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Bayesian Inference for SIR Epidemic Model with dependent parameters

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Abstract. This paper is concerned with the Bayesian inference for the dependent parameters of stochastic SIR epidemic model in a closed population. The estimation framework involves the introduction of $m-1$ latent data between every pair of observations. Kibble's bivariate gamma distribution is considered as a good candidate prior density of parameters, they give an appropriate frame to model the dependence between the parameters. A Markov chain Monte Carlo methods are then used to sample the posterior distribution of the model parameters. Simulated datasets are used to illustrate the proposed methodology.

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1. Introduction

In recent years there has been considerable research on the development of Bayesian inferential methods for the dynamics of the spread of infectious diseases data using stochastic epidemic models. Inference for epidemic models is complicated by the fact that, first, one or several model variables may be unobserved, and second, data are often available at discrete

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time points, while the underlying true process is continuous in time. In the case where data are observed in continuous time, parameter estimates can be obtained for complete data (see Becker [3]) and in the case of incomplete data, estimates have also been developed using martingale methods (see Andersson and Britton [1]), exact forward filtering (see Fearnhead and Meligkotsidou [16]), or MCMC methods which offer enormous power and flexibility compared to other approaches (see Gibson and Renshaw [18]; O'Neill and Roberts [27]; Streftaris and Gibson [32]; Neal and Wilkinson [26]). Recently, the Bayesian inference of the Susceptible-Infected-Removed (SIR) epidemic model has been treated by several authors using Markov chain Monte Carlo (MCMC) methods (see O'Neill and Roberts [27]; Lekone and Roberts [22]; Demiris and O'Neill [9]; Demiris and O'Neill [10]; Demiris and O'Neill [11]; Clancy and O'Neill [7]; Komorowski *et al*. [21]; Woodcock *et al*. [33]; Choi and Rempala [6]; El Maroufy *et al*. [13]; Qaffou *et al*. [29] and references therein).

The Bayesian approaches mentioned above are different from the one we present in this paper, since data are only available at discrete times, we introduce a set of $m-1$ auxiliary latent data point between each pair of observations. The idea of raising the observed low frequency data with simulated high-frequency ones was previously pursued by Pedersen [28]. This task is performed by the application of MCMC techniques (see Eraker [15]; El Maroufy *et al*. [13] and Qaffou *et al*. [29]) which alternately update the data and are usually feasible within a moderate computing time. Moreover, we examine a simple closed-population model for an epidemic in which the infection rate depends upon the number of removals that have occurred. In a modelling context, this infection mechanism reflects behavior change in response to the perceived state of the epidemic. In particular, this approach caters to epidemics where the current number of infectives is unknown, but where some information about the number of removed individuals is available. Data concerning sexually transmitted diseases are often of this type. Deterministic models for sexually transmitted diseases that consider behavior change have been proposed in Blythe, Brauer and Castillo-Chavez [4], Brauer, Blythe, Castillo-Chavez and Velasco-Hernandez [5]. In particular, these models allow the rate of recruitment into the sexually active part of the population to depend upon the current perceived state of the epidemic. In several circumstances the researcher has to deal with paired dependent data. Such cases usually arise in clinical trials involving survival analysis (paired lifetimes) and hydrology (flows in two distinct districts of the same river) among others.

In this paper, to model the dependence between the infection and removal rate parameters in SIR epidemic model, we adopt a Kibble's bivariate gamma distribution (KBGD) as a joint prior distribution for the model parameters. The popularity of the KBGD among practitioners derives in part from the fact that it allows for a convenient way to model dependence (conditional on observed characteristics) between the infective and the removal rate in SIR epidemic model. Moreover, we use the density given in Risken [30] as an approximation of transition density. We also develop MCMC methods used to explore the posterior distribution of the model parameters.

The rest of the paper is structured as follows. Section 2 briefly introduces the stochastic SIR epidemic model. In Section 3, we provide Bayesian inference of the parameters, in detail,

subsection 3.1 gives the prior density of parameters, subsection 3.2 establishes the posterior density of parameters and the algorithm in subsection 3.3, while the MCMC simulations are presented in Section 4 with application to the simulated data. The paper concludes with Section 5. Finally, proofs of some mathematical statements are given in the Appendix.

2. Basic SIR epidemic model

Mathematically, a SIR epidemic model is defined as follows: At time t, there are $S(t)$ susceptibles, $I(t)$ infectives and $R(t) = n + a - S(t) - I(t)$ removed individuals with $S(0) = n$ and $I(0) = a$. The numbers n and a are positive integers. The epidemic process is thus completely determined by $\{(S(t), I(t)); t \geq 0\}$, which is supposed to be a bidimensional continuous-time Markov jump process on the space $\mathbf{E}_{n,a} = \{(i,l);\ 0 \leq i \leq n,\ 0 \leq l \leq n + a - i\}$. The transition probabilities from time t to $t + h$ are given by

$$\begin{array}{ccccc} & \text{Transition} & & & \text{Probability} \\ (i,l) & \longrightarrow & (i-1,l+1) & & \beta\dfrac{il}{n}h + o(h) \\ (i,l) & \longrightarrow & (i,l-1) & & \mu l h + o(h) \\ (i,l) & \longrightarrow & (i,l) & & 1 - \left(\dfrac{\beta il}{n} + \mu l\right) h + o(h), \end{array} \tag{2.1}$$

all other transitions having probability $o(h)$ and the parameter μ being known as the removal rate and β is considered as the infection rate.
For $(i,l) \in \mathbf{E}_{n,a}$, we define $P_{(i,l)}(t) = \mathbb{P}\{S(t) = i, I(t) = l\}$. It follows directly from (2.1) that these transition probabilities satisfy the set of Kolmogorov forward equation:

$$P'_{(i,l)}(t) = \frac{\beta(i+1)(l-1)}{n} P_{(i+1,l-1)}(t) + \mu(l+1)P_{(i,l+1)}(t) - (\mu l + \frac{\beta il}{n})P_{(i,l)}(t),$$

for $(i,l) \in \mathbf{E}_{n,a}$ with $P_{(i,l)}(t) = 0$, if $(i,l) \notin \mathbf{E}_{n,a}$ and $P_{(n,a)}(0) = 1$.
In effect, during an infinitesimal time dt, the possible transitions to the state (i,l) are:

- $(i+1, l-1) \to (i,l)$ (one susceptible is infected) with probability $\beta(i+1)(l-1)dt$,
- $(i,l+1) \to (i,l)$ (one infected is recovered) with probability $\mu(l+1)dt$,
- and finally the transition $(i,l) \to (i,l)$ (no epidemic event occurs) with probability $1 - \left(\frac{\beta il}{n} + \mu l\right) dt$.

Thus :

$$P_{(i,l)}(t+dt) = \frac{\beta(i+1)(l-1)}{n} dt P_{(i+1,l-1)}(t) + \mu(l+1)dt P_{(i,l+1)}(t) + \left(1 - \left(\frac{\beta il}{n} + \mu l\right) dt\right) P_{(i,l)}(t)$$

Hence:

$$\frac{P_{(i,l)}(t+dt) - P_{(i,l)}(t)}{dt} = \frac{\beta(i+1)(l-1)}{n} P_{(i+1,l-1)}(t) + \mu(l+1)P_{(i,l+1)}(t) - \left(\frac{\beta il}{n} + \mu l\right) P_{(i,l)}(t)$$

For $dt \to 0$, we obtain the result.
A Markov process with the above described dynamics determines the general stochastic epidemic. For this model, the inference of the parameters based on the likelihood is impracticable,

because the latest requires the knowledge of the transition probabilities which are unavailable in simple form as established in El Maroufy *et al* [14]. For this reason we will use a diffusion approximation to the discret space process as in El Maroufy *et al* [12]. To do this, we normalize the process by the transformations $x(t) = S(t)/n$ and $y(t) = I(t)/n$. So, for sufficiently large population, we establish (see Fuchs [17] for rigorous proofs) that the process (x, y) satisfy the following Itô equation

$$\begin{pmatrix} dx \\ dy \end{pmatrix} = U(x, y, \theta)dt + \sigma(x, y, \theta)\begin{pmatrix} dW^1 \\ dW^2 \end{pmatrix}, \tag{2.2}$$

where $U(x, y, \theta) = \begin{pmatrix} -\beta xy \\ \beta xy - \mu y \end{pmatrix}, \sigma(x, y, \theta) = \frac{1}{\sqrt{n}} \begin{pmatrix} \sqrt{\beta xy} & 0 \\ -\sqrt{\beta xy} & \sqrt{\mu y} \end{pmatrix}$ and $\theta = (\beta, \mu)$.
The transition density $p(x, y, t)$ verifies the Fokker-Plank equation:

$$\frac{\partial p(\tilde{\mathbf{y}}, t)}{\partial t} = -\frac{\partial}{\partial t}[U(\tilde{\mathbf{y}}, \theta)p(\tilde{\mathbf{y}}, t)] + \frac{1}{2}\frac{\partial^2}{\partial \tilde{\mathbf{y}}^2}[\Sigma(\tilde{\mathbf{y}}, \theta)p(\tilde{\mathbf{y}}, t)]$$

with $\tilde{\mathbf{y}} = (x, y)$ and $\Sigma = \sigma \times \sigma'$. The conditions to solve the SDE given by (2.2) are satisfied (see Andersson and Britton [1]). The right hand side of the differential equation (2.2) consists of the deterministic and stochastic components (see Bailey [2]) in which W^1 and W^2 are two standard independent Brownian motions representing stochasticity in disease transmission and recovery.

3. Bayesian inference

There are many inference approaches employed to obtain estimation of the diffusion model parameters given by (2.2) from discrete of time data with low frequency as likelihood inference and martingale technics. Unfortunately in many applications in epidemic models the time between consecutive observations are rather large. Such approaches considered is hence not expected to yield satisfactory results in those cases. More advanced estimation procedure can be considered to address this problem. We propose the MCMC method to estimate the diffusion after discretizing using the transition density given in Risken [30, Section 4.7]. The method consists of increasing the low-frequency observations by the insertion of a finite number of latent data between two consecutive observations.
In order to apply this approximation to our model, we consider the transformation:

$$\tilde{\mathbf{y}}_{t_i} = (x_{t_i}, z_{t_i}) = (x_{t_i}, 1 + \frac{a}{n} - x_{t_i} - y_{t_i}) \text{ as the real data at a time } 0 = t_0, t_1, ..., t_N = T.$$

By using the Fokker-Plank equation and the equation (4.109) given in Risken [30], the transition density is given as follows:

$$\begin{aligned} p(\tilde{\mathbf{y}}_{t_i}|\tilde{\mathbf{y}}_{t_{i-1}}, \theta) &= p(x_{t_i}, z_{t_i}|x_{t_{i-1}}, z_{t_{i-1}}, \beta, \mu) \\ &= \left[2\sqrt{\pi \Delta t_i}\right]^{-2} \mid \Sigma_{i-1} \mid^{-\frac{1}{2}} \mathrm{e}^{\frac{-1}{4\Delta t_i}(\Delta x_{t_i} - \mu_{i-1}, \Delta z_{t_i} - \mu'_{i-1})(\Sigma_{i-1})^{-1}\binom{\Delta x_{t_i} - \mu_{i-1}}{\Delta z_{t_i} - \mu'_{i-1}}} \end{aligned} \tag{3.1}$$

where

$$\Sigma_{i-1} = \begin{pmatrix} \frac{\beta}{n}x_{t_{i-1}}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}}) & 0 \\ 0 & \frac{\mu}{n}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}}) \end{pmatrix},$$

$\Delta x_{t_i} = x_{t_i} - x_{t_{i-1}}$, $\Delta z_{t_i} = z_{t_i} - z_{t_{i-1}}$, $\mu_{i-1} = -\beta x_{t_{i-1}}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})\Delta t_i$
and $\mu'_{i-1} = \mu(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})\Delta t_i$.
In effect, given a stochastic diffusion process:

$$dx_t = U(x)dt + \sigma(x)dW_t \text{ with } x \in \mathbb{R}^N.$$

The density $p(x,t)$ of the process satisfies the following Fokker-Planck equation:

$$\frac{\partial p(x,t)}{\partial t} = L_{FP}(x,t)p(x,t).$$

Where: $L_{FP}(x,t) = -\sum_{i=1}^{N}\frac{\partial U(x)}{\partial x_i} + \sum_{i=1}^{N}\frac{\partial^2\Sigma(x)}{\partial x_i \partial x_j}$ here $\Sigma(x) = \frac{1}{2}\sigma(x)\sigma'(x)$.
Following the equation (4.109) given in Risken [30], the transition density $p(x,t|x',t')$ for $t > t'$ of the process, can be approximated with a multivariate normal distribution with mean $U(x')$ and covariance matrix $2(t-t')\Sigma(x')$.
We apply this approximation result for:
$\tilde{y} = (x,z)$, $U(\tilde{y}) = \begin{pmatrix} -\beta x(1+\frac{a}{n}-x-z) \\ \mu(1+\frac{a}{n}-x-z) \end{pmatrix}$ and $\Sigma(\tilde{y}) = \frac{1}{2}\begin{pmatrix} \frac{\beta x}{n}(1+\frac{a}{n}-x-z) & 0 \\ 0 & \frac{\mu}{n}(1+\frac{a}{n}-x-z) \end{pmatrix}$
and using Itô formula, we found that $d\tilde{\mathbf{y}}_{t_i} = U(\tilde{\mathbf{y}}_{t_i},\theta)dt_i + \sigma(\tilde{\mathbf{y}}_{t_i},\theta)dW_{t_i}$, where

$$U(\tilde{\mathbf{y}}_{t_i},\theta) = \begin{pmatrix} -\beta x_{t_i}(1+\frac{a}{n}-x_{t_i}-z_{t_i}) \\ \mu(1+\frac{a}{n}-x_{t_i}-z_{t_i}) \end{pmatrix}$$

and

$$\sigma(\tilde{\mathbf{y}}_{t_i},\theta) = \begin{pmatrix} -\sqrt{\frac{\beta x_{t_i}(1+\frac{a}{n}-x_{t_i}-z_{t_i})}{n}} & 0 \\ 0 & \sqrt{\frac{\mu(1+\frac{a}{n}-x_{t_i}-z_{t_i})}{n}} \end{pmatrix}.$$

Then the equation (3.1) is proved.
Since Σ_{i-1} is diagonal, it follows immediately from (3.1) that

$$p(\tilde{\mathbf{y}}_{t_i}|\tilde{\mathbf{y}}_{t_{i-1}},\theta) = \tilde{p_1}(\tilde{\mathbf{y}}_{t_i}|\tilde{\mathbf{y}}_{t_{i-1}},\beta) \times \tilde{p_2}(\tilde{\mathbf{y}}_{t_i}|\tilde{\mathbf{y}}_{t_{i-1}},\mu) \tag{3.2}$$

with

$$p_1(\tilde{\mathbf{y}}_{t_i}|\tilde{\mathbf{y}}_{t_{i-1}},\beta) = \left[2\sqrt{\pi\Delta t_i}\right]^{-1} \mathrm{e}^{-\frac{n}{2}\Delta x_{t_i}}\left(\frac{\beta}{n}x_{t_{i-1}}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})\right)^{-1/2} \times \mathrm{e}^{\frac{-n}{4\Delta t_i}\left(\frac{\Delta x_{t_i}^2}{\frac{x_{t_{i-1}}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})}{\beta}+x_{t_{i-1}}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})\Delta t_i^2\beta}\right)} \tag{3.3}$$

and

$$p_2(\tilde{\mathbf{y}}_{t_i}|\tilde{\mathbf{y}}_{t_{i-1}},\mu) = \left[2\sqrt{\pi\Delta t_i}\right]^{-1} \mathrm{e}^{-\frac{n}{2}\Delta z_{t_i}}\left(\frac{\mu}{n}(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})\right)^{-1/2}$$

$$\times \, e^{\frac{-n}{4\Delta t_i}\left(\frac{\Delta z_{t_i}^2}{\frac{(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})}{\mu}+(1+\frac{a}{n}-x_{t_{i-1}}-z_{t_{i-1}})\Delta t_i^2\mu}\right)}. \tag{3.4}$$

3.1. Prior density of the parameters. Bivariate gamma distributions (BGDs) are good candidates priors densities of parameters, they give an appropriate frame to model the dependence between the parameters. However, extensions defining multivariate gamma distributions (MGDs) are more controversial. In order to reduce the size of the family of MGDs. These distributions have found useful applications in several areas; for example, in the modeling of rainfall at two nearby rain gauges (see, Izawa [19]), data obtained from rainmaking experiments (see, Moran [24] [25]), the dependence between annual streamfow and areal precipitation (see, Clarke [8]), wind gust data (see, Smith and Adelfang [31]) and the dependence between rainfall and runoff (see, Mathai [23]). They have also found applications in reliability theory, renewal processes and stochastic routing problems. Here we use the Kibble's bivariate gamma distribution (KBGD) that has been introduced by Kibble [20], it's joint density is given by:

$$f(x,y|\nu,\lambda_1,\lambda_2,\rho) = \frac{(\lambda_1\lambda_2)^\nu}{(1-\rho)\Gamma(\nu)}\left(\frac{xy}{\rho\lambda_1\lambda_2}\right)^{\frac{\nu-1}{2}} e^{-\frac{\lambda_1 x+\lambda_2 y}{1-\rho}} I_{\nu-1}\left(\frac{2\sqrt{\rho\lambda_1\lambda_2 xy}}{1-\rho}\right), \tag{3.5}$$

where $x,y,\lambda_1,\lambda_2 \geq 0$, $0 \leq \rho < 1$, $\nu \geq 0$ and $I_\nu(.)$ is the modified Bessel function of the first kind with order ν defined as $I_\nu(\alpha) = \sum_{k=0}^{\infty} \frac{(\alpha/2)^{2k+\nu}}{\Gamma(k+\nu+1)k!}$, $\alpha \geq 0$.
In the present work, we suppose that the infective rate β and the removal rate μ in SIR epidemic model follow as priori distribution KBGD (3.5). The correlation between β and μ is ρ, then β and μ are independent if $\rho = 0$. Using the series representation of the Bessel function, (3.5) takes the form

$$f(\beta,\mu|\nu,\lambda_1,\lambda_2,\rho) = \sum_{k=0}^{\infty} f(k|\rho) f(\beta|\nu+k,\frac{\lambda_1}{1-\rho}) f(\mu|\nu+k,\frac{\lambda_2}{1-\rho})$$

where $f(k|\rho) = \frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)}(1-\rho)^\nu\rho^k$, $k \in \mathbb{N}$, is the probability mass function of the negative binomial distribution $\mathcal{NB}(\nu,1-\rho)$ and $f(\beta|\nu+k,\frac{\lambda_1}{1-\rho}), f(\mu|\nu+k,\frac{\lambda_2}{1-\rho})$ are the probabilities densities functions of gamma distributions $\Gamma(\nu+k,\frac{\lambda_1}{1-\rho})$, $\Gamma(\nu+k,\frac{\lambda_2}{1-\rho})$ respectively. Then, we have

$$\begin{aligned} f(\beta,\mu|\nu,\lambda_1,\lambda_2,\rho) &\propto \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)}(1-\rho)^\nu\rho^k\beta^{\nu+k-1} e^{-\frac{\lambda_1\beta}{1-\rho}} \mu^{\nu+k-1} e^{-\frac{\lambda_2\mu}{1-\rho}} \\ &\propto (1-\rho)^\nu(\beta\mu)^{\nu-1} e^{-\frac{\lambda 1\beta+\lambda 2\mu}{1-\rho}} \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)}(\rho\beta\mu)^k. \end{aligned} \tag{3.6}$$

3.2. Posterior density of the parameters. Due to the form of transition density in (3.2) and under the KBGD as prior of β and μ, the Bayes' theorem produces a posterior distribution of β and μ in the following result (proof is left to Appendix):

Proposition 3.1. *If β and μ follow a priori KBGD, then its a posterior distribution takes the form:*

$$p(\theta|\tilde{y}) \propto \sum_{k=0}^{\infty} c_k GIG(\beta| -\frac{N}{2}+\nu+k, A, B) GIG(\mu| -\frac{N}{2}+\nu+k, C, D) \tag{3.7}$$

where A, B, C, D and c_k are given in Appendix, and $GIG(.|p,a,b)$ is the probability density functions of generalized inverse Gaussian.

3.3. Algorithm.

(1) Initialize β and μ using linear interpolation between observed values of $\tilde{y}_i$ to initialize $\widehat{\tilde{y}}_i$,
(2) For all $i = 1, 2, ..., N-1$, at iteration h draw $\widehat{\tilde{y}}_i^{(h)}|(\widehat{\tilde{y}}_{i-1}^{(h-1)}, \widehat{\tilde{y}}_{i+1}^{(h-1)}, \beta, \mu)$ using the AR-MH algorithm with proposal density $\mathcal{N}\left(\frac{1}{2}(\widehat{\tilde{y}}_{i-1}^{(h)} + \widehat{\tilde{y}}_{i+1}^{(h-1)}), \frac{\Delta t}{2}\sum_{i-1}^{(h-1)}\right)$,
(3) Draw $\beta^{(h)}$ and $\mu^{(h)}$ using (3.7) as a mixture of two independent GIG distributions,
(4) Increase the value of h and go back to step (2).

4. MCMC simulation

In order to study the performance of the estimation methodology, we first generated artificial data. The data is sampled from the original discrete double Markov chain with true values of β and μ as given in Tables 1, 2 and 3. The estimation is obtained after 20000 iterations of our algorithm, with $\nu = 1$ and $\lambda_1 = \lambda_2 = 2$ for tree cases $\rho = 0.1$, $\rho = 0.5$ or $\rho = 0.9$.

	$\rho = 0.1$					
	true value of β	$\hat{\beta}$	true value of μ	$\hat{\mu}$	R_0	$\hat{R}_0$
Posterior mean	1	0.9499	1	0.9400	1	1.0152
Sd error		0.0504		0.0599		0.0158
Posterior mean	0.3	0.3078	0.8	0.8455	0.375	0.3729
Sd error		0.0078		0.0454		0.0021
Posterior mean	1.3	1.2989	0.8	0.7485	1.625	1.7378
Sd error		0.0011		0.0513		0.1126

TABLE 1. Posterior mean and standard error for β, μ and R_0 for $\rho = 0.1$.

$\rho = 0.5$						
	true value of β	$\hat{\beta}$	true value of μ	$\hat{\mu}$	R_0	$\hat{R}_0$
Posterior mean	1	0.9496	1	0.9415	1	1.0136
Sd error		0.0504		0.0585		0.0136
Posterior mean	0.3	0.3076	0.8	0.8616	0.375	0.3651
Sd error		0.0076		0.0616		0.0099
Posterior mean	1.3	1.2988	0.8	0.7499	1.625	1.7351
Sd error		0.0011		0.0501		0.1100

TABLE 2. Posterior mean and standard error for β, μ and R_0 for $\rho = 0.5$.

$\rho = 0.9$						
	true value of β	$\hat{\beta}$	true value of μ	$\hat{\mu}$	R_0	$\hat{R}_0$
Posterior mean	1	0.9523	1	0.9548	1	1.0012
Sd error		0.0476		0.0454		0.0027
Posterior mean	0.3	0.3058	0.8	0.9246	0.375	0.3349
Sd error		0.0058		0.1246		0.0400
Posterior mean	1.3	1.2987	0.8	0.7543	1.625	1.724
Sd error		0.0013		0.0456		0.0990

TABLE 3. Posterior mean and standard error for β, μ and R_0 for $\rho = 0.9$.

Looking at Tables 1, 2 and 3 and Figures 1, 2 and 3 they show that the estimations of the parameters are generally much closer to their true values in the tree cases $\rho = 0.1$, $\rho = 0.5$ and $\rho = 0.9$. Figures 1, 2 and 3 display the histograms densities of parameters posterior densities, which reveal the convergence of the algorithm toward a limit distribution.

5. Conclusion

The present paper described Bayesian estimation for the dependent parameters of stochastic SIR epidemic model. The proposed estimator is based on simulation-based inference through MCMC methods. The estimation framework involves the introduction of latent or missing observations. We adopt the approximation of transition density given in Risken [30] during the process of estimating the parameters of the SIR epidemic model which gives more accurate values. Furthermore, to lead to a better estimation, we have proposed Kibble's bivariate gamma distribution as a good prior density of parameters, that can be written as a discrete mixture of the negative binomial distribution and two gamma distributions. Hereafter, we prove that the posterior density of the parameters can be written as a discrete mixture of the negative binomial distribution and two GIG distributions.
Moreover, we have shown the efficiency of MCMC methods in simulating synthetic data from the SIR epidemic model, the estimations of the parameters are generally much closer to their

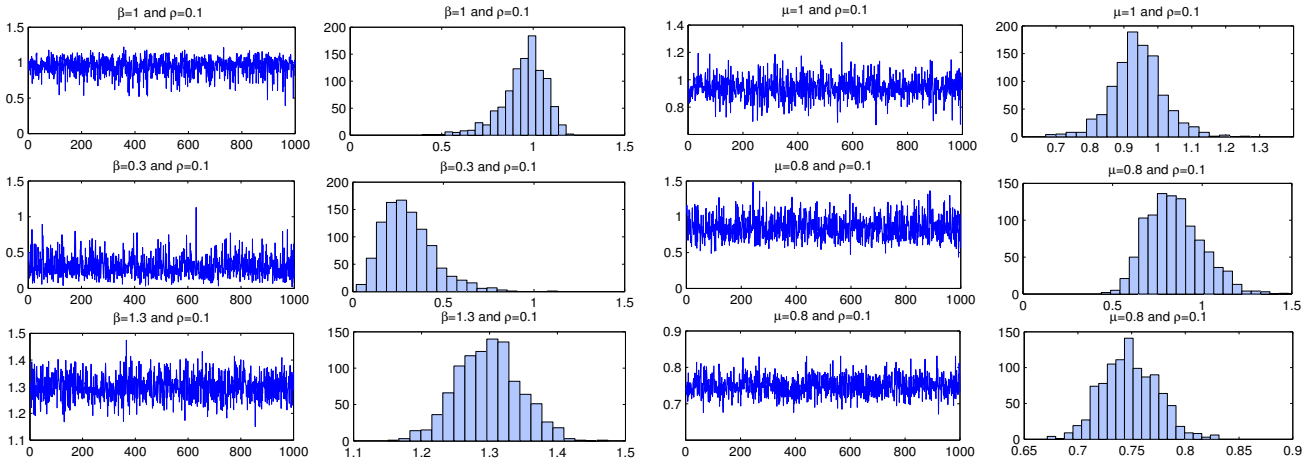


FIGURE 1. Frequency histogram for posterior densities estimates of β and μ for the same exact parameters in Table 1 with $\rho = 0.1$ and 20000 iterations in all cases.

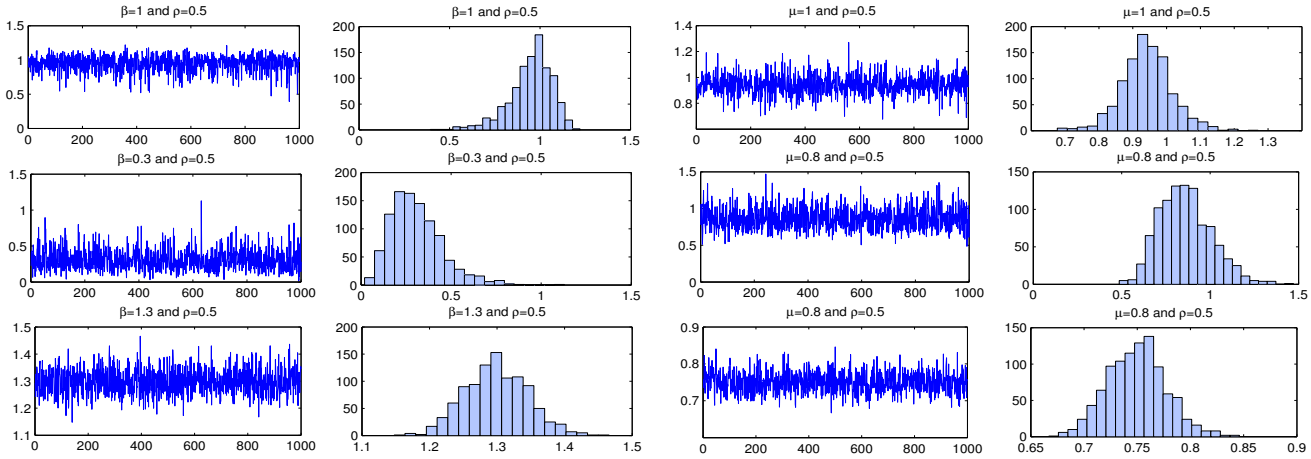


FIGURE 2. Frequency histogram for posterior densities estimates of β and μ for the same exact parameters in Table 2 with $\rho = 0.5$ and 20000 iterations in all cases.

true values in the two cases when $\rho \simeq 0.5$ and $\rho \simeq 0.9$.
This method is thus likely to be applicable to a rather wider range of models and to larger data sets than we have considered here. Further research will be devoted to improving the parametric inference by considering a higher parameter dimension. Also, we will generalise it to more complex epidemic models.

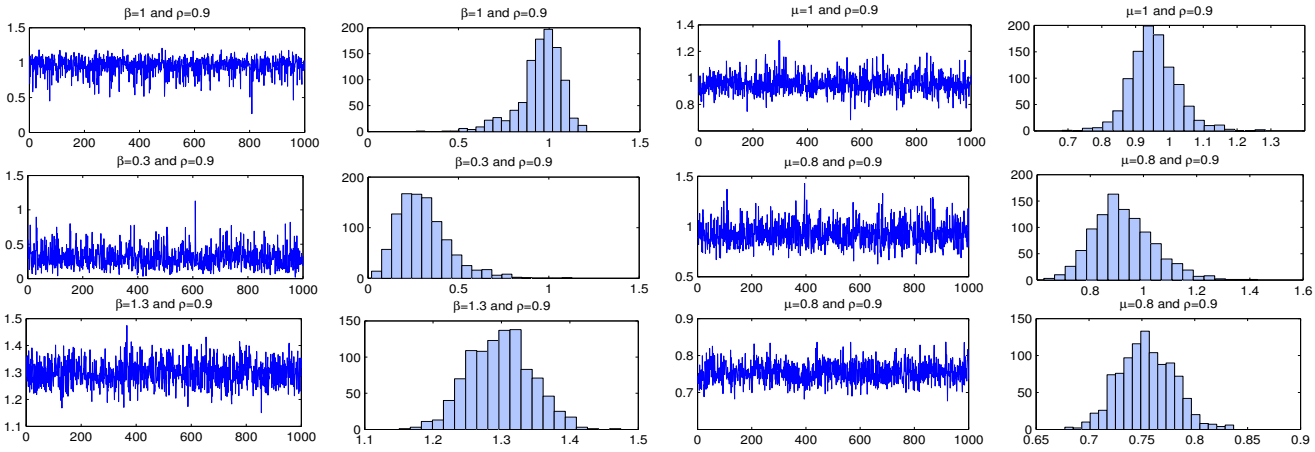


FIGURE 3. Frequency histogram for posterior densities estimates of β and μ for the same exact parameters in Table 3 with $\rho = 0.9$ and 20000 iterations in all cases.

Appendix

Proof of the Proposition 3.1 Let $\tilde{y}_{t_0}, ..., \tilde{y}_{t_N}$ be a random sample from (3.5), the joint posterior density of $\theta = (\beta, \mu)$ is given by $p(\theta|\tilde{y}) \propto \prod_{i=1}^{N} p(\tilde{y}_{t_i}|\tilde{y}_{t_{i-1}}, \theta)\pi(\theta)$ where $p(\tilde{y}_{t_i}|\tilde{y}_{t_{i-1}}, \theta)$ is the transition density given in (3.2) and $\pi(\theta)$ is the prior density of $\theta = (\beta, \mu)$ given by (3.6), taking $y_{t_{i-1}} = 1 + \frac{a}{n} - x_{t_{i-1}} - z_{t_{i-1}}$ in (3.3) and (3.4), and omiting all terms independent to β and μ, we obtain

$$p(\theta|\tilde{y}) \propto \prod_{i=1}^{N} p_1(\tilde{y}_{t_i}|\tilde{y}_{t_{i-1}}, \beta) p_2(\tilde{y}_{t_i}|\tilde{y}_{t_{i-1}}, \mu) p(\theta)$$

$$\propto \prod_{i=1}^{N} \beta^{-1/2} \, \mathrm{e}^{\frac{-n}{4\Delta t_i}\left(\frac{\Delta x_{t_i}^2}{x_{t_{i-1}} y_{t_{i-1}}/\beta} + x_{t_{i-1}} y_{t_{i-1}} \Delta t_i^2 \beta\right)} \mu^{-1/2} \, \mathrm{e}^{\frac{-n}{4\Delta t_i}\left(\frac{\Delta z_{t_i}^2}{y_{t_{i-1}}/\mu} + y_{t_{i-1}} \Delta t_i^2 \mu\right)}$$

$$\times (1-\rho)^{\nu} (\beta\mu)^{\nu-1} \, \mathrm{e}^{-\frac{\lambda 1 \beta + \lambda 2 \mu}{1-\rho}} \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)} (\rho\beta\mu)^k.$$

By taking:
$A = \sum_{i=1}^{N} \frac{n\Delta x_{t_i}^2}{2\Delta t_i x_{t_{i-1}} y_{t_{i-1}}}$, $B = \sum_{i=1}^{N} \frac{n}{2} x_{t_{i-1}} y_{t_{i-1}} \Delta t_i + \frac{2\lambda_1}{1-\rho}$, $C = \sum_{i=1}^{N} \frac{n\Delta z_{t_i}^2}{2\Delta t_i y_{t_{i-1}}}$, $D = \sum_{i=1}^{N} \frac{n}{2} \Delta t_i y_{t_{i-1}} + \frac{2\lambda_2}{1-\rho}$.
After simplification, we obtain

$$p(\theta|\tilde{y}) \propto \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)} \rho^k \beta^{-\frac{N}{2}+\nu+k-1} \, \mathrm{e}^{-\frac{1}{2}\left(\frac{A}{\beta} + B\beta\right)} \mu^{-\frac{N}{2}+\nu+k-1} \, \mathrm{e}^{-\frac{1}{2}\left(\frac{C}{\mu} + D\mu\right)}.$$

Approximatively, we can write

$$p(\theta|\tilde{y}) \propto \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)} \rho^k c_k^1 c_k^2 GIG(\beta| - \frac{N}{2} + \nu + k, A, B) GIG(\mu| - \frac{N}{2} + \nu + k, C, D),$$

with $c_k^1 = \frac{2I_{-\frac{N}{2}+\nu+k}(\sqrt{AB})}{\left(\sqrt{\frac{B}{A}}\right)^{-\frac{N}{2}+\nu+k}}$ and $c_k^2 = \frac{2I_{-\frac{N}{2}+\nu+k}(\sqrt{CD})}{\left(\sqrt{\frac{D}{C}}\right)^{-\frac{N}{2}+\nu+k}}$ are the inverse normalization constant of $GIG(\beta| - \frac{N}{2} + \nu + k, A, B)$ and $GIG(\mu| - \frac{N}{2} + \nu + k, C, D)$ respectively. $I_p(.)$ is the modified Bessel function of the second kind of order p.
Hence

$$\begin{aligned}\frac{\Gamma(\nu+k)}{\Gamma(\nu)\Gamma(k)} \rho^k c_k^1 c_k^2 &\propto \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(k)} \rho^k \left(\sqrt{\frac{A}{B}}\right)^k I_{-\frac{N}{2}+\nu+k}(\sqrt{AB}) \left(\sqrt{\frac{C}{D}}\right)^k K_{-\frac{N}{2}+\nu+k}(\sqrt{CD}) \\ &\propto \sum_{k=0}^{\infty} \frac{\Gamma(\nu+k)}{\Gamma(k)} \left(\sqrt{\frac{AC}{BD}}\rho\right)^k I_{-\frac{N}{2}+\nu+k}(\sqrt{AB}) K_{-\frac{N}{2}+\nu+k}(\sqrt{CD}).\end{aligned}$$

Then

$$p(\theta|\tilde{y}) \propto \sum_{k=0}^{\infty} c_k GIG(\beta| - \frac{N}{2} + \nu + k, A, B) GIG(\mu| - \frac{N}{2} + \nu + k, C, D),$$

with

$$c_k = \frac{\Gamma(\nu+k)}{\Gamma(k)} \left(\sqrt{\frac{AC}{BD}}\rho\right)^k I_{-\frac{N}{2}+\nu+k}(\sqrt{AB}) I_{-\frac{N}{2}+\nu+k}(\sqrt{CD}).$$

Finally $p(\theta|\tilde{y})$ is a discrete mixture of the two independent distributions:
$GIG(\beta| - \frac{N}{2} + \nu + k, A, B)$ and $GIG(\mu| - \frac{N}{2} + \nu + k, C, D)$.

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