Journal homepage http://revistas.unitru.edu.pe/index.php/SSMM

SELECCIONES MATEMÁTICAS
Universidad Nacional de Trujillo
ISSN: 2411-1783 (Online)
2023; Vol. 10(1): 41-50.

Special issue: Peruvian Conference on Scientific Computing 2022, Cusco - Peru

Bayesian estimation of parameters in a SI mathematical model for the transmission dynamics of an infectious disease in Peru

Estimación Bayesiana de parámetros en un modelo matemático SI, para la dinámica de transmisión de una enfermedad infecciosa en el Perú

Emma Cambillo-Moyano, Ysela Agüero-Palacios, Alicia Riojas-Cañari, Pedro Pesantes-Grados and Roxana López-Cruz

Received, Jan. 16, 2023 *Accepted, Apr. 16, 2023*

How to cite this article:
Cambillo-Moyano E. et al. *Bayesian estimation of parameters in a SI mathematical model for the transmission dynamics of an infectious disease in Peru*. Selecciones Matemáticas. 2023;10(1):41–50. http://dx.doi.org/10.17268/sel.mat.2023.01.04

Abstract

The objective of the research is to estimate the transmission rate of an infection (β) in the SI epidemical model, using Bayesian statistical methods from observed data in Peru. After studying the SI mathematical model and Bayesian statistical inference methods, a Bayesian estimator is proposed to estimate the transmission rate of an infection in this model and a procedure is proposed to estimate this rate using Montecarlo simulation based on Markov chains - MCMC.

Keywords . Ordinary differential equation, multiple level, stability, SI model, Montecarlo Simulation, Bayesian estimator, MCMC.

Resumen

El objetivo de la investigación es estimar la tasa de transmisión de una infección (β) en el modelo SI, utilizando métodos estadísticos bayesianos a partir de datos observados en el Perú. Luego de estudiar el modelo matemático SI y los métodos de inferencias estadística bayesiana se propone un estimador bayesiano para estimar la tasa de transmisión de una infección en este modelo y se propone un procedimiento para estimación de dicha tasa utilizando simulación Montecarlo basado en cadenas de Markov - MCMC.

Palabras clave. Ecuación diferencial ordinaria, múltiple nivel, estabilidad, modelo SI, Simulación Montecarlo , estimador Bayesiano, MCMC.

1. Introduction. Currently, the spread of infectious diseases is a major concern in public health analysis, including the design of strategies to manage the threat of infectious diseases, and this is possible by mathematical modeling of diseases. Since D'Alembert was one of the first to describe the spread of infectious diseases by means of a mathematical model in the 18th century. In this same century, Bernoulli proposed mathematical models based on differential equations to represent the evolution of some infectious diseases. These results are still useful today. Ross, with the study of human malaria, obtained the Nobel

*Departamento de Estadística, Universidad Nacional Mayor de San Marcos, Lima, Perú (ecambillom@unmsm.edu.pe).
†Departamento de Estadística, Universidad Nacional Mayor de San Marcos, Lima, Perú (yaguerop@unmsm.edu.pe).
‡Departamento de Investigación de Operaciones, Universidad Nacional Mayor de San Marcos, Lima, Perú (ariojasc@unmsm.edu.pe).
§Unidad de Posgrado de la Facultad de Ciencias Matemáticas, Universidad Nacional Mayor de San Marcos, Lima, Perú (pedro.pesantes@unmsm.edu.pe).
¶Departamento de Matemática, Universidad Nacional Mayor de San Marcos, Lima, Perú (rlopezc@unmsm.edu.pe).

Prize in 1902, Kermack and McKendrick, considered the endemic diseases and several interesting findings were related to experimental data with rats. The outstanding result was the famous threshold theorem, according to which the introduction of infectious individuals into a population of susceptibles could lead to an epidemic only if the density of susceptibles exceeds a certain threshold value. If the threshold is exceeded, then an outbreak occurs, otherwise it disappears. ([1]).

Acquired Immunodeficiency Syndrome (AIDS) is the final and most serious stage of the disease caused by the Human Immunodeficiency Virus (HIV) ([2]), and has experienced a rapid growth in the world since 1981. The main form of infection is sexual, producing progressive destruction of the immune system. Currently the number of infected people worldwide is approximately 40 million, calling the attention of scientists, physicians and world health organizations to counteract the advance of this dreaded retrovirus. It is a major social problem, so it is important to understand the dynamics of the spread of this disease, which together with the analysis of epidemiological studies will result in strategic plans for awareness and prevention of the spread of the virus.

Nowadays, mathematical models are of great importance for the study of problems in medicine, biology, epidemiology, among other areas of knowledge, since they allow describing, explaining and predicting the dynamics of transmission and control of infectious diseases. Health data modeling is based on mathematical sciences with the objective of defining future scenarios based on historical information and thus better understand the behavior and spread of diseases ([3]).

Epidemiological models assume that individuals are in one of several possible states. Depending on these states, the population can be included in categories: susceptible (S), infected (I) or removed (R) individuals, etc. The most important models are: SI, SIS and SIR, which can be modeled deterministically or stochastically and in all of them it is assumed that the interaction between individuals is random ([1]).

For most sexually transmitted diseases (STDs), the SIS model is more useful, since only a small number of STDs confer post-infection immunity. HIV is a clear exception and can still be adequately described, at least in the western world, by a model called SI.

2. MCMC Estimation. There are several methods for estimating the parameters of mathematical models for infectious and contagious diseases, among which the most widely used method is the least squares, which minimizes the sum of squares of the deviations of the data from the proposed model [4], [5].

Another method used for fitting models for infectious diseases is the maximum likelihood , using the iterative algorithm of maximizing the expectation of the score function (EM). This method was used by [6], during the period 1708 - 1748 in London to estimate the parameters of a model for smallpox, with data on deaths from this disease. A variant of this method was used by [7] to estimate the parameters of a long-term dynamic model of HIV. A more sophisticated method for obtaining good estimates for the unknown parameters of mathematical models for infectious diseases is to adopt a Bayesian approach using Montecarlo Markov chain (MCMC) simulations.

Montecarlo Markov chain (MCMC) simulation with Bayesian approach is one of the most modern and advanced methods used to obtain good estimates for unknown parameters of mathematical models for infectious diseases, in which the parameter of interest is considered to have an a priori probability distribution, based on the researcher's knowledge. Subsequently, based on a random sample of the population, parameter of interest and the a priori distribution and using Bayes'Theorem, aposteriori of the estimator and the estimation of the corresponding parameter. MCMC methods are a class of algorithms for sampling from probability distributions based on a Markov chain with stationary distribution. In Bayesian models, the MCMC method estimates the a posteriori probability distribution of the parameters [8]. According to [9] the reasons why Bayesian MCMC has become an attractive option for estimating the parameters of models for infectious diseases is that

- is easy to implement and provides a great deal of modeling flexibility.
- allows the analysis of all model parameters and parameter functions.
- does not provide point estimates of the parameters, but their probability distributions, which capture the uncertainty.
- a posteriori summaries such as means, medians, maxima, minima, credibility intervals, etc., can be easily obtained for individual parameters or for joint distributions of parameters.
- if the amount of available data is limited, this is reflected in the result, since the a posteriori distributions of the parameters show greater variability.

Model fitting by the MCMC method involves [9]

1. to build a mathematical model of the disease.
2. to have appropriate epidemiological data on the disease.
3. to perform Bayesian inference, in which information on model parameters obtained from previous studies is considered as a priori knowledge and combined with epidemiological data to update information on unknown model parameters.

The Monte Carlo Markov chain (MCMC) method is used to update the parameter distributions.

Let, a model be given by a set of differential equations, and let $D_i = D(t_i) : i = 1, 2, \ldots, n$; epidemiological data at discrete time points $t_1, t_2, \ldots, t_n$, the objective is to find a set of free parameters such that the model fits the data at those time points. Let $y(t_i/\theta)$ be the data series produced by the proposed mathematical model at the discrete time point, t_i.

a) The objective function, E^2, is constructed by calculating the sum of squares of the deviations of the observed data (D_i) from the data produced by the proposed model $(y(t_i/\theta))$

$$E^2 = \sum_{i=1}^{n} (D_i - y(t_i/\theta))^2 \tag{2.1}$$

b) A likelihood function for the model parameters. The likelihood function is obtained by assigning some probability distribution to the perturbations of model (2.1). This function can be, for example, a normal, binomial, poisson or other probability distribution. In many practical situations, a standard normal distribution is assumed for (2.1) and the likelihood function is written as:

$$L(\theta) = Pr(D/\theta) = exp\big(-E^2\big) \tag{2.2}$$

c) An a priori probability function for the model parameters, $Pr(\theta)$, is established. In the uninformative case, a non-informative a priori distribution can be used.

d) Finally, the a posteriori distribution of the unknown parameters is calculated, which is the conditional distribution of the parameter values, given the data (likelihood function). By Bayes' theorem [10].

$$Pr(\theta/D) = \frac{Pr(D/\theta)Pr(\theta)}{Pr(D)} \tag{2.3}$$

where:
$Pr(\theta/D)$ is the posteriori distribution of θ,
$Pr(D/\theta)$ is the distribution function of D given the value of θ
$Pr(\theta)$ is the a priori distribution y
$Pr(D)$ is the empirical evidence and is expressed as :

$$Pr(D) = \int Pr(D/\theta)Pr(\theta)d\theta. \tag{2.4}$$

The a posteriori distribution can be estimated by calculating the expression (2.3).
Unfortunately, $Pr(D)$ is computationally difficult, if not impossible, to calculate. However, we do know that the a posteriori distribution is proportional to the numerator of the expression (2.3)

$$Pr(\theta/D) \propto Pr(D/\theta)Pr(\theta). \tag{2.5}$$

Using the expression (2.5) and by using a simple Metropolis algorithm; a Markov chain is formed that converges asymptotically to the a posteriori distribution.

The Metropolis algorithm is an iterative procedure that uses an acceptance/rejection rule to achieve convergence to the required distribution. [8].

The algorithm consists of the following steps:

1. Start with an initial θ^0 estimate for the parameter values. This initial estimate is drawn at random from the a priori distribution, $Pr(\theta)$.
2. For each iteration, $i = 1, 2, 3, \ldots$
   a. A new set of θ^* parameter values is generated by sampling from a proposed distribution, $J(\theta^*/\theta^{n-1})$. In order to use this algorithm, the proposed distribution $J(\theta^*/\theta^{n-1})$ must be symmetric, i.e., $J(\theta^*/\theta^{n-1}) = J(\theta^{n-1}/\theta^*)$.
   b. Using the likelihood function, an r value is calculated which is the minimum between 1 and the ratio of the a posteriori probabilities.

$$r = min\left\{\frac{Pr(\theta^*/D)Pr(\theta^*)}{Pr(\theta^{n-1}/D)Pr(\theta^{n-1})}, 1\right\} \tag{2.6}$$

   c. A random number with uniform distribution, $\alpha(0, 1)$, is generated. Then the values of the parameters for this iteration are

$$\theta^n = \begin{cases} \theta^* & \text{si } \alpha < r \\ \theta^{n-1} & \text{en other case} \end{cases} \tag{2.7}$$

The iterative algorithm should be repeated until the estimated parameter values converge to the a posteriori distribution so that errors are minimized.

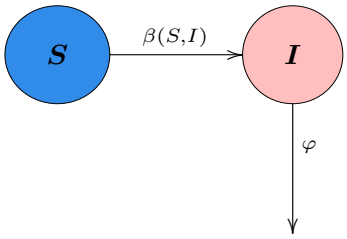


Figure 3.1: Flowchart of the SI model without life dynamics, where $\beta(S, I) = \beta I$.

3. Mathematical epidemiological Model SI. An SI model [3] is applied to a contagious disease from which the infected never recover. It is the simplest model, where the population consists of susceptibles (S) and infected (I), if an individual becomes infected, the disease is permanent. The diagram representing the dynamics of the SI model without life dynamics is as follows where the parameter β controls how fast people move from being susceptible (S) to infected (I); is the transmission rate, average number of contacts suitable for infection of a person per unit time and, the parameter φ controls deaths from infection, is the rate of death from infection. The state variables at time t are :

$S(t)$is the number of susceptible individuals.

$I(t)$ is the number of infected individuals.

Continuous and discrete SI epidemic model without vital dynamics. The continuous SI model is expressed in the following system of ordinary differential equations

$$\frac{dS}{dt} = -\beta SI, \tag{3.1}$$

$$\frac{dI}{dt} = \beta SI - \varphi I, \tag{3.2}$$

where; (3.1) is the average change in the susceptible population (S) per unit time (t), this change is given in relation to the probability of becoming infected, upon contact between a susceptible (S) and an infected (I), which is represented as βSI and (3.2) is the average change of the infected population (I) per unit of time (t), the expression βSI represents the susceptibles that became infected to which is subtracted the expression φI that represents the infected that die from the infection.

The applicability of these models is achieved by establishing a good approximation of the values of the model parameters or at least those that are more sensitive with respect to the initial conditions [11], [7]. The equivalent of continuous versus discrete dynamics is obtained by starting from the continuous model

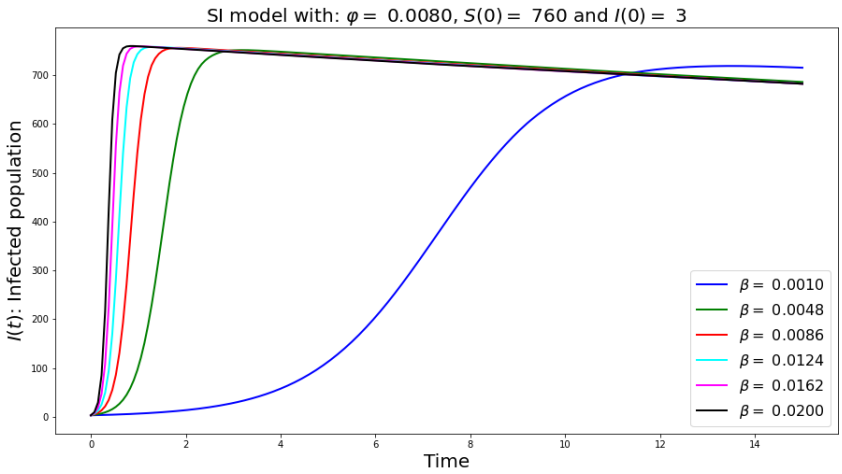


Figure 3.2: Infected populations trajectories under several values of parameter β (sensibility of β).

$$\frac{dS}{dt} = -\beta SI$$
$$dS \approx -\beta SI \quad dt.$$

We integrate from t to $t+1$

$$\int_t^{t+1} \frac{dS}{S} dt = \int_t^{t+1} -\beta I(t) dt,$$

we obtain

$$S(t+1) = (1 - \beta I(t))S(t).$$

This is the equivalent model to the continuous model considered in (3.1). And it indicates that the number of susceptible individuals passing to the infected at time t is $betaS(t)I(t)$. Likewise, the displacement of infected individuals, including their death by infection, is given by

$$I\,(t+1) = (1 + \beta S\,(t) - \varphi)I(t).$$

As can be seen, the variables depend on each other, therefore the discrete SI system is studied without vital dynamics.

$$\begin{cases} S(t+1) = (1 - \beta I(t))S(t), \\ I(t+1) = (1 + \beta S(t) - \varphi)I(t). \end{cases} \tag{3.3}$$

Another SI Model without vital dynamics. The flow diagram of the modified SI model without life dynamics [12] life dynamics and death by infection [3] is explained in the Fig(3.3).
where

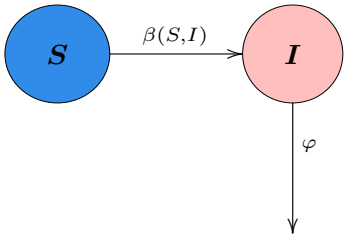


Figure 3.3: Flowchart of the SI model without life dynamics, where $\beta(S,I) = k\,ln\left(1 + \frac{\beta I}{k}\right)$.

$N = S + I$ is the total population
β is the transmission rate, the average number of contacts suitable for infection of a person per unit of time
k is the overdispersion parameter, i.e. the measure of the degree of contagion.
φ is the death rate due to infection
The continuous version is given by the following system of ordinary differential equations

$$\frac{dS}{dt} = -kS\,ln\left(1 + \frac{\beta I}{k}\right), \tag{3.4}$$

$$\frac{dI}{dt} = kS\,ln\left(1 + \frac{\beta I}{k}\right) - \varphi I. \tag{3.5}$$

Without loss of generality, it is assumed that the total number of infected individuals is constant and integrating (3.4) over a unit time interval:

$$S(t+1) = S(t)\left(\frac{k}{k + \beta I(t)}\right)^k.$$

This implies that the fraction of susceptible individuals surviving in that time span is $\left(\frac{k}{k+\beta I(t)}\right)^k$. Likewise, consider that the average number of newly infected individuals is $1 - S(t)\left(\frac{k}{k+\beta I(t)}\right)^k$, therefore, the discrete version of the SI model (3.4-3.5), is

$$\begin{cases} S(t+1) = S(t)\left(\frac{k}{k+\beta I(t)}\right)^k \\ \\ I(t+1) = S(t)\left[1 - \left(\frac{k}{k+\beta I(t)}\right)^k\right] - \varphi I(t) \end{cases} \tag{3.6}$$

$$\frac{dS}{dt} = \lim_{h\to 0} \frac{S(t+h) - S(t)}{h}$$

which represents the instantaneous change in continuous dynamics.

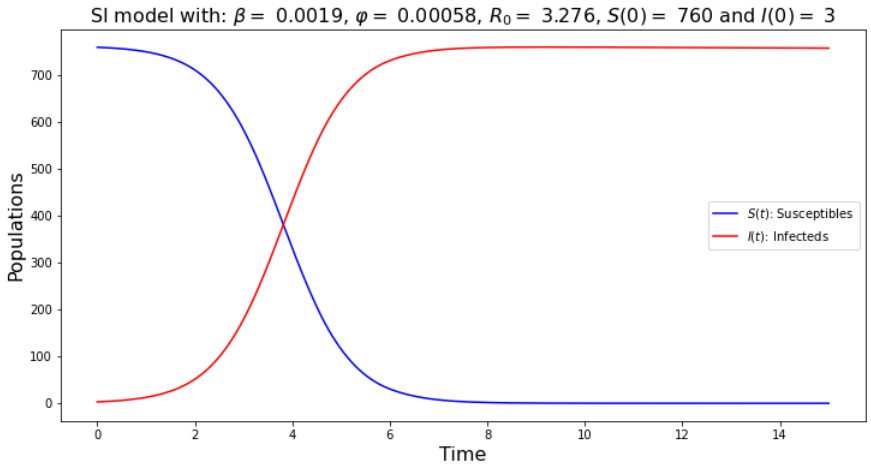


Figure 3.4: Solutions trajectories of the basic SI model. System (3.1 - 3.2).

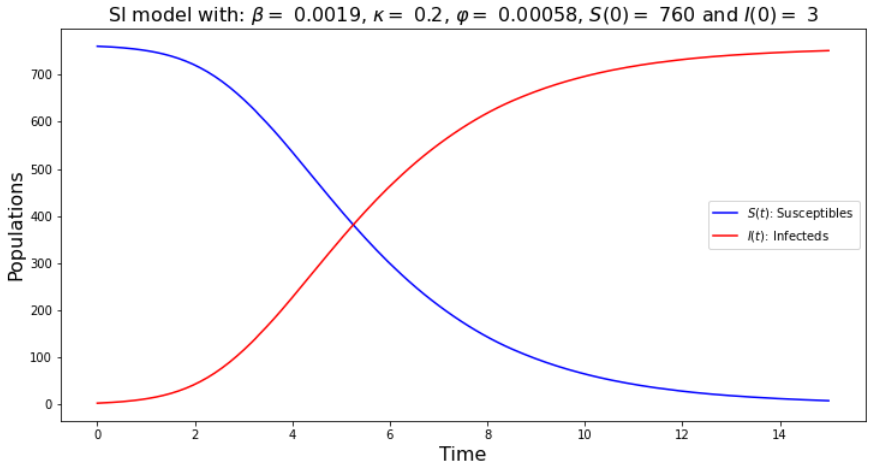


Figure 3.5: Solutions trajectories of the basic SI model. System (3.4 - 3.5).

In Fig.3.4 and Fig.3.5, we appreciate the second system is sensible to parameter k (contagion index) which control the incidence rate β.

Bayesian Estimation of parameters in the system (3.6). If $S(t) = s, I(t) = i$, the new infections at time $(t + 1)$, is obtained from

$$\hat{I}|s, i \sim B(s, p_i\,(i, \beta, k)),$$

where

$$p_i\,(i, \beta, k) = 1 - \left(\frac{k}{k + \beta i}\right)^k.$$

Then, let be the number of new infected at time T,

$$\hat{i}_t = S\,(t - 1) - S(t)$$

The likelihood function for data observed at time T is given by

$$\prod_{t=1}^{T} B(t|S(t-1), p_i\,(I(t-1), \beta, k))$$

Samples for $beta$ and k can be obtained from the Metropolis-Hastings algorithm, thus the conditional based on previous sample values (β, k) is (β^*, k^*), which can be obtained by the Metropolis algorithm inside the Gibbs Sampler using:

$$P(\beta^*|k) \propto \prod_{t=1}^{T} B(\hat{i}_t|S(t-1), p_i\,(I\,(t-1)\,, \beta^*, k)),$$

and

$$P(k^*|\beta^*) \propto \prod_{t=1}^{T} B(\hat{i}_t|S(t-1), p_i\,(I\,(t-1)\,, \beta^*, k^*)).$$

4. Application of the Bayesian estimation of Parameters. In the present section, the methodology exposed in section 2 is implemented to the model given in (3.1) and (3.2), where the parameters and initial conditions for the model are given in the Table (4.1).

Parameter	Meaning	Value	Reference
β	Per capita transmission rate	0.000055047 (year×person) $^{-1}$	Estimated
φ	Per capita HIV-related death rate	0.029789 (year^{-1})	Assumed
$S(0)$	Initial susceptible population	9000 (person)	Assumed
$I(0)$	Initial infected population	1 (person)	[13]

Table 4.1: System parameters and initial conditions for SI model without vital dynamics.

Frequently, it is difficult to have data of all variables related to an specific model. In epidemiology context, morbidity and mortality data is usually available, for this reason, the following example uses real data based on the monitoring of HIV (human immunodeficiency virus) and AIDS (acquired immunodeficiency syndrome) in the Peruvian population [13]. On the other hand, the transmission rate is the most important parameter in epidemiology models, it depends on the contact rate and the probability to be infected, and those factors are not easy to be estimated [3]. Taking this into account, the authors developed a case study where the per capita HIV-related death rate is known and the transmission rate is estimated, using the infected-HIV people data to fit the model.

The data was tabulated, processed and plotted using the packages Pandas 1.1.0 and the Bayesian parameter estimation was performed with PyMC3 3.11.5 [14] and ArviZ 0.11.0 [15] in Python language. The data is shown in Figure 4.1 and the initial infected population was taken from this data. The initial susceptible population used to the estimation and simulation was taken arbitrarily because is difficult to access this information in a close population during these years.

The parameter φ can be interpreted and assumed as the average remaining period off life for a HIV-infected person, whose value can be calculated as the inverse mean infection period for the HIV [16]. The

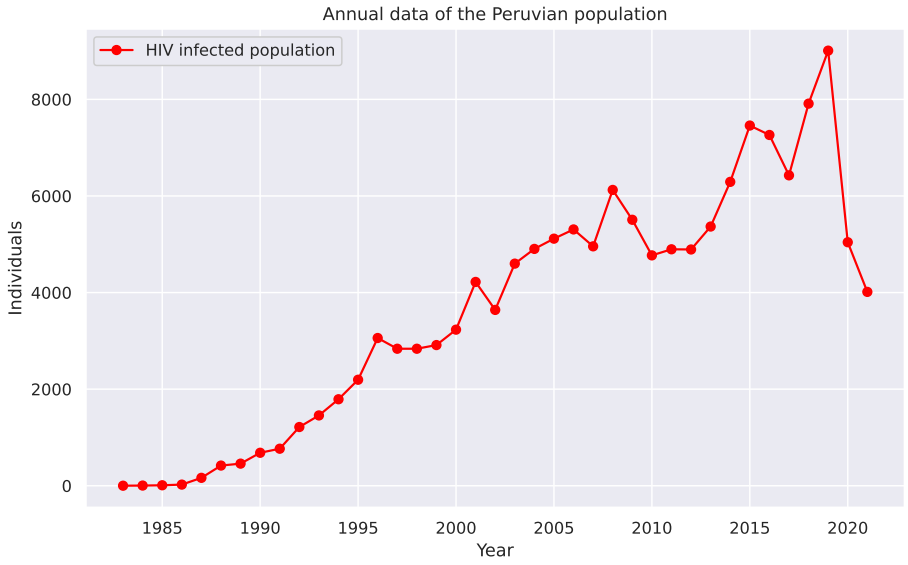
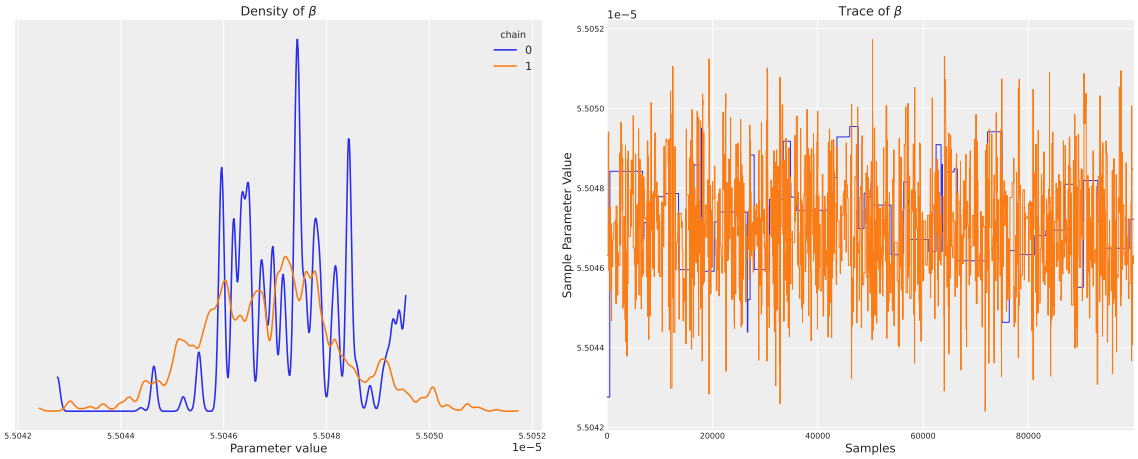
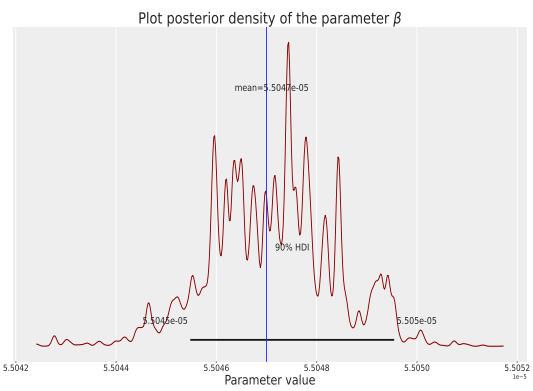


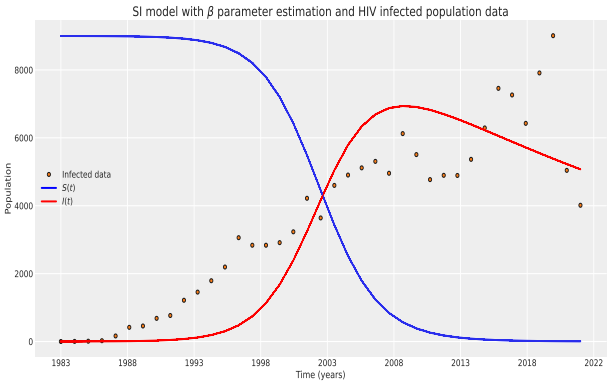
Figure 4.1: HIV-infected Peruvian population from 1983 to 2021



(a) Trace and density plots for parameter β.

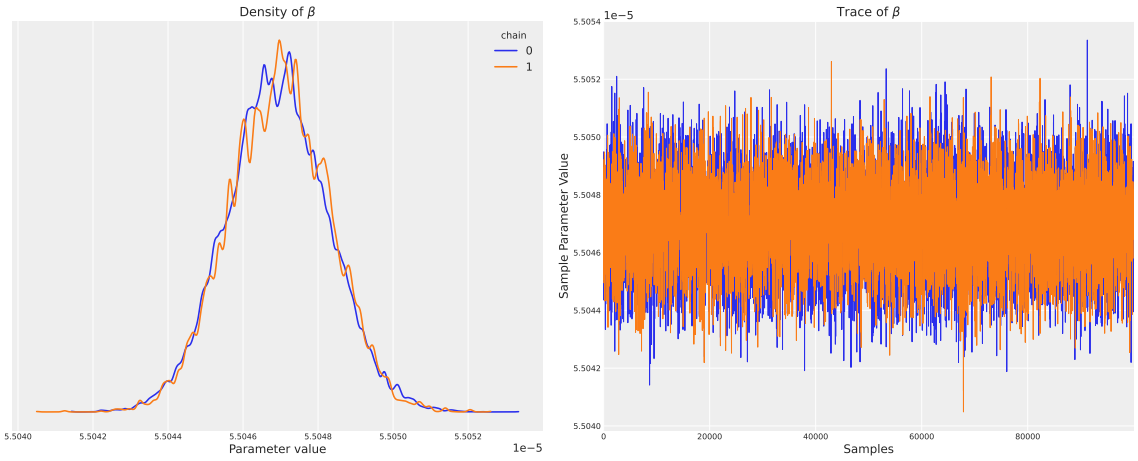


(b) Posterior density for parameter β.

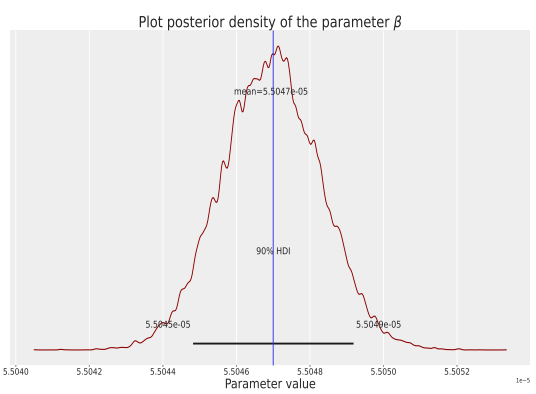


(c) Plot of the fitted SI model and the data.

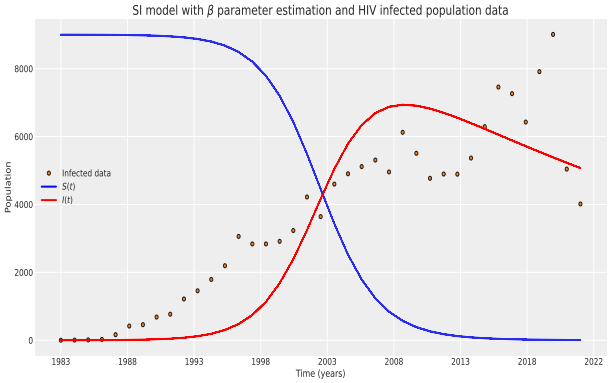
Figure 4.2: Bayesian parameter estimation plots and model fit considering a Normal prior distribution for the parameter β.



(a) Trace and density plots for parameter β.



(b) Posterior density for parameter β.



(c) Plot of the fitted SI model and the data.

Figure 4.3: Bayesian parameter estimation plots and model fit considering a Uniform prior distribution for the parameter β.

parameter β was estimated using the Bayesian approximation and its mean value is shown in the Table 4.1.

In order to estimate β, two different a priori distribution were used: Normal (Figure 4.2), and Uniform (Figure 4.3). The error function is given by equation (2.1), while the likelihood function was implemented using the Log-Normal with mean equal 0 and standard deviation equal one, from equation (2.2) is possible to derive the following likelihood expression:

$$Loglik\left(\theta\right) = \log\left(L\left(\theta\right)\right) = \log\left(Pr\left(D/\theta\right)\right) = -E^2.$$

A random seed equal 369 was used in all the simulations, and the sample method to run the MCMC was Metropolis-Hastings with 100000 samples and two Markov chains are shown. The initial guess for parameter β was 0.0005, and the Uniform distribution was implemented with a lower bound equal to 0 and an upper bound equal to 1. Also, the mean position of the β value is specified as a vertical blue line in the posterior density plots together with the high density intervals (HDI) at the 90%, which means that there is 90% probability the belief is between 5.5045×10^{-5} and 5.5049×10^{-5} for the mean β value, for example (Figure 4.3b).

5. Conclusions. The estimate for the transmission rate of an infection in the SI model can be obtained from the conditional distributions using the Metropolis Hasting algorithm within the Gibbs Sampler. Also, a procedure has been derived to estimate this rate using Monte Carlo simulation based on Markov chains - MCMC.

As a result of this work, Bayesian estimation works well to estimate the parameter: HIV transmission rate per inhabitant in Perú, from a priori normal distribution and based on the posterior distribution it can be concluded that the posterior mean is 0.000055 per year, so it can be interpreted that if an individual is infected with HIV, he/she infects another with a rate of 0.000055 per year.

Acknowledgment. The research was funded by the Vice Rectorate for Research and Graduate Studies. Project No. B17141831 (04274-R-17) . The authors also thank the anonymous reviewers and the handling editor for their constructive comments, suggestions and valuable corrections which have enhanced this work.

ORCID and License
Emma Cambillo-Moyano https://orcid.org/0000-0003-3173-9425
Ysela Agüero-Palacios https://orcid.org/0000-0001-6067-1218
Alicia Riojas-Cañari https://orcid.org/0000-0002-1110-7255
Pedro Pesantes-Grados https://orcid.org/0000-0003-2370-1419
Roxana López-Cruz https://orcid.org/0000-0002-7703-5784

References

[1] Montesinos-López OA, Hernández-Suárez CM. Modelos matemáticos para enfermedades infecciosas. Salud pública de México. 2007 Jul;49(3):218-26.
[2] Mesa-Mazo MJ, Vergaño-Salazar JG, Sánchez-Botero CE, Muñoz-Loaiza A. Modelo matemático para la dinámica de transmisión del VIH/SIDA en una población sexualmente activa. Revista de Salud Pública. 2010 Apr;12(2):308-16.
[3] López R, Vidal M, Valdez W. Nociones básicas de modelamiento matemático aplicado a la epidemiología. MInisterio de Salud-Perú. 2015.
[4] Chowell G, Diaz-Duenas P, Miller JC, Alcazar-Velazco A, Hyman JM, Fenimore PW, Castillo-Chavez C. Estimation of the reproduction number of dengue fever from spatial epidemic data. Mathematical biosciences. 2007 Aug 1;208(2):571-89.
[5] Mubayi A, Castillo-Chavez C, Chowell G, Kribs-Zavaleta C, Siddiqui NA, Kumar N, Das P. Transmission dynamics and underreporting of Kala-azar in the Indian state of Bihar. Journal of theoretical biology. 2010 Jan 7;262(1):177-85.
[6] Duncan S, Gyongy M. Using the EM algorithm to estimate the disease parameters for smallpox in 17th century London. In2006 IEEE Conference on Computer Aided Control System Design, 2006 IEEE International Conference on Control Applications, 2006 IEEE International Symposium on Intelligent Control 2006 Oct 4 (pp. 3312-3317). IEEE.
[7] Lavielle M, Samson A, Karina Fermin A, Mentré F. Maximum likelihood estimation of long-term HIV dynamic models and antiviral response. Biometrics. 2011 Mar;67(1):250-9.
[8] Gelman A, Rubin DB. Markov chain Monte Carlo methods in biostatistics. Statistical methods in medical research. 1996 Dec;5(4):339-55.
[9] Pandey A. Modeling dengue transmission and vaccination (Doctoral dissertation, Clemson University).
[10] Jiménez Luna J. Métodos Monte Carlo basados en cadenas de Markov[Trabajo Fin de Grado Inédito]. Universidad de Sevilla, Sevilla, 2015. https://idus.us.es/handle/11441/40818
[11] Amiri Mehra AH, Shafieirad M, Abbasi Z, Zamani I. Parameter estimation and prediction of COVID-19 epidemic turning point and ending time of a case study on SIR/SQAIR epidemic models. Computational and Mathematical Methods in Medicine. 2020 Dec 29;2020.
[12] Talawar AS, Aundhakar UR. Parameter estimation of SIR epidemic model using MCMC methods. Glob J Pure Appl Math. 2016;12:1299-306.
[13] MINSA-CDC. Situación epidemiológica del VIH-Sida en el Perú (SE43). Ministerio de Salud de la República del Perú, Viceministerio de Salud Pública - Centro Nacional de Epidemiología, Prevención y Control de enfermedades. Lima, Perú. 2021. [cited 2023 Jan 14]. Available from: http://www.dge.gob.pe/portal/docs/tools/teleconferencia/2021/SE432021/03.pdf
[14] Salvatier J, Wiecki TV, Fonnesbeck C. Probabilistic programming in Python using PyMC3. PeerJ Computer Science. 2016 Apr 6;2:e55.
[15] Kumar R, Carroll C, Hartikainen A, Martín OA. ArviZ a unified library for exploratory analysis of Bayesian models in Python. Journal of Open Source Software. 2019; 4(33):1143. Available from: https://doi.org/10.21105/joss.01143
[16] López Roxana, Yang Kuang, Abdessamad Tridane. A Simple SI Model with Two Age Groups and Its Application to US HIV Epidemics: To Treat or Not to Treat?. Journal of Biological Systems. 2007; 15(02): 169-184.