mosquito population in Kenya between 2010 to 2022 c.f Figure 1.

This time the unknowns ,θ, are *both* the parameters and the initial state cf. Eq. (1). We used uniform priors for the parameters corresponding with the ranges given in Section 2.1 and half-Cauchy for initial state reflecting a high uncertainty. We used the *MCMC*-samples after convergence to construct the posterior predictive distribution shown. As expected the uncertainty increases over time. When the system approaches the steady state corresponding with the parameter values in the ground truth the uncertainty decreases again as expected since the observations from then continue to fluctuate around constant values for I_h and I_m.

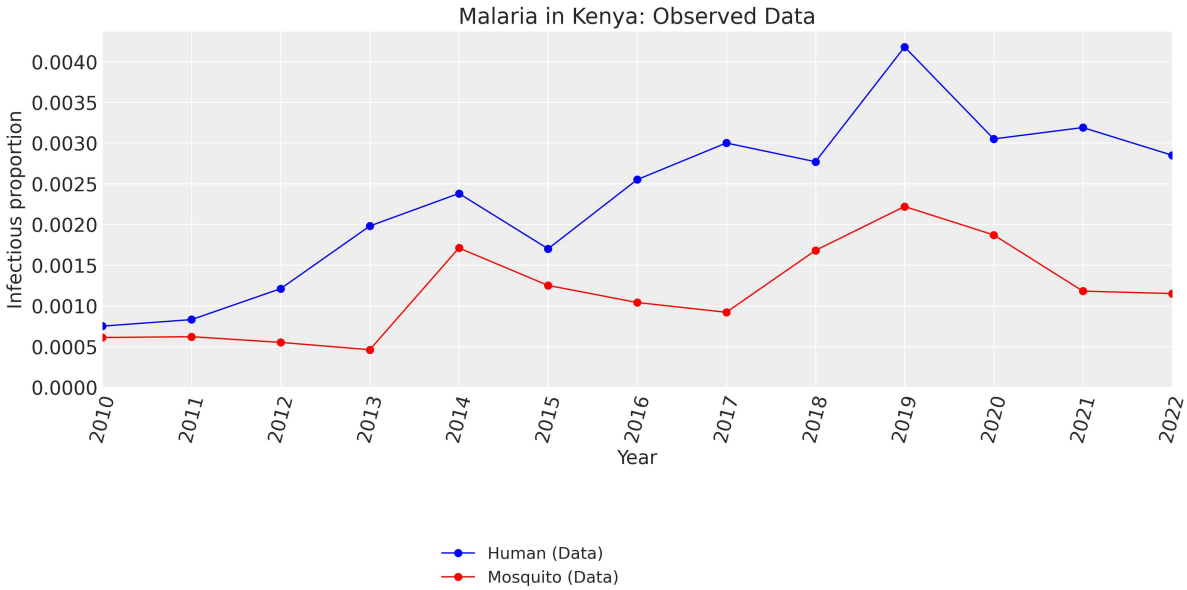

FIGURE 1. The observed Malaria Cases and infected Mosquito population in Kenya.

Figure 1 show the The observed Malaria Cases and infected Mosquito population in Kenya from 2010 to 2022. The blue shows the human cases and red the infected mosquitoes. These

datasets were sourced from

https://www.statista.com/statistics/1240010/number-of-malaria-cases-in-kenya/

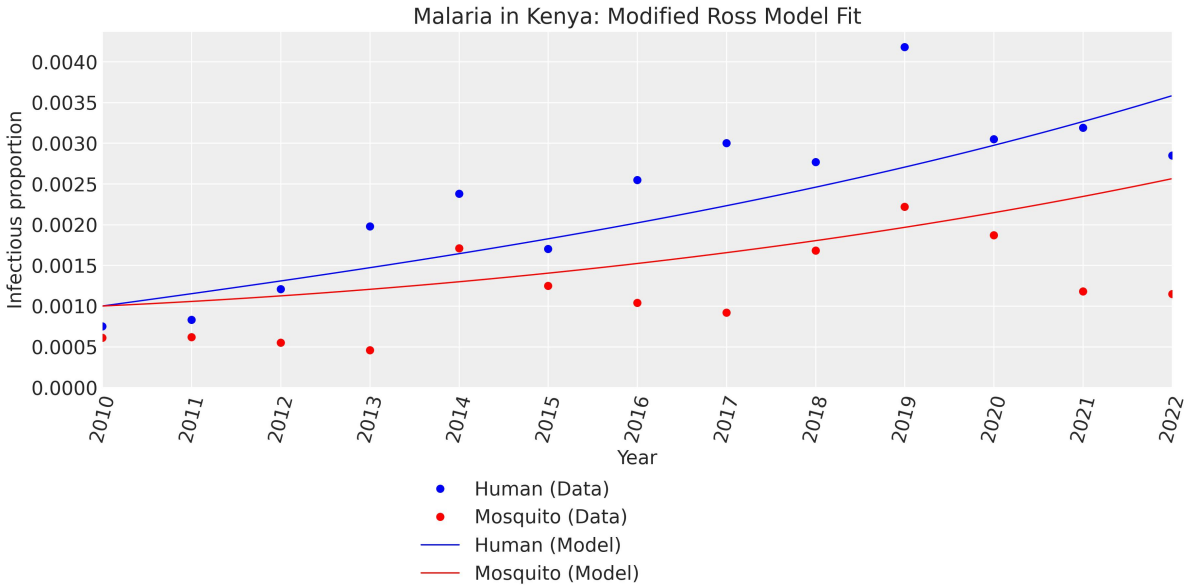

FIGURE 2. This figure shows both the observed malaria infections in human (blue dots) and mosquito (red dots) populations. The ODE fitted lines for humans and mosquitoes are shown by the red and blue lines.

We subsequently fitted our ODE model using observed malaria infection data from both human and mosquito populations. The ODE model presented in Figure 2 demonstrates poor fit to the observed data. Therefore, we opted to use the Least square method to fit the observed data. in Figure 1. The resulting OLS-optimized ODE trajectories in Figure 3 exhibit a precise match to the dataset. Table 2 shows the calibrated OLS parameter estimates.

TABLE 2. Least Squares Solution of the best parameters estimates

Parameter	OLS estimate
a	0.2797
b	0.7709
c	0.5000
m	2.0568
r	0.05
μ	0.5000

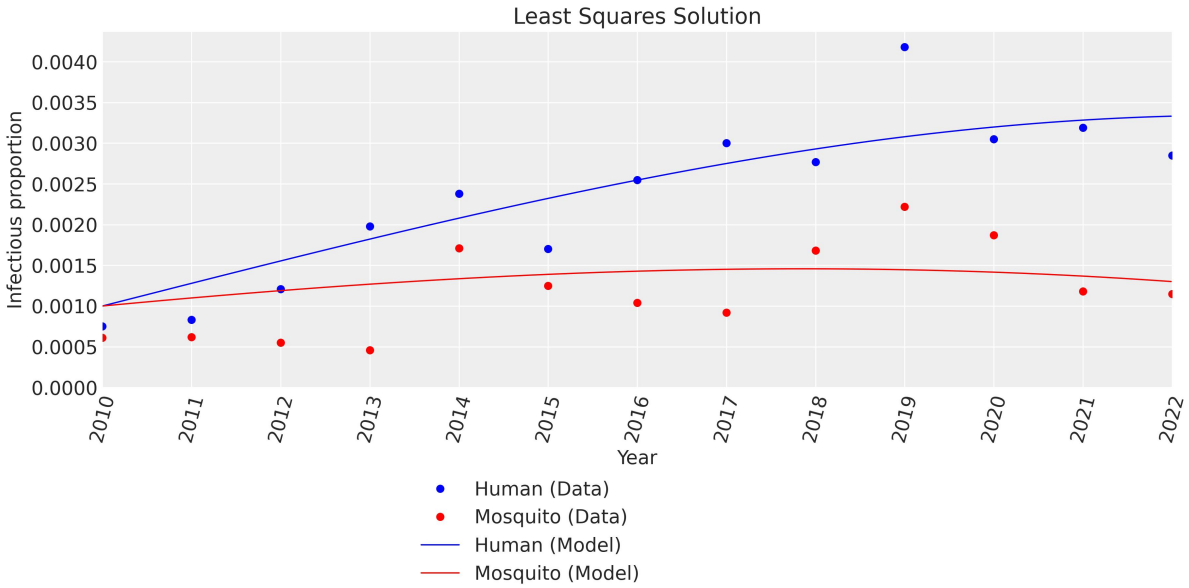

FIGURE 3. This figure shows both the observed malaria infections in human (green dots) and mosquito (blue dots) populations. The OLS fitted ODE lines for humans and mosquitoes are shown by the green and blue lines.

TABLE 3. MCMC and highest Solution of the best parameters estimates†

Parameter	Mean	SD	2.5% HDI	97.5% HDI	MCSE Mean	$\hat{r}$
a	0.280	0.001	0.278	0.281	0.0	1.01
b	0.770	0.004	0.763	0.778	0.0	1.00
m	2.055	0.009	2.041	2.072	0.0	1.00
r	0.164	0.001	0.162	0.165	0.0	1.00
σ	0.002	0.000	0.001	0.002	0.0	1.00

† $c = 0.5000$ and $\mu = 0.500$ maintained the same values as OLS.

To estimate the posterior distributions of the model parameters, we implemented Markov Chain Monte Carlo (MCMC) sampling, which generated a robust set of parameter samples through iterative simulations. Subsequently, we summarized the results in a Table (see Table 3) and visualized them by plotting kernel density estimates (KDEs) to assess the uncertainty and shape of the posterior distributions, alongside trace plots to evaluate chain convergence and ensure sampling stability across iterations (see Figure 4).

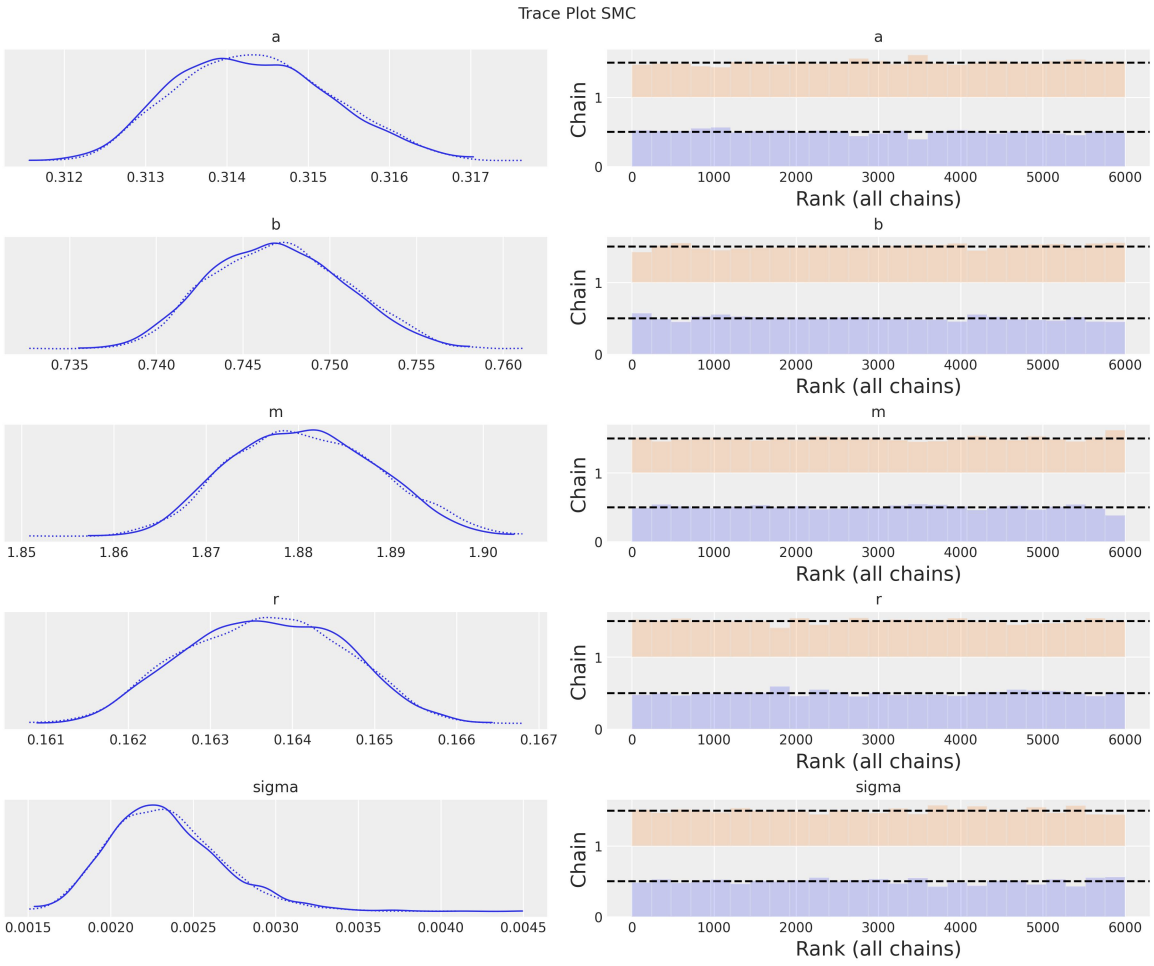

FIGURE 4. The MMCMC density and trace plots of the posterior parameter estimates.

In Figure 5, we present the final results of the MCMC simulations, which illustrate the posterior estimates derived from 30 independent sampling iterations. The blue and red lines correspond to the inferred trajectories for human and mosquito infections, respectively, demonstrating variability across the sampled parameter sets.

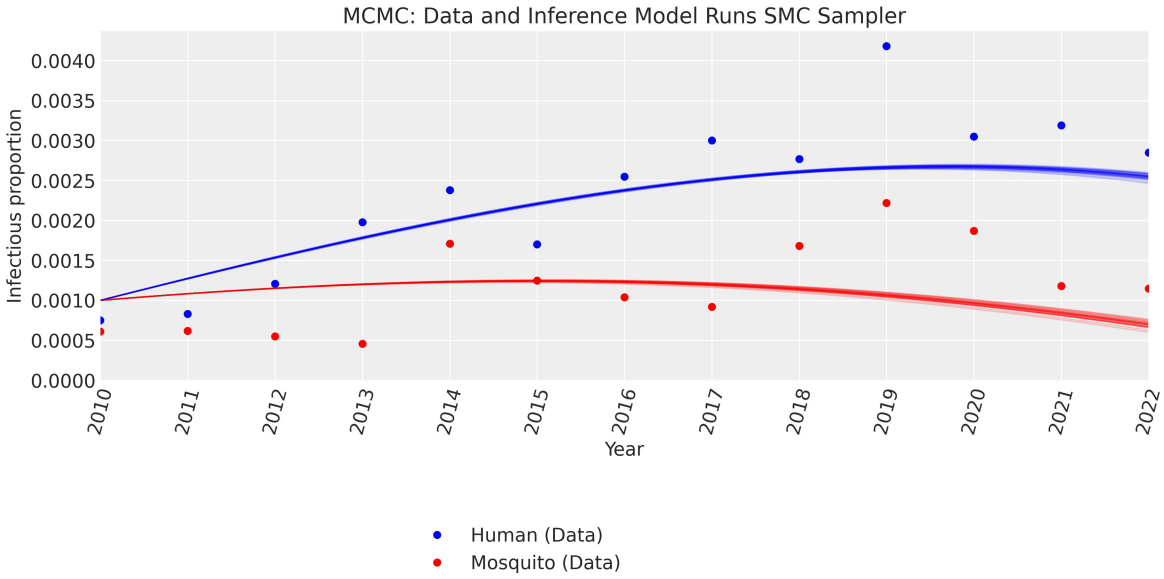

FIGURE 5. This figure shows both the observed malaria infections in human (blue dots) and mosquito (red dots) populations.

5. CONCLUSION AND FUTURE WORK

This study demonstrates the critical role of Bayesian inference and Markov Chain Monte Carlo (MCMC) methods in addressing uncertainties inherent in malaria transmission modelling. By applying these techniques to the Ross-Macdonald SIR model, we successfully estimated key parameters—such as mosquito biting rates, transmission probabilities, and recovery rates—while rigorously quantifying uncertainties through posterior distributions. The comparison between Ordinary Least Squares (OLS) and Bayesian approaches revealed that while OLS provided precise point estimates, Bayesian methods offered a more comprehensive understanding of parameter variability, particularly when integrating prior knowledge and synthetic data. The convergence of MCMC chains and the stability of posterior distributions underscored the reliability of these estimates, even under Kenya's heterogeneous transmission patterns and limited empirical data.

The findings hold significant implications for malaria control strategies in Kenya. By capturing uncertainties in transmission dynamics, Bayesian frameworks enable policymakers to evaluate intervention impacts probabilistically, accounting for both spatial and temporal variability. For instance, the posterior estimates of the basic reproductive number ($R0$) and mosquito-human

ratios provide actionable insights for prioritizing bed net distribution or indoor residual spraying in high-risk regions. Furthermore, the integration of prior knowledge—such as biologically plausible parameter ranges—enhances model robustness in data-scarce settings, ensuring that interventions are both evidence-based and adaptable to evolving transmission landscapes.

Future research should expand these methodologies to more complex models, such as stochastic or agent-based frameworks, to better capture individual-level interactions and climate-driven transmission shifts. Additionally, applying Approximate Bayesian Computation (ABC) could address limitations posed by non-Gaussian noise in real-world mosquito population data. By advancing Bayesian approaches in malaria modelling, this work paves the way for scalable, data-informed strategies that align with Kenya's public health goals and global malaria eradication efforts. Such innovations will be vital in navigating the dual challenges of drug resistance and climate change, ultimately fostering sustainable, community-tailored solutions.

CONFLICT OF INTERESTS

The authors declare that there is no conflict of interests.

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