Bayesian Formulation of Time-Dependent Carrier-Borne Epidemic Model with a Single Carrier

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Abstract: In this paper, the time dependent carrier-borne epidemic model defined by Weiss in 1965 has been adopted into a Bayesian framework for the estimation of its parameters. A complete methodological structure has been proposed for estimating the relative infection rate and probability of survival of *k* out of *m* susceptibles after time *t* from the start of the epidemic. The methodology has been proposed assuming a single carrier to simplify the study of the behavioral validity of the fitted Bayesian model with respect to time and relative infection rate. Further, the proposed model has been implemented on two real data sets- the typhoid epidemic data from Zermatt in Switzerland and the Covid-19 epidemic data from Kerala in India. Results show that the proposed methodology produces reliable predictions which are consistent with those of the maximum likelihood estimates and with expected epidemiological patterns.

Keywords: Carrier-borne epidemic model, infection rate and removal/recovery rate, Priors, Conjugate priors, Posteriors, Bayesian Estimation.

1. INTRODUCTION

Prediction of progression of an epidemic is of paramount importance in developing strategies to fight the spread of infection. Carrier-borne epidemic models are among the earliest mathematical and statistical models developed for studying the progression dynamics of epidemics. Carrier- borne diseases are contagious diseases caused by pathogens, like viruses, protozoa and bacteria, which are communicated by human, or animal agents known as carriers. Basically, carriers are individuals with inapparent infection who are capable of spreading the infection to others. For example, pathogens such as hepatitis B virus, herpes simplex virus, and HIV are frequently transmitted by asymptomatic human carriers.

Currently, deterministic and stochastic compartmental models, like Susceptible, Infectious, or Recovered (SIR), are being popularly used to study the progression dynamics and epidemiological parameters of epidemics. Extensive use of such models is apparent in a huge volume of research done in the context of the current pandemic, COVID-19. However, when it comes to studying epidemics caused by carrier-borne infections, carrier-borne epidemic models can serve a better purpose, especially if the objective is to predict the probabilities of survival of susceptibles given the number of carriers in the population. Although few authors published their work on stochastic epidemic models as early as in the years 1926, 1949 [1, 2], G.H. Weiss is credited with laying the foundations of carrier-borne epidemic models through his pioneer work published in the year 1965 [3]. He developed the overall deterministic formulation of the carrier-borne epidemic model and presented a stochastic framework for estimating the ultimate size of a carrier-borne epidemic using the concept of Markov process. Weiss formulated his model under the assumption that all carriers can be identified and removed from the population at some rate (removal rate) using the available public health measures. Further, he assumed a closed population where infections are spread by initially introduced carriers and no new carriers in the form of infectives are introduced in the population. This model of Weiss has been extended further by many authors, under different assumptions regarding the carriers and the types of population [4-20].

In summary, there are various methods available for estimating the infection rate of susceptible and recovery rate of a carrier for Weiss's stochastic model for carrier-borne epidemics. However, such methods are not available for complete time dependent model. Grover *et al*. (2021) [27] have proposed a maximum likelihood estimation method for estimating the probability of susceptible not being infected but it does not consider time varying infection and recovery rates. In such a case, the usual maximum likelihood estimation method does not provide reliable estimate for the probability of susceptible not being infected at different time points during the epidemic.

In this paper, our primary objective is to propose a more robust and computationally rich methodology for estimating the parameters of the classic carrier-borne epidemic model of Weiss. For this purpose, Weiss's carrier-borne model has been adopted in a Bayesian framework, and the parameters have been estimated from their posterior distributions using Gibbs sampling

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MCMC technique. Although Bayesian Hierarchical formulation of compartmental epidemic models (SIR and its variants) have been introduced by some authors in recent times [21-26], Bayesian approach has not been explored for the carrier-borne epidemic models. Since the Bayesian formulation allows to combine past information about epidemic parameters, like infection rate, recovery rate etc., with the likelihood from the sample through prior distributions, it provides more flexibility to account for errors at multiple levels in the models. The methodology proposed in this paper can be further applied to the more generalized extensions of the carrier-borne epidemic models.

2. METHODOLOGY

2.1. Bayesian Framework for the Carrier-Borne Epidemic Model

Suppose that an epidemic is initiated by n=1 carrier in the presence of m susceptibles. It is assumed that the epidemic can terminate in one of the two ways- either carrier is eliminated or the entire population gets infected from the disease.

We define $\pi_{k|\alpha,t}(m,1)$ to be the probability that the population of m susceptibles is reduced to k in time period t with infection rate α, when the epidemic was initiated with m susceptibles and one carrier [3].

$$\pi_{k|t}(m,1) = \binom{m}{k}.(e^{-\alpha t})^k \cdot (1-e^{-\alpha t})^{m-k} \cdots \quad (1)$$

Where k= 0, 1, 2, $\cdots, m$;

For computational conveniences, we define τ = βt, and rewrite the expression as follows.

$$\pi_{k|\tau,\sigma}(m,1) = \binom{m}{k}.(e^{-\sigma\tau})^k \cdot (1-e^{-\sigma\tau})^{m-k} \cdots \quad (2)$$

Where, k = 0, 1, 2, $\cdots, m,$ and $\sigma = \frac{\alpha}{\beta}$ is the relative infection rate (α is the infection rate and β is the recovery/removal rate).

Let $\theta = e^{-\sigma\tau}$ be the probability of a susceptible not being infected in time period τ, when the relative infection rate is σ. Now, using this in equation (2), we get the following expression.

$$\pi_{k|\theta}(m,1) = \binom{m}{k}.(\theta)^k \cdot (1-\theta)^{m-k} \cdots \quad (3)$$

Where, k = 0, 1, 2, $\cdots, m$;

Let us assume that the prior distribution of $\theta = e^{-\sigma\tau}$ is Beta with parameter σ (initial infection rate) i.e.

$$\theta \sim beta(1,\sigma) \text{ with pdf } \pi(\theta); \text{ where } 0<\theta<1;\ \sigma>0. \quad (4)$$

The likelihood function for estimating θ will be

$$\mathrm{L}(\theta\ |\mathrm{k}) = \binom{m}{k}.(\theta)^k \cdot (1-\theta)^{m-k} \cdots \quad (5)$$

Now the posterior distribution of θ is given as

$$\pi(\theta|data) \propto \pi(\theta).\mathrm{L}(\theta\ |\mathrm{k})$$

$$\propto \{\frac{\Gamma(1+\sigma)}{\Gamma(\sigma)}\}.\{(1-\theta)^{\sigma-1}\}.\binom{m}{k}.(\theta)^k \cdot (1-\theta)^{m-k}$$

$$\propto \{\frac{\Gamma(1+\sigma)}{\Gamma(\sigma)}\}.\binom{m}{k}(\theta)^k \cdot (1-\theta)^{\sigma+m-k-1} \cdots \quad (6)$$

From equation (6) it is clear that the posterior distribution of θ is Beta distribution with parameters $k+1$ and $\sigma+m-k$.

$$i.e.\ \pi(\theta|data) \sim beta(k+1, \sigma+m-k) \cdots \quad (7)$$

Therefore, the posterior mean and variance of θ are given as follows:

$$posterior\ mean\ (\theta(z)) = \frac{k+1}{\sigma+m+1} \cdots \quad (8)$$

$$posterior\ variance\ (\theta(z)) = \frac{(k+1).(\sigma+m-k)}{(\sigma+m+2).(\sigma+m+1)^2} \cdots \quad (9)$$

2.2. Bayesian Estimate of θ

By assuming squared error loss function, the posterior mean of θ qualifies to be the Bayesian estimate of θ. That is,

$$\hat{\theta}_{\boldsymbol{b}} = \frac{k+1}{\sigma+m+1} \text{ (from equation (8)) } \cdots \quad (10)$$

2.3. Maximum Likelihood Estimate of θ

Let K be the observed value of the number of susceptibles remaining in the population during time period τ since the start of the epidemic. Then, the maximum likelihood estimate of θ [27] is

$$\hat{\theta}_{\boldsymbol{mle}} = \frac{k}{m} \cdots \quad (11)$$

3. APPROXIMATE ESTIMATION OF THE PARAMETER OF THE CARRIER BORNE EPIDEMIC MODEL

The probability of susceptible not being infected, when the no. of susceptible in a population is sufficiently large, can also be estimated by using the following approximations.

3.1. Using Poisson Approximation

As we know that the Binomial distribution converges to Poisson distribution when number of trials goes to infinity and np(mean) converges to a finite limit. Therefore, Binomial (m, θ), when m (no. of susceptible) is sufficiently large and θ (the probability of not being infected) is *very small*, converges to Poisson distribution for reduced no. of susceptible K with parameter λ=mθ.

$$\text{i.e. } \pi_{k|\theta}(m,1) = e^{-m\theta}.\frac{(m\theta)^k}{k!} \text{ ; k=0,1, 2, ...} \quad (12)$$

Then, the likelihood function for estimating θ can be defined as

$$L_1(\theta|\,\mathrm{k}) = e^{-m\theta}.\frac{(m\theta)^k}{k!} \cdots \quad (13)$$

With the prior distribution

$\theta \sim \pi(\theta) \equiv beta(1,\sigma)$; where $0 < \theta < 1$; $\sigma > 0$.

The posterior distribution of θ is obtained as

$$\pi(\theta|data) \propto \pi(\theta)\,.L_1(\theta\,|\mathrm{k})$$

$$\propto \{\frac{\Gamma(1+\sigma)}{\Gamma(\sigma)}\}.\{(1-\theta)^{\sigma-1}\}.e^{-m\theta}.\frac{(m\theta)^k}{k!}$$

$$\propto \{\frac{\Gamma(1+\sigma)}{\Gamma(\sigma)}\}.\{(1-\theta)^{\sigma-1}.e^{-m\theta}.\frac{(m\theta)^k}{k!}\} \cdots \quad (14)$$

3.2. Using Normal Approximation

The Binomial (m, θ), when m (no. of susceptible) is sufficiently large and θ (the probability of not being infected) is *not very small*, converges to Normal distribution for reduced no. of susceptible K with mean= mθ and variance= mθ(1-θ).

i.e. $\pi_{k|\theta}(m,1) = \frac{1}{\sqrt{2\pi.m\theta(1-\theta)}}.\ \exp\{-\frac{1}{2}\left(\frac{k-m\theta}{m\theta(1-\theta)}\right)^2\}$; k>0 $\cdots$ (15)

The likelihood function for estimating θ can be defined as

$$L_2(\theta|\mathrm{k}) = \frac{1}{\sqrt{2\pi.m\theta(1-\theta)}}.\ \exp\{-\frac{1}{2}\left(\frac{k-m\theta}{m\theta(1-\theta)}\right)^2\} \cdots \quad (16)$$

With the prior distribution

$\theta \sim \pi(\theta) \equiv beta(1,\sigma)$; where $0 < \theta < 1$; $\sigma > 0$.

And the posterior distribution of θ is obtained as

$$\pi(\theta|data) \propto \pi(\theta)\times L_2(\theta\,|\mathrm{k})$$

$$\propto \{\frac{\Gamma(1+\sigma)}{\Gamma(\sigma)}\}.\{(1-\theta)^{\sigma-1}\}\times\frac{1}{\sqrt{2\pi.m\theta(1-\theta)}}$$
$$\exp\{-\frac{1}{2}\left(\frac{k-m\theta}{m\theta(1-\theta)}\right)^2\} \quad (17)$$

Note: In both the above cases, the posterior estimation of the probability of susceptible not being infected can be obtained by using MCMC methods or Open Bugs of any software.

4. APPLICATION

This section aims to evaluate the performance of the Bayesian estimator of relative infection rate of carrier-borne epidemic model. Two data sets are considered viz. Typhoid epidemic in Zermatt and COVID19 epidemic in Kerala, India.

4.1. Typhoid Epidemic in Zermatt

For the data of typhoid epidemic in Zermatt out of 1500 susceptibles approximately 100 cases of typhoid were reported [3].

Table 1: Estimate of θ for m=1500, k=1400, *σ= 1/15 =0.067*

Likelihood function	$\widehat{\theta}_{true\ value}$	$\widehat{\theta}_b$
Binomial	0.935507	0.933377 (With M.S.E.=0.000047)
Normal	0.935507	0.9333 (With M.S.E.=0.0000063)
Poisson	0.935507	0.954 (With M.S.E.=0.001303)

with $\widehat{\theta}_{mle}$ = 0.933333.

From Table **1** it can be observed that we get minimum standard error with respect to Normal distribution as compared to Binomial and Poisson distribution.

4.2. Covid19 Epidemic in Kerala, India

We have taken this data from the Kerala Government's official website (https: dashboard.kerala.gov.in; Kerala: COVID-19 Battle). Kerala population in 2022 is estimated to be 35 million (3.5 Crores), according to Unique Identification Aadhar India. Here, we have used the data updated till December 18, 2021 with the following details

Total Population of Kerala estimated 35 million
No. of Susceptibles (m) 35 million

Active cases	33098
Relative infection rate (*σ*)	0.00095

Table 2: Estimate of θ for m=35.0 million, k=34966902 million, *σ= 0.00095*

Likelihood function	$\widehat{\theta}_{true\ value}$	$\widehat{\theta}_b$
Binomial	0.9990505	0.9857157 (With M.S.E.=0.0027)
Normal	0.9990505	0.986 (With M.S.E.=0.00017)
Poisson	0.9990505	0.986 (With M.S.E.=0.00017)

with $\widehat{\theta}_{mle}$ =0.9857143 (with S.E.=0.00002).

From Table **2** it can be observed that we get same standard error with respect to Normal and Poisson distribution which is smaller than that for the Binomial distribution.

4.3 Visual Interpretation

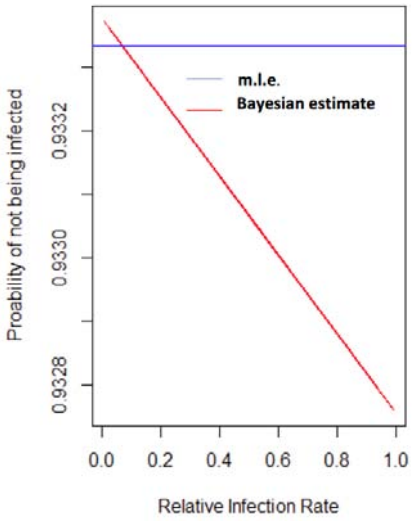

Figure 1: Effect of relative infection rate on the probability of not being infected for Typhoid in Zermatt.

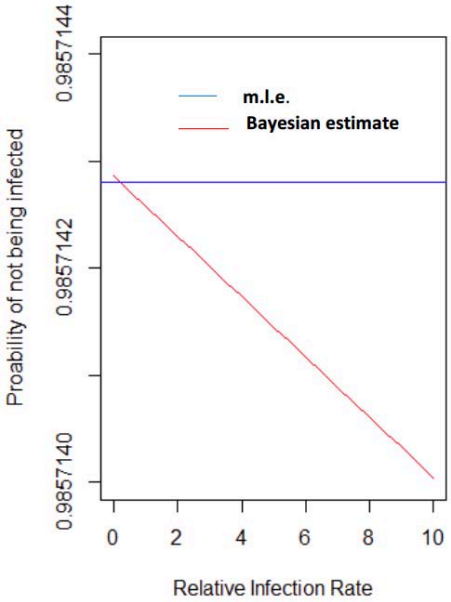

Figure 2: Effect of relative infection rate on the probability of not being infected for Covid19 in Kerala, India.

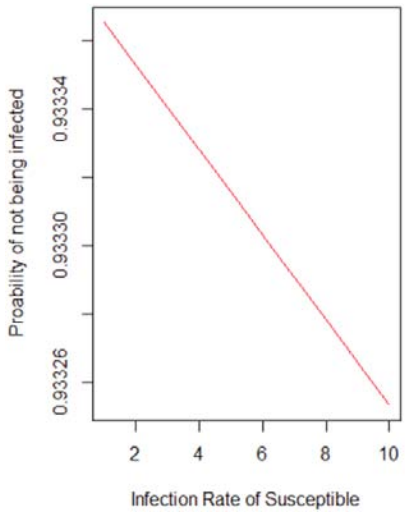

Figure 3: Effect of infection rate on the probability of not being infected for Typhoid in Zermatt.

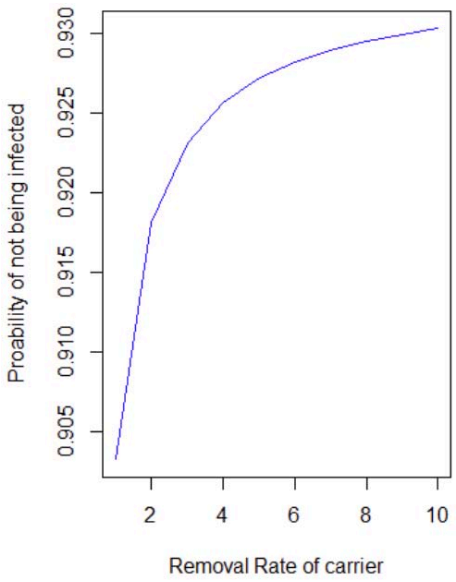

Figure 4: Effect of removal rate of carrier on the probability of not being infected for Typhoid in Zermatt.

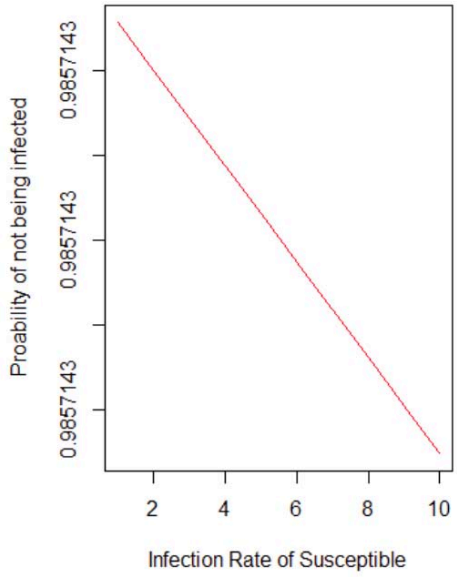

Figure 5: Effect of infection rate on the probability of not being infected for Covid19 in Kerala, India.

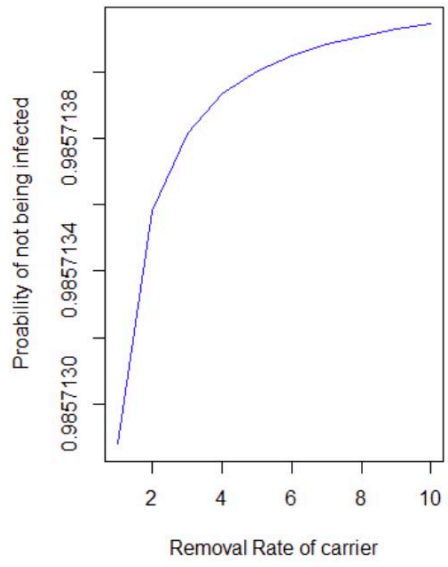

Figure 6: Effect of removal rate of carrier on the probability of not being infected for Covid19 in Kerala, India.

5. DISCUSSION

The whole idea behind this study is to introduce a computationally rigorous methodology for the estimation of parameters of carrier-borne epidemic model. From section 4, it can be observed that the posterior estimates of the parameter of the carrier-borne model, obtained for both datasets are consistent, and are very close to the true value of the parameter. It can be observed from Figures **1** and **2** that m.l.e. does not depict the change in the probability of not being infected with change in the relative infection rate whereas Bayes estimator is capable of capturing the change in the probability not being infected with change in the relative infected rate. We can conclude that the posterior estimate is more reliable than the m.l.e. That is, the Bayesian methodology provides a better estimator than maximum likelihood method. This provides us with a strong ground to believe that in a more complex set-up where time-dependent parameters are introduced in the model and where finding closed-form solutions of maximum likelihood estimates may become difficult, the proposed Bayesian methodology, or an extension of the proposed Bayesian methodology can be used for reliable estimation and prediction.

6. CONCLUSION

This paper provides a new method based on the Bayesian approach to estimate the parameters of the carrier-borne epidemic model as well as the approximation form of the carrier-borne epidemic model in the presence of a single carrier for the specified infection period. In the carrier-borne epidemic model, we assume all infectives are isolated from the population. But the disease is still spreading, which means the carrier is present in the population. By this method, we can estimate the probability of susceptibles to be infected by the carrier in case of increasing or decreasing infection rate of susceptible and recovery/ removal rate of the carrier. Moreover, we have shown that the Bayes estimation method is more reliable than the maximum likelihood method.

This study adopted the Beta conjugate prior for Binomial distribution for the Bayesian analysis. Priors with other distributions may also be considered.

Further, this method can also be employed for more complex and realistic carrier-borne epidemic models with completely time-dependent parameters.

DISCLOSURE

The authors have no conflict of interest.

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CONFLICTS OF INTEREST

The authors declare that they have no known competing interests that could influence the work reported in this paper.

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