Calculation Method and Application of Basic Regeneration Number for a Class of Stochastic Systems

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Abstract: - Considering the influence of random noise on SIR, SEIR and SEIAR infectious disease models, we establish SIR, SEIR and SEIAR models with random disturbance, and deduce the calculation formula of the basic regeneration number of the random infectious disease model in the sense of mean value by using *Itô* formula. The effectiveness of the basic regeneration number calculation method is verified by numerical simulation of the system evolution process.

Key-Words: - Random infectious disease model, Noise, *Itô* formula, The basic regeneration number.

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1 Introduction

Infectious diseases are one of the threats to human health and have a non-negligible impact on our lives. Historically, infectious diseases such as dengue[1], Severe Acute Respiratory Syndrome (SARS)[2], pneumonia[3] threaten human life safety. Therefore, it is of great significance for the study of infectious diseases. By exploring the transmission rules of infectious diseases and predicting their development trend, it can provide a theoretical basis for disease control. In recent years, many mathematical scholars have studied the dynamics behavior of epidemic models for infections by establishing mathematical models. Kermack and McKendrick established the SIR epidemic model for infections by dynamics methods in 1927 [4]; literature [5] established the SEI model to study the impact of media reports on the transmission and control of infectious diseases in specific regions. The SIR model with stochastic perturbations is discussed [6]. The global dynamics of an SIRS epidemic model for infections with non permanent acquired immunity was investigated [7]. Literature [8] will describe Tuberculosis transmission using the Susceptible-Exposed-Infected-Recovered (SEIR) model. The SEIR model for transmission of Tuberculosis was analyzed and performed simulations using data on the number of TB cases in South Sulawesi.

In the epidemic model, the basic regeneration number R_0 is one of the important parameters to determine the prevalence of infectious diseases. The calculation of the basic regeneration number is instructive for the prevention and control of infectious diseases. Literature [9] introduces the calculation method of the basic regeneration number in the deterministic model. This paper mainly introduces the basic regeneration number of several stochastic epidemic models. When $R_0 < 1$, the disease disappears and $R_0 > 1$ spreads.

2 The Basic Reproduction Number of the Stochastic Model

2.1 The SIR model

The SIR model with vaccination:

$$\begin{cases} S'(t) = (1-p)b - \mu S - \beta SI + \gamma R \\ I'(t) = \beta SI - (\mu + c + \alpha)I \\ R'(t) = pb - (\mu + \gamma)R + \alpha I \end{cases} \quad (1)$$

In the SIR model, the population is divided into three compartments: susceptible (S), infectious (I) and recovered with immunity (R), where β represents the rate of infection, b is considered as the proportion of new individuals entering the population, vaccination proportion coefficient is p, μ is considered as the emigration rate, the immune loss rate is γ, c is considered as the emigration rate due to illness, the recovery rate is α. N is the total population size such that $N = S(t) + I(t) + R(t)$ for all t. Assuming the propagation coefficient β is assumed to be disturbed by stochastic noise. We define

$$\beta \to \beta + \sigma \dot{B}(t),$$

where $B(t)$ is the standard Brownian motion and σ is the fluctuation intensity of the white noise. We can build the following stochastic SIR model:

$$\begin{cases} dS = [(1-p)b - \mu S - \beta SI + \gamma R]dt - \sigma SIdB(t) \\ dI = [\beta SI - (\mu + c + \alpha)I]dt + \sigma SIdB(t) \\ dR = [pb - (\mu + \gamma)R + \alpha I]dt \end{cases} \quad (2)$$

The state space of the model (2) is

$$X \equiv R_+^3 = \{(S, I, R) : S \geq 0, I \geq 0, R \geq 0\}.$$

Define the C^2 function

$$V : V(S(t), I(t)) = \ln(S(t), I(t)),$$

and using the Itô formula can be given as:

$$d\ln S = (S^{-1}((1-p)b - \mu S - \beta SI + \gamma R) + 0.5\sigma^2 I^2)dt - \sigma IdB(t) \quad (3)$$

$$d\ln I = (I^{-1}(\beta SI - (\mu + c + \alpha)I) - 0..5\sigma^2 S^2)dt + \sigma SdB(t) \quad (4)$$

The Eq.(3) and the Eq.(4) are transformed to Stratonovich stochastic differential equation and take the mean. Thus, the study of model (2) can be turned into a study of the following systems:

$$\begin{cases} dS = [(1-p)b - \mu S - \beta SI + \gamma R + 0.5\sigma^2 SI^2]dt \\ dI = [\beta SI - (\mu + c + \alpha)I - 0.5\sigma^2 S^2 I]dt \\ dR = [pb - (\mu + \gamma)R + \alpha I]dt \end{cases} \quad (5)$$

The disease-free equilibrium point of the model (1) and the model (5) can be calculated:

$$E_0^{SIR} = (S_1, I_1, R_1) = (\frac{b((1-p)\mu + \gamma)}{\mu(\mu + \gamma)}, 0, \frac{pb}{\mu + \gamma}).$$

The basic reproduction number of the model (1) can be calculated:

$$R_0^{SIR} = \frac{\beta b((1-p)\mu + \gamma)}{\mu(\mu + \gamma)(\mu + c + \alpha)}.$$

We note $x = (I, S, R)^T$,the system (5) may be represented as $x' = \mathcal{F}_1(x) - \mathcal{V}_1(x)$,where

$$\mathcal{F}_1(x) = \begin{pmatrix} \beta SI \\ 0 \\ 0 \end{pmatrix};$$

$$\mathcal{V}_1(x) = \begin{pmatrix} (\mu + c + \alpha)I + 0.5\sigma^2 S^2 I \\ -(1-p)b + \mu S + \beta SI - \gamma R - 0.5\sigma^2 SI^2 \\ -pb + (\mu + \gamma)R - \alpha I \end{pmatrix}.$$

The Jacobian matrix of $\mathcal{F}_1(x), \mathcal{V}_1(x)$ in E_0^{SIR} note F_1, V_1 , we have:

$$F_1 = \begin{pmatrix} \beta S_1 & 0 & 0 \\ 0 & 0 & 0 \\ 0 & 0 & 0 \end{pmatrix};$$

$$V_1 = \begin{pmatrix} \mu + c + \alpha + 0.5\sigma^2 S_1^2 & 0 & 0 \\ \beta S_1 & \mu & -\gamma \\ -\alpha & 0 & \mu + \gamma \end{pmatrix}.$$

The next generation matrix can be calculated:

$$F_1 V_1^{-1} = \begin{pmatrix} R_0^{SIR} - \frac{\sigma^2 b^2((1-p)\mu + \gamma)^2}{2\mu^2(\mu + \gamma)^2(\mu + c + \alpha)} & 0 \\ 0 & 0 \end{pmatrix},$$

thus, the basic reproduction number of the stochastic SIR model (2) is:

$$R_S^{SIR} = \rho(F_1 V_1^{-1}) = R_0^{SIR} - \frac{\sigma^2 b^2((1-p)\mu + \gamma)^2}{2\mu^2(\mu + \gamma)^2(\mu + c + \alpha)}.$$

2.2 The SEIR Model

The model discussed in the previous section ignores the disease latency. Given the latency of many infectious diseases, many scholars introduce a latent compartment E to indicate the latent status. After susceptible individuals are infected, they enter the latent status and into the infection compartment pass the $1/q$ day incubation period. The transmission process of these infectious diseases can be expressed in the following model:

$$\begin{cases} S'(t) = (1-p)b - \mu S - \beta SI + \gamma R \\ E'(t) = \beta SI - (\mu + q)E \\ I'(t) = qE - (\mu + c + \alpha)I \\ R'(t) = pb - (\mu + \gamma)R + \alpha I \end{cases} \quad (6)$$

Similar to the reasoning in 2.1, we present the following system of stochastic differential equations for SEIR models with stochastic perturbations:

$$\begin{cases} dS = [(1-p)b - \mu S - \beta SI + \gamma R]dt - \sigma SIdB(t) \\ dE = [\beta SI - (\mu + q)E]dt + \sigma SIdB(t) \\ dI = [qE - (\mu + c + \alpha)I]dt \\ dR = [pb - (\mu + \gamma)R + \alpha I]dt \end{cases} \quad (7)$$

Define the C^2 function

$$V : V(S(t), E(t)) = \ln(S(t), E(t)),$$

and using the *Itô* formula can be expressed as:

$$d\ln S = [S^{-1}((1-p)b - \mu S - \beta SI + \gamma R) + 0.5\sigma^2 I^2]dt - \sigma IdB(t) \quad (8)$$

$$d\ln E = [E^{-1}(\beta SI - (\mu + q)I) - 0.5E^{-2}\sigma^2 S^2 I^2]dt + E^{-1}\sigma SIdB(t) \quad (9)$$

The Eq.(8) and the Eq.(9) are transformed to Stratonovich stochastic differential equation and take the mean.Therefore we only need to discuss systems such as:

$$\begin{cases} dS = [(1-p)b - \mu S - \beta SI + \gamma R + 0.5\sigma^2 SI^2]dt \\ dE = [\beta SI - (\mu + q)E - 0.5E^{-1}\sigma^2 S^2 I^2]dt \\ dI = [qE - (\mu + c + \alpha)I]dt \\ dR = [pb - (\mu + \gamma)R + \alpha I]dt \end{cases} \quad (10)$$

Suppose

$$\lim_{I \to 0} \frac{I}{E} = c_1 \quad (11)$$

where c_1 is constant, so the disease-free equilibrium point of the model (6) and the model (10) can be calculated:

$$E_0^{SEIR} = (S_2, E_2, I_2, R_2) = (\frac{b((1-p)\mu+\gamma)}{\mu(\mu+\gamma)}, 0, 0, \frac{pb}{\mu+\gamma}).$$

The basic reproduction number of the model (6) is

$$R_0^{SEIR} = \frac{\beta bq((1-p)\mu+\gamma)}{\mu(\mu+q)(\mu+\gamma)(\mu+c+\alpha)}.$$

We note $x = (E, I, S, R)^T$,the system (10) may be represented as:

$$x' = \mathcal{F}_2(x) - \mathcal{V}_2(x),$$

where

$$\mathcal{F}_2(x) = \begin{pmatrix} \beta SI \\ 0 \\ 0 \\ 0 \end{pmatrix};$$

$$\mathcal{V}_2(x) = \begin{pmatrix} (\mu+q)E + 0.5E^{-1}\sigma^2 S^2 I^2 \\ (\mu+c+\alpha)I - qE \\ -(1-p)b + \mu S + \beta SI - \gamma R - 0.5\sigma^2 SI^2 \\ -pb + (\mu+\gamma)R - \alpha I \end{pmatrix}.$$

The Jacobian matrix of $\mathcal{F}_2(x), \mathcal{V}_2(x)$ in E_0^{SEIR} note F_2, V_2, we have:

$$F_2 = \begin{pmatrix} 0 & \beta S_2 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 \end{pmatrix};$$

$$V_2 = \begin{pmatrix} q+\mu-0.5c_1^2 S_2^2\sigma^2 & c_1^2 S_2^2\sigma^2 & 0 & 0 \\ -q & \mu+c+\alpha & 0 & 0 \\ 0 & \beta S_2 & \mu & -\gamma \\ 0 & -\alpha & 0 & \mu+\gamma \end{pmatrix}.$$

The basic reproduction number of the stochastic SEIR model (7) is the spectral radius of the next generation matrix $F_2 V_2^{-1}$, then

$$R_S^{SEIR} = \rho(F_2 V_2^{-1}) = \frac{\beta bq((1-p)\mu+\gamma)}{L_2 + M_2 - N_2},$$

where

$$L_2 = \frac{b^2 qc_1(\mu+\gamma)((1-p)\mu+\gamma)^2\sigma^2}{\mu(\mu+\gamma)},$$

$$M_2 = \mu(\mu+c+\gamma)(\mu+\gamma)(\mu+q),$$

$$N_2 = \frac{b^2 c_1^2(\mu+c+\alpha)((1-p)\mu+\gamma)^2\sigma^2}{2\mu(\mu+\gamma)}.$$

2.3 The SEIAR Model

Some scholars believe that asymptomatic infected individuals can also spread the virus. Therefore, if we add a compartment A of asymptomatic infected individuals, the model take the form:

$$\begin{cases} S'(t) = (1-p)b - \mu S - \beta SI - \beta_A SA + \gamma R \\ E'(t) = \beta SI + \beta_A SA - (\mu+q)E \\ I'(t) = dqE - (\mu+c+\alpha)I \\ A'(t) = (1-d)qE - (\mu+\alpha_A)A \\ R'(t) = pb - (\mu+\gamma)R + \alpha I + \alpha_A A \end{cases} \quad (12)$$

New infections in compartment E arise by contacts between susceptible and infected individuals in compartments S and A at a rate $\beta_A SA$. Individuals progress from compartment E to I at a rate d . Asymptomatic individuals are recovered at a rate α_A. Assuming the propagation coefficient β and β_A are assumed to be disturbed by stochastic noise. We define:

$$\beta \to \beta + \sigma_1 \dot{B}_1(t), \beta_A \to \beta_A + \sigma_2 \dot{B}_2(t).$$

The following stochastic SEIAR model can be established:

$$\begin{cases} dS = [(1-p)b - \mu S - \beta SI - \beta_A SA + \gamma R]dt - \sigma_1 SIdB_1(t) - \sigma_2 SAdB_2(t) \\ dE = [\beta SI + \beta_A SA - (\mu+q)E]dt + \sigma_1 SIdB_1(t) + \sigma_2 SAdB_2(t) \\ dI = [dqE - (\mu+c+\alpha)I]dt \\ dA = [(1-d)qE - (\mu+\alpha_A)A]dt \\ dR = [pb - (\mu+\gamma)R + \alpha I + \alpha_A A]dt \end{cases} \quad (13)$$

Define the C^2 function

$$V : V(S(t), E(t)) = \ln(S(t), E(t)),$$

and using the *Itô* formula can be expressed as:

$$d\ln S = [S^{-1}((1-p)b - \mu S - \beta SI - \beta_A SA + \gamma R) + 0.5S^{-2}(\sigma_1^2 S^2 I^2 + \sigma_2^2 S^2 A^2)]dt - \sigma_1 IdB_1(t) - \sigma_2 AdB_2(t) \quad (14)$$

$$d\ln E = [E^{-1}(\beta SI + \beta_A SA - (\mu+q)E) - 0.5E^{-2}(\sigma_1^2 S^2 I^2 + \sigma_2^2 S^2 A^2)]dt - E^{-1}\sigma_1 SIdB_1(t) - E^{-1}\sigma_2 SAdB_2(t) \quad (15)$$

The Eq.(14) and Eq.(15) are transformed to Stratonovich stochastic differential equation and take the mean,we can study the following systems:

$$\begin{cases} dS = [(1-p)b - \mu S - \beta SI - \beta_A SA + \gamma R + 0.5(\sigma_1^2 SI^2 + \sigma_2^2 SA^2)]dt \\ dE = [\beta SI + \beta_A SA - (\mu+q)E - 0.5E^{-1}(\sigma_1^2 S^2 I^2 + \sigma_2^2 S^2 A^2)]dt \\ dI = [dqE - (\mu+c+\alpha)I]dt \\ dA = [(1-d)qE - (\mu+\alpha_A)A]dt \\ dR = [pb - (\mu+\gamma)R + \alpha I + \alpha_A A]dt \end{cases} \quad (16)$$

Suppose

$$\lim_{A\to 0} \frac{A}{E} = c_2 \quad (17)$$

where c_2 is constant.

According to Eq.(11) and Eq.(17), the system (12) and (16) has a unique disease-free equilibrium point, with

$$E_0^{SEIAR} = (S_3, E_3, I_3, A_3, R_3) = (\frac{b((1-p)\mu+\gamma)}{\mu(\mu+\gamma)}, 0, 0, 0, \frac{pb}{\mu+\gamma}).$$

The basic reproduction number of the model (12) is

$$R_0^{SEIAR} = \frac{bq((1-p)\mu+\gamma)(\beta_A(\mu+c+\alpha)+d((\mu+\alpha_A)\beta-(\mu+c+\alpha)\beta_A))}{\mu(\mu+q)(\mu+c+\alpha)(\mu+\alpha_A)(\mu+\gamma)}.$$

We note $x=(E,I,A,S,R)^T$ thus, the system (16) may be represented as:

$$x' = \mathcal{F}_3(x) - \mathcal{V}_3(x),$$

where

$$\mathcal{F}_3 = \begin{pmatrix} \beta SI + \beta_A SA \\ 0 \\ 0 \\ 0 \\ 0 \end{pmatrix};$$

$$\mathcal{V}_3 = \begin{pmatrix} (\mu+q)E + 0.5E^{-1}(\sigma_1^2S^2I^2 + \sigma_2^2S^2A^2) \\ (\mu+c+\alpha)I - dqE \\ (\mu+\alpha_A)A - (1-d)qE \\ -(1-p)b + \mu S + \beta SI + \beta_A SA - \gamma R - 0.5(\sigma_1^2SI^2 + \sigma_2^2SA^2) \\ -pb + (\mu+\gamma)R - \alpha I - \alpha_A A \end{pmatrix}$$

.

The Jacobian matrix of $\mathcal{F}_3(x), \mathcal{V}_3(x)$ in E_0^{SEIAR} note F_3, V_3, we have:

$$F_3 = \begin{pmatrix} 0 & \beta S_3 & \beta_A S_3 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \\ 0 & 0 & 0 & 0 & 0 \end{pmatrix};$$

$$V_3 = \begin{pmatrix} q+\mu-0.5S_3^2(c_1^2\sigma_1^2+c_2^2\sigma_2^2) & c_1S_3^2\sigma_1^2 & c_2S_3^2\sigma_2^2 & 0 & 0 \\ -dq & \mu+c+\alpha & 0 & 0 & 0 \\ -(1-d)q & 0 & \alpha_A+\mu & 0 & 0 \\ 0 & \beta S_3 & \beta_A S_3 & \mu & -\gamma \\ 0 & -\alpha & -\alpha_A & 0 & \mu+\gamma \end{pmatrix}.$$

The basic reproduction number of the stochastic SEIAR model (13) is:

$$R_S^{SEIAR} = \rho(F_3V_3^{-1}) = \frac{2bq\mu(\mu+\gamma)((1-p)\mu+\gamma)(\beta_A(1-d)(\mu+c+\alpha)+d\beta(\mu+\alpha_A))}{L_3+M_3-N_3}$$

where

$$L_3 = b^2c_1(\mu+\alpha_A)((1-p)\mu+\gamma)^2\sigma_1^2(2dq-c_1(\mu+c+\alpha)),$$

$$M_3 = b^2c_2(\mu+c+\alpha)((1-p)\mu+\gamma)^2\sigma_2^2(2q(1-d)-c_2(\mu+\alpha_A))$$

,

$$N_3 = 2\mu^2(\mu+\alpha_A)(\mu+c+\alpha)(\mu+\gamma)^2(\mu+q).$$

3 Numerical Simulation

Taking the model (2) as an example, we analyzed the effect of the vaccination rate p and the noise intensity σ on R_S^{SIR}. We take $b=2$, $\mu=0.04$, $\beta=0.025$, $c=0.01$, $\gamma=0.001$, $\alpha=0.9$. Fig.1 shows the change of the basic regeneration number R_S^{SIR} with vaccination rate p at $\sigma=0.02$, and Fig.2 shows the change of R_S^{SIR} with noise intensity σ at $p=0.5$. It indicates that R_S^{SIR} decreases monotonically with increasing p and σ, which is also in line with the actual situation. In Fig. 1c we show the results of R_S^{SIR} as a function of p and σ. As seen from Fig.3, the R_S^{SIR} decrease monotonically with the increase of noise intensity σ for different values of vaccination rate p, which shows that the increase of noise intensity σ can effectively control the spread of the disease.

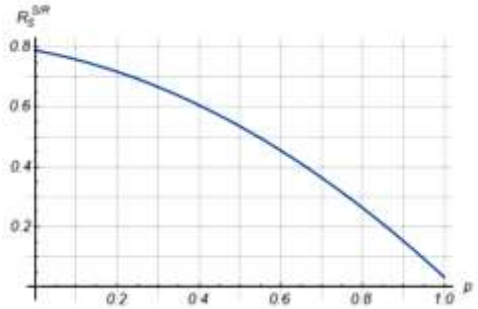


Fig. 1: The change of R_S^{SIR} with vaccination rate p at $\sigma=0.02$.

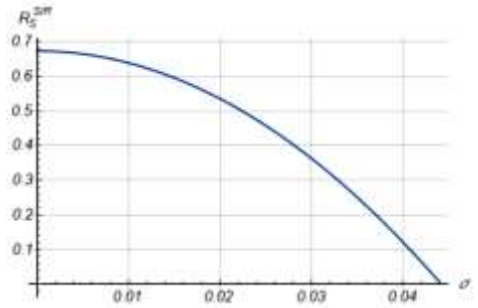


Fig. 2: The change of R_S^{SIR} with noise intensity σ at $p=0.5$.

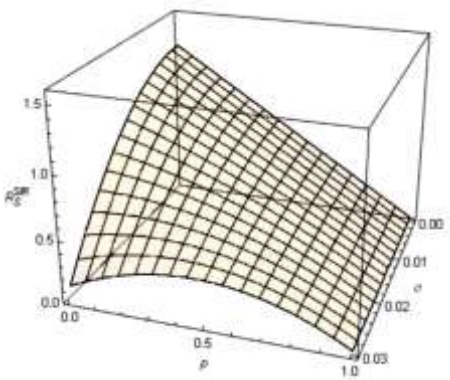
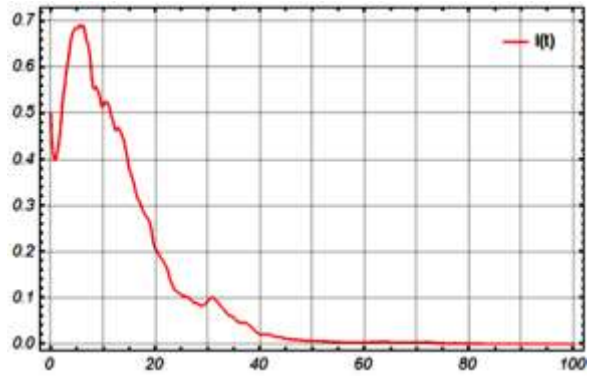


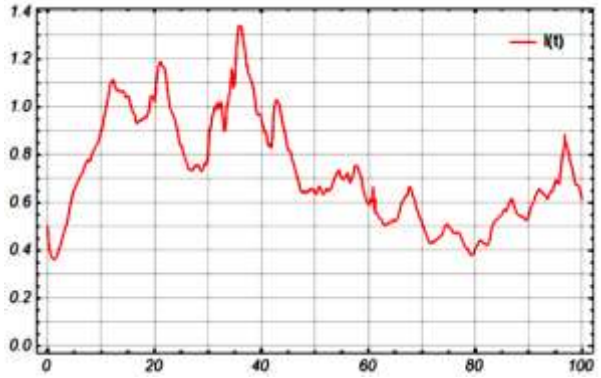
Fig. 3: Three-dimensional plot of R_S^{SIR} as a function of p and σ.

To verify the effect of the basic regeneration number on the infectious diseases, now we will perform some numerical simulations. The numerical

simulations are given by the Milstein's scheme. For the model (13), take $p = 0.7$, $b = 3$, $\mu = 0.04$, $\beta = 0.025$, $\beta_A = 0.015$, $c = 0.01$, $\gamma = 0.001$, $\alpha = 0.9$, $\alpha_A = 0.95$, $q = 0.21$, $d = 0.7$, $c_1 = c_2 = 0.01$, $\sigma_1 = \sigma_2 = 0.02$. By calculating $R_S^{SEIAR} = 0.4579 < 1$, We can see that the disease gradually goes extinct (Fig. 4a). When we take $p = 0.1$, therefore, the basic reproduction number of the random system (13) $R_S^{SEIAR} = 1.2861 > 1$, the number of infections continues to grow and will eventually lead to an outbreak (Fig. 4b). Fig.4(a, b) shows the mean value of the numerical simulation results when the vaccination rate are equal to 0.7 and 0.1 for 100 runs, respectively.



(a): $R_S^{SEIAR} = 0.4579 < 1$ when $p = 0.7$.



(b): $R_S^{SEIAR} = 1.2861 > 1$ when $p = 0.1$.

Fig. 4: Evolution of infected individuals after 100 number of simulations and taking the mean value, with $p = 0.7$, $b = 3$, $\mu = 0.04$, $\beta = 0.025$, $\beta_A = 0.015$, $c = 0.01$, $\gamma = 0.001$, $\alpha = 0.9$. $\alpha_A = 0.95$, $q = 0.21$, $d = 0.7$, $c_1 = c_2 = 0.01$, $\sigma_1 = \sigma_2 = 0.02$.

4 Conclusion

We study the SIR, SEIR, and SEIAR infectious disease models disturbed by random noise, and give the calculation of the basic regeneration number of the three stochastic models, when $R_S < 1$ the maximum proportion of people who can infect a patient in the average disease period is less than 1, the disease will not spread. If,the disease will spread. Numerical simulation results show that:

(1) By increasing the vaccination rate p, the basic regeneration number will be reduced. This means that increasing the vaccination rate can effectively inhibit the spread of the disease;

(2) Increased noise intensity σ can also reduce the number of infected people.

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-Jiaxin Shi has organized and executed the experiments of Section 2.

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