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BAYESIAN MARKOV CHAIN MONTE CARLO SIMULATION OF NONLIENAR MODEL FOR INFECTIOUS DISEASES WITH QUARANTINE

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ABSTRACT

The SIQS (Susceptible, Infective, Quarantine, and Susceptible) non-linear model is used to describe the dynamics of infectious diseases, especially optimizing individuals who are quarantined. Discretization of the SIQS model using the Runge-Kutta method and its physical interpretation is very useful if the model parameters can be estimated. Bayesian Markov Chain Monte Carlo for its numerical simulation. After 10,000 iterations, convergent and significant parameters were obtained, namely beta = 94.37, beta0 = -10.19, mu = -0.23 and b = 0.5.

Keywords: Bayesian, Disease, Markov Chain Monte Carlo, Runge-Kutta, SIQS.

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INTRODUCTION

In general, the characteristics of infectious diseases have different clinical symptoms according to the causative factors of the disease (Mukhsar et al, 2016; Mukhsar et al, 2013; Mukhsar et al 2022). Based on clinical manifestations, the characteristics of infectious diseases consist of: 1) The spectrum of infectious diseases, 2) Covert infections (without clinical symptoms), 3) Sources of transmission. The phenomenon of the spread of infectious diseases can be described through modeling to find out the physical interpretation. This physical interpretation is used to describe phenomena that occur in everyday life (Allen, 2003; Hethcote, 2000; Mukhsar, 2018).

One of the models used in the spread of infectious diseases is the SIQS (Susceptible, Infective, Quarantine, and Susceptible) model with the characteristic that every individual is susceptible to being infected with a disease. Individuals in the infection class can recover through quarantine, but are not immune, so they may be re infected and enter the infection class (Bain and Engelhardt, 2000). Bayesian Markov Chain Monte Carlo is used for numerical simulations in obtaining the estimation of parameter model.

MATERIALS AND METHODS

Modeling uses Bayesian concepts, for example $x' = (y_1, y_2, \dots, y_n)$ is a vector of n cases that has distribution $f(x \mid \theta)$ and parameter requirements $\theta' = (\theta_1, \theta_2, \dots, \theta_k)$, defined probability distribution of $f(\theta)$ as

$$f(x \mid \theta) f(\theta) = f(x, \theta) = f(\theta|x) f(x)$$

or

$$f(\theta|x) = \frac{f(x|\theta) f(\theta)}{f(x)}$$

with

$$f(x) = \begin{cases} \int f(x|\theta) f(\theta)\, d\theta, & \theta \quad \text{continue} \\ \sum f(x|\theta) f(\theta), & \theta \quad \text{descrete} \end{cases}$$

The likelihood function of the *n* random variables $x_1, x_2, \dots, x_n$ is defined as the joint density function. The joint density function $f(x_1, x_2, \dots, x_n)$ considers of the θ. For example, we have *n* random samples $x_1, x_2, \dots, x_n$ and probability density function of $f(x_i, \theta)$, then the likelihood function is defined

$$L(\theta) = f(x_1; \theta) f(x_2; \theta) \dots f(x_n; \theta)$$
$$= \prod_{i=1}^{n} f(x_i; \theta)$$

The Bayesian concept is then used to estimate the parameters of the SIQS model in Figure 1.

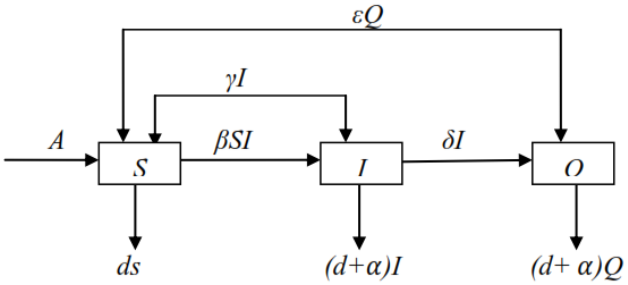

Figure 1. SIQS schema

From the schematic in Figure 1, the differential equations of the SIQS epidemic model are obtained as follows:

$$\frac{dS}{dt} = A - \beta SI - dS + \gamma I + \varepsilon Q$$

$$\frac{dI}{dt} = [\beta S - (\gamma + \delta + d + \alpha)]I \qquad (1)$$

$$\frac{dQ}{dt} = \delta I - (\varepsilon + d + \alpha)Q$$

The physical meaning of each symbol in equation (1) is described in Table 1.

Table 1. Physical interpretation of model 1

Symbol	Interpretation
A	the natural birth rate
β	the rate of transmission from an infected to a susceptible individual
d	natural mortality rate in susceptible individual
γ	the rate of recovery from infected to susceptible individual without being quarantined
ε	the degree of prevention and control of the spread of the disease in susceptible individual
δ	infection rate from infected to quarantined individual
α_1	natural mortality rate in infected individual
α_2	natural mortality rates in quarantined individual
S	the number of individuals who are susceptible to disease
I	the number of infected individuals who be transmitted the disease to other individual
Q	the number of individuals quarantined

Non-linear differential equation (1) is linearized using the Runge-Kutta principle [Box and Tiao, 1973; Nakamura, 1991],

$$y_{n+1}^{(k)} - y_n = \frac{h}{2}\left[f\left(y_{n+1}^{(k-1)}, t_{n+1}\right) + f(y_n, t_n)\right]$$

with $y_{n+1}^{(k)}$ is the k-th iteration approximation for y_{n+1}, and $y_{n+1}^{(0)}$ is an initial number of y_{n+1}. Iterations are declared convergent when $\left|y_{n+1}^{(k)} - y_{n+1}^{(k-1)}\right|$ less than the tolerance value set. The decritization of model (1), respectively, is
$\frac{S_{n+1}-S_n}{h} = S_n'$, $S_n' = f(t_n)$, obtained

$$\frac{S_{t+1} - S_t}{h} = A - \beta S_t I_t - dS_t + \gamma I_t + \varepsilon Q_t$$
$$S_{t+1} = S_t\lambda_1 + hA + h\gamma I_t + h\varepsilon Q_t,\ \lambda_1 = 1 - h\beta I_t - hd$$

and

$$\frac{I_{t+1} - I_t}{h} = [\beta S_t - (\gamma + \delta + d + \alpha)]I_t$$
$$I_{t+1} = I_t(1 - h\gamma - h\delta - hd - h\alpha) + h\beta S_t I_t$$

and

$$\frac{Q_{t+1} - Q_t}{h} = \delta I_t - (\varepsilon + d + \alpha)Q_t$$
$$Q_{t+1} = Q_t(1 - h\varepsilon - hd - h\alpha) + h\delta I_t$$
$$Q_{t+1} = Q_t\lambda_3 + h\delta I_t,\ \lambda_3 = 1 - h\varepsilon - hd - h\alpha$$

In the term of S_{t+1}, let $S_t\lambda_1 = G_1$ in Poisson distribution $G_1 \sim Poisson(\lambda_1)$, then probability density function of G_1 is written as

$$f(G_1; \lambda_1) = \frac{e^{-\lambda_1}{\lambda_1}^{G_1}}{G_1!} = \frac{e^{-(1-h\beta I_t - hd)}(1 - h\beta I_t - hd)^{G_1}}{G_1!}$$

Likewise for I_{t+1}, let $I_t\lambda_2 = G_2$, we have Poisson $G_2 \sim Poisson(\lambda_2)$, then probability density function of G_2 is written as

$$f(G_2;\lambda_2)=\frac{e^{-\lambda_2}{\lambda_2}^{G_2}}{G_2!}=\frac{e^{-(1-h\gamma-h\delta-hd-h\alpha)}(\,1-h\gamma-h\delta-hd-h\alpha)^{G_2}}{G_2!}$$

For Q_{t+1}, let $Q_t\lambda_3=G_3$, we have $G_3{\sim}Poisson(\lambda_3)$ and probability density function for G_3 written as

$$f(G_3;\lambda_3)=\frac{e^{-\lambda_3}{\lambda_3}^{G_3}}{G_3!}=\frac{e^{-(1-h\varepsilon-hd-h\alpha)}(\,1-h\varepsilon-hd-h\alpha)^{G_3}}{G_3!}$$

The likelihood of $f(G_1;\lambda_1)$ is written as

$$\begin{aligned}L_{G_1}(\lambda_1)&=\prod_{i=1}^{n}f(G_{1_i};\lambda_1)=\prod_{i=1}^{n}\frac{e^{-\lambda_1}{\lambda_1}^{G_{1i}}}{G_{1_i}!}\\&=\prod_{i=1}^{n}\frac{e^{-(1-\,h\beta I_t-hd)}(1-\,h\beta I_t-hd)^{G_{1i}}}{G_{1_i}!}\\&\frac{e^{-(1-\,h\beta I_t-hd)}(1-\,h\beta I_t-hd)^{G_{1_2}}}{G_{1_2}!}\times\ldots\times\frac{e^{-(1-\,h\beta I_t-hd)}(1-\,h\beta I_t-hd)^{G_{1_n}}}{G_{1_n}!}\\&=\frac{e^{-n(1-\,h\beta I_t-hd)}(1-\,h\beta I_t-hd)^{\sum_{i=1}^{n}G_{1i}}}{\prod_{i=1}^{n}G_{1_i}!}\end{aligned}$$

The likelihood of $f(G_2;\lambda_2)$ written as

$$\begin{aligned}L_{G_2}(\lambda_2)&=\prod_{i=1}^{n}f(G_{2_i};\lambda_2)=\prod_{i=1}^{n}\frac{e^{-\lambda_2}{\lambda_2}^{G_{2i}}}{G_{2_i}!}\\&=\frac{e^{-n(1-h\gamma-h\delta-hd-h\alpha)}(1-h\gamma-h\delta-hd-h\alpha)^{\sum_{i=1}^{n}G_{2i}}}{\prod_{i=1}^{n}G_{2_i}\,!}\end{aligned}$$

The likelihood of $f(G_3;\lambda_3)$written as

$$\begin{aligned}L_{G_3}(\lambda_3)&=\prod_{i=1}^{n}f(G_{3_i};\lambda_3)=\prod_{i=1}^{n}\frac{e^{-\lambda_3}{\lambda_3}^{G_{3i}}}{G_{3_i}!}\\&=\frac{e^{-n(1-h\varepsilon-hd-h\alpha)}(1-h\varepsilon-hd-h\alpha)^{\sum_{i=1}^{n}G_{3i}}}{\prod_{i=1}^{n}G_{3_i}\,!}\end{aligned}$$

RESULTS AND DISCUSSION

The prior distribution used is a non-informative prior. In the SIQS model there are several parameters used to describe the model, namely α which describes the natural death rate in individuals, β which describes the level of transmission from individuals infected with the disease to susceptible individuals, δ which describes the level of infection from infected individuals to quarantined individuals, γ which describes the recovery rate from infected individuals to susceptible individuals without being quarantined and ε which describes the level of prevention and control of the spread of disease to susceptible individuals.

The parameters are assumed to be normally distributed:

$$f(\theta)=\begin{cases}f(\alpha){\sim}N(0,\sigma^2)\\f(\beta){\sim}N(0,\sigma^2)\\f(\gamma){\sim}N(0,\sigma^2)\\f(\delta){\sim}N(0,\sigma^2)\\f(\varepsilon){\sim}N(0,\sigma^2)\end{cases}$$

Thus, the probability density function is respectively as, $f(\alpha) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\alpha_i}{\sigma}\right)^2}$, $f(\beta) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\beta_i}{\sigma}\right)^2}$, $f(\gamma) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\gamma_i}{\sigma}\right)^2}$, $f(\delta) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\delta_i}{\sigma}\right)^2}$, and $f(\varepsilon) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\varepsilon_i}{\sigma}\right)^2}$.

The prior distribution of *f*(θ) is the product of all the probability distribution models

$$f(\theta) = f(\alpha) \times f(\beta) \times f(\gamma) \times f(\delta) \times f(\varepsilon)$$

$$f(\theta) = \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\alpha_i}{\sigma}\right)^2} \times \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\beta_i}{\sigma}\right)^2} \times \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\gamma_i}{\sigma}\right)^2} \times \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\delta_i}{\sigma}\right)^2} \times \frac{1}{\sqrt{2\pi\sigma^2}} e^{-\frac{1}{2}\left(\frac{\varepsilon_i}{\sigma}\right)^2}$$

$$f(\theta) = \frac{e^{-\left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}\right)}}{2\pi\sigma^5\sqrt{2\pi}}$$

The posterior distribution is the product of the likelihood function and its prior distribution. Then joint posterior for $P(\lambda_1; G_{1_i}) = L_{G_1}(\lambda_1) \times f(\theta)$ is obtained

$$P(\lambda_1; G_{1_i}) = \frac{e^{-n(1-h\beta I_t - hd)}(1 - h\beta I_t - hd)^{\sum_{i=1}^n G_{1i}}}{\prod_{i=1}^n G_{1_i}!} \times \frac{e^{-\left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}\right)}}{2\pi\sigma^5\sqrt{2\pi}}$$

$$= \frac{e^{-n(1-h\beta I_t - hd) - \left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^{2S}}\right)}(1 - h\beta I_t - hd)^{\sum_{i=1}^n G_{1i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^n G_{1_i}!}$$

$$= \frac{e^{\frac{-2n\sigma^2(1-h\beta I_t - hd) - (\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2)}{2\sigma^2}}(1 - h\beta I_t - hd)^{\sum_{i=1}^n G_{1i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^n G_{1_i}!}$$

Furthermore for $P(\lambda_2; G_{2_i}) = L_{G_2}(\lambda_2) \times f(\theta)$ is written as

$$P(\lambda_2; G_{2_i}) = \frac{e^{-n(1-h\gamma-h\delta-hd-h\alpha)}(1 - h\gamma - h\delta - hd - h\alpha)^{\sum_{i=1}^n G_{2i}}}{\prod_{i=1}^n G_{2_i}!} \times \frac{e^{-\left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}\right)}}{2\pi\sigma^5\sqrt{2\pi}}$$

$$= \frac{e^{-n(1-h\gamma-h\delta-hd-h\alpha) - \left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}\right)}(1 - h\gamma - h\delta - hd - h\alpha)^{\sum_{i=1}^n G_{2i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^n G_{2_i}!}$$

$$= \frac{e^{\frac{-2n\sigma^2(1-h\gamma-h\delta-hd-h\alpha) - \alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}}(1 - h\gamma - h\delta - hd - h\alpha)^{\sum_{i=1}^n G_{2i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^n G_{2_i}!}$$

and we have $P(\lambda_3; G_{3_i}) = L_{G_3}(\lambda_3) \times f(\theta)$ as

$$P(\lambda_3; G_{3_i}) = \frac{e^{-n(1-h\varepsilon-hd-h\alpha)}(1 - h\varepsilon - hd - h\alpha)^{\sum_{i=1}^n G_{3i}}}{\prod_{i=1}^n G_{3_i}!} \times \frac{e^{-\left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}\right)}}{2\pi\sigma^5\sqrt{2\pi}}$$

$$= \frac{e^{-n(1-h\varepsilon-hd-h\alpha) - \left(\frac{\alpha_i{}^2+\beta_i{}^2+\gamma_i{}^2+\delta_i{}^2+\varepsilon_i{}^2}{2\sigma^2}\right)}(1 - h\varepsilon - hd - h\alpha)^{\sum_{i=1}^n G_{3i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^n G_{3_i}!}$$

$$= \frac{e^{\frac{-2n\sigma^2(1-h\varepsilon-hd-h\alpha)-{\alpha_i}^2+{\beta_i}^2+{\gamma_i}^2+{\delta_i}^2+{\varepsilon_i}^2}{2\sigma^2}}(1-h\varepsilon-hd-h\alpha)^{\sum_{i=1}^{n} G_{3i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^{n} G_{3_i}\,!}$$

Marginal Posterior for $P(\lambda_1; G_{1_i})$ is

$$P(\lambda_1; G_{1_i}) = \frac{e^{\frac{-2n\sigma^2(1-\,h\beta I_t-hd)-\left({\alpha_i}^2+{\beta_i}^2+{\gamma_i}^2+{\delta_i}^2+{\varepsilon_i}^2\right)}{2\sigma^2}}(1-\,h\beta I_t-hd)^{\sum_{i=1}^{n} G_{1i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^{n} G_{1_i}!}$$

Marginal posterior for $P(\beta; G_{1_i}) = P(\lambda_1; G_{1_i})$ is

$$p(\beta; G_{1_i}) = \frac{e^{\frac{-2n\sigma^2(1-\,h\beta I_t-hd)-\left({\alpha_i}^2+{\beta_i}^2+{\gamma_i}^2+{\delta_i}^2+{\varepsilon_i}^2\right)}{2\sigma^2}}(1-\,h\beta I_t-hd)^{\sum_{i=1}^{n} G_{1i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^{n} G_{1_i}!}$$

Marginal Posterior for $P(\lambda_2; G_{2_i})$ is obtained

$$P(\lambda_2; G_{2_i}) = \frac{e^{\frac{-2n\sigma^2(1-h\gamma-h\delta-hd-h\alpha)-{\alpha_i}^2+{\beta_i}^2+{\gamma_i}^2+{\delta_i}^2+{\varepsilon_i}^2}{2\sigma^2}}(1-h\gamma-h\delta-hd-h\alpha)^{\sum_{i=1}^{n} G_{2i}}}{\left(2\pi\sigma^5\sqrt{2\pi}\right)\prod_{i=1}^{n} G_{2_i}\,!}$$

We use monthly measles data from of Kendari from 10 sub-districts for 2016-2018 to estimate model parameters of model (1). Markov Chain Monte Carlo is used to estimate of the parameters. The Win BUGS software is implemented for the numerical simulation, as shown

```
model {
Sh[1]<-N[1]-I[1]-Q[1]
I[1]<-0.00252*N[1]
Q[1]<-0.00252*N[1]

for (i in 1:n) {

#HUMAN POPULATIONS
S[i]<-(1+mu+beta*Q[i-1])*S[i-1]-newI[i]
I[i]<-(1-b*Q[i-1])*I[i-1]+newI[i]
Q[i]<-(1-b*I[i-1])-beta*S[i-1])*Q[i-1]
newI[i]~dpois(lambdanew[i])
log(lambdanew[i])<-beta0+Ch[i]
}
#CAR prior distribution for random effects Ch. The sum of Ch is always 0
Ch[1:n]~car.normal(adj[], weights[], num[], varCh)
# Weights
for (h in 1:SumNumNeigh){
weights[h]<-1}
#Other priors
beta0~dflat()                                    #Flat prior for the intercept
varCh~dgamma(0.01,0.01)          #Prior on precision for spatial random effect Ch
mu<-0.2
beta<-0.2
b<-0.2
}
DATA
list(newI=structure(.Data=c(),.Dim=c(10,36)),n=10,T=36,SumNumNeigh=32,
adj = c(), num = c())
h=c()
INITIAL
List()
```

Figure 2. Trace plot of parameters model (1)

The model parameter estimates at 10,000 iterations have reached convergence, as shown from the historical trace plot at constant zones (Figure 3).

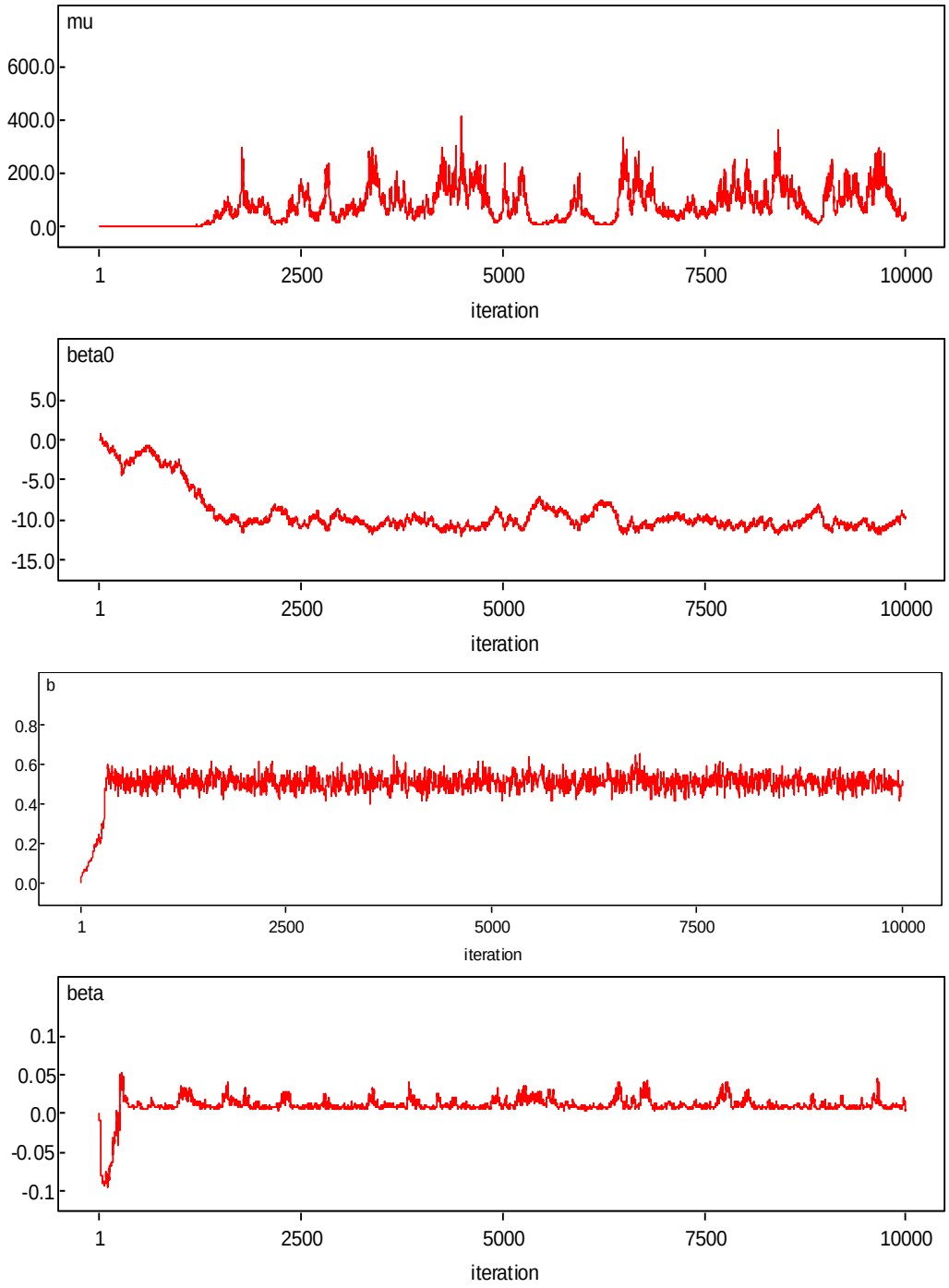

Figure 3. Trace plot of parameters model (1)

The estimated parameter is significant, as evidenced by the confidence interval between 2.5% and 97.5% does not contain 0 (Table 2).

Table 2. Estimated parameters of model (1)

Node	mean	SD	MC error	2.5%	median	97.5%	Start	Sample
Beta	94.38	63.72	6.36	7.615	83.9	235.1	4001	10000
beta0	-10.19	0.906	0.09617	-11.43	-10.38	-7.969	4001	10000
mu	-0.231	0.04547	0.003957	0.28	0.2469	0.1269	4001	10000
b	0.5129	0.03377	0.001566	0.4484	0.5127	0.5779	4001	10000

CONCLUSION

Discretization of the nonlinear model (1) for parameter estimation is purposed. The physical interpretation of the nonlinear model (1) is very useful if the mode parameters can be estimated. In this study, discretization of the nonlinear model (1) uses the Runge-Kutta method. Bayesian Markov Chain Monte Carlo for its numerical simulation. We use monthly measles data from of Kendari from 10 sub-districts for 2016-2018. After 10,000 iterations, convergent and significant parameters were obtained, namely beta = 94.37, beta0 = -10.19, mu = -0.23 and b = 0.5.

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