

## On the Qualitative Behaviour of SIR Epidemics with Generalized Infection Rate Functions

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We consider an SIR stochastic epidemic model in which new infection occurs at rate  $f_n(x, y)$ , where  $x$  and  $y$  are respectively the number of susceptibles and infectives at time of infection and  $f_n$  is a positive sequence of real functions. Threshold theorems analogous to those of Whittle and Williams are fairly proved for this model. Also we examine the shape of the total size distribution for various values of removal rate and suitable values of other important parameters.

**Keywords:** Epidemic model, generalized infection rate, threshold theorems, total size.

### 1 Introduction

The purpose of this note is to examine the qualitative properties of stochastic models with generalized infection rate in which the population is divided into three classes of individuals: susceptible, infective and removed individuals. This model can be used to model the transmission of complex diseases. Mathematically it is defined as follows. At time  $t$  there are  $X(t)$  susceptibles,  $Y(t)$  infectives and  $n - X(t) - Y(t)$  removed individuals with  $X(0) = n$  and  $Y(0) = a$ . The epidemial process is thus completely determined by  $\{(X(t), Y(t)); t \geq 0\}$ , which is supposed to be a continuous-time Markov process on the state space:  $\mathbf{E}_{n,a} = \{(x, y), 0 \leq x \leq n, 0 \leq y \leq n + a - x\}$  with the transition

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probabilities

$$\left\{ \begin{array}{l} \Pr\left\{ (X(t + \delta t), Y(t + \delta t)) = (x - 1, y + 1) \mid (X(t), Y(t)) = (x, y) \right\} \\ \qquad \qquad \qquad = f_n(x, y)\delta t + o(\delta t), \\ \Pr\left\{ (X(t + \delta t), Y(t + \delta t)) = (x, y - 1) \mid (X(t), Y(t)) = (x, y) \right\} \\ \qquad \qquad \qquad = \mu y \delta t + o(\delta t), \end{array} \right. \quad (1.1)$$

all other transition probabilities are of  $o(\delta t)$  and the parameter  $\mu$  is known as the removal rate. The process terminates when the number of infectives becomes zero, which almost surely happens within a finite time. Throughout this paper we adopt the assumption that  $f_n(x, 0) = f_n(0, y) = 0$  and  $f_n(x, y) > 0$  for  $x > 0$  and  $y > 0$ .

If  $f_n(x, y) = \beta xy$  is chosen, where  $\beta$  is an infection parameter, the model is reduced to the general model (see, e.g., [1, p. 88]). There are two threshold theorems for general epidemics, Whittle's theorem [25] and Williams' theorem [26], that govern the qualitative behaviour of the epidemic. These two theorems are based respectively on the asymptotic approximation of the distribution of the intensity of the epidemic,  $I = n - X(\infty)/n$ , and the total size distribution. These results show that a small change in relative removal rate  $\rho = \mu/\beta$  leads to a qualitative change of the epidemic. They are generalized by Ball and O'Neill [5] and O'Neill [20, 21] to allow the case when  $f_n(x, y) = \beta xy/(x + y)$ .

The above theorems all require that the population size approaches infinity, given that a small finite size is so large that this limiting result is an acceptable approximation. In this situation Näsell [18], using numerical methods, studied the threshold of the epidemic by illustrating the form of the total size distribution.

If we consider the SIR model with generalized infection rate, we claim that the classical theorem of Williams and a fair proof of Whittle's theorem are not yet obtained. Apart from the paper of Gani and Purdue [15] that gives an intuitive proof of Whittle's result, our contribution aims to see how these results can be extended to the model as described by (1.1). Under some condition on the infection rate  $f_n(x, y)$  we give an algebraic proof of Williams' theorem in Section 2, which outlines the explicit formula for the Laplace transforms of the transitions probabilities obtained by El Maroufy and others [11]. In the Section 3 we give a rigorous proof of Whittle's theorem using the coupling method. A qualitative study in the case of small size is examined in the Section 4.

## 2 Williams' Threshold Theorem

In order to establish the Williams threshold theorem for our model we need to restrict the behaviour of the infection rate  $f_n(x, y)$ . For a sufficiently large  $n$  and a suitable choice of  $(x, y)$ ,  $f_n(x, y)$  should be closer to  $\beta(n)y$ , where  $\beta(n)$  is a positive constant that may depend on  $n$ . To this end we now define the class of sequences of functions  $f_n$ .

**Definition 2.1.** Let  $\mathcal{L}$  be the set of all real-valued sequences  $(x_n, n \geq 0)$  for which there exists  $k \in \mathbb{N}$  such that  $|x_n - n| < k$  for all  $n \in \mathbb{N}$ .

**Definition 2.2.** Let  $(f_n)_{n \geq 0}$  be sequences of positive real-valued functions. Then  $(f_n)_{n \geq 0} \in \mathcal{L}_0$  if for all  $(x_n)_{n \geq 0} \in \mathcal{L}$

$$f_n(x_n, y) \sim \beta(n)y \text{ when } n \rightarrow \infty \text{ and } y \in \mathbb{N}. \tag{2.1}$$

Let  $P_{il}(t) = \Pr\{X(t) = i, Y(t) = l\}$  be the probability that the epidemic with the state  $(n, a)$  at time 0 passes to the state  $(i, l)$  at time  $t$  and for  $r = 0, 1, \dots, n$  and let  $\Pi_r$  be the probability of an epidemic with final size  $r$ . By using the explicit form  $\hat{P}_{r0}(v)$  for the Laplace transform of  $P_{r0}(t)$  derived in [11, Theorem 1] we see that for any  $r = 0, \dots, n$

$$\begin{aligned} \Pi_r &= \Pr(n - X(\infty) = r) \\ &= \lim_{t \rightarrow \infty} P_{n-r,0}(t) = \mu \hat{P}_{n-r,1}(0) \\ &= \sum_{L \in \hat{D}_{0a+r}} \mu^{a+r} a! \prod_{w=1}^r \frac{f_n(n-r+w, l_w-w)}{l_w-w} \times \\ &\quad \prod_{(w,k) \in \hat{D}_r} \left[ \mu + \frac{f_n(n-r+w, k+l_w-w)}{k+l_w-w} \right]^{-1}, \tag{2.2} \end{aligned}$$

where

$$\hat{D}_{0a+r} = D_{0a+r} \cap \{(l_1, l_2, \dots, l_r), l_1 > 1, l_2 > 2, \dots, l_r > r\} \text{ and } \hat{D}_r = D_r \setminus \{(0, 0)\}$$

with

$$D_{0a+r} = \{(l_1, l_2, \dots, l_r), 0 \leq l_1 \leq l_2 \leq \dots \leq l_r \leq a+r\}$$

and

$$\hat{D}_r = \{(w, k)/w = 0, \dots, r, k = 0, \dots, l_{w+1} - l_w\}.$$

Since  $(w, k) \in \hat{D}_r$  and  $L = (l_0, \dots, l_r) \in \hat{D}_{0a+r}$ , then  $(x_n)_{n \geq 0} = (n - r + w)_{n \geq 0} \in \mathcal{L}$ . Moreover, if we suppose that  $(f_n)_{n \geq 0} \in \mathcal{L}_0$ , we obtain for sufficiently large  $n$ ,

$$\mu + \frac{f_n(n-r+w, k+l_w-w)}{k+l_w-w} \sim \mu + \beta(n) \text{ and } \frac{f_n(n-r+w, l_w-w)}{l_w-w} \sim \beta(n).$$

By injecting the last two approximations into (2.2) and using the fact that the cardinal  $|\hat{D}_r|$  of  $\hat{D}_r$  is equal to  $2r + a$  it follows that for a sufficiently large  $n$

$$\Pi_r \approx |\hat{D}_{0a+r}| \rho(n)^{a+r} (\rho(n) + 1)^{-(2r+a)}, \tag{2.3}$$

where  $\rho(n) = \mu/\beta(n)$ .

**Lemma 2.1.** For any  $r = 0, \dots, n$

$$|\hat{D}_{0a+r}| = \frac{(2r+a-1)!a}{r!(a+r)!}. \quad (2.4)$$

Let  $\alpha_0, \alpha_1, \dots, \alpha_r$  be the nonnegative numbers such that

$$\alpha_0 = a + r - l_r, \dots, \alpha_w = l_{w+1} - l_w, \dots, \alpha_r = l_r$$

with  $l = (l_0, \dots, l_r) \in \hat{D}_{0a+r}$ . Then the set of vectors  $\alpha = (\alpha_0, \dots, \alpha_r)$  has the same cardinal as the set  $A_r$  defined in [19]. However, according to Foster [14] (see also [5]) the  $A_r$  set is identical to the set of all paths from  $(n, a)$  to  $(n-r, 0)$  when the epidemial process is viewed as a random walk on  $E_{n,a}$ . Then the ballot theorem (Feller [13]) implies that  $|A_r| = \mathcal{C}_r^{2r+a-1}(a/(a+r))$ . It results from (2.3) and (2.4) that

$$\Pi_r \approx \frac{(2r+a-1)!a}{r!(r+a)!} \left( \frac{\rho(n)}{\rho(n)+1} \right)^{a+r} \left( \frac{1}{\rho(n)+1} \right)^r, \quad r = 0, 1, \dots \quad (2.5)$$

With the same algebraic techniques as used by Bailey [1, p. 107] it may be seen that the right member of (2.5) is the  $r$ th term in the expansion of

$$\left( \frac{\{1 + \rho(n) - |\rho(n) - 1|\}}{2} \right)^a = (\min\{1, \rho(n)\})^a$$

and  $\sum_{r=0}^{\infty} \Pi_r = (\min\{1, \rho(n)\})^a$ . So the following result is obtained.

**Theorem 2.1.** Suppose that  $(f_n)_n \in \mathcal{L}_0$ . Then for sufficiently large  $n$  the probability of a minor epidemic is given by

$$\Pr\{\mathbf{T} < \infty\} \approx (\min\{1, \rho(n)\})^a. \quad (2.6)$$

If we suppose that  $f_n(x, y) = \beta xy/(x+y)^\alpha$  for  $\alpha \geq 0$ , then  $(f_n)_n \in \mathcal{L}_0$  so that (2.6) becomes  $\Pr\{T < \infty\} \approx (\min\{1, \rho n^{\alpha-1}\})^a$ . In this case, if  $\alpha = 0$  or  $\alpha = 1$ , the above probability is the same as that obtained respectively by Rajarshi [19] for the general epidemic and by Ball and O'Neill [5] for the modified epidemic.

The limiting distribution is similar to that found by Ball and Näsell [4] and corresponds to the distribution of the final size of the birth-death process with the extinction probability given by (2.6). This interpretation involves that, when  $n$  tends to infinity and  $f_n$  checks the conditions of Definition 2, the epidemic process is approached by a birth and death process with birth rate 1 and death rate  $\rho(n)$  and initial population size  $a$ . So a major epidemic can occur with probability  $1 - \rho(n)$  if and only if  $\rho(n) < 1$ .

### 3 Whittle's Threshold Theorem

In this section we restrict ourselves to the case  $f_n(x, y) = \beta_n(x, y)xy$  with  $\beta_n(x, y) = 0$  if  $x$  or  $y = 0$ , where  $\beta_n$  is a specified function that determines the type of infection

mechanism. It comprises some infection mechanisms mentioned in epidemial literature. For instance Clancy [8] took  $\beta_n(x, y) = \beta/(x + y)^\alpha$  where  $\beta$ , as defined in Dietz [10], is the product of the contact rate and the probability that a successive number of contacts leads to infection and  $\alpha > 0$ . In this case, if  $\alpha = 1$ , this gives the model considered by Gleißner [16], Ball and O'Neill [5] and Sani and others [22]. When  $\alpha = 0$ , the model is reduced to the general epidemial model. The case  $\alpha = 1/2$  was considered by Saunders [23].

In order to give a rigorous proof of Whittle's threshold theorem, we begin by defining our model using a construction due to Sellke [24] (see also [3] and [6]). Label the initial infectives  $-(a - 1), \dots, 0$  and the initial susceptibles  $1, \dots, n$ . Let  $R_{-(a-1)}, \dots, R_0$  and  $R_1, \dots, R_n$  be independent sequences of independent negative exponential random variables with mean  $\mu^{-1}$ . For  $j = -(a - 1), \dots, 0$  the initial infective remains infectious for a period  $R_j$  and it is then removed while for  $j = 1, \dots, n$   $R_j$  is the infectious period of the  $j$ th susceptible to become infected. For  $j = 1, \dots, n$  let  $Q_j$  denote the infection tolerance of susceptible  $j$ , the  $Q_j$  are independent copies of some nonnegative exponential random variables having mean 1 and denoted by  $Q_{(1)} \dots, Q_{(n)}$  the order statistic associated to  $(Q_j, 1 \leq j \leq n)$ .

For  $i = -(a - 1) \dots, 0, 1, \dots, n$ , let  $\tau_j$  be the time of individual  $j$ 's infection, with  $\tau_j = 0$  if  $j = -(a - 1), \dots, 0$ , and  $\tau_j = +\infty$  if susceptible  $j$  avoids infection. For  $t \geq 0$  any remaining infective accumulates exposure to infection at rate  $\beta_n(X, Y)$ . Our epidemic now proceeds as follows: knowing that  $j$  infections occur before  $t$ , the  $j + 1$  susceptible becomes infected when its total exposure to infection (see, e.g. [5] and [6])

$$\chi_j(t) = \int_0^{t_j} \beta_n(X(u), Y(u))Y(u)du \text{ with } t_j = \min \left\{ t, \max_{-(a-1) \leq i \leq j} (\tau_i + R_i) \right\} \quad (3.1)$$

reaches  $Q_{(j+1)}$ . The epidemic ceases as soon as no more infectives are left in the population.

With these arguments the final size of the epidemic is equal to

$$T = \min \{r \in \{0, \dots, n\} : Q_{(r+1)} > \chi_r(\infty)\}. \quad (3.2)$$

Thus

$$\{T \geq k\} = \bigcap_{r=1}^k \{Q_{(r)} \leq \chi_{r-1}(\infty)\} \quad \forall k \in [0, N]. \quad (3.3)$$

We now consider the intensity  $I$  of the epidemic as defined in Section 1. We have for  $t \geq 0$

$$n(1 - \mathbf{I}) \leq X(t) \leq n \text{ and } 0 \leq X(t) + Y(t) \leq n + a \text{ for } t \geq 0$$

and

$$n(1 - \mathbf{I})m_{\mathbf{I}}Y(t) \leq \beta_n(X(t), Y(t))X(t)Y(t) \leq MY(t), \quad (3.4)$$

where  $m_I$  and  $M$  are respectively suitable lower and upper bounds of  $\beta_n(x, y)$  and  $\beta_n(x, y)x$  over the set  $A_I = \{(x, y); n(1 - I) \leq x \leq n \text{ and } 0 \leq x + y \leq n + a\}$  and  $E_{n,a}$  respectively.

Hence it follows from (3.4) that the process can be sandwiched between two other epidemial processes each having removal rate  $\mu$ . The first is slow and the second is fast with the total exposure to infection such that  $j$  infections occur before  $t$ , respectively equal to

$$\check{\chi}_j^I(t) = (1 - I)m_I \int_0^{t_j} \frac{Y(u)}{X(u)} du \tag{3.5}$$

and

$$\hat{\chi}_j(t) = M \int_0^{t_j} \frac{Y(u)}{X(u)} du. \tag{3.6}$$

Hence it follows from (3.1) and (3.4)-(3.6) that

$$\check{\chi}_j^I(\infty) \leq \chi_j(\infty) \leq \hat{\chi}_j(\infty). \tag{3.7}$$

We let  $\check{T}^I = \min\{r \in \{0, \dots, n\} : Q_{(r+1)} > \check{\chi}_r^I(\infty)\}$  and  $\hat{T} = \min\{r \in \{0, \dots, n\} : Q_{(r+1)} > \hat{\chi}_r(\infty)\}$  be, respectively, the final sizes of the two epidemics. Then by (3.3) and (3.7) we find that

$$\{\hat{T} \leq k\} \subseteq \{T \leq K\} \subseteq \{\check{T}^I \leq K\} \text{ for } k \in \mathbb{N}. \tag{3.8}$$

The second inclusion of (3.8) implies for  $i \in ]0, 1[$  that

$$\begin{aligned} \Pr\{T \leq ni\} &= \Pr\{T \leq ni, \check{T}^I \leq ni\} = \Pr\{I \leq i, \check{T}^I \leq ni\} \\ &\leq \Pr\{I \leq i, \check{T}^i \leq ni\} \leq \Pr\{\check{T}^i \leq ni\}, \end{aligned} \tag{3.9}$$

where  $\check{T}^i$  is the final size of the epidemic with infection rate  $n(1 - i)m_i$ .

Combining (3.8) and (3.9) we obtain  $\Pr\{\hat{T} \leq ni\} \leq \Pr\{T \leq ni\} \leq \Pr\{\check{T}^i \leq ni\}$  on the other hand  $\Pr\{\hat{T} \leq ni\} = \Pr\{\hat{T} < \infty\} - \Pr\{ni < \hat{T} < \infty\}$  and, when  $n$  is sufficiently large,  $\Pr\{ni < \hat{T} < \infty\} \approx 0$ . Moreover  $\Pr\{\check{T}^i \leq ni\} \leq \Pr\{\check{T}^i < \infty\}$ . Consequently by considering the following distribution  $\pi_i = \Pr\{I \leq i\} = \Pr\{T \leq ni\} = \sum_{r=0}^{[ni]} \Pi_r$  and using Theorem 2.1 the following result is obtained:

**Theorem 3.1.** *For sufficiently large  $n$*

$$\left(\min\left\{\frac{\mu}{M}, 1\right\}\right)^a \leq \pi_i \leq \left(\min\left\{\frac{\mu}{n(1-i)m_i}, 1\right\}\right)^a. \tag{3.10}$$

The statement in (3.10) constitutes Whittle's stochastic threshold theorem. It may be interpreted by saying that, if  $\mu > M$ , then  $\pi_i = 1$  so that there is zero probability of an epidemic exceeding any intensity  $i \in ]0, 1[$ .

In a particular case such as  $\beta_n(X(t), Y(t)) = \beta n^{\alpha-1}/(X(t) + Y(t))^\alpha$ , where  $\alpha$  is defined as previously, we obtain  $m_i = \beta n^{\alpha-1}/(n + a)^\alpha$  and  $M = \beta$ . Then for sufficiently large  $n$  (3.10) becomes

$$(\min\{\rho, 1\})^a \leq \pi_i \leq \left( \min \left\{ \frac{\rho(n + a)^\alpha}{n^\alpha(1 - i)}, 1 \right\} \right)^a. \tag{3.11}$$

We see in this case that the probability that an epidemic exceeds the size  $ni$  is approximately  $1 - \rho^a$ . When  $\alpha = 1$  and for sufficiently large  $n$ , the upper boundary in (3.10) is close to  $(\min\{1, \rho/(1 - i)\})^a$  which is obtained by Ball and O’Neill [20].

### 4 The Shape of the Total Size Distribution

In this Section we are concerned with the shape of the distribution curve of the total size considering the following particular infection rate

$$f_n(x, y) = \frac{\beta xy}{(x + y)^\alpha} \text{ for } \alpha \geq 0, \tag{4.12}$$

where  $\beta$  and  $\alpha$  are as previously defined. For an epidemial model with particular functions of the infection rate Bailey [1], Ball and O’Neill [5], Nåsell [18] and Clancy [9] give the total size distribution for various values of the removed rate  $\rho$ , remarking that the distribution curve can, for a small number of initial infectives, take one of the two shapes called J-shape and U-shape. The J-shaped curve, i.e. with a mode at the origin or a mode at some small positive value of the argument and decreasing monotonically thereafter, can be interpreted as describing a minor epidemic while the U-shaped curve, i.e. bimodal, is associated to a minor or major epidemic. More extensive results are shown in Figures 4.1-4.3 over a suitable range of  $\alpha$ .

All the probabilities used here were originally calculated using the following two-dimensional recursive equation of the  $g_{i,l} = \lim_{v \rightarrow 0}(v \hat{P}_{il}(v))$ , which are derived from the generalized recursive equations proved by EL Maroufy and Ziad [12, Section 5],

$$g_{n,l} = \mu^{a-l} \frac{a!}{l!} \prod_{k=l}^a (f_n(n, k) + \mu k)^{-1}, \quad l = 1, \dots, a,$$

for  $l = 0, \dots, a$  and

$$g_{i,l} = \sum_{\max(2,l) \leq h \leq n+a-i} \mu^{h-l} \frac{h!}{l!} f_n(i + 1, h - 1) \frac{g_{i+1,h-1}}{\prod_{k=l}^h (\mu k + f_n(i, k))}$$

for  $l = 0, \dots, n + a - i$ . For  $i = 1, \dots, n$  the terms of the distribution of the total size are then given by  $P(T = i) = g_{0,n-i}$ . The two-dimensional system above is perfectly adequate for computing purposes and its implementation is fast and numerically

stable. Since the threshold behaviour of the four epidemics is controlled respectively by  $\rho_0/n$ ,  $\rho_{1/2}/\sqrt{n}$ ,  $\rho_1$  and  $\rho_2 n$ , if we set  $\rho_\alpha = n^{1-\alpha}\rho_1$ ,  $\rho_\alpha$  is above its threshold value  $\rho_\alpha = n^{1-\alpha}$  if and only if  $\rho_1$  is above its threshold  $\rho_1 = 1$ . Under this condition the curves of the total size distribution have the same shape for all four models.

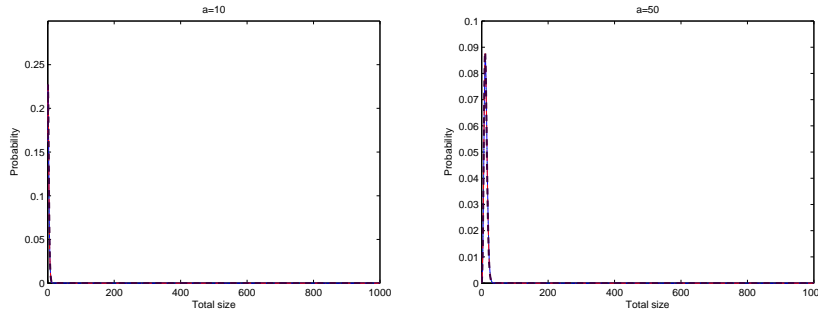


Figure 4.1: Distribution of the final sizes,  $n = 1000$ , —  $\rho_0 = 600$  (representing general model),  $\cdots$   $\rho_{1/2} = 54.7$  (Saunders’s model),  $\cdot\cdot\cdot$   $\rho_1 = 5$  (modified model), —  $\rho_2 = 0.041$ , (our proposed model).

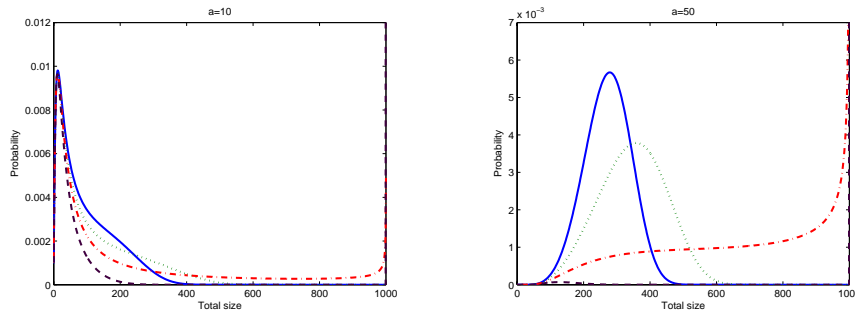


Figure 4.2: Distribution of the final sizes,  $n = 1000$ , —  $\rho_0 = 120$  (representing general model),  $\cdots$   $\rho_{1/2} = 11$  (Saunders’s model),  $\cdot\cdot\cdot$   $\rho_1 = 1$  (modified model), —  $\rho_2 = 0.008$ , (our proposed model)

From Figure 4.1 it is clear that, when  $\rho_\alpha = n^{1-\alpha}$ ,  $\alpha = 0, 1/2, 1, 2$ , is above its threshold, then all curves fall rapidly and tend to be null as the total increases. In other words the curve is J-shaped (Figure 4.1); this illustrates the fact that the epidemic dies out quickly and becomes minor. However, on one hand, when the relative rates  $\rho_0/n$ ,  $\rho_{1/2}/\sqrt{n}$ ,  $\rho_1$  and  $\rho_2 n$  are respectively below their thresholds  $n$ ,  $n^{1/2}$ ,  $1$  and  $n^{-1}$ , the curves are U-shaped (Figure 4.3), but not more pronounced (Figure 4.2,  $a = 10$ ). On the other hand Figure 4.3 illustrates the fact that the epidemic is major with increasing degree  $\alpha$ , in the sense that



there is higher probability of none of the initial susceptibles contracting the disease in the general epidemic and Saunders epidemic than in others.

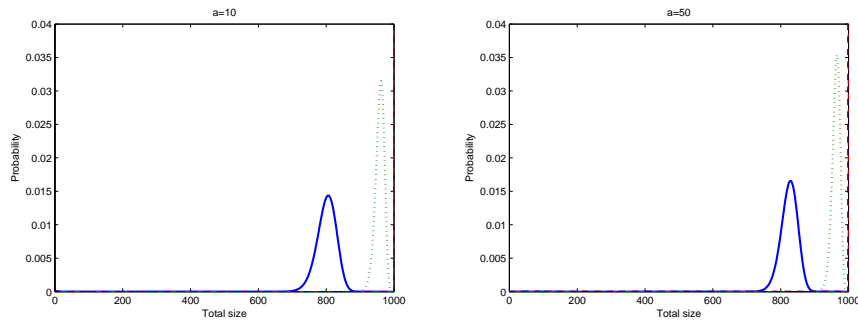


Figure 4.3: Distribution of the final sizes,  $n = 1000$ ,  $— \rho_0 = 60$  (representing general model),  $\cdots \rho_{1/2} = 5.54$ , (Saunders's model)  $- - \rho_1 = 0.5$ , (modified model)  $- \cdot - \rho_2 = 0.0041$ , (our proposed model)

## 5 Conclusions

In this note we have examined the qualitative properties described for an **SIR** epidemic model with a generalized infection mechanism. We may obtain the same result by considering a more generalized removal rate  $\mu_n(x_n, y)$  with  $\mu_n(x_n, y) \sim \mu(n)y$  when  $n$  is sufficiently large for all sequences  $(x_n)_{n \geq 0} \in \mathcal{L}$ . As illustrated in Sections 2 and 3, the method used to prove rigorously Williams' and Wittle's threshold theorems is versatile and can be adapted to various multipopulation SIR epidemic models. This will be investigated in future research.

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