Study of the convergence of stochastic compartmental models in epidemiology

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Abstract

The use of compartmental models is well known in epidemiology. In this paper, we present a numerical method for the convergence analysis of stochasistic extensions of these models. Considering three stochastic extensions of the SIR model such as the model with a pure-jump Markov chain, the model with Ito's integral, and the Poisson stochastic model; we studied the convergences of these models towards the basic deterministic model. Simulations highlight the differences in the speed of convergence of the three stochastic extensions considered. This technique constitutes a method for analyzing the strengths and limitations of stochastic compartmental models.

Keywords

Stochastic epidemic model, Pure jump Markov chain, Poisson process, Itô's integral

I INTRODUCTION

Mathematical modelling of infectious diseases has been used for decades to study the mechanisms of disease spread, to predict the evolution of an epidemic, to evaluate control strategies and to help design public health interventions. Daniel Bernouilli was the first to bring mathematical research to epidemiology[5]. A well-established method of making inferences about epidemic patterns is to divide the population of interest by the abstract notion of compartments, defined by the health status of the pathogen in the system, the demographic or epidemiological characteristics. The cornerstone of these compartmental models was developed by Kermack WO in 1927[3].

Recently, under the magnitude of the covid'19 pandemic, various extensions of the SIR models have been proposed to describe the evolution of this disease in different countries[9]. In the event that we have uncertainties on certain model parameters or we only have a limited number of data, stochastic compartmental models are preferred[8]. However, in many cases, the convergences of these so-called stochastic models are difficult to prove.

In this article, our objective is to study the strengths and limitations of stochastic compartmental models using simulations. Starting from the basic deterministic model, we consider three stochastic extensions: the continuous-time markov chain model, the stochastic model with Ito's integral and the model with the model with the Poisson process. After estimating the different parameters of these models, we carry out analyzes on the long-term behavior of the models.

II DETERMINISTIC BASELINE MODEL

All compartmental epidemic models are derived from the Kermack model described in the figure 1 below[3].

Figure 1: SIR model of Kermack WO

The model can be formulated using ordinary differential equations (ODE). A closed population is assumed, i.e. at all times t :

$$\begin{cases} \frac{dS(t)}{dt} &= -\beta S(t)\frac{I(t)}{N} \\ \frac{dI(t)}{dt} &= \beta S(t)\frac{I(t)}{N} - \gamma I(t) \\ \frac{dR(t)}{dt} &= \gamma I(t) \end{cases} \tag{1}$$

Several assumptions have been made in the formulation of the above equations. The population of a compartment is differentiable with respect to time and the epidemic process is deterministic. The compartments are homogeneous, which means that an individual in the population contracts the disease with a rate of β, being the infection rate of the disease. A fraction equal to γ representing the average recovery/mortality rate of infectious individuals leaving that compartment per unit time to enter the recovered compartment.

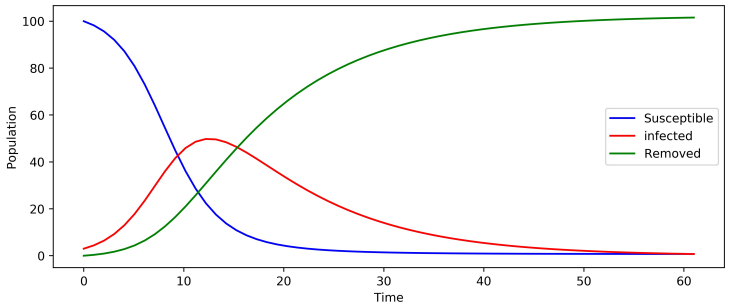

Figure 2: Numerical simulation with S(0)=97, I(0)=3 and R_0=5

An important parameter of the model that determines the magnitude of the epidemic is the basic reproduction number R_0 given by:

$$R_0 = \frac{\beta}{\gamma} \tag{2}$$

This is the number of new infections produced by an infected individual in an intact population of susceptible individuals only. When $R_0 > 1$, an epidemic occurs and when $R_0 < 1$, there is no epidemic.

III PURE JUMP STOCHASTIC MARKOV CHAIN MODEL

In the case of the continuous time Markov chain (CTMC) model, we consider a new infection or a new cure in a sufficiently small time Δt. There, the term $o(\Delta t)$ is included in the definition and $(\lim_{t\to\infty}(o(\Delta t)/\Delta t) = 0)$.

The CTMC epidemic processes are defined on a continuous time scale $t \in [0, \infty)$, but the states S(t),I(t) and R(t) are discrete variables, i.e. $S(t), I(t), R(t) \in 0, 1, 2, ..., N$.

The infinitesimal transition probabilities are defined as follows:

$$P(s+j, i+k \mid s, i) = \begin{cases} (\frac{\beta SI}{N})\Delta t + o(\Delta t) & (j,k) = (-1,1) \\ (\gamma I)\Delta t + o(\Delta t) & (j,k) = (0,-1) \\ (1 - (\frac{\beta SI}{N} + \gamma I))\Delta t + o(\Delta t) & (j,k) = (0,0) \end{cases} \tag{3}$$

The event times $0 < T_1 < T_2 < ...$ during which an individual moves from one state to another are modelled as a renewal process with exponentially distributed increments:

$$P(T_k - T_{k-1} > t \mid T_j, j \leq k-1) = e^{-\Theta(T_{k-1})}$$

où

$$\Theta(T_{k-1}) = \left(\frac{\beta S(T_{k-1}) I(T_{k-1})}{N} + \gamma I(T_{k-1}) \right)$$

Algorithm 1: CTMC SIR Model

Choose times;
$i \leftarrow 0$;
$X_0 \leftarrow (S_0, I_0, R_0)$
while $i < times$ **do**
  $p_1 = \frac{\beta S(i) I(i)}{N}$
  $p_2 = \gamma I(i)$
  $\lambda = p_1 + p_2$
  $t_{i+1} - t_i \sim Exp(\lambda)$
  if $U_{[p_1,p_2]} = p_1$ **then**
    $X_{i+1} \leftarrow (S_i - 1, I_i + 1, R_i)$
  else
    $X_{i+1} \leftarrow (S_i, I_i - 1, R_i + 1)$
  i++

3.1 Probability of an outbreak

In the birth and death model, the process approaches state 0 or approaches infinity. The probability of absorption in state 0 depends on the birth probability p, death probability q and the initial position. If we take $X(t) = x_0 > 0$, then we can show that :

$$\lim_{t \to \infty} \{X(t) = 0\} = \begin{cases} 1 & if \quad p \leq q \\ (\frac{q}{p})^{x_0} & if \quad p \geq q \end{cases}$$

This identity is also valid for in a CTMC (Continuous Time Markov Chain) model, where p and q is replaced by λ_i and γ_i, where i is the position. In a linear birth and death process, the infinitesimal transition probabilities satisfy:

$$p_{i+j,i}(\Delta t) = \begin{cases} \lambda i \Delta t + o(\Delta t), & j = 1 \\ \gamma i \Delta t + o(\Delta t), & j = -1 \\ 1 - (\lambda + \gamma) i \Delta t + o(\Delta t), & j = 0 \end{cases}$$

The probability of absorption is one if $\lambda \leq \gamma$. But if $\lambda > \gamma$ the probability of absorption decreases to $(\gamma/\lambda)^{x_0}$. In the latter case, the probability of persistence of the population is $1 - (\gamma/\lambda)^{x_0}$.

This identity can be used to estimate the probability of an epidemic in CTMC SIS and SIR epidemic models, where population persistence can be interpreted as an epidemic.

Assume that the initial number of infected individuals i_0 is small and the population size N is large. Then the birth and death functions in a SIR epidemic model are given by:

- Birth=$\frac{\beta i(N-i)}{N} \simeq \beta i$
- Death=γi

Applying the previous approximations for the birth and death functions leads to the approximation $\lambda/\gamma = \gamma/\alpha = 1/R_0$, then:

$$Prob\{I(t) = 0\} \simeq \begin{cases} 1 & if \quad R_0 \leq 1 \\ (\frac{1}{R_0})^{i_0} & if \quad R_0 > 1 \end{cases}$$

Therefore, the probability of an epidemic is:

$$\text{Probability of an outbreak } \simeq \begin{cases} 0 & if \quad R_0 \leq 1 \\ 1 - (\frac{1}{R_0})^{i_0} & if \quad R_0 > 1 \end{cases}$$

There is close agreement between the numerical values and the estimated probability of an epidemic when $i_0 = 1, 2, 3$ alors $[1 - (1/R_0)^{i_0} = 0.8, 0.96, 0.992]$ with $R_0 = 5$

3.2 Study of convergence

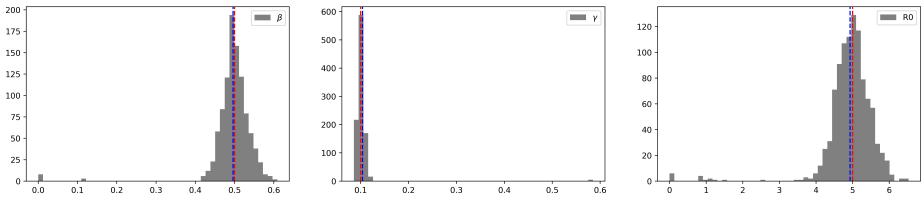

Figure 3: Estimating the parameters of $\beta = 0.50$, $\gamma = 0.10$ and $R_0 = 5$ for model CTMC SIR with S(0)=97 and I(0)=3 on 1000 simulation trajectory, the red line represents the parameter and the blue line represents the mean of the estimate

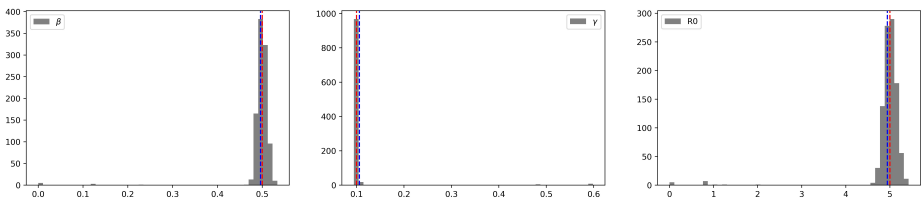

Figure 4: Estimating the parameters of $\beta = 0.50$, $\gamma = 0.10$ and $R_0 = 5$ for model CTMC SIR with S(0)=997 and I(0)=3 on 1000 simulation trajectory, the red line represents the parameter and the blue line represents the mean of the estimate

By the law of large numbers, in the infinite limit, the stochasticity disappears. Thus, the model fails to correctly reproduce the stochastic dynamics, the model converges to the deterministic model in the infinite limit. Indeed, we observe a decrease in the relative stochasticity of trajectories when studying a large population.

The parameter R_0 is determined in a similar way to the deterministic model except for the probability of an epidemic. As shown in the figure above, there is a probability where R_0 is less than 1 i.e. there is no epidemic.

IV STOCHASTIC DIFFERENTIAL EQUATION MODEL

There is a need to investigate other approaches that include stochastic noise that does not vanish for large populations. The idea, which will be developed in this section, is to add white noise to the transition rates in a stochastic SIR model[1][7].

Suppose that the time variables are continuous, $S(t), I(t), R(t)$ are discret random variables, that is to say..,

$$S(t), I(t), R(t) \in [0, N]$$

Assumptions similar to the previous section are made regarding the variation of the random variables on the variation of ΔS and ΔI. In addition, we assume that the variation of these random variables is approximately normally distributed.

Let's consider $\Delta X(t) = (\Delta S, \Delta I)^T$. Then, the mean of $\Delta X(t)$ to the order of Δt is:

$$E(\Delta X(t)) = \begin{pmatrix} -\frac{\beta}{N} SI \\ \frac{\beta}{N} SI - \gamma I \end{pmatrix} \Delta t$$

The covariance matrix of $\Delta X(t)$ is $V(\Delta X(t)) = E(\Delta X(t)[\Delta X(t)])^T - E(\Delta X(t))E(\Delta X(t))^T \simeq E(\Delta X(t)[\Delta X(t)]^T)$ because the element of the second term is $o([\Delta t]^2)$. So the covariance matrix of $\Delta X(t)$ to the order of Δt is

$$V(\Delta X(t)) = \begin{pmatrix} \frac{\beta}{N} SI & -\frac{\beta}{N} SI \\ -\frac{\beta}{N} SI & \frac{\beta}{N} SI + \gamma I \end{pmatrix} \Delta t$$

The random vector $X(t + \Delta t)$ can be approximated as follows:

$$X(t + \Delta t) = X(t) + \Delta X(t) \simeq X(t) + E(\Delta X(t)) + \sqrt{V(\Delta X(t))} \tag{4}$$

Since the covariance matrix is symmetric and positive definite, it has a unique square root $B\sqrt{\Delta t} = \sqrt{V}$. This is an Euler approximation of the Itô integrals. For sufficiently smooth coefficients, the solution $X(t)$ of (4) converges to the solution of the following system of Itô's DSE:

$$\begin{cases} \frac{dS(t)}{dt} &= -\beta S(t)\frac{I(t)}{N} + B_{11}\frac{dW_1}{dt} + B_{12}\frac{dW_2}{dt} \\ \frac{dI(t)}{dt} &= \beta S(t)\frac{I(t)}{N} - \gamma I(t) + B_{21}\frac{dW_1}{dt} + B_{22}\frac{dW_2}{dt} \end{cases} \tag{5}$$

where W_1 and W_2 are independent Wiener processes.

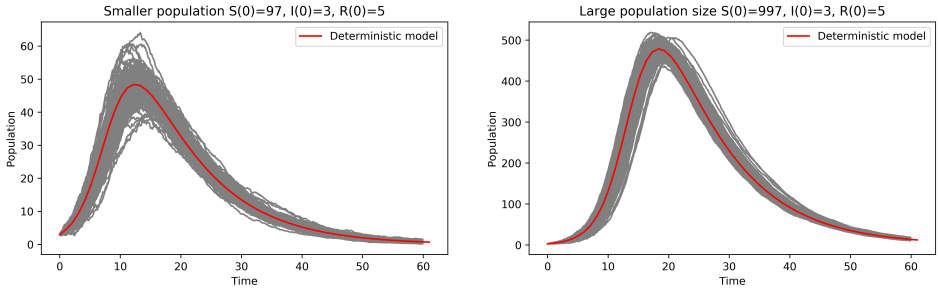

Figure 5: 100 model simulation trajectories for two different population sizes

The model had the deterministic model as the mean, but the noise builds up a variance that allows for stochastic dynamics even in large population numbers.

V STOCHASTIC MODELS POISON PROCESSES

5.1 Presentation of the model

Let $\tau_0 < \tau_1 < \tau_2 < \cdots$ the successive times of infection. Given λ_i, $(i \geq 0)$ the i-th infected individual who had contact with the others according to the Poisson process $P(\int_0^t \lambda_i(s-\tau_i)ds)$. The individual has contact with others in the population according to the Poisson process P(Ct). If the contact is with a susceptible individual, it leads to a new infection with the probability of $p_i(t-\tau_i)$.[4].

Let S(t), I(t) and R(t) be the number of susceptible, infectious and Recovered individuals at time t. Consider $S(t) + I(t) + R(t) = N$ for all $t \geq 0$ and $S(0) > 0$, $I(0) > 0$ and $R(0) = 0$.

With P_{inf} and P_{rec} two independent Poisson processes:

$$\begin{cases} S(t) &= S(0) - P_{inf}(\beta \int_0^t \frac{S(s)I(s)}{N} ds) \\ I(t) &= I(0) + P_{inf}(\beta \int_0^t \frac{S(s)I(s)}{N} ds) - P_{rec}(\gamma \int_0^t I(s) ds) \\ R(t) &= P_{rec}(\gamma \int_0^t I(s) ds) \end{cases} \tag{6}$$

5.2 Study of convergence

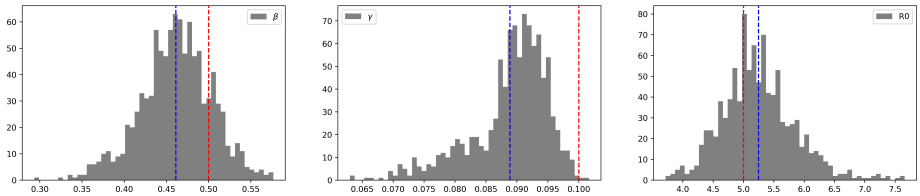

Figure 6: Estimating the parameters of $\beta = 0.50$, $\gamma = 0.10$ and $R_0 = 5$ for model CTMC SIR with S(0)=97 and I(0)=3 on 1000 simulation trajectory, the red line represents the parameter and the blue line represents the mean of the estimate

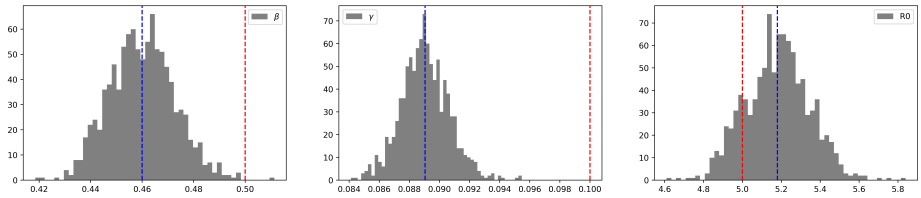

Figure 7: Estimating the parameters of $\beta = 0.50$, $\gamma = 0.10$ and $R_0 = 5$ for model CTMC SIR with S(0)=997 and I(0)=3 on 1000 simulation trajectory, the red line represents the parameter and the blue line represents the mean of the estimate

We know that if (X_n) is a sequence of random variables following the Poisson laws of parameters λ_n. If $\lim_{n\to\infty} \lambda_n = \infty$, then $\frac{X_n - \lambda_n}{\sqrt{\lambda_n}}$ converges in law to $\mathcal{N}(0,1)$. We see then that the model does not lose the stochastic dynamics in large population. So the model does not converge to the deterministic ODE model.

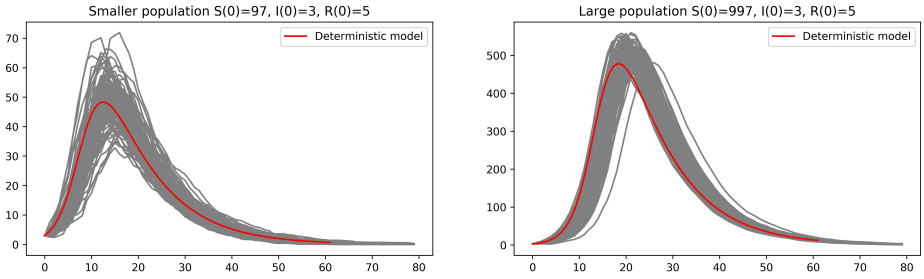

Figure 8: 100 model simulation trajectories for two different population sizes

In large populations, the R0 increases i.e. the epidemic increases in contagiousness and programming accelerates.

VI CONCLUSION AND PERSPECTIVE

In analysing the stochastic compartmental models, we find that the Markov model allows for a natural modelling of the evolution of the epidemic and the results already established in probability theory allow for further studies. It is a powerful and complete model for compartmental epidemiological modelling but the speed of convergence to the deterministic model is very fast in large numbers. The model does not allow for the reproduction of stochastic dynamics. In the model, the infection disappears much earlier than in the corresponding deterministic models. The model can also be used to represent the probability of an outbreak. Furthermore, the extinction time of the epidemic could also be estimated since in the model all states are transient except the $I(t) = 0$ state, a study already investigated in Moujahid, Abdelmalik and Vadillo[6].

Stochastic differential equation models can be used to approximate the stochasticity of the Markov model and will allow parameter estimates with continuous data. But it is a simple model close to the deterministic model which just allows to integrate a noise in the dynamics of the epidemic. The poissonian model presented here is more interesting in the situation where we want to study a large population. This model keeps the stochasticity in a large population. It will also allow a simple method to estimate the parameters of the model. Now we can prove mathematically the convergence speeds of the different stochastic compartmental models.

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A APPENDIX: MAXIMUM LIKELIHOOD ESTIMATION OF THE PURE JUMP MARKOV CHAIN MODEL

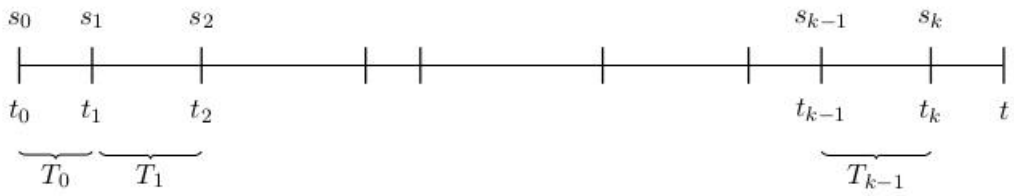

Figure 9: IIllustration of a continuous time stochastic process observed between units of time t_0 and units of time t.

Consider a CTMC SIR model with a trajectory

$$U = (s_0, T_0, s_1, T_1, ..., s_{k-1}, T_{k-1}, s_k)$$

The system starts in state s_0 at time unit t_0 and enters the last state s_k at t_k, as shown in Figure 9. There are a total of k transitions in this process. At any time, all observations occur in the time interval (t_0, t) where $t \geq t_k$, and there are no transitions in the interval t_k, t.

The likelihood function is:

$$L(\beta, \gamma) = \prod_{i=0}^{k-1} (\lambda_{s_i} e^{-\lambda_{s_i} T_i})(p_{s_{i+i} \leftarrow s_i})(e^{-\lambda_{s_k}(t - \sum_{i=0}^{k-1} T_i)}) \tag{7}$$

where $\lambda_{s_i} e^{-\lambda_{s_i} T_i}$ is the probability that the holding time T_i in state s_i, $p_{s_{i+i} \leftarrow s_i}$ is the probability of s_i transitioning to s_{i+1} and $e^{-\lambda_{s_k}(t - \sum_{i=0}^{k-1} T_i)}$ is the probability that no further transitions P occur after time s_k until time t. We observe that $\sum_{i=0}^{k-1} T_i = t_k$. Let $t - t_k = T_k$ be taken, then:

$$e^{-\lambda_{s_k}(t - \sum_{i=0}^{k-1} T_i)} = e^{-\lambda_k (T_k)}$$

and

$$L(\beta, \gamma) = e^{-\lambda_{s_k}(T_k)} \prod_{i=0}^{k-1} (\lambda_{s_i} e^{-\lambda_{s_i} T_i})(p_{s_{i+i} \leftarrow s_i}) \tag{8}$$

Let $t_{\beta_1}, t_{\beta_2}, ..., t_{\beta_n}$ be the set of moments where there is a transition $i \rightarrow i + 1$ and $t_{\gamma_1}, t_{\gamma_2}, ..., t_{\gamma_n}$ is the set of moments where there is a transition $i \rightarrow i - 1$. This means that the first transition from i to i + 1 in the system occurred at time t_{β_1}, the first transition from $i \rightarrow i - 1$ in the system occurred at time t_{γ_1} and so on. There are n transitions of $i \rightarrow i + 1$ and m transitions of $i \rightarrow i - 1$. There are a total of k transitions in the system from the state s_0 to the state s_k.

The transition probability from (s,i) to (s-1,i+1) is:

$$p_{(s,i) \rightarrow (s-1, i+1)} = \frac{(\frac{\beta si}{N})}{(\frac{\beta si}{N} + \gamma i)}$$

And the transition probability from (s,i) to (s,i-1) is:

$$p_{(s,i) \rightarrow (s, i-1)} = \frac{\gamma i}{(\frac{\beta si}{N} + \gamma i)}$$

The likelihood function can be written as follows:

$$L(\beta, \gamma) = \exp\left(-\left(\frac{\beta S(t_k) I(t_k)}{N} + \gamma I(t_k)\right) T_k\right) \prod_{a=t_{\beta_1}}^{t_{\beta_n}} \left[\frac{\beta S(a) I(a)}{N} \exp\left(-\left(\frac{\beta S(a) I(a)}{N} + \gamma I(a)\right) T_a\right)\right]$$

$$\times \prod_{b=t_{\gamma_1}}^{t_{\gamma_n}} \left[\frac{\beta S(b) I(b)}{N} \exp\left(-\left(\frac{\beta S(b) I(b)}{N} + \gamma I(b)\right) T_b\right)\right]$$

Taking the logarithm of the likelihood function, we have:

$$LogL(\beta,\gamma) = -\left(\frac{\beta S(t_k)I(t_k)}{N} + \gamma I(t_k)\right)T_k + \sum_{a=t_{\beta_1}}^{t_{\beta_n}}\left[log\left(\frac{\beta S(a)I(a)}{N}\right) - \left(\frac{\beta S(a)I(a)}{N} + \gamma I(a)\right)T_a\right]$$

$$+ \sum_{b=t_{\gamma_1}}^{t_{\gamma_n}}\left[log\left(\frac{\beta S(b)I(b)}{N}\right) - \left(\frac{\beta S(b)I(b)}{N} + \gamma I(b)\right)T_b\right]$$

Taking the partial derivative of the logarithm of the likelihood function with respect to β and γ, we have :

$$\frac{\partial logL(\beta,\gamma)}{\partial\beta} = \sum_{a=t_{\beta_1}}^{t_{\beta_n}}\left[\left(\frac{1}{\beta}\right) - \left(\frac{S(a)I(a)}{N}\right)T_a\right] + \sum_{b=t_{\gamma_1}}^{t_{\gamma_m}}\left[-\left(\frac{S(b)I(b)}{N}T_b\right)\right] - \left(\frac{S(t_k)I(t_k)}{N}\right)T_k$$

$$\frac{\partial logL(\beta,\gamma)}{\partial\gamma} = -I(t_k)T_k + \sum_{b=t_{\gamma_1}}^{t_{\gamma_m}}\left(\frac{1}{\gamma}\right) - \left(\sum_{a=t_{\beta_1}}^{t_{\beta_n}}[I(a)T_a] + \right)\sum_{a=t_{\gamma_1}}^{t_{\gamma_m}}[I(b)T_b]$$

After calculation we have the estimator of β and γ:

$$\hat{\beta} = \frac{n}{\sum_{i=0}^{k}\left[\frac{S(t_i)I(t_i)T_i}{N}\right]} \tag{9}$$

where $n = \sum_{a=t_{\beta_1}}^{t_{\beta_n}}$

$$\hat{\gamma} = \frac{m}{\sum_{i=0}^{k}[I(t_i)T_i]} \tag{10}$$

où $m = \sum_{a=t_{\gamma_1}}^{t_{\gamma_n}}$