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The Stochastic SIR Household Epidemics With $T_I \equiv 4.1$ and T_I Having GAMMA(a, b) Infectious Period Distribution.

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Abstract

Model estimates, their functions are in no doubt affected by wrong choice of the infectious period distribution, T_I when the actual one is unknown. This is a misspecification problem which is often accompanied with biased and imprecise estimates. This work does not completely examined this problem but explored the choice of constant infectious period, $T_I \equiv 4.1$ and T_I distributed as $\Gamma(2, 2.05)$ for the household epidemic and then examined their effects on the behaviours of the model functions and quality of its maximum likelihood estimates in order to see if there are considerable disparities in the maximum likelihood estimates and behaviours of the functions giving these scenarios and whether constant infectious period is a reasonable assumption for the stochastic SIR household epidemic.

Keywords:

Infectious period, Global infection, household epidemic, threshold parameter.

1. Introduction

This work broadly examined two scenarios namely, the behaviours of the mean final size of the stochastic SIR household epidemic, its function β, the likelihood function, its maximum, the corresponding estimates of the parameters, when the infectious period T_I is constant and when it is distributed as $\Gamma(a, b)$. We do this using [1] final size epidemic data, by firstly examining the model, its community based variant, its household structure, the behaviour of the epidemic in the early stage, its approximation by a branching process, its

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threshold parameter and condition for a global epidemic.

We also discussed the proportion infected and its computation method, the associated likelihood function, their plots, computation and the calculation of the final size probabilities.

we examined the computation of the likelihood function and the effects of the choice of initial approximate estimates of the parameters for the maximum likelihood algorithm given the two scenarios, using [1] final size household epidemic data.

The stochastic SIR household epidemic model of [3, 4, 5] and [6, 2] assumed a closed and finite population (without birth or death) partitioned into small groups referred to as households. Each household is made of susceptibles, infective and removed individuals. Where a susceptible is one who can be infected with the disease, an infective is one who has the disease and a removed individual is one who has recovered and is immune from further re-infection or isolated or has died, [7].

It assume that contacts occur at random between the susceptibles and infectives at the points of homogeneous Poisson processes having rates λ_L and $\frac{\lambda_G}{N}$. Where λ_L is the local contact rate (contacts between individuals in the households), λ_G is the total number of global contacts from the household epidemic and N is the total population of individuals in the households and

Any individual contacted if susceptible will immediately become infectious, for period T_I, referred to as the infectious period (as there is no latency for the disease) after which the individual is removed (died or quarantined or immune) at the end of the infectious period, as it no longer plays any part in the epidemic process. We assumed no disease latency, as the distribution of the final size of the epidemic is invariant to general assumptions concerning the latency period [5].

The infectious period of each infective is assumed to be independent and identically distributed according to the random variable T_I which is assumed to be arbitrary but must be specified [5]. The Poisson processes describing contacts and the infectious period are assumed to be mutually independent [5, 6].

Community based variant of [5] with permanent immunity assumed heterogeneity in contact and also multiple source of infection. Here, the population is stratified according to different group of individuals $(i = 1, \ldots, m)$ with each individual in exactly one group and susceptible to the infectious disease of interest [1] and [11].

They assumed that an epidemic can be started by one or more individuals, a_i, $i = 1, 2, \ldots, m$, becoming infected from a specified source outside the population similar to that of [4, 8]. Where a_i, $i = 1, 2, \ldots, m$, are the initial number of infectives in group i. While [9] focused on design of vaccination studies.

The initial number of susceptible individuals are assumed to be, $\mathbf{N} = (N_1, \ldots, N_m)^{'}$ with the total population size, $N = \sum_{i=1}^{m} N_i$, $i = 1, 2, \ldots, m$ [1]. While the length of the infectious period of an i infective residing in $k = 1, 2, \ldots, m$ group is assumed to be $T_{i,k}$, with moment generating function, $\phi_i(t) = E(\exp(-tT_{i,k}))$.

Progress of epidemic in each household in the community based model of [1] is assumed independent in contrast to [5] dependency assumption of epidemic between households. The epidemic is then governed by extra-population escape probability,(defined as the probability that a susceptible of type $i = 1, 2, \ldots m$ escapes infection from outside the population during the course of the epidemic), $\mathbf{B} = (\beta_1, \ldots, \beta_m)^{'}$.

Where each $\beta_i, i = 1, \ldots m$ is the extra-population escape probability for susceptibles of type $i = 1, \ldots, m$. Secondly, the within-population disease transmission (defined as the rate at which a susceptible from group of type i comes in contact with an infective from a group of type k) is represented by [1] as $\beta_{i,k}$.

Other extension with temporary immunity is proposed by [10]. They assumed that every susceptible in the household has equal probability of avoiding infection from the community. Where $b_t = 1 - a_t$, a_t is the probability that a susceptible from a household becomes infected from the community, $t = 0, 1, \ldots, T$, is the time period of infection, $B = f(b_t)$ is the probability that an infective is not infected from the community [10].

1.1. Household Structure

Let M_n be the number of households of size n, and $M = \sum_{i=1}^{n} M_n$ be the sum of the households. The proportion of household of size n, $\alpha_n = \frac{M_n}{M}$ and the total population size , $N = \sum_{n=1}^{\infty} nM_n$.

In line with [5, 6], the probability that a global contact is with an individual residing in a household of

size n is

$$\tilde{\alpha}_n = \frac{nM_n}{N}. \tag{1}$$

1.2. Epidemics in the Early Stages

If the population is large and the number of the initial infectives is small then during the early stages of the epidemic, the probability that global contact is with individual residing in a previously infected household is small hence [5] showed that the early stages of the epidemic can be approximated by a branching process.

The epidemic is started at time $t = 0$, with an initial infective who infects its household members and other household members. Those infected also infect susceptibles household members and in other households. The process of creating new infections locally and globally follows a branching process until the first contact with an infective or removed individual called a ghost [5, 2].

During its infectious period, an infectious individual makes contact with distinct individual in the households independently and at random at the points of a Poisson process having rates λ_L. The total number of global contacts from the household epidemic, R_n follows a Poisson distribution with mean $\lambda_G T_A$ [5, 2]. Where T_A the is the sum of the infectious period of the infectives or the severity of the epidemic, R_n is the offspring random variable for the approximating branching process in the epidemic process.

The threshold parameter $R_* = E(R)$ is then defined as the mean number of infected households from the household epidemic.

Let $E(\theta^R) = h(\theta)$ be the probability generating function of the offspring random variable R. In line with the branching process theory, a global epidemic occurs if in the limit as the number of households, $m \to \infty$, the epidemic infects infinitely many households [5, 6].

Thus, a global epidemic occurs for the stochastic household epidemic if the threshold parameters, $R_* > 1$. Here,

$$R_* = \sum_{n=1}^{\infty} \tilde{\alpha}_n E(R_n) \tag{2}$$

$$= \sum_{n=1}^{\infty} \bar{\alpha}_n \lambda_G E(T_A), \tag{3}$$

Since $E(T_A) = E(T_n)E(T_I)$, from Wald identity for epidemic [5, 6, 2],

we then have $R_* = \lambda_G E(T_I) \sum_{n=1}^{\infty} \tilde{\alpha}_n \mu_n$, $\mu_n = E(T_n)$, $n = 1, 2, \ldots$.

Where, $R_0 = \lambda_G E(T_I)$ is the threshold parameter for the stochastic SIR single household epidemic and $\sum_{n=1}^{\infty} \tilde{\alpha}_n \mu_n$ is the mean amplification factor owing to internal spread within households, $\mu_n = \mu_{n-1,1}$ is the mean final size of the household epidemic with $n-1$ initial susceptibles and 1 infective.

For n initial susceptibles and a infectives, the the mean final size is given by,

$$\mu_{n,a} = n + a - \sum_{k=0}^{n} \binom{n}{k} \beta_k \phi(\lambda_L k)^{n+a-k}. \tag{4}$$

Where, $\beta_1, \ldots,$ are obtained recursively from,

$$\sum_{i=0}^{k} \binom{k}{i} \beta_i \phi(\lambda_L i)^{k-i} = k. \tag{5}$$

1.3. Proportion Ultimately Infected

This is a weighted average of the number of infectives in a single household epidemic with k binomial distributed number of infectives [5, 6], while the remaining $n - k$ susceptibles avoid infection from outside

the household. It is given by,

$$z = \sum_{n=1}^{\infty} \tilde{\alpha}_n n^{-1} \sum_{k=1}^{n} \binom{n}{k} (1-\phi)^k \phi^{n-k} \mu_{n-k,k}. \tag{6}$$

Where,

$$\phi(\lambda_G, z, T_I) = \exp(-\frac{\lambda_G}{N} z N E(T_I). \tag{7}$$

$$= \exp(-\lambda_G z E(T_I)). \tag{8}$$

Then, $NzE(T_I)$ is the total person units of infection present throughout the epidemic, N is the population, z is defined in equation 6.

2. The Final Size Probabilities

In line with the assumptions in [1] and [5], the triangular equation for the probability of the final size household epidemic, assuming the value ω given m groups of different types of individuals is,

$$1 = \sum_{\boldsymbol{\omega}=0}^{\mathbf{j}} \binom{\boldsymbol{j}}{\boldsymbol{\omega}} P^{\mathbf{N}}_{\boldsymbol{\omega}_i \ldots \boldsymbol{\omega}_m} / \boldsymbol{\phi}(\boldsymbol{\beta}'(\mathbf{N}-\mathbf{J}))^{\boldsymbol{\omega}+\boldsymbol{a}} \mathbf{B}^{(\mathbf{N}-\mathbf{J})}, \ \mathbf{j} \geq 0,$$

where $\omega = (\omega_1, \ldots, \omega_m)$, $\boldsymbol{\beta}$ is an $m \times m$ of contact rates, $\mathbf{B}$ is a vector of all the extra-escape population probabilities, while $\mathbf{N}$ is the vector of all the initial susceptibles in the m groups of different types of individuals.

For population with single type of individual, $m = 1$ for which $a = 0$, the final size probabilities satisfy the triangular equation,

$$1 = \sum_{\omega=0}^{j} \binom{j}{\omega} P^n_{\omega} / \phi(\lambda_L(n-j))^{\omega} \pi^{n-j}, \ j \geq 0, \tag{9}$$

which simplifies to,

$$P^n_k = \left(1 - \sum_{w=0}^{k-1} \frac{\binom{k}{w} P^n_w}{\phi(\lambda_L(n-k))^w \pi^{n-k}}\right) \phi(\lambda_L(n-k))^k \pi^{n-k}, \ k = 0, 1 \ldots n, \tag{10}$$

where n is the number of the initial susceptibles in the household and $\phi(\lambda_L) = E(\exp(-\lambda_L T_I))$.

where λ_L is the local contact rate, π is the probability of avoiding infection from outside the household and P^n_w, are the final size probabilities of the epidemic outcomes $w = 0, 1, 2 \ldots, n$ and n is the household size [4, 5, 6].

Taking into account all the possible ways an individual can become infected, the final size probabilities are given by [4, 5, 6] as,

$$P_{n,i} = \binom{n}{i} P^n_i. \tag{11}$$

3. Maximum Likehood Estimation

Each household sizes has a separate multinomial distribution [8] for $X_{n,0}, X_{n,1}, \ldots, X_{n,j}, j = 0, 1, \ldots, \max$. Hence

$$P(X_{n,0} = x_{n,0}, X_{n,1} = x_{n,1}, \ldots, X_{n,j} = x_{n,j}) = \frac{M_n!}{\prod_{j=1}^{max} x_{n,j}} \prod_{j=0}^{n} P_{nj}^{x_{n,j}}. \tag{12}$$

Where $X_{n,j}$ is the total number of j cases in the household of size n and $p_{n,j}$ is the probability of j cases in the household of size n,

The approximate likelihood function is,

$$L(\lambda_L, \pi) = \frac{M_n!}{\prod_{j=1}^{max} x_{n,j}} \prod_{i=1}^{\max} \prod_{j=0}^{n} P_{n,j}(\lambda_L, \pi)^{x_{n,j}}. \tag{13}$$

Where,

$$P_{i,j}(n) = \sum_{k=0}^{i} \binom{j}{i-k} \binom{n-j}{k} \varepsilon^{j-i+2k}(1-\varepsilon)^{n-j+i-2k}, \quad i,j = 0,1,\ldots,n. \tag{14}$$

Alternatively written as,

$$P_{i,j}(n) = \sum_{k=0}^{i} \binom{j}{k} \binom{n-j}{i-k} \varepsilon^{j+i-2k}(1-\varepsilon)^{n-j-i+2k}, \quad i,j = 0,1,\ldots,n, \tag{15}$$

if the final size data is misclassified. Here ϵ is the misclassification probability, defned as the probability of observing an infective as susceptible or a susceptible as an infective.

Here,

$$\sum_{i=0}^{n} P_{i,j}(n) = 1, \forall j \in \{0,1,\ldots,n\}.$$

4. When $T_I \equiv 4.1$ and T_I having $\Gamma(a,b)$ Infectious Period Distribution

Inference of the parameters of the stochastic SIR household epidemic model with constant and varying infection period having $\Gamma(a,b)$ distribution can be found in [1] and [5] without adequate attention to the their theoretical properties and those of functions of the model given these scenarios.

For example, how does the magnitude of the contact parameters contribute to minor and major epidemics and what are their effects on other functions of the model, given their theoretical lower and upper boundaries. Also how does these influence the likelihood function, its maximum and corresponding parameter estimates ?

We examined these questions for the β_k, $\mu_{n,a}$ functions and also the likelihood function, its maximum and corresponding estimates of the model parameters. We do this using [1] final size epidemic data and with maximum likelihood algorithm in which independent and Binomial distribution number of infectives in each household is assumed.

We assumed, $T_I \equiv 4.1$ and also T_I with $\Gamma(a,b)$ infectious period distribution and explored their likelihood functions, compute their maximum and hence obtained their corresponding estimates using [1] household final size epidemic data.

5. The Beta and Mean Final Size Function

The function, β_k is obtained from the triangular equation,

$$k - i\sum_{i=0}^{k} \binom{k}{i} \beta_i \phi(\lambda_L.i) = k, k = 1,0,\ldots,n \tag{16}$$

where $\phi(\theta)$ is defined as the moment generating function of the infectious period distribution T_I, also referred to as the Laplace transform of the infectious period.

Simplification of equation (16) gives β_k in general form,

$$\beta_k = k - \sum_{i=1}^{k-1} \binom{k}{i} \beta_i \phi(\lambda_L.i)^{k-i} \tag{17}$$

If $\lambda_L \to 0$, then $\phi(\lambda_L) \to 1$ and so β_k reduces,

$$\beta_k = k - \sum_{i=1}^{k-1} \binom{k}{i} \beta_i \tag{18}$$

With constant infectious period in [1] we have,

$\beta_k = 0, \forall k \in \mathbf{Z}_+ - \{1\}$, and $\beta_1 = 1$, similar to when $\Gamma(a, b)$ is assumed as the infectious period distribution .

If, $\lambda_L \to \infty$, then $\phi(\lambda_L) \to 0$, similar to when the infectious period distribution is assumed to be $\Gamma(a, b)$.

Thus, $\beta_k = k, \forall k \in \mathbf{Z}_+$, is a dependent function of the mean final size, which is defined as the average number of susceptibles individuals ultimately infected, given in [4, 5, 6] as,

$$\mu_{n,a} = n + a - \sum_{k=0}^{n} \binom{n}{k} \beta_k \phi(\lambda_L.k)^{n-k}, \tag{19}$$

n is the household size, a is the initial number of infectives,

Hence, $\lambda_L \to 0$, gives $\beta_k = 0, \forall k \in \mathbf{Z}_+ - \{1\}$, while $\beta_1 = 1$.

From equation (19), we see that $\phi(\lambda_L) \to 1$, reduces equation (19) to,

$$\mu_{n,a} = n + a - \sum_{k=0}^{n} \binom{n}{k} \beta_k, \tag{20}$$

similar to when the infectious period is assumed Gamma(a, b).

Now substituting the value of β_k in equation (20) gives only the term, $\binom{n}{1}\beta_1 = n$, with others zero. Thus, the mean final size with constant infectious period is given by,

$$\mu_{n,a} = n + a - n = n \tag{21}$$

Same as when the infectious period is distributed as $\Gamma(a, b)$.

This means that in both scenarios, without local contact, there will be no new infections generated other than the initial number of infectives.

Also, if $\lambda_L \to \infty$, $\phi(\lambda_L) \to 0$ equation (19), will be left with $n + a$, number of infectives similar to when the infectious period is distributed as $\Gamma(a, b)$.

The properties of β_k and the $\mu_{n,a}$ with constant and varying infectious period distributed as $\Gamma(a, b)$ are similar.

6. When The Infectious Period, $T_I = 4.1$

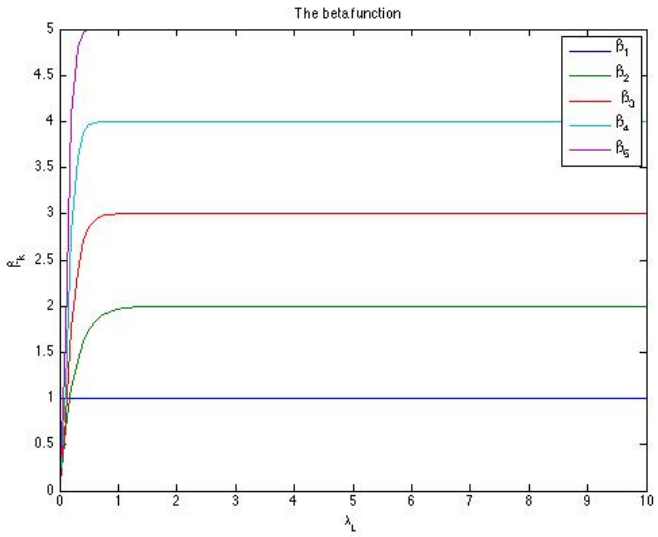

Figure 1: The β function with $T_I \equiv 4.1$, $\lambda_L = 10, n = 5$.

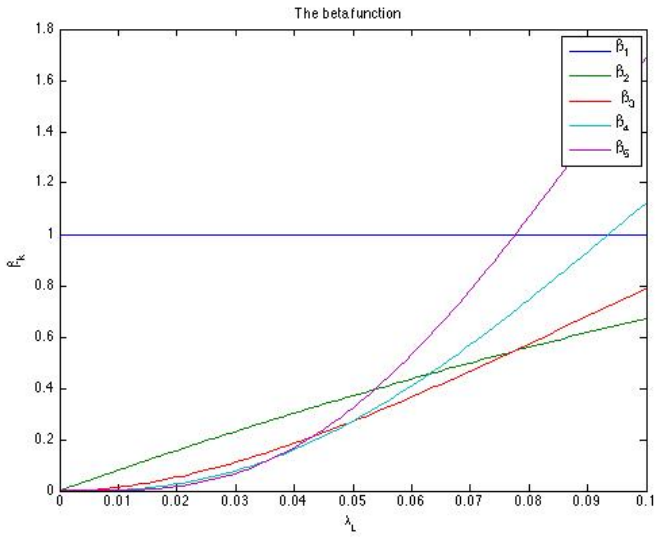

Figure 2: The β function with $T_I \equiv 4.1$, $\lambda_L = 0.1$, $n = 5$.

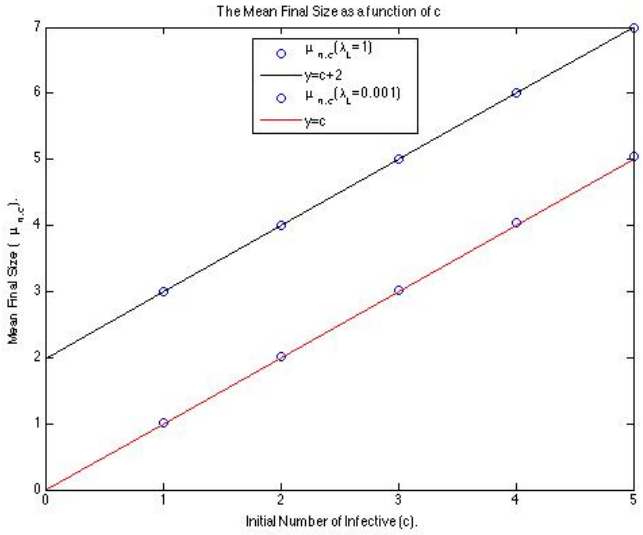

Figure 3: The μ_n with varying c, $T_I \equiv 4.1$, $\lambda_L = 10$, $n = 5$.

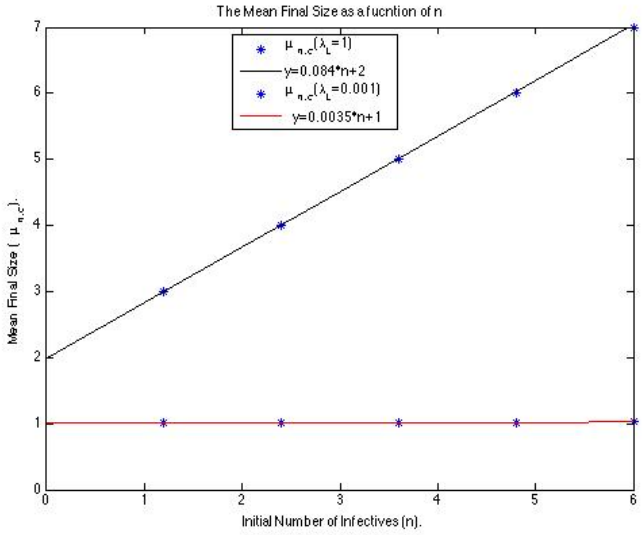

Figure 4: The μ_n with varying n, $T_I \equiv 4.1$, $\lambda_L = 1$, $n = 5$.

	Number of Infectives					
	0	1	2	3	4	5
1	110	23	0	0	0	0
2	149	27	13	0	0	0
3	72	23	6	7	0	0
4	60	20	16	8	2	0
5	13	9	5	2	1	1

Table 1: Each coefficient in the table represents number of households of size $n = 1, 2, \ldots, 5$ with $i = 1, 2, \ldots, 5$ number of infectives by the end of the epidemic.

7. Data Analysis

7.1. Computation of The Likehood Function From Final Size Data

We adopt the assumptions and techniques in [1] to construct matrix of the maximum likelihood estimates of the parameters over a grid of λ_L and π points using the final size data in table 1 and then obtained their maximum by inspection .

The idea here is to get a more robust initial starting estimates of the parameters for the Nelder Mead fminsearch simplex non linear algorithm which numerically estimate the parameters.

These approximate estimates are obtained from the contour and surface plots of the likelihood functions associated with given final size epidemic data by inspection.

We have in this section followed these procedures, by first chosen the approximate estimates of the model parameters from the two dimensional contour and three dimensional surface plots of the loglikelihood functions by inspection and then employed the Nelder Mead fminsearch simplex linear algorithm to get the desired maximum likelihood estimates for the two cases of the infectious period, T_I.

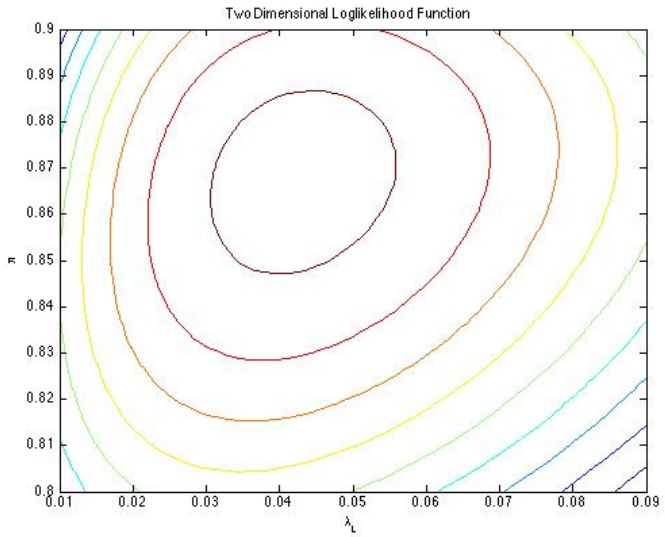

Figure 5: Two Dimensional Loglikelihood function with $T_I = 4.1$ and $n = 5$

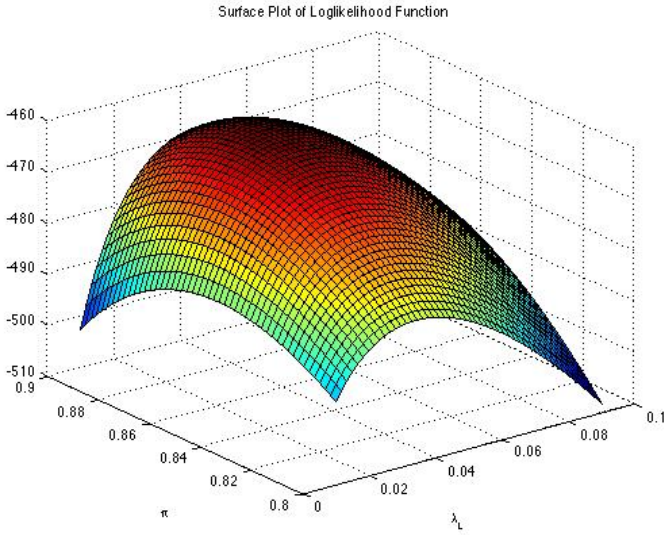

Figure 6: Surface Plot of the Loglikelihood function with $T_I = 4.1$ and $n = 5$

7.2. When The Infectious Period T_I is Distributed as $\Gamma(2, 2.05)$

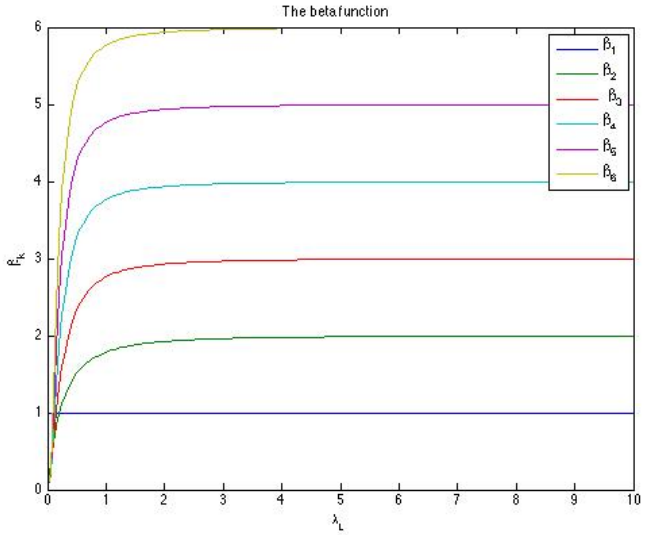

Figure 7: The β function with T_I, distributed as $\Gamma(a, b)$ where $a = 2$, $b = 2.05$.

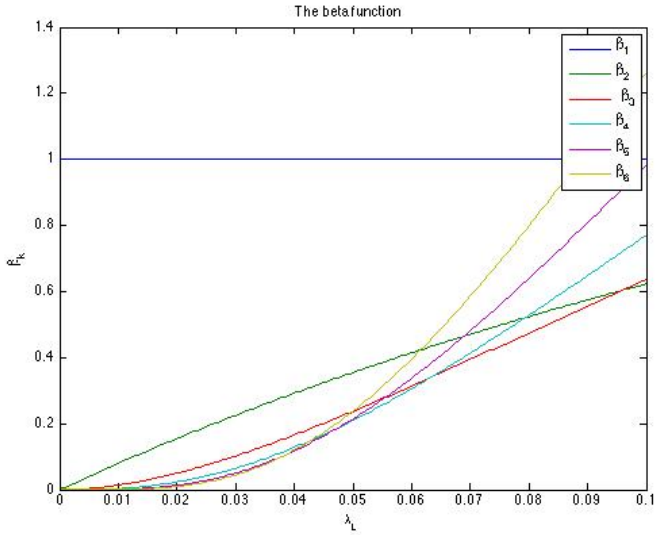

Figure 8: The β function with T_I, distributed as $\Gamma(2, 2.05)$ in figure 7.

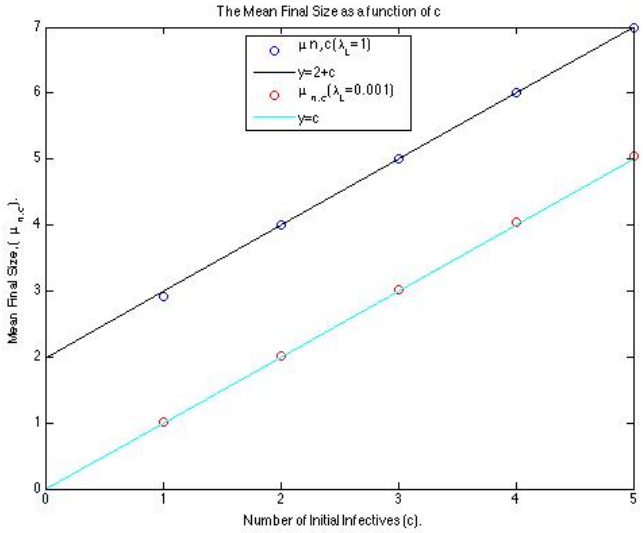

Figure 9: The mean final size with varying c, with $\lambda_L =, 0.001, 0.05, 1, 20$, and T_I, distributed as $\Gamma(a, b)$, $a = 2$, $b = 2.05$.

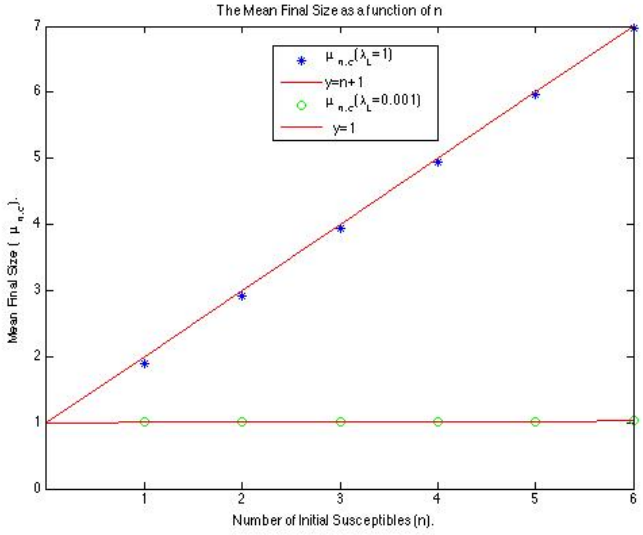

Figure 10: The mean final size for $\lambda_L = 0.2, 0.3, 1, 20$ with varying n, and T_I, distributed as $\Gamma(a, b)$, $a = 2$, $b = 2.05$, $c = 1$.

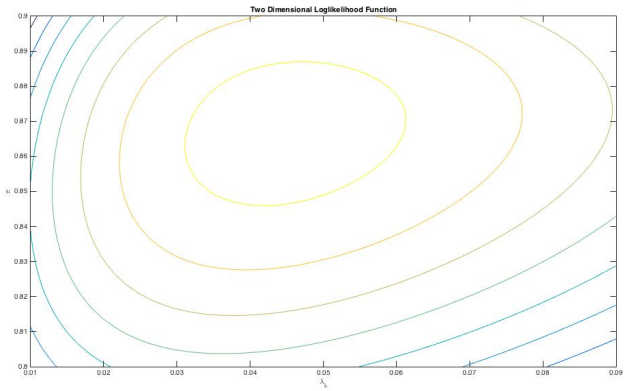

Figure 11: Two Dimensional Loglikelihood function with T_I distributed as $\Gamma(2, 2.05)$ and $n = 5$

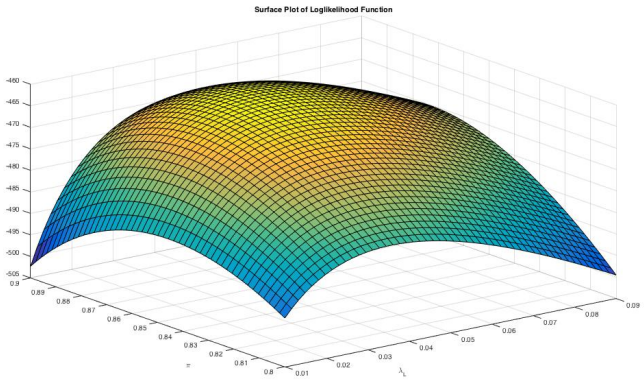

Figure 12: Surface Plot of the Loglikelihood function with T_I distributed as $\Gamma(2, 2.05)$ and $n = 5$

In figure 8, we see that, if λ_L tends to zero then β_k also tends to zero except β_1 which assumes the value 1, in line with its theoretical properties also similar to figure 2.

In figure 7, the β function increases with increasing λ_L, similar to figure 1 with constant infectious period.

In figure 9, three linear plots with asymptotic behaviours for the mean final size are studied. Here the mean final size either lies on a line for a given value of λ_L or it lies close to it. As the contact rates increases it becomes asymptotic to the line, $y = 2 + c$, which act as its upper bound, with 2 as the number of initial susceptibles. Same behaviour is observed in figure 3 with constant T_I. The notation c has the same meaning as a in [4, 5, 6], referred to as the number of the initial infectives.

In figure 10, the mean final size approaches the line $y = n + 1$, as $\lambda_L \to \infty$, which is its upper bound. Where 1 is the initial number of infectives. Silimiarly the line $y = 1$ is its lower bound. Same behaviour is also obseved in figure 4.

8. Results and Discussion

We take the approximate estimates of λ_L and π from figure (6) by inspection and optimised them using Nelder Mead fminsearch simplex nonlinear algorithm in line with [1]. Here, these approximations are, $\lambda_L = 0.04$, $\pi = 0.87$ respectively. The optimized estimates are, $\lambda_L = 0.0423$, $\pi = 0.867$, which are approximately the same with those of [1] using constant infectious period distribution, given as $\lambda_L = 0.0423$, $\pi = 0.8677$ respectively.

The proportion of the susceptibles ultimately infected including the initial number of infectives, z and the global contact rate λ_G, are, $z = 0.1783$, $\lambda_G = 0.1952$, the threshold parameter, $R_* = 1.1320$

The estimate of the observed proportion of the population infected is $z = 0.1768$, while [1] obtained, $z = 0.1775$ using $\Gamma(2, 2.05)$ infectious period distribution.

However, [5] computes the threshold parameter, $R_* = 1.1303$ using $\Gamma(2, 2.05)$ infectious period distribution, while we obtained $R_* = 1.1304$.

9. Conclusion

In general, maximum likelihood estimates with constant infectious period does not differ substantially from the infectious period distributed having $\Gamma(2, 2.05)$ adopted in [1]. It can be shown that same behaviours holds for infectious period distributed as $\Gamma(k, 4.1/k), k = 1, 2, 5$. Thus the assumption of a constant infectious period is reasonable.

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