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Diffusion Approximation of Stochastic SIR Epidemic Model

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Abstract

In this work we consider the general stochastic SIR (Susceptible - Infected - Removed) epidemic model with the transition intensity $q_{(S,I),(S-1,I+1)} = \beta g(S)I$, where $g(x)$ is a function density dependent. An approximation of the final size by a diffusion process is given. Finally, I introduce some numerical simulation graphics to illustrate the main result.

Keywords: Epidemic model, Final size, SIR, Stochastic model, Markov process, Density dependent, Diffusion approximation.

2010 Mathematics Subject Classification: 53C25; 83C05; 57N16

1 Introduction

A significant class of simple epidemic models relates to the infectious diseases is the SIR (Susceptible - Infected - Removed) epidemic model (see, Kermack and McKendrick [1]). Their principal characteristics are as follows: a closed population is subdivided in three classes, the susceptible individuals (healthy individuals but exposed to the infection), the infected individuals (individuals carrying the pathogenic matter: virus, parasitic, etc...) and the removed individuals (infected individuals which

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leave their state of infection by immunization, death or quarantine). Each infected individual remains infectious for a random period of time called infection period. During this period, the infected individuals transmit the infectious germs to susceptible individuals which, in this case, become infected and infectious. When the infection period of an individual is finished, he is eliminated from the infection process in a permanent way: according to the type of the disease, the individual cured and immunized, deceased or in a critical state quarantined.
Suppose that initially say at time $t = 0$; there are n susceptible individuals, m infected individuals and 0 removed individuals in the population respectively.
For each $t \in \mathbb{R}^+$, let $S(t)$ and $I(t)$ be the numbers of susceptible individuals and infected individuals at time t and let $R(t)$ the total number of removed individuals in the time interval $[0, t]$.
The population is supposed to be closed. Then for each $t \geq 0$,

$$S(t) + I(t) + R(t) = n + m.$$

Consequently the epidemic is completely described by the dynamic of the process $((S(t), I(t)), t \geq 0)$.
Suppose that $((S(t), I(t)), t \geq 0)$ is a Markov process with the following transition intensities:

$$q_{(S,I),(S-1,I+1)} = \beta g(S)I,$$

$$q_{(S,I),(S,I-1)} = \mu I,$$

where $g(x)$ is density dependent, i.e. $g(x) = ng(x/n)$.
This epidemic process continues until the time

$$\widetilde{T} = \inf\{t \geq 0, I(t) = 0\}$$

which is the time of extinction of the epidemic (an epidemic dies out if there does not remain any more infected in the population). $S_{\widetilde{T}}$ is thus the number of individuals who have escaped from any infectious contact with the infected. The quantity $Z = n - S_{\widetilde{T}}$ indicates the final size of the epidemic. It is the total number of new cases of infection which take place throughout the propagation of the epidemic.
A considerable number of authors interested in the study of the distribution of the final size Z: Bailey [2], Williams [3], Ball [4], Ball and clancy [5], Lindholm [6], Ma and Earn [7], Demiris and O'Neill [8], Gordillo et *al*. [9] and Artalejo et *al* [10]. In the following section, we aim to approximate the epidemic final size distribution, using an approximation diffusion of stochastic SIR epidemic model after a suitable time scale transformation when the number of susceptible n is sufficiently large. In the section 3, a brief discussion and numerical simulations are presented. Finally, we close with a brief conclusion.

2 Diffusion Approximation

In this section, instead of natural numbers $S(t)$ and $I(t)$ of susceptible and infectious individuals, we consider the respective fractions $x(t) = \frac{S(t)}{n}$ and $y(t) = \frac{I(t)}{n}$, and define $\omega(t) = \int_0^t y(u)du$ and transform the time scale to $\omega(t)$ by defining $\tilde{x}(\omega(t)) = x(t)$ and $\tilde{y}(\omega(t)) = y(t)$. Then we can verify that

$$x(\tau) = \tilde{x}(\omega(\tau)) = \tilde{x}(\tilde{\tau})$$

where, $\tau = \inf\{t : y(t) = 0\}$ and $\tilde{\tau} = \inf\{t : \tilde{y}(t) = 0\}$.
The Markov process $((\tilde{x}(t), \tilde{y}(t)), t \geq 0)$ has the initial conditions $\tilde{x}(0) = 1$ and $\tilde{y}(0) = m/n$, and has the following transition probabilities:

$$\begin{cases} P\{(\tilde{x}(t+dt), \tilde{y}(t+dt)) = (x' - \epsilon, y' + \epsilon)/(\tilde{x}(t), \tilde{y}(t)) = (x', y')\} \\ \qquad\qquad = \beta n g(x')dt + o(dt), \\ P\{(\tilde{x}(t+dt), \tilde{y}(t+dt)) = (x', y' - \epsilon)/(\tilde{x}(t), \tilde{y}(t)) = (x', y')\} \\ \qquad\qquad = \mu dt + o(dt). \end{cases} \tag{2.1}$$

with $\epsilon = 1/n$.
One way to characterize the process with the above transition probabilities is by means of Poisson process, see for example Ethier and Kurtz [11].
Let $Y_l = \{Y_l(t), t \geq 0\}$ be independent standard Poisson process defined for each transition $l = (-1, 1)$ and $l = (0, -1)$. Then $(\tilde{x}, \tilde{y})$ can be written as

$$\left\{ \begin{array}{ll} \tilde{x}(t) = & \tilde{x}(0) - \frac{1}{n} Y_{(-1,1)} \left(n\beta \int_0^t g(\tilde{x}(s))ds \right) \\ \tilde{y}(t) = & \tilde{y}(0) + \frac{1}{n} Y_{(-1,1)} \left(n\beta \int_0^t g(\tilde{x}(s))ds \right) - \frac{1}{n} Y_{(0,-1)}(n\mu t) \end{array} \right. \tag{2.2}$$

The form of the generator of $(\tilde{x}, \tilde{y})$ is

$$A_\epsilon h(x, y) = \epsilon^{-1} \beta g(x)(h(x - \epsilon, y + \epsilon) - h(x, y)) + \epsilon^{-1} \mu (h(x, y - \epsilon) - h(x, y))$$

For sufficiently small ϵ the generator A_ϵ is approached by the operator of the following form

$$\begin{aligned} \mathcal{L} &= -\beta g(x) \frac{\partial}{\partial x} + (\beta g(x) - \mu) \frac{\partial}{\partial y} \\ &\quad + \frac{\epsilon}{2} \left[\beta g(x) \frac{\partial^2}{\partial x^2} + \beta g(x) \frac{\partial^2}{\partial y^2} + \mu \frac{\partial^2}{\partial y^2} - 2\beta g(x) \frac{\partial^2}{\partial x \partial y} \right] \\ &= A \nabla + \frac{1}{2} \nabla' \Sigma \nabla \end{aligned}$$

where

$$\nabla = \begin{pmatrix} \frac{\partial}{\partial x} \\ \frac{\partial}{\partial y} \end{pmatrix}, \qquad A = \begin{pmatrix} -\beta g(x) & \beta g(x) - \mu \end{pmatrix}$$

and

$$\Sigma = \epsilon \begin{pmatrix} \beta g(x) & -\beta g(x) \\ -\beta g(x) & \beta g(x) + \mu \end{pmatrix}$$

which corresponds, according to Øksendal [12], to the generator of the Markov process which is the solution of the bivariate SDEs,

$$\left\{ \begin{array}{ll} d\hat{x} = & -\beta g(\hat{x})dt + \sqrt{\frac{\beta g(\hat{x})}{n}} dW_1(t) \\ d\hat{y} = & \beta g(\hat{x})dt - \sqrt{\frac{\beta g(\hat{x})}{n}} dW_1(t) + \sqrt{\frac{\mu}{n}} dW_2(t) \end{array} \right. \tag{2.3}$$

where W_1 and W_2 are independent Brownian motions. Then, we can consider now the stopping time $\hat{\tau} = \inf\{t \geq 0 : \hat{y}(t) = 0\}$ and approximate the final size Z by $\hat{Z} = n - n\hat{x}(\hat{\tau})$. In the following section we will plot the distribution of Z and $\hat{Z}$ on the same figure for some values of β and μ.

3 Numerical Simulations

In this section we made a comparison between the exact distribution of the final size given in [9] and the distribution obtained using the system 2.3 for $p(x) = x$. The exact final size distributions have been determined numerically by programming the algorithm given in [9] in MATLAB. To simulate the diffusion process governed by the system 2.3, we employ the Milstein Scheme (see Kloeden and Platen [13]). The distribution of the final size using diffusion approximation is based on 1000 simulation of system 2.3 until the time of extinction.
Figures 1-6 show the exact distribution of the final size against the approximate distribution for various values of parameters and population size $n = 50$, $n = 100$ and $n = 1000$.
The figures 3-6 show that the final size by the diffusion approximation is well for $n \geq 100$. So the diffusion approximation allows to calculate the final size for n rather large (see figures 7 and 8).

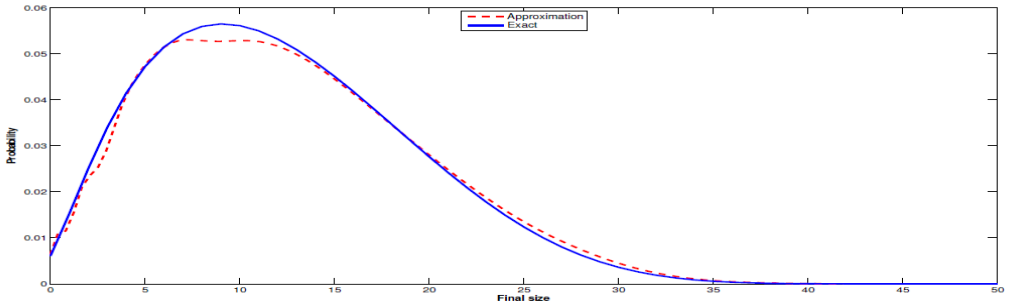

Figure 1: Distribution of the final size and its diffusion approximation, for $n = 50$, $m = 10$, $\beta = 0.2$, $\mu = 0.3$.

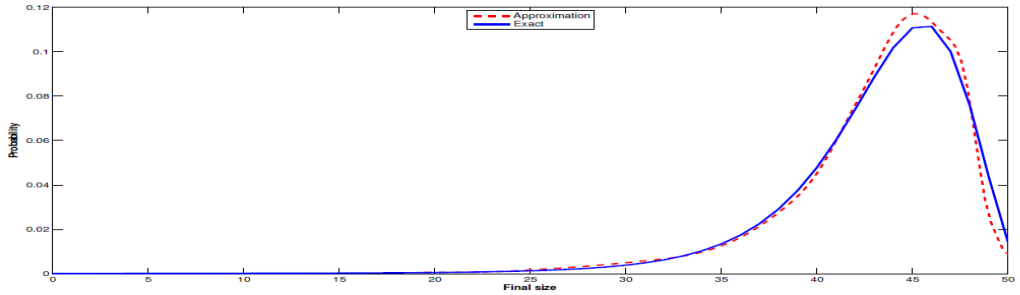

Figure 2: Distribution of the final size and its diffusion approximation, for $n = 50$, $m = 10$, $\beta = 0.2$, $\mu = 0.1$.

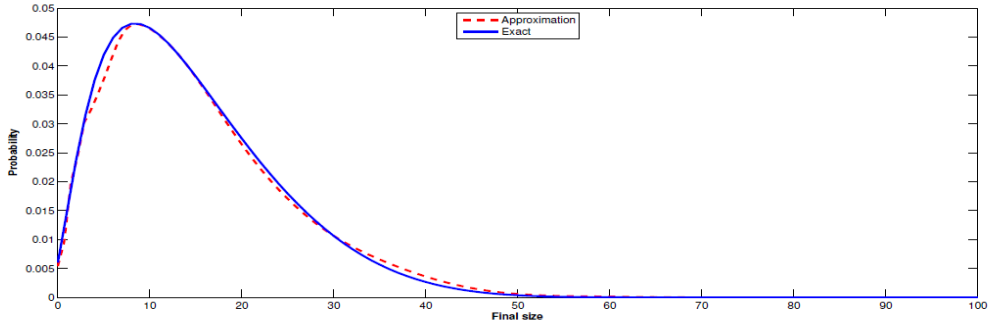

Figure 3: Distribution of the final size and its diffusion approximation, for $n = 100$, $m = 10$, $\beta = 0.2$, $\mu = 0.3$.

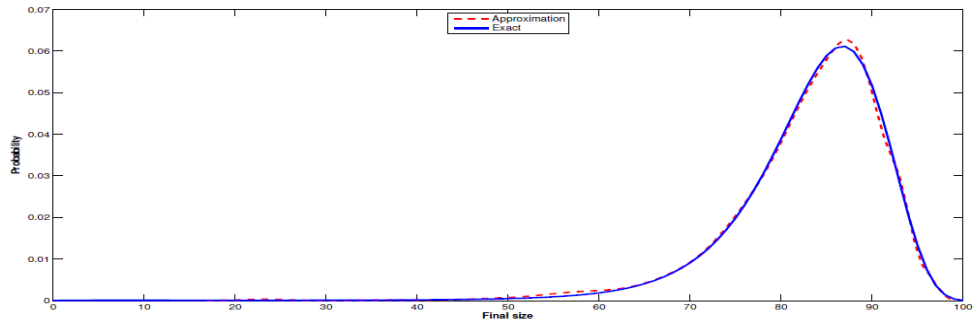

Figure 4: Distribution of the final size and its diffusion approximation, for $n = 100$, $m = 10$, $\beta = 0.2$, $\mu = 0.1$.

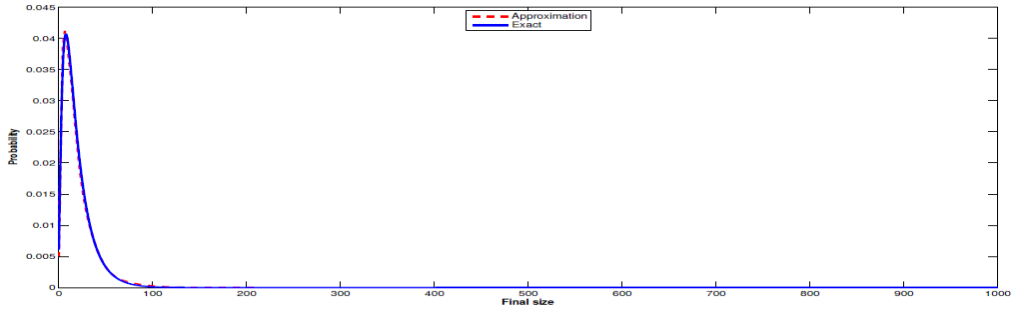

Figure 5: Distribution of the final size and its diffusion approximation, for $n = 1000$, $m = 10$, $\beta = 0.2$, $\mu = 0.3$.

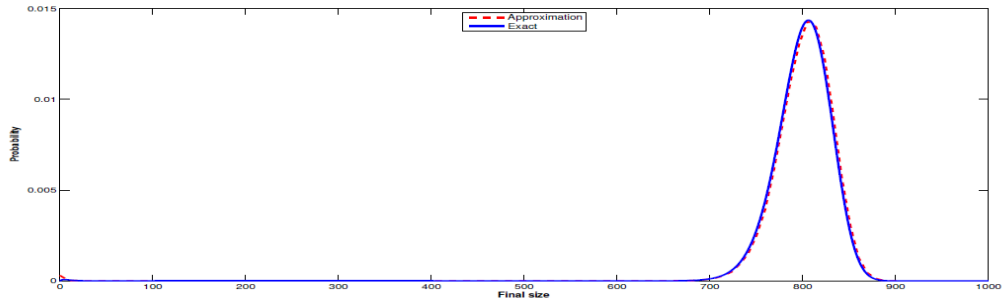

Figure 6: Distribution of the final size and its diffusion approximation, for $n = 1000$, $m = 10$, $\beta = 0.2$, $\mu = 0.1$.

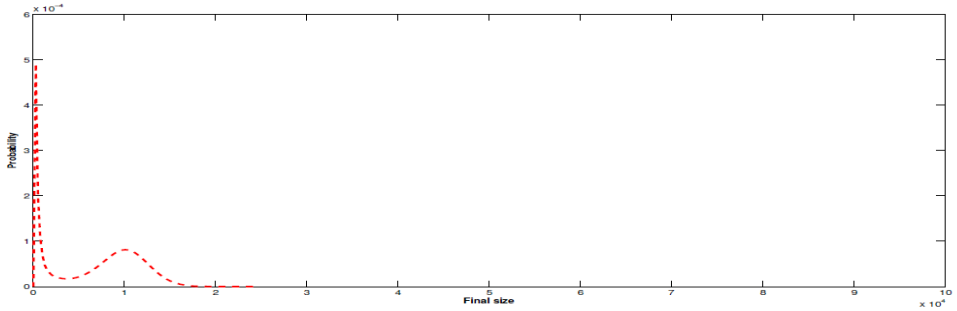

Figure 7: Distribution of the final size by diffusion approximation, for $n = 10^5$, $m = 10$, $\beta = 1.05$, $\mu = 1$.

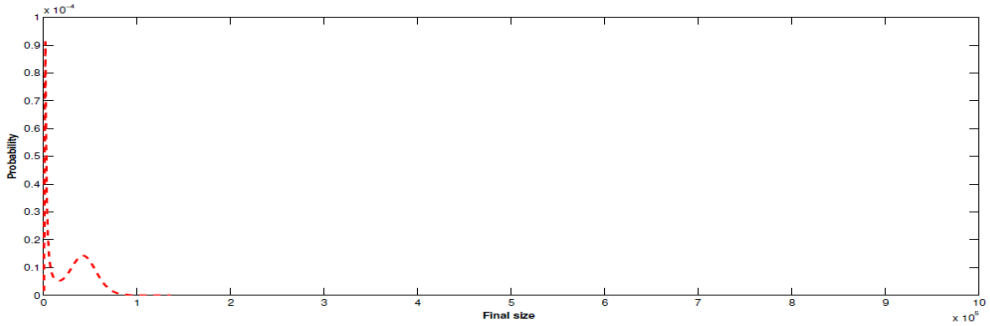

Figure 8: Distribution of the final size by diffusion approximation, for $n = 10^6$, $m = 10$, $\beta = 1.02$, $\mu = 1$.

4 Conclusion

In this paper, a stochastic SIR epidemic model through a diffusion process is approached. An approximation of the final size when the number of individuals initially susceptibles n is large is deduced. When n is more than 100 the diffusion approximation is well.

Competing Interests

The author declares that no competing interests exist.

References

[1] Kermack, W.O. and McKendrick, A.G.(1927). Contribution to mathematical theory of epidemics. P. Roy. Soc. Lond. A Mat., 115, pp. 700-721.

[2] Bailey NTJ. The Mathematical Theory of Infectious Diseases and its Applications, 2nd edn. Hafner Press, New York; 1975.

[3] Williams T. An algebraic proof of the threshold theorem for the general stochastic epidemic, Adv. appl. Prob. 1971;3:223.

[4] Ball FG. A Note on the Total Size Distribution of Epidemic Models. Journal of Appl. Prob.1986;23(3):832-836.

[5] Ball F, Clancy D. The final size and severity of a generalised stochastic multitype epidemic models, Adv. App. Prob.1993;25:721-736.

[6] Lindholm M. Some approximation results concerning near critical epidemics, Examensarbete. Department of Mathematical Statistics, Stocholm University. 2004;21.

[7] Ma J, Earn DJ. Generality of the final size formula for an epidemic of a newly invading infectious disease. Bull. Math. Biol. 2006;68(3):679-702.

[8] Demiris N, O'Neill PD. Computation of final outcome probabilities for the generalised stochastic epidemic. Stat Comput. 2006;16:309-317.

[9] Gordillo LF, Marion SA, Martin-Lof A, Greenwood PE. Bimodal Epidemic Size Distributions for Near-Critical SIR with Vaccination. Bulletin of Mathematical Biology. 2008;70:589-602.

[10] Artalejo JR, Economou A, Lopez-Herrero MJ. Stochastic epidemic models with random environment: quasi-stationarity, extinction and final size. J. Math. Biol. 2013;67(4):799-831.

[11] Ethier SN, Kurtz TG. Markov Processes Caracterisation and Convergence, Jhon Wiley and Sons, New york; 1986.

[12] Øksendal B. Stochastic Differential Equations: An Introduction with Applications. Springer-Verlag Heidelberg New York; 2000.

[13] Kloeden PE, Platen E. Numerical Solution of Stochastic Differential Equations, Springer, Berlin; 1995.

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