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The effect of individual variation in epidemic modelling

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Abstract

This paper investigates a stochastic epidemic model of SIR type; Susceptible → Infectious → Removed, modified with the addition of a latency period prior to the infectious period. The periods of latency and infectiousness are modeled as gamma distributed random variables. The main purpose is to reveal how the probability for a large outbreak, and the growth rate of the epidemic, depend on parameters of the latency period and the infectious period. Analysis is based on the theory of biological branching processes, due to their resemblance with the propagation of the epidemic in the early stages. The main results are that growth rate of the epidemic is increasing with the coefficient of variation of the latency period and decreasing with the coefficient of variation of the infectious period. Furthermore is the probability for a large outbreak independent of the latency period and decreasing with the coefficient of variation of the infectious period. These theoretically derived results are supported by the results from simulations of the epidemic.

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Contents

1 Introduction

This article is an analysis of an SIR, Susceptible → Infectious → Removed, stochastic epidemic model modified with the addition of a latency period, where the population is closed and homogenously mixing (see Andersson and Britton (2000) for more on stochastic epidemic modelling). In an SIR model, the population is divided into compartments as mentioned above, which is applicable when concerned with diseases caused by microparasites, such as viral and bacterial parasites. Microparasites are defined by direct reproduction within the host at high rates, and by short generation times, why the life cycle of the individual microparasite need not be taken into account when studying the host population (Anderson and May, 1991). Some examples of diseases caused by microparasites are Chicken Pox, Measles and Rubella.

The aim of the paper is to explain how the probability for a large outbreak, and the growth rate of the epidemic, depend on the coefficient of variation of the latency period and the infectious period. The latency period and the infectious period are modeled as independent gamma distributed random variables. Furthermore, individuals within the population are assumed to make contact according to a poisson process at a constant rate during the infectious period, though some of the results are compared with ones obtained with this rate modeled as a random variable.

It is concluded that the probability for a large outbreak of the epidemic, and the growth rate of the epidemic, is decreasing with the coefficient of variation of the infectious period. The result concerning the outbreak probability is in accordance with the ones obtained in Asikainen (2006), where the outbreak probability is compared for different distributions of the infectious period. We also show that the growth rate of the epidemic is decreasing with the coefficient of variation of the latency period.

In Section 2, the model is defined and the branching process approximation of the epidemic is intuitively justified. The quantities corresponding to the probability for a large outbreak, and the growth rate of the epidemic, are also identified in the theory of branching processes. Results, based on the calculations in Section A, are presented in Section 3. These results are supported by the results from simulations of the epidemic in Section 4, and discussed in Section 5.

2 Theoretical framework

2.1 The SIR model

Initially we assume that one individual carrying an infectious disease enters a population, and that the disease is of SIR type. The name SIR refers to that an individual who is infected with this disease will go through the chain of states: Susceptible → Infectious → Removed. By assumption, the whole population that is monitored is susceptible at first, and when the infectious individual enters the population some will become infected and others not (we emphasize the difference between the *infectious* and *infected*, where the first refer to an individual that is ill and able to infect others at the present, and the second refers to an individual that has become infected sometime in the past. In the latter case the individual may either still be infectious, recovered and immune, or latent). Those who become infected will be able to infect others during their periods of infectiousness, and after that be removed which corresponds to immunization or death. This leads to that the whole population is divided into the three classes of the susceptible, the infectious and the removed.

We assume that each pair of individuals is equally likely to make contact, i.e. the population is homogeneously mixing. We also assume that no individual enters or leaves the population, i.e. the population is closed. All imaginable pairs of individuals make contact according to homogeneous and independent Poisson processes. The rates of these processes are set to $\frac{\lambda}{N}$, for some rate λ, when the population size is N. As a consequence, the rate at which one infectious make contact with susceptible individuals, is independent of the size of the population and initially equal to λ. This rate will eventually decrease, since by assumption some part of the susceptible individuals will get infected.

We will investigate a more general case of the epidemic model described above, assuming that when infected an individual is at first latent for a random length of time before being able to infect others. This will define an epidemic model of SEIR type; Susceptible → Exposed → Infectious → Removed, described more thoroughly by Ping and Shengqiang (2006). As the SIR epidemic model is more common, and still captures the main aspects of our model, we will somewhat incorrectly use that terminology.

The latency period L and the infectious period I are both modeled as gamma distributed random variables, i.e. $L \sim \Gamma(K_L, B_L)$ and $I \sim \Gamma(K_I, B_I)$, where K_L and K_I are integer valued. It follows that L and I can be regarded as sums of independent exponentially distributed random variables, which will prove useful when we analyze and simulate the epidemic. The contact rate λ is deterministic, but in some parts of the text compared with the more general case with the contact rates, then denoted by Λ, modeled as Pareto

distributed random variable, i.e. $\Lambda \sim Pa(m, \phi)$ i.i.d for different contact processes.

2.2 Branching processes approximation

The propagation of the epidemic can be approximated by a branching process in the early stages (Andersson and Britton, 2000), which we exploit in the analysis. We begin by establishing this fact in a intuitive way as follows. Consider a large population of size N entered by an infectious individual and assume that all the properties of our SIR model stated above are fulfilled. By definition of the SIR model, the individuals are homogeneously mixing according to independent poisson processes with rates $\frac{\lambda}{N}$. As the population size N is assumed large compared to λ, the probability for any specific pair to make contact is small. It hence follows that, as long as only a few individuals have been infected, the probability for an infectious individual to make contact with an already infected one is negligible. This implies that infectious individuals will spread the disease almost independently in the initial stages of the epidemic, which induce the behaviour of a branching process.

If a large outbreak occurs, the total number of infectious individuals in the population will at first increase, steadily making the ratio between the number of infected and the total population size larger. As the probability for an infectious individual to make contact with an already infected grows, our assumption that infectious individuals spread the disease independently becomes less valid, thus the branching process approximation eventually breaks down. The propagation of the epidemic continues until the last infectious has recovered.

We identify the branching processes corresponding to our epidemic model in a treatise by Jagers (1975) (where one finds a more detailed discussion of biological branching processes) as the *Sevast'yanov* model, which is defined as follows. We consider a biological branching process $\{z_t\}$, the number of individuals alive at time t, originating from one ancestor. All individuals including the ancestor are living a random length of time, denoted I. Each individual gives birth at random points during their lifetime according to a poisson process, denoted ξ.

For the branching process $\{z_t\}$ to behave like our epidemic, we set the lifetime equal to the infectious period. Birth will correspond with a contact between an infectious individual and an susceptible individual, and death with an infectious individual being removed. It hence follows that births will occur according to a Poisson process ξ with rate λ. The mean number of births by an individual in the process $\{z_t\}$ corresponds to the *basic reproduction number* $R_0 = E[I\lambda]$. We are now able to analyze the behaviour of the epidemic using the theory of branching processes.

2.3 Outbreak probability

When an infectious individual enters a population that satisfy the SIR conditions stated in Section 2.1, one of the following events will occur; either the epidemic terminates with only a few individuals infected, or else a large and nearly deterministic proportion of the population becomes infected before the epidemic terminates (Andersson and Britton, 2000). The probability for a large outbreak to occur is henceforth denoted by π.

We let E denote the event of extinction of a population which reproduce according to the process $\{z_t\}$, defined is Section 2.2. Then, recalling the correspondence between a living individual in the branching process $\{z_t\}$ and an infectious individual in the our epidemic model stated in Section 2.2, we have that the probability for extinction of the population $P(E)$=1-π. The probability $P(E)$ is determined as the smallest non-negative root of

$$P(E) = E[P(E)^{\xi(\infty)}], \tag{2.1}$$

stated by Jagers (1975), where $\xi(\infty)$ is the total number of children born by an arbitrary individual. The following argument explains intuitively why $P(E)$ is the solution to (2.1). We suppose that the number of children born by the ancestor, which we denote by $\xi_0(\infty)$, is equal to n. In order for the branching process $\{z_t\}$ to die out each of these n new branching processes, starting with the n children, has to die out. These events happens independently with probability $P(E)$. As a consequence $P(E|\xi_0(\infty) = n) = P(E)^n$, which yields, by replacing n by $\xi(\infty)$ and taking the expected value, that $P(E)$ is a solution to (2.1).

We reformulate (2.1) as

$$\pi + E[(1-\pi)^{\xi(\infty)}] = 1, \tag{2.2}$$

where $\xi(\infty)$ accordingly denote the total number of produced infections. It is assumed that the contact rate λ and the infectious period I are independent of the latency period L. It hence follows that $\xi(\infty)$ is independent of L. As π is derived from (2.2), all stochasticity in π origins from $\xi(\infty)$. Thus, we conclude that π is independent of L. Conditioning on I yields

$$p(\xi(\infty) = k|I = x) = \frac{(x\lambda)^k e^{x\lambda}}{k!}, \qquad k = 0, 1, 2, \ldots, \tag{2.3}$$

by definition of a poisson process on a fixed interval. We notice that (2.3) is symmetrical in the parameters I and λ. As a consequence, π depends on I and λ only trough their product.

If the population is entered by m infectious individuals instead of 1, each of the m individuals will independently cause a large outbreak with probability

π (see Section 2.2). The probability for a large outbreak, which we denote by π_m, is thus calculated numerically as the solution to

$$\pi_m = 1 - (1 - \pi)^m, \qquad 0 < \pi_m < 1, \tag{2.4}$$

where π is defined above.

2.4 Epidemic growth rate

If an outbreak of the epidemic described in the previous sections occurs, then the number of infected will grow at a certain rate. We want analyze how this rate depends on the stochasticity in the latency period, and the infectious period, of an infected individual. In Section 2.2, we argued that the epidemic be approximated by the branching process $\{z_t\}$ in the initial stage. The event of an outbreak then corresponds to an explosion of $\{z_t\}$, growing at the exponential rate e^α, where $\alpha > 0$. For this to happen R_0 has to be larger than 1 (Jagers, 1975). Since R_0 is the mean number of produced infections by an infectious individual, $R_0 \leq 1$ would intuitively suggest that the number of infectious individual should decrease, or remain constant. The parameter α, which defines the Malthusian parameter, satisfies

$$\int_0^\infty e^{-\alpha t} \mu(dt) = 1, \tag{2.5}$$

stated by Jagers (1975), where $\mu(dt) = E[\xi([t, t + dt])]$ and $\xi([t, t + dt])$ is the number of infections caused by an infectious individual in $[t, t + dt]$. An infectious individual is, by assumption, able to infect others at any point in time during the infectious period. Thus $\mu(dt) = \mu(t)dt$, where $\mu(t) = E[\xi([0, t])]$ is the reproduction function. (As $\mu(t)$ is the mean number of infections caused by an infectious individual up to and including time t, it follows that $R_0 = \mu(\infty)$). We conclude that (2.5) equals

$$\int_0^\infty e^{-\alpha t} \mu'(t)dt = 1. \tag{2.6}$$

The quantity $\mu'(t)$ is interpreted as the mean number of produced infections during the infinitely short interval $(t, t+dt)$. We recall our basic assumption of the epidemic; each infected individual is at first latent during L, then infectious during I where new infections are produced according to a poisson process at the rate λ. Thus, $\mu'(t|\ t \in (0, L)) = \mu'(t|\ t \in (L + I, \infty)) = 0$ and $\mu'(t|\ t \in (L, L + I)) = \lambda$. We conclude, since L and I are stochastic, that $\mu'(t) = \lambda P(L < t < L + I)$.

3 Results

3.1 Outbreak probability

To explain how the probability for a large outbreak, π, depend on the coefficient of variation of the infectious period CV_I, where I is a gamma distributed random variable, we derive the relation

$$\pi + \left(\frac{1}{1+\pi R_0 CV_I}\right)^{(CV_I)^{-2}} = 1, \qquad 0 < \pi < 1, \tag{3.1}$$

which origins from (2.2) (see Section $A.1$). It follows from (3.1) that π is determined by the basic reproduction number $R_0 = E[I]\lambda$ and $CV_I = \frac{\sqrt{Var(I)}}{E[I]}$. We notice that E$[I]$ is a common factor of R_0 and CV_I. As a consequence, to display the desired relation between π and CV_I with R_0 and the contact rate λ fixed, E$[I]$ must be kept constant. In the remainder of the text E$[I] = 1$, thus functioning as the time unit, without loss of generality. Relation (3.1) is illustrated in Figure 1 with $R_0 = 2$. We see that π is monotonically decreasing with CV_I. This holds in general which is proved in the end of Section $A.1$, supporting the result by Asikainen (2006). It hence follows that the probability for a large outbreak decline with the variability, in proportion to the mean length, of the infectious period.

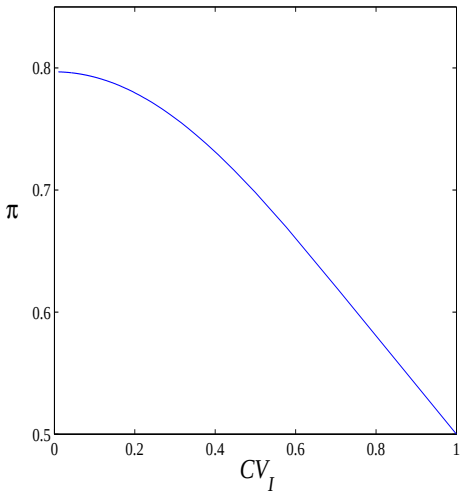

Figure 1: Probability π of an outbreak as a function of the coefficient of variation of the infectious period CV_I. R_0=2 is kept fixed.

If the population is entered by m infectious individuals instead of 1, the

probability for a large outbreak, denoted π_m, is calculated from (2.4) where π is assumed to be known. Figure 2 display the relation between π_m and m with $\pi = 0.5$. We see that π_m growths rapidly as a function of m, and is close to 1 when $m = 10$ despite that π is fairly small. Thus, even when the probability for a single infectious individual to cause an outbreak is moderate, a small group of infectious individuals will cause an outbreak almost for certain.

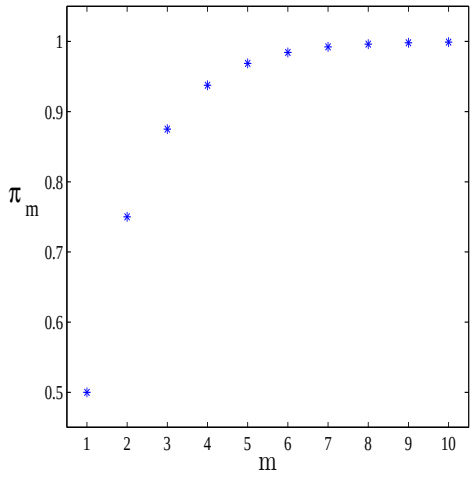

Figure 2: The probability π_m of an outbreak when m infectious individuals enters the population, with $\pi = 0.5$.

Next we want to see how π is affected by the assumption that the contact rate, here denoted by Λ, is stochastic. We have from Section 2.3 that π depends on I and Λ only trough their product. We are then interested in how π depends on the coefficient of variation of $I\Lambda$, $CV_{I\Lambda}$. By independence of I and Λ, $CV_{I\Lambda}$ is derived to $CV_{I\Lambda} = CV_I CV_\Lambda \sqrt{1 + (CV_I)^{-2} + (CV_\Lambda)^{-2}}$, $CV_I > 0$ and $CV_\Lambda > 0$ (see equation (A.21)).

We model Λ as a Pareto distributed random variable, which takes into account that Λ, by definition, is a positive real number. Thus $\Lambda \sim \text{Pa}(m, \phi)$, where $\Lambda > m$, by definition of the Pareto distribution, for some choices of $\phi > 0$ and $m > 0$. The restriction on $\Lambda > m$ might seem unnatural, and lacks a biological motivation, although our aim, to explain how π is affected by the stochasticity in Λ, will be accomplished regardless.

Table 1 shows the relation between π and $CV_{I\Lambda}$ for a small selection of values $CV_{I\Lambda}$, with $R_0 = 2$. The values on $CV_\Lambda = 0$ corresponds to that Λ is deterministic. They are included for the sake of comparison against the case with Pareto distributed Λ, which is illustrated by $\Delta\pi$.

CV_I	CV_Λ	$CV_{I\Lambda}$	π	$\Delta\pi$
1	0	1	0.5000	
1	$\frac{1}{\sqrt{3}}$	$\sqrt{\frac{5}{3}}$	0,4619	0,0381
$\frac{1}{\sqrt{2}}$	0	$\frac{1}{\sqrt{2}}$	0,6180	
$\frac{1}{\sqrt{2}}$	$\frac{1}{\sqrt{8}}$	$\sqrt{\frac{11}{16}}$	0,5932	0,0248
$\frac{1}{\sqrt{3}}$	0	$\frac{1}{\sqrt{3}}$	0,6695	
$\frac{1}{\sqrt{3}}$	$\frac{1}{\sqrt{15}}$	$\sqrt{\frac{19}{45}}$	0,6529	0,0166
$\frac{1}{2}$	0	$\frac{1}{2}$	0,6981	
$\frac{1}{2}$	$\frac{1}{\sqrt{80}}$	$\sqrt{\frac{17}{64}}$	0,6941	0,0040
$\frac{1}{\sqrt{5}}$	0	$\frac{1}{\sqrt{5}}$	0,7162	
$\frac{1}{\sqrt{5}}$	$\frac{1}{\sqrt{440}}$	$\sqrt{\frac{223}{1100}}$	0,7154	0,0010

Table 1: Probability π as a function of $CV_{I\Lambda}$, compared with π a a function of CV_I when $E[\Lambda] = \lambda = 2$.

3.2 The Malthusian parameter

As proposed in Section 2.4, if the disease takes of, the number of infectious will begin to grow exponentially at the rate e^α. One of our main questions is how α, the Malthusian parameter, depends on the coefficient of variation of the latency period L and the infectious period I, denoted CV_L and CV_I respectively. We have from Section 2.4 that α is the solution to (2.6), which can be expressed explicitly as

$$\left(\frac{R_0}{\alpha}\right)\left(1+\alpha CV_L^2 E[L]\right)^{-CV_L^{-2}}\left(1-\left(1+\alpha CV_I^2\right)^{-CV_I^{-2}}\right)=1, \qquad (3.2)$$

(see Section A.3). The mean of the infectious period $E[I]$ is set to 1, thus functioning as the time unit of the growth. Thus, $R_0 = E[I]\lambda = \lambda$. It hence follows that α, which is determined by (3.2), depends on R_0, CV_L, $E[L]$ and CV_I, where $E[L]$ is measured relative to $E[I]$.

We begin to investigate α by assigning $R_0 = 10$, $E[L] = 1$, and $CV_I = CV_L = \frac{1}{3}$ as default values (with $E[I] = E[L] = 1$ the coefficients of variation of I and L simplifies to the respective standard deviations; $CV_I = Std(I)$ and $CV_L = Std(L)$). A few common diseases where $E[I] \approx E[L]$ are Chicken pox, Measles and Rubella (Anderson and May, 1991, p.31), why having $E[I] = E[L]$ might be relevant.

Figure 3 shows that α, determining the growth rate of the epidemic e^{α}, is a decreasing function of mean latency period $E[L]$ for that chosen parameter values. This holds in general which is proved in the end of Section A.3. The latency period L delays an infected individual in transmitting the disease further, thus to contribute to the epidemic growth, which explains the relation between α and $E[L]$.

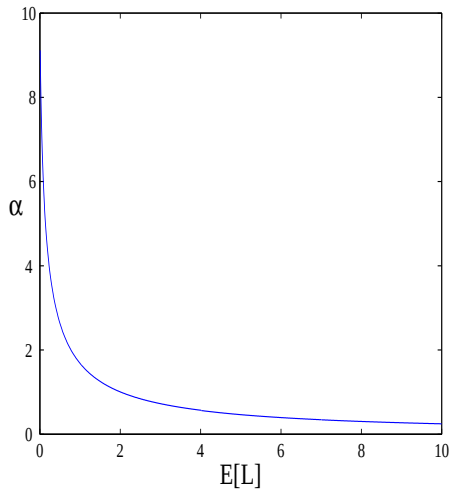

Figure 3: The Malthusian parameter α as a function of the mean length of the latency period, measured relative the mean length of the infectious period.

From Figure 4 (left) and Figure 4 (right), we have that α is a increasing function of CV_L, and a decreasing function of CV_I, for these particular parameter values. These relation hold in general, for the chosen distribution of L and I, which is proved in the end of Section A.3. Thus, a larger variability, in proportion to the mean, in the length of the latency period results in a faster epidemic growth, and a larger variability in proportion to the mean, in the length of the infectious period results in a slower epidemic growth. One way to get intuitive sense of why we obtain these results is to do the following simple comparison.

We consider two infectious individuals with a deterministic infectious period, denoted $I_a = 2t$, and two infectious individuals with a random infectious period, denoted I_b, with $P(I_b = t) = P(I_b = 3_t) = 0,5$. The latency period of both pairs are set to 0, and all 4 satisfy our conditions of the SIR epidemic stated in Section 2.1. The first pair represent a population with smaller variability in the infectious period, and the second pair a population with larger variability in the infectious period, although the mean infectious of both pairs is $2t$. Thus, we have that $CV_{I_b} > CV_{I_a} = 0$. We set the mean

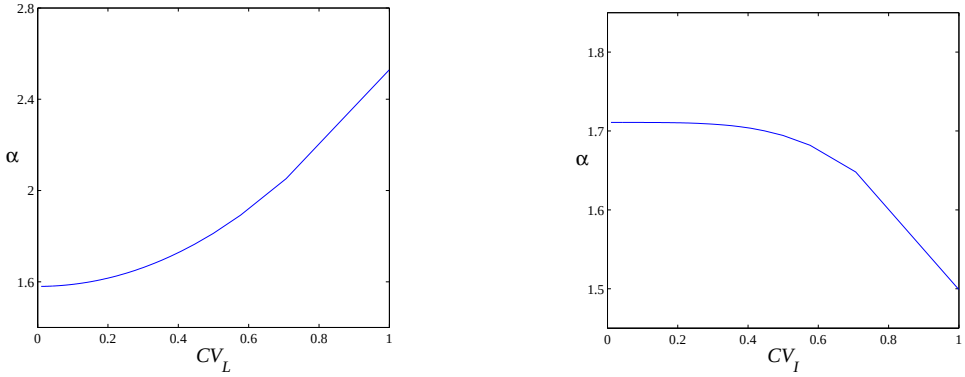

Figure 4: The Malthusian parameter α as a function of the coefficient of variation of the latency period (left), and the coefficient of variation of the infectious period (right), with $R_0 = 10$ kept constant.

number of infections caused during a period of length t to m. As the means of the latency periods $E[I_a] = E[I_b] = 2t$, we would expect, on an average equally many infections produced by the first pair as the second pair. The comparison is illustrated in Figure 3.2 (left). We realize that the pair having a random infectious period is delayed in producing m new infections a period t, which results in slower epidemic growth. The result concerning the latency period is perhaps less obvious. We assume the first pair have a deterministic latency period $L_a = t$, and the second pair have a random latency period L_b, with $P(L_b = 0) = P(L_b = 2t) = 0.5$, the infectious period of both pairs is set to 1. If we match one infectious from each pair with one from the other, Figure 3.2 (right) shows that one infectious from each pair has a head start of a period t in the production of m new infections. The pair with a random latency period gets their head start in $(0, t)$, instead of in $(t, 2t)$ like the pair with a deterministic latency period, which results in a head start for the next generation infectious in further spread of the disease. Expressed in a more general fashion, the individuals with a short latency period overcompensate the ones with a long latency period in transmitting the disease.

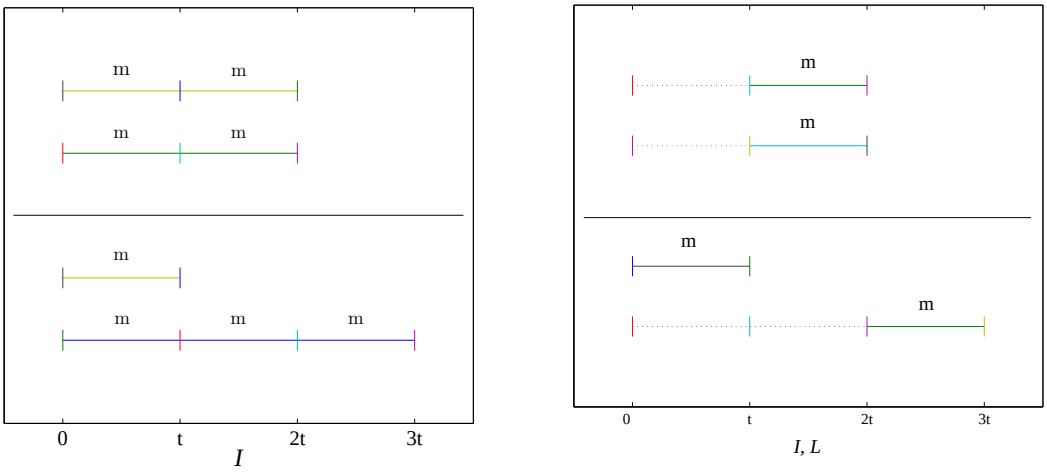

Figure 5: Comparison of the spread of a disease by a pair of individuals with deterministic infectious period $2t$, and a pair of individuals with stochastic infectious period $P(I = t) = P(I = 2t) = 0,5$ (left), and a similar comparison regarding the latency period (right). The mean number of produced infections during t is m.

4 Simulations

4.1 Outbreak probability

To gain more confidence in our theoretically derived results we simulate our epidemic model. We recollect, from Section 2.1, the restriction on the parameters K_L and K_I in the gamma distributions to model the latency period L and the infectious period I, to be positive integers. It hence follows, as mentioned in Section 2.1, that I and L can be regarded as sums of independent exponentially distributed random variables. Thus one infected individual passes through each of the K_L states during latency and the K_I states during infectiousness. Due to the property of the exponential random variable to be memoryless, the propagation of the epidemic is Markovian. Figure 6 shows one realization of the epidemic, i.e. the number of infectious individuals over time, denoted $I(t)$. The size of the population is set to 50000, and the coefficients of variation and the expected values of L and I are set to $CV_L = CV_I = \frac{1}{3}$ and $E[L] = E[I] = 1$. Furthermore is the contact rate $\lambda = 10$.

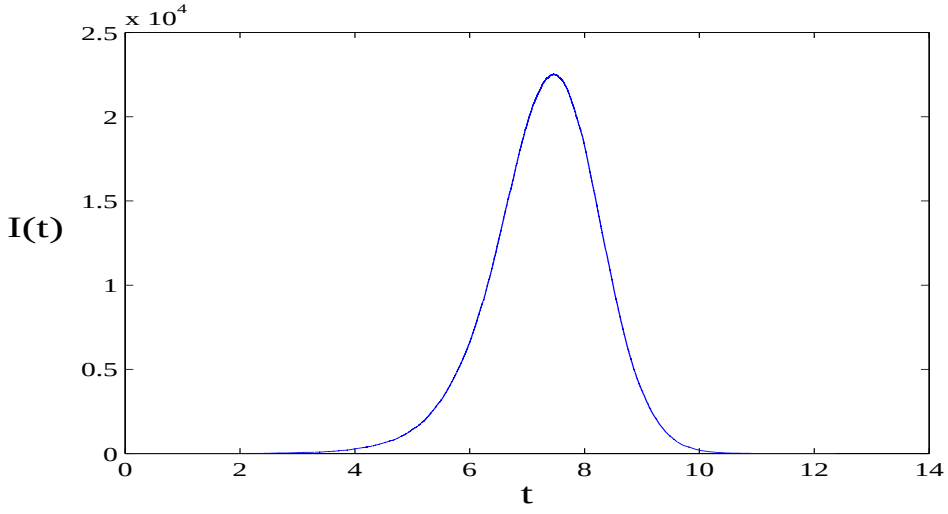

Figure 6: Number infectious over time from one simulation of the epidemic, in a population of 100000 individuals.

We compare the probability for a large outbreak, π, derived theoretically with the frequency of simulation resulting in a large outbreak from M simulations, denoted $\tilde{\pi}$. Figure 7 suggests that an outbreak larger than 100, in a population of 1000, should be considered large. If we let Q denote the number of the M simulations of the epidemic resulting in a large outbreak,

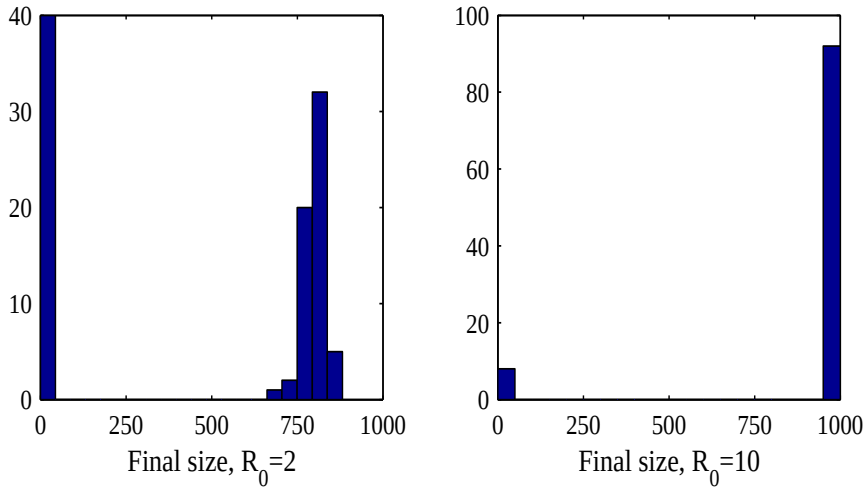

Figure 7: The final size of 100 simulated epidemics in a population of 1000 individuals, $R_0 = 2$ (left), $R_0 = 10$ (right), and $CV_I = \frac{1}{3}$.

Q is binomial distributed with parameters M and π, i.e $Q \sim \text{Bin}(M, \pi)$. According to custom, a normal approximation of the $\text{Bin}(M, \pi)$ distribution is viable if $M\pi > 10$, and $M(1-\pi) > 10$, or equivalently if $\frac{10}{M} < \pi < 1 - \frac{10}{M}$. Thus, we have that $\tilde{\pi}$ is approximately normal, $\tilde{\pi} \sim N(\pi, \frac{\pi(1-\pi)}{M})$, when $\frac{10}{M} < \pi < 1 - \frac{10}{M}$.

Table 2 display the comparison between π and $\tilde{\pi}$, for a small selection of sets of parameter values, from $M = 1000$ simulations. In the lower half of the table, the contact rate is modeled as a Pareto distributed random variable, (as contact rate by default is deterministic, the coefficient of variation of the contact rate $CV_\Lambda = 0$ in the upper part of table). We choose the parameters so that π are safely within $(\frac{10}{M}, 1 - \frac{10}{M}) = (0.01, 0.99)$, why the normal approximation enables us to calculate approximate 95 % confidence intervals. We see that all the confidence intervals cover their respective values of π in evidence of the theoretically derived relation between π and the underlying stochastic quantities.

CV_I	CV_Λ	$CV_{I\Lambda}$	$\tilde{\pi}$	95 % CI	π
1	0	1	0,485	(0,454 0,516)	0,500
$\frac{1}{2}$	0	$\frac{1}{2}$	0,679	(0,650 0,708)	0,698
$\frac{1}{3}$	0	$\frac{1}{3}$	0,748	(0,721 0,775)	0,751
1	$\frac{1}{\sqrt{3}}$	$\sqrt{\frac{5}{3}}$	0,446	(0,415 0,477)	0,462
$\frac{1}{2}$	$\frac{1}{\sqrt{8}}$	$\sqrt{\frac{13}{32}}$	0,674	(0,645 0,703)	0,670
$\frac{1}{3}$	$\frac{1}{\sqrt{24}}$	$\sqrt{\frac{17}{108}}$	0,745	(0,718 0,772)	0,738

Table 2: Comparison of π derived theoretically and $\tilde{\pi}$ derived from simulations, (95 % confidence interval within parenthesis).

4.2 The Malthusian parameter

The results concerning the growth rate of the epidemic can be established more firmly, if supported by the behaviour of the simulated epidemic. We have from the previous sections that the epidemic grows exponentially in the initial stage, at the rate e^{α}, where we are interested in the Malthusian parameter α. An estimate of α can be obtained from a simulation of the epidemic which results in a large outbreak. As mentioned in Section 2.2 the branching approximation, which justify the use of e^{α} as a measure of the growth rate, is valid only in the initial stage of the outbreak. It follows that the estimate of α, denoted $\tilde{\alpha}$, should be assessed from the the initial part of the simulation. Thus, with the number of infectious at t denoted $I(t)$, we have that $I(t) \approx e^{\alpha t}$, why $\tilde{\alpha}$ is obtained as

$$\tilde{\alpha} = \frac{\ln I(t^{'})}{t^{'}}, \tag{4.1}$$

at some suitable value of $t^{'}$. Table 3 illustrates how $\tilde{\alpha}$, derived as the mean of 20 estimates from simulations, and the theoretically derived α, varies together for a small selection of values on the coefficients of variation of the infectious period and latency period, CV_I and CV_L. Furthermore $R_0 = 10$, $E[L] = E[I] = 1$, and the population size $N = 10000$. The values of $\tilde{\alpha}$ are calculated from (4.1) with $t^{'} = \{\min(t); I(t) > N \times 0.02\}$, where the branching process approximation still holds acceptably. Examining table 3 gives that the values of means of $\tilde{\alpha}$ are fairly close to the values of α, and captures the trend in α from altering the values of CV_I and CV_L. The discrepancy $\Delta\alpha$ can be explained partly by the stochastic nature of simulations, and the arbitrariness in the choice of $t^{'}$, in the assessment of $\tilde{\alpha}$.

CV_I	CV_L	α	$\sum_{i=1}^{20} \tilde{\alpha}_i/20$	$\Delta\alpha$
1	$\frac{1}{3}$	$1,499$	$1,220$	$0,279$
1	$\frac{1}{2}$	$1,601$	$1,331$	$0,270$
$\frac{1}{3}$	$\frac{1}{3}$	$1,682$	$1,426$	$0,256$
$\frac{1}{2}$	$\frac{1}{2}$	$1,773$	$1,470$	$0,303$
1	1	$2,162$	$1,873$	$0,289$
$\frac{1}{2}$	1	$2,464$	$2,181$	$0,283$
$\frac{1}{3}$	1	$2,529$	$2,291$	$0,238$

Table 3: Comparison between $\tilde{\alpha}$ estimated from simulations and α derived theoretically.

5 Discussion

The aim of this paper was to analyze the effect of random properties on a stochastic epidemic model. The main results were that the probability for a large outbreak of the epidemic is independent of the latency period, and decreasing with the coefficient of variation of the infectious period. Also that the growth rate of the initial phase of the epidemic is increasing with the coefficient of variation of the latency period and decreasing with the coefficient of variation of the infectious period and the expected value of the latency period. Although these results were derived assuming that both the infectious period and the latency period were gamma distributed random variables, one might suspect the they hold for arbitrary distributions, which is hinted in the end of Section 3. The contact rate between individuals in the population was assumed constant during the infectious period, when analyzing the growth rate of the epidemic. A more general, and realistic, model would take into account the stochasticity in the contact rate. Modelling the contact rate as random would probably not yield different results, but a more refined model and perhaps a subject of further research. It is mentioned by Anderson and May (1991) that individual variability, in proportion to the mean, of the infectious period and latency period, is small for many common viral and bacterial diseases. This fact together with the difficulties in estimation of the parameters within the model, suggests that the results might be hard to incorporate in disease control and prediction, but are nonetheless of theoretical interest.

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A Derivations

A.1 Outbreak probability

To establish an explicit equation from which the probability for a large outbreak, π, can be calculated, we start with

$$E[(1-\pi)^{\xi(\infty)}] + \pi = 1, \qquad 0 < \pi < 1, \tag{A.1}$$

from (2.2), with s is substituted by $1-\pi$. To solve (A.1), we need the explicit probability function of $\xi(\infty)$. As the infectious period I is gamma distributed, $I \sim \Gamma(K_I, \beta_I)$, the probability function of $\xi(\infty)$, $P(\xi(\infty) = k)$,

$k = 0, 1, 2, \ldots$, is derived from (2.3) as follows.

$$\begin{aligned} P(\xi(\infty) = k) &= \int_0^\infty f_I(x) p(\xi(\infty) = k \mid I = x) dx \\ &= \int_0^\infty \frac{\beta_I^{K_I}}{\Gamma(K_I)} x^{K_I - 1} e^{-\beta x} \frac{(\lambda x)^k}{k!} e^{-\lambda x} dx \\ &= \int_0^\infty \frac{(\beta_I + \lambda)^{K_I + k}}{\Gamma(K_I + k)} x^{K_I + k - 1} e^{-(\beta_I + \lambda)x} dx \left(\frac{\lambda^k}{k!} \frac{\beta^{K_I}}{\Gamma(K_I)} \frac{\Gamma(K_I + k)}{(\beta_I + \lambda)^{K_I + k}} \right) \\ &= \binom{K_I + k - 1}{k} \left(\frac{\beta_I}{\beta_I + \lambda} \right)^{K_I} \left(\frac{\lambda}{\beta_I + \lambda} \right)^k \end{aligned}$$

We conclude that $\xi(\infty)$ has a negative binomial probability function, $\xi(\infty) \sim \text{Nbin}\left(K_L, \left(\frac{\beta_I}{\beta_I + \lambda} \right) \right)$. The probability generating function $E[(1-\pi)^{\xi(\infty)}]$ is then, (Gut, 1995),

$$\begin{aligned} E[(1-\pi)^{\xi(\infty)}] &= \left(\frac{\frac{\beta_I}{\beta_I + \lambda}}{1 - \frac{\lambda}{\beta_I + \lambda}(1 - \pi)} \right)^{K_I} \\ &= \left(\frac{\beta_I}{\beta_I + \lambda - \lambda(1 - \pi)} \right)^{K_I} \\ &= \left(\frac{1}{1 + \pi \frac{(\lambda)}{\beta_I}} \right)^{K_I}. \end{aligned} \tag{A.2}$$

It hence follows that (A.1) can be expressed as

$$\left(\frac{1}{1 + \pi \frac{(\lambda)}{\beta_I}} \right)^{K_I} + \pi = 1, \qquad 0 < \pi < 1, \tag{A.3}$$

As we want to establish a relation between π and the coefficient of variation of I, CV_I, we rewrite (A.3), defining $E[I] = 1$ without any restriction and using that

$$\begin{cases} E[I] = \frac{K_I}{\beta_I} \\ Var(I) = \frac{K_I}{\beta_I^2} \\ CV_I = \frac{\sqrt{Var(I)}}{E[I]} = \frac{1}{\sqrt{K_I}} \\ R_0 = \lambda E[I] = \lambda \end{cases}$$

by definition of the gamma distribution, as

$$\pi + \left(\frac{1}{1 + \pi R_0 C V_I^2} \right)^{CV_I^{-2}} = 1, \qquad 0 < \pi < 1. \tag{A.4}$$

To be determine how π depends on CV_I, we define a function $G(\pi, CV_I) = (\pi-1)(1+\pi R_0 CV_I^2)^{CV_I^{-2}}+1$ on the set $D = \{(\pi, CV_I)|\ 0 < \pi < 1,\ 0 < CV_I \leqslant 1\}$, where $G = 0$ is relation (A.4) rewritten. If we can show that $G'_\pi \neq 0$ on $G = 0$, applying the Implicit Function Theorem (Persson and Böiers, 2001) gives that there exist an implicit function $h(\cdot)$ such that $\pi = h(CV_I)$ and

$$h'(CV_I) = -\frac{G'_{CV_I}}{G'_\pi}. \tag{A.5}$$

We have that

$$\begin{aligned} G'_\pi &= (1+\pi R_0 CV_I^2)^{CV_I^{-2}} + (\pi-1)(1+\pi R_0 CV_I^2)^{CV_I^{-2}-1} R_0 \\ &= (1+\pi R_0 CV_I^2)^{CV_I^{-2}-1}(1+\pi R_0 CV_I^2 + \pi R_0 - R_0), \end{aligned} \tag{A.6}$$

thus $G'_\pi = 0$ when

$$1+\pi R_0 CV_I^2 + \pi R_0 - R_0 = 0. \tag{A.7}$$

Simple algebra gives, from rewriting $G = 0$, that $R_0 = \frac{(1-\pi)^{-CV_I^2}-1}{\pi CV_I^2}$. Thus (A.7) can be reformulated as

$$1+\pi\frac{(1-\pi)^{-CV_I^2}-1}{\pi CV_I^2}CV_I^2+\pi\frac{(1-\pi)^{-CV_I^2}-1}{\pi CV_I^2}-\frac{(1-\pi)^{-CV_I^2}-1}{\pi CV_I^2} = 0, \tag{A.8}$$

or, after some algebra, as

$$\frac{\pi(CV_I^2+1)-1+(1-\pi)^{CV_I^2+1}}{(\pi CV_I^2)(1-\pi)^{CV_I^2}} = 0. \tag{A.9}$$

We the define $q = CV_I^2 + 1$, $1 < q < 2$, and $A(\pi) = \pi q - 1 + (1-\pi)^q$, with $A(0) = 0q + (1-0)^q - 1 = 1 - 1 = 0$. As $A'_\pi = q - q(1-\pi)^{q-1} > 0$ when $0 < \pi < 1$, and $A(0) = 0$, $A(\pi) > 0$ for $0 < \pi < 1$. As a consequence, (A.9) does not hold on D. Thus, $G'_\pi \neq 0$ on D, and in particular on the curve $G = 0$. It hence follows, since G'_π is continuous on $G = 0$, that G'_π does not change sign on $G = 0$. As $\pi = 1 - \frac{1}{R_0} > 0$ when $CV_I = 1$, from rewriting $G(\pi, 1) = 0$, and $G'_\pi(1-\frac{1}{R_0}, 1) > 0$, we conclude that $G'_\pi > 0$ on the curve $G = 0$. Furthermore,

$$\begin{aligned} G'_{CV_I} &= (\pi-1)(1+\pi R_0 CV_I^2)^{CV_I^{-2}} \\ &\quad \times\Big[-2CV_I \ln(1+\pi R_0 CV_I^2) - \frac{CV_I^2}{(1+\pi R_0 CV_I^2)}\Big] \\ &= (\pi-1)(1+\pi R_0 CV_I^2)^{CV_I^{-2}}(-2CV_I^{-1}) \\ &\quad \times\Big[\ln(1+\pi R_0 CV_I^2) - \frac{\pi R_0 CV_I^2}{(1+\pi R_0 CV_I^2)}\Big] \\ &\quad > 0 \end{aligned} \tag{A.10}$$

since $\pi < 1$ and, $\ln(x) - \frac{x}{1+x} > 0$ for $x > 0$, here $x = \pi R_0 CV_I^2$. We finally get from (A.5) that $h'(CV_I) < 0$, which is, π is a decreasing function of CV_I.

A.2 Outbreak probability with a stochastic contact rate

Next, we want to derive an expression for the outbreak probability, π, within a more general model, assuming the contact rate, Λ, is random instead of being deterministic. We model Λ as a Pareto distributed random variable, $\Lambda \sim Pa(m, \phi)$, independent of the infectious period I. As for the simpler model, we need to express (A.1) explicitly. We start with the probability generating function $E[(1-\pi)^{\xi(\infty)}]$ from (A.1), recalling that the number of produced infections, $\xi(\infty)$, is poisson distributed.

$$\begin{aligned} E[(1-\pi)^{\xi(\infty)}] &= \sum_{k=0}^{\infty} P(\xi(\infty)=k)(1-\pi)^k \\ &= \sum_{k=0}^{\infty} E[P(\xi(\infty)=k|I,\Lambda)](1-\pi)^k \\ &= \sum_{k=0}^{\infty} \Big[\int_m^{\infty} \Big(\int_0^{\infty} f_I(x) \frac{(x\lambda)^k}{k!} e^{-\lambda x} dx \Big) f_\Lambda(\lambda)\ d\lambda \ \Big] (1-\pi)^k \\ &= \int_m^{\infty} \Big[\sum_{k=0}^{\infty} \Big(\int_0^{\infty} f_I(x) \frac{(x\lambda)^k}{k!} e^{-\lambda x} dx \Big)\ (1-\pi)^k \Big] f_\Lambda(\lambda) d\lambda, \quad \text{(A.11)} \end{aligned}$$

where interchangeability of summands an integrals, of integrable functions, motivates the last equality. We have from (A.2) that (A.11) simplifies to

$$\begin{aligned} E[(1-\pi)^{\xi(\infty)}] &= \int_m^{\infty} \left(\frac{1}{1+\pi\frac{\lambda}{\beta_I}} \right)^{K_I} f_\Lambda(\lambda) d\lambda \\ &= \int_m^{\infty} \left(1+\lambda\frac{\pi}{\beta_I} \right)^{-K_I} \frac{\phi m^\phi}{\lambda^{\phi+1}}\ d\lambda, \end{aligned}$$

which, by defining

$$\begin{cases} x = \lambda\frac{\pi}{\beta_I} \\ c = \frac{m\pi}{\beta_I}, \end{cases}$$

and substitute λ by x, gives

$$\begin{aligned} E[(1-\pi)^{\xi(\infty)}] &= \int_{m\frac{\pi}{\beta_I}}^{\infty} (1+x)^{-K_I} \frac{\phi m^\phi}{\left(\frac{x\beta_I}{\pi}\right)^{\phi+1}} \frac{\beta_I}{\pi}\ dx \\ &= \phi\Big(\frac{m\pi}{\beta_I}\Big)^{\phi} \int_c^{\infty} (1+x)^{-K_I} x^{-\phi-1}\ dx. \quad \text{(A.12)} \end{aligned}$$

An explicit expression for (A.12) is derived, at first through iterated partial integration, where K_I from the gamma distribution of the latency period is

$K_I = 3, 4 \ldots$. We perform the two first partial integrations as follows.

$$\begin{aligned}\int_c^\infty (1+x)^{-K_I} x^{-\phi-1}\, dx &= \frac{(1+c)^{-K_I+1}}{(K_I-1)} c^{-\phi-1} \\ &\quad - \int_c^\infty \frac{(1+x)^{-K_I+1}}{(K_I-1)} (\phi+1) x^{-\phi-2} dx \\ &= \frac{(1+c)^{-K_I+1}}{(K_I-1)} c^{-\phi-1} - \\ &\quad - \frac{(1+c)^{-K_I+2}}{(K_I-2)(K_I-1)} (\phi+1) c^{-\phi-2} + \\ &\quad + \int_c^\infty \frac{(1+x)^{-K_I+2}}{(K_I-1)(K_I-2)} (\phi+1)(\phi+2) x^{-\phi-3} dx. \end{aligned} \quad \text{(A.13)}$$

This pattern suggests that the left hand side of (A.13), $K_I - 1$ times partially integrated, satisfy

$$\int_c^\infty (1+x)^{-K_I} x^{-\phi-1}\, dx = \sum_{i=2}^{K_I} a(i)(-1)^{K_I-i} + S(-1)^{K_I-1},\ 2 \leqslant K_I, \quad \text{(A.14)}$$

where

$$a(i) = \frac{1}{(K_I - i + 1)} \frac{\binom{K_I+\phi-i}{\phi}}{\binom{K_I-1}{i-2}} (1+c)^{-(i-1)} c^{-(\phi+K_I-i+1)}$$

and

$$S = \binom{K_I + \phi - 1}{\phi} \int_c^\infty (1+x)^{-1} x^{-(\phi+K_I)} dx.$$

It remains to solve S, which is done using partial fraction expansion as follows.

$$\begin{aligned}\int_c^\infty (1+x)^{-1} x^{-(\phi+K_I)} dx &= \int_c^\infty \frac{1}{(1+x)x^{(\phi+K_I)}} dx \\ &= \int_c^\infty \frac{Bx^{\phi+K_I} + \sum_{i=1}^{\phi+K_I} (1+x) A_i x^{\phi+K_I-i}}{(1+x)x^{\phi+K_I}} dx \quad \text{(A.15)} \\ &= \int_c^\infty \Big(\frac{B}{(1+x)} + \sum_{i=1}^{\phi+K_I} \frac{A_i}{x^i} \Big) dx,\end{aligned}$$

where B and $A_1, A_2, \ldots, A_{\phi+K_I}$ are constants satisfying

$$\begin{cases} A_{\phi+K_I} = 1 \\ A_{\phi+K_I} + A_{\phi+K_I-1} = 0 \quad \Rightarrow \quad A_{\phi+K_I-1} = -1 \\ A_{\phi+K_I-1} + A_{\phi+K_I-2} = 0 \quad \Rightarrow \quad A_{\phi+K_I-2} = 1 \\ \vdots \\ A_k = (-1)^{\phi+K_I-k}, \quad k \in (1, \phi + K_I) \\ \vdots \\ A_1 = (-1)^{\phi+K_I-1} \\ A_1 + B = 0 \quad \Rightarrow \quad B = (-1)^{\phi+K_I}. \end{cases}$$

forced by (A.15). It hence follows that (A.15) can be reformulated as

$$\begin{aligned} S &= \binom{K_I + \phi - 1}{\phi} \int_c^\infty \left(\frac{(-1)^{\phi+K_I}}{(1+x)} + \sum_{i=1}^{\phi+K_I} \frac{(-1)^{\phi+K_I-i}}{x^i} \right) dx \\ &= \binom{K_I + \phi - 1}{\phi} \left[(-1)^{\phi+K_I} \ln\left(\frac{1+x}{x}\right) + \sum_{i=2}^{\phi+K_I} \frac{(-1)^{\phi+K_I-i+1}}{(i-1)x^{i-1}} \right]_c^\infty . \end{aligned} \quad \text{(A.16)}$$

As we change index from i $\rightarrow$ j, defining $j = i - 1$, and use the fact that $\lim_{t\to\infty} \ln\left(\frac{1+t}{t}\right) = \ln(1) = 0$, we have from (A.16) that

$$S = \binom{K_I + \phi - 1}{\phi} (-1)^{\phi+K_I+1} \left(\ln\left(1 + \frac{1}{c}\right) + \sum_{j=1}^{\phi+K_I-1} \frac{(-1)^j}{jc^j} \right), \quad \text{(A.17)}$$

which yields, from (A.14), recalling the definition of c, when $2 \leqslant K_I$, that

$$\begin{aligned} E[(1-\pi)^{\xi(\infty)}] &= \phi\Big(\frac{m\pi}{\beta_I}\Big)^\phi \left[\sum_{i=2}^{K_I} \frac{\left(\frac{m\pi}{\beta_I}\right)^{-(\phi+K_I-i+1)}}{(K_I - i + 1)} \frac{\binom{K_I+\phi-i}{\phi}}{\binom{K_I-1}{i-2}} \left(1 + \frac{m\pi}{\beta_I}\right)^{-(i-1)} (-1)^{K_I-i} \right. \\ &\quad \left. + (-1)^\phi \binom{K_I + \phi - 1}{\phi} \left(\ln\left(1 + \frac{\beta_I}{m\pi}\right) + \sum_{j=1}^{\phi+K_I-1} \frac{1}{j} \Big(\frac{-\beta_I}{m\pi}\Big)^j \right) \right]. \end{aligned} \quad \text{(A.18)}$$

When $K_I = 1$, which implies that the infectious period I is exponentially distributed, we have that

$$E[(1-\pi)^{\xi(\infty)}] = \phi\Big(\frac{-m\pi}{\beta_I}\Big)^\phi \left[\ln\left(1 + \frac{\beta_I}{m\pi}\right) + \sum_{j=1}^{\phi} \frac{1}{j} \Big(\frac{-\beta_I}{m\pi}\Big)^j \right]. \quad \text{(A.19)}$$

The outbreak probability π is then solved numerically from (A.1), with the explicit expression for $E[(1-\pi)^{\xi(\infty)}]$ from (A.18) or (A.19), depending on whether K_I is equal to, or larger than 1.

We want to establish how π depend on the coefficient of variation of the product of I and Λ, $CV_{I\Lambda} = \frac{\sqrt{Var(I\Lambda)}}{E[I\Lambda]}$. From the independence of I and Λ, it follows that

$$\begin{cases} Var(I\Lambda) = Var(I)Var(\Lambda) + Var(I)E[\Lambda]^2 + E[I]^2 Var(\Lambda) \\ R_0 = E[I\Lambda] = E[I]E[\Lambda], \end{cases}$$

where the first equality is relies on the result stated by Bohrnstedt and Goldberger (1969), concerning the variance of a product of two stochastically independent random variables. As in the previous sections, $E[I]$ is set to 1, which yields, recalling the expressions for the mean and the variance from the Pareto distribution and the gamma distribution, that

$$\begin{aligned} CV_{I\Lambda} &= \frac{\sqrt{\frac{R_0^2}{K_I\phi(\phi-2)} + \frac{R_0^2}{K_I} + \frac{R_0^2}{\phi(\phi-2)}}}{R_0} \\ &= \sqrt{\frac{1+\phi(\phi-2)+K_I}{\phi(\phi-2)K_I}}, \qquad \phi = 3, 4, \ldots \; K_I = 1, 2, \ldots . \end{aligned} \tag{A.20}$$

When comparing π derived within this model, with π derived within simpler model, where the contact rate Λ is deterministic, we need to keep R_0 fixed. As a consequence, the parameter m from the Pareto distribution describing the random Λ, is determined by R_0 and ϕ through $m = \frac{R_0(\phi-1)}{\phi}$.

The coefficient of variation of $CV_{I\Lambda}$, with unspecified distribution functions of I and Λ, is derived as follows.

$$\begin{aligned} CV_{I\Lambda} &= \frac{\sqrt{Var(I\Lambda)}}{E[I\Lambda]} \\ &= \frac{\sqrt{Var(I)Var(\Lambda) + Var(I)E[\Lambda]^2 + E[I]^2 Var(\Lambda)}}{E[I]E[\Lambda]} \\ &= \frac{\sqrt{Var(I)Var(\Lambda)(1 + \frac{E[\Lambda]^2}{Var(I)} + \frac{E[I]^2}{Var(\Lambda)})}}{E[I]E[\Lambda]} \\ &= CV_I CV_\Lambda \sqrt{1 + (CV_I)^{-2} + (CV_\Lambda)^{-2}} \end{aligned} \tag{A.21}$$

A.3 The Malthusian parameter.

The Malthusian parameter, α, is the solution to

$$\int_0^\infty e^{-\alpha t} \mu'(t) dt = 1, \tag{A.22}$$

stated in Section 2.4, where we also defined $\mu'(t)$, the mean number of produced infections during $(t, t+dt)$, as $\mu'(t) = \lambda P(L < t < L + I)$, when the contact rate is λ, the infectious period I and the latency period L. We begin by deriving an explicit expression for $\mu'(t)$ as follows.

$$\begin{aligned}\mu'(t) &= \lambda P(L < t < L + I) \\ &= \Lambda \int_0^t (1 - F_I(t-z)) f_L(z) dz, \end{aligned} \tag{A.23}$$

where the infectious period I and the latency period L are gamma distributed, $I \sim \Gamma(K_I, \beta_I)$ and $L \sim \Gamma(K_L, \beta_L)$. We use the fact that K_I is a positive integer to rewrite $F_I(t-y)$, (when K_I is an positive integer, we have that I has a Erlang distribution function), which yields that (A.23) can be expressed as, (Ross, 2002),

$$\begin{aligned}\mu'(t) &= \lambda \int_0^t \left(e^{-\beta_I (t-z)} \sum_{j=0}^{K_I - 1} \frac{(\beta_I (t-z))^j}{j!} \right) \frac{\beta_L^{K_L}}{\Gamma(K_L)} z^{K_L - 1} e^{-\beta_L z} dz \\ &= \lambda e^{-\beta_I t} \frac{\beta_L^{K_L}}{\Gamma(K_L)} \sum_{j=0}^{K_I - 1} \frac{\beta_I^j}{j!} \int_0^t e^{\beta_I z} (t-z)^j z^{K_L - 1} e^{-\beta_L z} dz \qquad \text{(A.24)} \\ &= \lambda e^{-\beta_I t} \frac{\beta_L^{K_L}}{\Gamma(K_L)} \sum_{j=0}^{K_I - 1} \frac{\beta_I^j}{j!} t^{K_L + j} \int_0^1 e^{yt(\beta_I - \beta_L)} y^{K_L - 1} (1-y)^j dy, \qquad \text{(A.25)} \end{aligned}$$

where the third equality follows from substitution of z by $\frac{y}{t}$. We let Y_j be a beta distributed random variable, $Y_j \sim \text{Beta}(K_L, j+1)$, with associated beta function $\text{B}(K_L, j+1) = \frac{\Gamma(K_L)\Gamma(j+1)}{\Gamma(K_L + j + 1)}$. Then (A.25) simplifies to

$$\mu'(t) = \lambda\, e^{-\beta_I t} \frac{\beta_L^{K_L}}{\Gamma(K_L)} \sum_{j=0}^{K_I - 1} \frac{\beta_I^j}{j!} t^{K_L + j} B(K_L, j+1) E[e^{Y_j t(\beta_I - \beta_L)}]. \tag{A.26}$$

The moment generating function of Y_j in (A.26), $E[e^{Y_j t(\beta_I - \beta_L)}]$, is calculated as follows.

$$\begin{aligned} E[e^{Y_j t(\beta_I - \beta_L)}] &= \int_0^1 \frac{\Gamma(K_L + j + 1)}{\Gamma(K_L)\Gamma(j+1)} y^{K_L - 1} (1-y)^j e^{Y_j t(\beta_I - \beta_L)} dy \\ &= \int_0^1 \frac{\Gamma(K_L + j + 1)}{\Gamma(K_L)\Gamma(j+1)} y^{K_L - 1} (1-y)^j \sum_{k=0}^{\infty} \frac{(yt(\beta_I - \beta_L))^k}{k!} dy \\ &= \sum_{k=0}^{\infty} \frac{\Gamma(K_L + k)\Gamma(K_L + j + 1)}{\Gamma(K_L)\Gamma(K_L + k + j + 1)} \frac{(t(\beta_I - \beta_L))^k}{k!} \times \\ &\quad \times \int_0^1 \frac{\Gamma(K_L + k + j + 1)}{\Gamma(K_L + k)\Gamma(j+1)} y^{K_L + k - 1} (1-y)^j dy \\ &= 1 + \sum_{k=0}^{\infty} \prod_{r=0}^{k-1} \left(\frac{K_L + r}{K_L + j + 1 + r} \right) \frac{(t(\beta_I - \beta_L))^k}{k!} \end{aligned}$$

Then we get the final expression for $\mu'(t)$ as

$$\begin{aligned}\mu'(t) &= \lambda\, e^{-\beta_I t}\frac{\beta_L^{K_L}}{\Gamma(K_L)}\sum_{j=0}^{K_I-1}\frac{\beta_I^j}{j!}t^{K_L+j}B(K_L,j+1)+\\ &\quad+\lambda\, e^{-\beta_I t}\frac{\beta_L^{K_L}}{\Gamma(K_L)}\sum_{j=0}^{K_I-1}\frac{\beta_I^j}{j!}t^{K_L+j}B(K_L,j+1)\sum_{k=0}^{\infty}\prod_{r=0}^{k-1}\left(\frac{K_L+r}{K_L+j+1+r}\right)\frac{(t(\beta_I-\beta_L))^k}{k!}\end{aligned}$$

We are now able to rewrite the right side of (A.22), splitting the integral into two parts, as

$$\begin{aligned}\int_0^\infty e^{-\alpha}\mu'(t)dt &= \lambda\frac{\beta_L^{K_L}}{\Gamma(K_L)}\sum_{j=0}^{K_I-1}\frac{\beta_I^j}{j!}B(K_L,j+1)\int_0^\infty e^{-(\alpha+\beta_I)t}\ t^{K_L+j}dt+\\ &\quad+\lambda\frac{\beta_L^{K_L}}{\Gamma(K_L)}\sum_{j=0}^{K_I-1}\frac{\beta_I^j}{j!}B(K_L,j+1)\sum_{k=1}^{\infty}\left(\prod_{r=0}^{k-1}\frac{K_L+r}{K_L+j+1+r}\right)\times\\ &\quad\times\frac{(\beta_I-\beta_L)^k}{k!}\int_0^\infty e^{-(\alpha+\beta_I)t}\ t^{K_L+j+k}dt \qquad\text{(A.27)}\end{aligned}$$

The two integrals of the right hand side of (A.27) are positive moments of exponential random variables, which can be expressed using the formula by Gut (1995). Then, with the beta functions and gamma functions expressed using factorials, we rewrite (A.27) as

$$\begin{aligned}\int_0^\infty e^{-\alpha}\mu'(t)dt &= \lambda\frac{\beta_L^{K_L}}{(K_L-1)!}\sum_{j=0}^{K_I-1}\frac{\beta_I^j}{j!}\frac{(K_L-1)!j!}{(K_L+j)!}\left(\frac{(K_L+j)!}{(\beta_I+\alpha)^{K_L+j+1}}\right)+\\ &\quad+\lambda\frac{\beta_L^{K_L}}{(K_L-1)!}\sum_{j=0}^{K_I-1}\frac{\beta_I^j}{j!}\frac{(K_L-1)!j!}{(K_L+j)!}\sum_{k=1}^{\infty}\left(\frac{(K_L+k-1)!(K_L+j)!}{(K_L-1)!(K_L+j+k)!}\right)\times\\ &\quad\times\frac{(\beta_I-\beta_L)^k}{k!}\left(\frac{(K_L+j+k)!}{(\beta_I+\alpha)^{K_L+j+k+1}}\right). \qquad\text{(A.28)}\end{aligned}$$

After some regrouping, and by putting together the factorials into a binomial coefficient, (A.28) simplifies to

$$\begin{aligned}\int_0^\infty e^{-\alpha}\mu'(t)dt &= \lambda\frac{\beta_L^{K_L}}{(\beta_I+\alpha)^{K_L+1}}\sum_{j=0}^{K_I-1}\left(\frac{\beta_I}{\beta_I+\alpha}\right)^j\left(1+\sum_{k=1}^{\infty}\binom{K_L+k-1}{k}\left(\frac{\beta_I-\beta_L}{\beta_I+\alpha}\right)^k\right)\\ &= \lambda\frac{\beta_L^{K_L}}{(\beta_I+\alpha)^{K_L+1}}\sum_{j=0}^{K_I-1}\left(\frac{\beta_I}{\beta_I+\alpha}\right)^j\sum_{k=0}^{\infty}\binom{K_L+k-1}{k}\left(\frac{\beta_I-\beta_L}{\beta_I+\alpha}\right)^k. \qquad\text{(A.29)}\end{aligned}$$

The geometric sum in (A.29) is simplified using the standard formula, and the combinatorial sum using the formula stated by Grimaldi (2003), which

yields

$$\begin{aligned}\int_0^\infty e^{-\alpha}\mu'(t)dt &= \lambda\frac{\beta_L^{K_L}}{(\beta_I+\alpha)^{K_L+1}}\frac{1-\left(\frac{\beta_I}{\beta_I+\alpha}\right)^{K_I}}{1-\left(\frac{\beta_I}{\beta_I+\alpha}\right)}\frac{1}{\left(1-\left(\frac{\beta_I-\beta_L}{\beta_I+\alpha}\right)\right)^{K_L}} \\ &= \left(\frac{\lambda}{\alpha}\right)\left(\frac{\beta_L}{\beta_L+\alpha}\right)^{K_L}\left(1-\left(\frac{\beta_I}{\beta_I+\alpha}\right)^{K_I}\right).\end{aligned}$$

Finally, (A.22) is formulated as

$$\left(\frac{\left(\lambda\right)}{\alpha}\right)\left(\frac{\beta_L}{\beta_L+\alpha}\right)^{K_L}\left(1-\left(\frac{\beta_I}{\beta_I+\alpha}\right)^{K_I}\right)=1. \tag{A.30}$$

We rewrite (A.30) in terms of CV_I and CV_I, using that

$$\begin{cases} E[I]=\frac{K_I}{\beta_I} \\ Var(I)=\frac{K_I}{\beta_I^2} \\ E[L]=\frac{K_L}{\beta_L} \\ Var(L)=\frac{K_L}{\beta_L^2} \\ CV_I=\frac{\sqrt{Var(I)}}{E[I]} \\ CV_L=\frac{\sqrt{Var(L)}}{E[L]} \\ R_0=\lambda E[I], \end{cases}$$

by definition of the gamma distribution, with $E[I]=1$ without any restriction, and

$$\begin{cases} K_I=(CV_I)^{-2} \\ K_L=(CV_L)^{-2} \\ \beta_L=\frac{(CV_L)^{-2}}{E[L]} \\ R_0=\lambda \end{cases} \tag{A.31}$$

as

$$\left(\frac{R_0}{\alpha}\right)\left(1+\alpha CV_L^2E[L]\right)^{-CV_L^{-2}}\left(1-\left(1+\alpha CV_I^2\right)^{-CV_I^{-2}}\right)=1, \tag{A.32}$$

which is stated in (3.2).

To derive how α depend on CV_L, $E[L]$, and CV_I, independently, we begin by defining the function

$$F(\alpha, CV_L, E[L], CV_I) = \int_0^\infty e^{-\alpha t}\mu'(t)dt - 1, \tag{A.33}$$

on the set $\Omega = \{(\alpha, CV_L, E[L], CV_I,)|\ 1 < \alpha,\ 0 < CV_L \leq 1,\ 0 < E[L],\ 0 < CV_I \leq 1\}$. When we want the relation between α and CV_L, we simply view the other variables as constant and so on. Then $F = 0$ can be regarded as a collection of level curves representing relation (A.22). We begin by deriving the relation between α and CV_L. We have that

$$\begin{aligned} F'_\alpha &= -\int_0^\infty te^{-\alpha t}\mu'(t)dt \\ &< 0. \end{aligned} \tag{A.34}$$

Since F is continuous on Ω, and from (A.34) $F'_\alpha \neq 0$ on Ω, it follows from Implicit Function Theorem (Böiers and Persson, 2001) that there exists an implicit function $f_1(\cdot)$ such that $\alpha = f_1(CV_L)$, and

$$f'_1(CV_L) = -\frac{F'_{CV_L}}{F'_\alpha}, \tag{A.35}$$

on Ω and specially on $F = 0$. Furthermore, we have from using the explicit expression for relation (A.22), (A.32), that

$$\begin{aligned} F'_{CV_L} &= \left(\frac{R_0}{\alpha}\right)\left(1 + \alpha CV_L^2 E[L]\right)^{-CV_L^{-2}}\left(1 - \left(1 + \alpha CV_I^2\right)^{-CV_I^{-2}}\right) \\ &\quad \times \left[2CV_L^{-3}\ln(1 + \alpha CV_L^2 E[L]) - \frac{CV_L^{-2}\alpha 2CV_L E[L]}{1 + \alpha CV_L^2 E[L]}\right] \\ &= 2CV_L^{-3}\left[\ln(1 + \alpha CV_L^2 E[L]) - \frac{\alpha CV_L^2 E[L]}{1 + \alpha CV_L^2 E[L]}\right] \\ &> 0. \end{aligned} \tag{A.36}$$

In the second equality we use (A.32), and the inequality follow since function $ln(1 + x) - \frac{x}{1+x} > 0$ when $0 < x$, here $x = \alpha CV_L^2 E[L]$. We conclude that $F'_{CV_I} > 0$ and $F'_\alpha < 0$ on the curve $F = 0$. Thus, from (A.35), it follows that $f'_1(CV_L) > 0$. As a consequence, α is a increasing function of CV_L. The relation between α and CV_I is derived in the same fashion. We have from

(A.32) that

$$\begin{aligned} F'_{CV_I} &= -\Big(\frac{R_0}{\alpha}\Big)\left(1+\alpha CV_L^2 E[L]\right)^{-CV_L^{-2}}\left(1+\alpha CV_I^2\right)^{-CV_I^{-2}} \\ &\quad \times 2CV_I^{-3}\left[\ln(1+\alpha CV_I^2) - \frac{CV_I^2\alpha}{1+\alpha CV_I^2}\right] \\ &< 0, \end{aligned} \tag{A.37}$$

where the inequality is justified by the fact that $ln(1+x) - \frac{x}{1+x} > 0$ when $0 > x$, here $x = \alpha CV_I^2$. We conclude by the same reasoning as above that there exists an implicit function $f_2(\cdot)$ such that $\alpha = f_2(CV_I)$, and from (A.35), using (A.34), that $g'(CV_I) < 0$. Thus, α is a decreasing function of CV_I. Finally we derive the relation between α and $E[L]$ in the same fashion. We have that

$$\begin{aligned} F'_{E[L]} &= -R_0\left(1+\alpha CV_L^2 E[L]\right)^{-CV_L^{-2}}\left(1-\left(1+\alpha CV_I^2\right)^{-CV_I^{-2}}\right) \\ &< 0, \end{aligned}$$

which gives, using (A.34), from (A.35), that there exists a function $f_3(\cdot)$ such that $\alpha = f_3(E[L])$ and $f'_3(E[L]) < 0$. Thus, α is a decreasing function of $E[L]$.