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# Parameter estimation of the Conformable fractional stochastic SIR model based on the Markov chain

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**----------*ABSTRACT*----------**
*In this paper, the fractional SIR model and fractional stochastic SIR model are given. The relationship between them is obtained by using a probability generating function. The maximum likelihood estimation of the fractional stochastic SIR model and the parameter estimation results of the MCWM algorithm are given. Finally, the parameter estimation results of the fractional stochastic SIR model and integer stochastic SIR model were compared by using British boarding school influenza data and Hong Kong SARS data.Results show that the order of fractionalstochastic SIR model within a certain range, the fitting effect of the original data is better than integerstochastic SIR model, and the parameter estimation error is smaller.*
***KEYWORDS:*** *Fractional stochastic SIR model, Markov Chain, Maximum likelihood estimation, MCWM algorithm*

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## I. INTRODUCTION

In recent years, as the epidemic has continued to spread around the world, the economic losses caused by the epidemic to countries have gradually increased. Therefore, the mathematical model of infectious diseases has become a hot research topic, and its model can be divided into a deterministic model and a stochastic model[1]. Due to the influence of various environmental uncertainties such as weather and region in real life, the random infectious disease model is more in line with the actual situation.

In 1927, Kermack and Mckendrick proposed the SIR model[2]. In 1931, the SIS chamber model and threshold theorem were proposed[3], which laid the foundation for the study of infectious disease dynamics. In 1957, MacDonald explained the basic regeneration number of infected people[4]. In 1976, Becker studied the estimation results of infectious disease models and defined the initial infection rate using the least squares and maximum likelihood estimation models[5]. In 1989, Yip estimated the initial infection rate of a class of random epidemiological models using a bicorrelation martingale-based method[6]. In 2000, Timmer discussed the problem of parameter estimation of nonlinear stochastic differential equations[7]. In 2007, Chowell et al. calculated the effective reproduction number using early exponential growth rates and a combination of stochastic SIER models and Bayesian estimation[8]. In 2012, Capistran et al. used Van Campen's inverse magnitude expansion to obtain approximations of the first and second moments of the state variables of the random SIR model and performed complete Bayesian inference using an informative priori[9]. In 2020, Mehra et al. used the least squares method to estimate unknown parameters, and used SSE and RMSE criteria to study the goodness of the fitted model, the range of unknown parameters is also given[10].

In 2017, Fazal et al. obtained an approximate solution of the nonlinear fractional SIR model by the Laplace-Adomian decomposition method[11]. In 2019, Srivastava et al. used the consistency fractional difference transformation method to calculate the approximate solution of the fractional SIR model of childhood diseases[12]. In 2020, Naik proposed a nonlinear fractional infectious disease model of HIV transmission and discussed global dynamics and partial optimal control[13]. In 2021, Naim et al. considered a Caputo fractional SIR epidemic model with a double epidemic hypothesis and a specific functional response and studied local and global stability analyses of four equilibrium points[14]. However, the parameter estimation problem of the fractional SIR model is not considered.

In 2014, Khalil et al. proposed the Conformable fractional derivative, which is a natural extension of the integer derivative[15]. It is possible to overcome some shortcomings of the Caputo derivative in operation, For example, the derivative formula that cannot satisfy the product of two known functions, the chain rule cannot be satisfied, and so on. Some definitions and properties are described below (see Literature [15] for details).

**Definition 1** Set functions $f(t):[0,\infty)\to\Re$, for $t>0$, $\alpha\in(0,1]$, the $\alpha$ order Conformable fractional derivative of $f(t)$ is defined as

$$T_\alpha f(t)=\lim_{\varepsilon\to 0}\frac{f(t+\varepsilon t^{1-\alpha})-f(t)}{\varepsilon}$$

when $t=0$, $T_\alpha f(0)=\lim_{t\to 0^+}T_\alpha f(t)$.

**Lemma 2** If the function $f(t)$ is derivable, then the $\alpha$ order Conformable fractional derivative of $f(t)$ and its first derivative have

$$T_\alpha f(t)=t^{1-\alpha}\frac{\mathrm{d}f(t)}{\mathrm{d}t}$$

in particular, $T_1 f(t)=\frac{\mathrm{d}f(t)}{\mathrm{d}t}$.

In this paper, considering the advantages of the fractional infectious disease model to flexibly adjust the order of fractional derivatives to improve the degree of fit, the conformable fractional SIR model is discussed. At the same time, considering that the model parameters are easily affected by environmental uncertainties, a stochastic SIR model in the sense of conformable score is given. The maximum likelihood estimation of the model and the parameter estimation of the MCWM algorithm are given. and used the flu data form British boarding schools and SARS data in Hong Kong for case analysis. The results show that when the order of the fractional stochastic SIR model is taken within a certain range, it fits the original data better than the integer stochastic SIR model, and the error of parameter estimation is smaller.

## II. MODELANALYSIS

**Fractional Stochastic SIR Model**

The SIR model constructed in 1927[2] is a widely adopted classic infectious disease model, including Susceptible( $S$ )、Infective( $I$ )、Removed( $R$ ). Determine the SIR model as follows

$$\begin{cases}\frac{\mathrm{d}S(t)}{\mathrm{d}t}=-\beta I(t)S(t)\\ \frac{\mathrm{d}I(t)}{\mathrm{d}t}=\beta I(t)S(t)-\gamma I(t)\\ \frac{\mathrm{d}R(t)}{\mathrm{d}t}=\gamma I(t)\end{cases}\tag{1}$$

where $(S(0),I(0),R(0))\geq(0,0,0)$, $\beta$ is the infection factor, $\gamma$ is the recovery factor, and the sum of the three groups of people meets $S(t)+I(t)+R(t)=N$ [16].

Considering the advantages of the fractional SIR model can flexibly adjust the order of fractional derivatives to improve the degree of fit. In this paper, according to the definition and properties of conformable fractional derivative, the fractional SIR model is obtained as follows

$$\begin{cases}T_\alpha S(t)=t^{1-\alpha}\frac{\mathrm{d}S(t)}{\mathrm{d}t}=-\beta I(t)S(t)\\ T_\alpha I(t)=t^{1-\alpha}\frac{\mathrm{d}I(t)}{\mathrm{d}t}=\beta I(t)S(t)-\gamma I(t)\\ T_\alpha R(t)=t^{1-\alpha}\frac{\mathrm{d}R(t)}{\mathrm{d}t}=\gamma I(t)\end{cases}\tag{2}$$

Randomized infectious disease studies are important when the number of infected people is small, or when environmental uncertainties affect the outcome of infectious diseases. Since the infection factor $\beta$ and recovery factor $\gamma$ are easily affected by environmental change, and there is a certain randomness in the next moment of susceptibility, infection and the number of people recovering, we give a conformable fractional stochastic SIR model.

The two-dimensional stochastic process $\{(S(t),I(t),t\geq 0\}$ is represented by a continuous-time Markov chain[17], $\Delta t$ represents the time interval between adjacent moments. The transition probability[18] of the fractional stochastic SIR model is as follows

$$P_{(s+k,i+j)}(\Delta t)=\begin{cases} t^{\alpha-1}\beta si\Delta t+o(\Delta t), & (k,j)=(-1,1) \\ t^{\alpha-1}\gamma i\Delta t+o(\Delta t), & (k,j)=(0,-1) \\ 1-t^{\alpha-1}(\beta si+\gamma i)\Delta t+o(\Delta t), & (k,j)=(0,0) \\ o(\Delta t), & \text{其它} \end{cases} \quad (3)$$

where $P_{(s+k,i+j)}(\Delta t)=P\{(S(t+\Delta t)=s+k,I(t+\Delta t)=i+j)\,|\,(S(t)=s,I(t)=i)\}$.

Next, the probability generating function is used to analyze the fractional stochastic SIR model.

**Fractional Stochastic SIR Model Analysis**

Let the $t+\Delta t$ moment state value be $(s,i)$, so the $t$ state transitions to the $t+\Delta t$ state in the following three cases:

1) The probability of state $(s+1,i-1)$ transferring to state $(s,i)$ is $t^{\alpha-1}\beta(s+1)(i-1)\Delta t+o(\Delta t)$,

2) The probability of state $(s,i+1)$ transferring to state $(s,i)$ is $t^{\alpha-1}\gamma(i+1)\Delta t+o(\Delta t)$,

3) The probability of state $(s,i)$ transferring to state $(s,i)$ is $1-t^{\alpha-1}(\beta si+\gamma i)\Delta t+o(\Delta t)$,

So the probability of state transition from time $t$ to time $t+\Delta t$ is

$$P_{(s,i)}(t+\Delta t)=P_{(s,i)}(t)+t^{\alpha-1}[\beta(s+1)(i-1)P_{(s+1,i-1)}(t)+\gamma(i+1)P_{(s,i+1)}(t)-(\beta si+\gamma i)P_{(s,i)}(t)]\Delta t+o(\Delta t)$$

Subtract $P_{(s,i)}(t)$ on both sides and divide $\Delta t$ to make $\Delta t\to 0$, it so that the Kolmogorov forward equation[17] of the model is

$$\frac{\mathrm{d}P_{(s,i)}(t)}{\mathrm{d}t}=t^{\alpha-1}[\beta(s+1)(i-1)P_{(s+1,i-1)}(t)+\gamma(i+1)P_{(s,i+1)}(t)-(\beta si+\gamma i)P_{(s,i)}(t)] \quad (4)$$

where $i,j=0,1,2,\cdots,N$, and $i+j\le N$.

French mathematician Laplace introduced generative functions in 1812 for the study of non-negative integer random variables[19].

**Definition 3** Let $(X,Y)$ be a two-dimensional discrete random variable with a probability distribution $p_{(i,j)}=P\{X=i,Y=j\}\{i,j=0,1,2,\cdots\}$, then the probability generating function of $(X,Y)$ is defined as follows

$$G_{X,Y}(s_1,s_2)=E(s_1^X s_2^Y)=\sum_{i=0}^{\infty}\sum_{j=0}^{\infty}p_{(i,j)}s_1^i s_2^j$$

where $-1\le s_1\le 1,-1\le s_2\le 1$.

The probability generating function of the state transition probability of the fractional stochastic SIR model is

$$G_{S(t),I(t)}(s_1,s_2;t)=E(s_1^{S(t)}s_2^{I(t)})=\sum_{s=0}^{N}\sum_{i=0}^{N-s}p_{(s,i)}(t)s_1^s s_2^i$$

The probability generation function $G_{S(t),I(t)}(s_1,s_2;t)$ satisfies

$$E(S(t))=\lim_{\substack{s_1\to 1\\ s_2\to 1}}\frac{\partial G}{\partial s_1},E(I(t))=\lim_{\substack{s_1\to 1\\ s_2\to 1}}\frac{\partial G}{\partial s_2},$$

$$E(S(t)I(t))=\lim_{\substack{s_1\to 1\\ s_2\to 1}}\frac{\partial^2 G}{\partial s_1\partial s_2}=E(S(t))E(I(t))+\mathrm{cov}(S(t),I(t)).$$

Derivation of time $t$ is available

$$\begin{aligned}\frac{\mathrm{d}E(S(t))}{\mathrm{d}t}&=\lim_{\substack{s_1\to 1\\ s_2\to 1}}\frac{\partial}{\partial s_1}(\frac{\partial G}{\partial t})=-t^{\alpha-1}\beta E(S(t))E(I(t))-t^{\alpha-1}\beta\,\mathrm{cov}(S(t),I(t)),\\ \frac{\mathrm{d}E(I(t))}{\mathrm{d}t}&=\lim_{\substack{s_1\to 1\\ s_2\to 1}}\frac{\partial}{\partial s_2}(\frac{\partial G}{\partial t})=t^{\alpha-1}\beta E(S(t))E(I(t))-t^{\alpha-1}\gamma E(I(t))+t^{\alpha-1}\beta\,\mathrm{cov}(S(t),I(t)).\end{aligned} \quad (5)$$

Observe equation (5) and fractional SIR model (3), taking into account the covariance $\mathrm{cov}(S(t),I(t))=0$, the fractional stochastic SIR model is the mean process of the fractional SIR model.

Affected by various factors, there will be a certain randomness in the development of infectious diseases, and the transfer of various groups of people in the next moment is also accidental, so the stochastic model is more ideal in actual modeling.

## III. PARAMETERESTIMATION

The Gillespie stochastic simulation algorithm[20] was used to obtain the simulation data of three types of populations of thefractional stochastic SIR model. Based on these simulation data, the parameters $\beta$ and $\gamma$ in the fractional stochastic SIR model were estimated by maximum likelihood estimation and MCWM algorithm, respectively. $\theta=(\beta,\gamma)$ is used below to indicate the parameters to be estimated.

Assuming that at moment $t$, the number of susceptible and infected people states $(S(t),I(t))$, After time $\Delta t$ has elapsed, it is transferred to the state $(S(t+\Delta t),I(t+\Delta t))$, The time interval $\Delta t$ of state transition follows an exponential distribution with parameter $t^{\alpha-1}(\beta S(t)I(t)+\gamma I(t))$. There are two possible values $(S(t)-1,I(t)+1)$ or $(S(t),I(t)-1)$ for the state $(S(t+\Delta t),I(t+\Delta t))$, from the values of the initial moment, a series of simulation values of susceptible and infected people in the fractional stochastic SIR model is generated.

**MaximumLikelihood Estimation**

We obtain the simulation data of the two-dimensional stochastic process $\{(S(t),I(t),t\geq 0\}$ through the Gillespie stochastic simulation algorithm within the period $[0,T]$. Suppose that a total of $Q$ transitions occur in a state, and the moment of the $k$ state transition is $t_k$, In the period $(t_{k-1},t_k)$, the values of $\{(S(t),I(t),t\geq 0\}$ are $(S(t_k),I(t_k))$, $k\in\{1,2,\cdots,Q\}$. The time interval of the state transition from $k$ to $k+1$ is denoted as $\Delta t_k=t_{k+1}-t_k$, and the total time interval is $\Delta T=T$. The time interval follows an exponential distribution with parameter $t^{\alpha-1}(\beta S(t)I(t)+\gamma I(t))$

$$P\{\Delta t_k\leq T\}=\mathrm{e}^{-t^{\alpha-1}(\beta S(t_k)I(t_k)+\gamma I(t_k))\Delta t_k}$$

The likelihood function for calculating the fractional stochastic SIR model is as follows

1) The probability that the state of $\{(S(t),I(t),t\geq 0\}$ does not shift within the period $(t_k,t_{k+1})$ is

$$L_1(\theta)=\prod_{k=0}^{Q-1}\mathrm{e}^{-t^{\alpha-1}(\beta S(t_k)I(t_k)+\gamma I(t_k))\Delta t_k}$$

2) The probability that the state of $\{(S(t),I(t),t\geq 0\}$ does shift within the period $(t_k,t_{k+1})$ is

$$L_2(\theta)=\prod_{k=0}^{Q-1}\xi_k$$

where $\xi_k=\begin{cases}t^{\alpha-1}\beta S(t_k)I(t_k)\Delta t_k, & (I(t_{k+1})=I(t_k)+1)\\ t^{\alpha-1}\gamma I(t_k)\Delta t_k, & (I(t_{k+1})=I(t_k)-1)\end{cases}$.

3) The probability that there is no transition of the state within the interval $(t_Q,T)$ at the final moment is

$$L_3(\theta)=\mathrm{e}^{-t^{\alpha-1}(S(t_Q)I(t_Q)+\gamma I(t_Q))(T-t_Q)}$$

Based on the above three cases, the likelihood function for maximum likelihood estimation can be deduced

$$L(\theta)=A\times\mathrm{e}^{-B\beta t^{\alpha-1}-C\gamma t^{\alpha-1}}\times(t^{\alpha-1}\beta)^D\times(t^{\alpha-1}\gamma)^E \quad (6)$$

where $A=(S(t_k)I(t_k))^D\times(I(t_k)\Delta t_k)^E$, $B=\sum_{k=0}^{Q-1}S(t_k)I(t_k)\Delta t_k+S(t_Q)I(t_Q)(T-t_Q)$,

$C=\sum_{k=0}^{Q-1}I(t_k)\Delta t_k+I(t_Q)(T-t_Q)$, $D=\sum_{k=0}^{Q-1}\mathrm{sgn}(I(t_k)<I(t_{k+1}))$, That is, the number of times I increases,

$E=\sum_{k=0}^{Q-1}\mathrm{sgn}(I(t_k)>I(t_{k+1}))$, That is, the number of times I decreased.

The log-likelihood function is calculated as follows

$$l(\theta) = -B\beta t^{\alpha-1} - C\gamma t^{\alpha-1} + D\ln\beta + D(\alpha-1)\ln t + E\ln\gamma + E(\alpha-1)\ln t$$

The maximum likelihood estimation of parameters $\beta$ and $\gamma$ is obtained

$$\hat{\beta} = DB^{-1}t^{1-\alpha}, \hat{\gamma} = EC^{-1}t^{1-\alpha} \quad (7)$$

By finding a suitable $\alpha$ value, the estimation error is as low as possible.

**MCWM Algorithm**

In 2017, Fintzi proposed the MCWM algorithm to overcome the convergence difficulties caused by the latent variables of the Gibbs algorithm and the MH algorithm in the MCMC algorithm and the high correlation of model parameters[21]. The MCWM algorithm essentially replaces the likelihood ratio in the standard Metropolis algorithm with an approximate likelihood ratio calculated based on simulated data.

To reduce the error of operation or recording errors, observation data $Y_k$ can be calculated from the infection data $I_{t_k}$ at the $k$ moment, where $k \in \{1,2,\cdots,Q\}$. Given observation data $Y_k$ follows a normal distribution with a mean of $I_{t_k}$ and a variance of $\sigma^2$, that is, $Y_k \sim N(I_{t_k}, \sigma^2)$.

Remember the real state transition process $Z = \{Z^1, Z^2, \cdots, Z^M\}$ of each individual as potential data, where $M$ is the total number of iterations. State $Z_t^m = (S_t^m, I_t^m, R_t^m)$, $m = 1,2,\cdots,M$, iteration $m$ at moment $t$, the transition probability for the state $Z_t^m$ is equation (3).

Let $P_{t_1}(S_{t_1}, I_{t_1}, R_{t_1})$ represent the probability that an individual is susceptible, infected, and recovered at the time of first observation, state $Z_{t_1}$ follows a categorical distribution at the time of first observation[14]. The observed data plus the latent data obtain the complete data, so the likelihood function of the complete data is

$$\begin{aligned} L(Z,Y \mid \theta) &= P(Y \mid Z, \sigma^2) \times P(Z_{t_1} \mid P_{t_1}) \times P(Z \mid Z_{t_1}, \theta) \\ &= P_S^{S_{t_1}} P_I^{I_{t_1}} P_R^{R_{t_1}} \times \prod_{k=1}^{K} \frac{1}{\sqrt{2\pi\sigma^2}} \exp\left(-\frac{(Y_k - I_{t_k})^2}{2\sigma^2}\right) \\ &\times A\mathrm{e}^{-B\beta t^{\alpha-1} - C\gamma t^{\alpha-1}} (t^{\alpha-1}\beta)^D (t^{\alpha-1}\gamma)^E \end{aligned} \quad (8)$$

The above equation integrates the potential data to obtain the desired likelihood function $P(Y \mid \theta)$, considering that the likelihood function expression is too complex, the MC method is used to approximate the likelihood function. Then given observations $Y$ and parameter set $\theta$, the MC estimate $\hat{P}(Y \mid \theta)$ for $P(Y \mid \theta)$ is

$$\begin{aligned} \hat{P}(Y \mid \theta) &= P(Z_{t_1} \mid P_{t_1}) \times \frac{1}{R} \sum_{r=1}^{R} P(Y \mid Z^r, \sigma^2) \\ &\propto \frac{P_S^{S_{t_1}} P_I^{I_{t_1}} P_R^{R_{t_1}}}{R} \times \sum_{r=1}^{R} \frac{1}{\sigma^K} \exp\left(-\sum_{k=1}^{K} \frac{(Y_k - I_{t_k})^2}{2\sigma^2}\right) \end{aligned} \quad (9)$$

where $\theta^{(m)}$ is the parameter sampling value of the $m$ time, $\theta'$ is the updated parameter candidate value, $R$ is the number of simulations, and the $r$ simulation $r \in \{1,2,\cdots,R\}$ is the second time. The state $Z^r$ is the data of various groups of people in the fractional stochastic SIR model simulated by the Gillespie algorithm according to the initial number and parameters of the three types of population, that $Z_{t_1} \mid P_{t_1} \sim Gillespie(Z_{t_1}, \theta^{(0)})$. Combine the prior information of the parameter $\theta$ and the likelihood function to obtain the posterior probability $P(\theta \mid Y)$. So the acceptance probability of the MCWM algorithm is

$$a(\theta', \theta^{(i)}) = \min\{1, \frac{q(\theta^{(i)} \mid \theta')P(Y \mid \theta')P(\theta')}{q(\theta' \mid \theta^{(i)})P(Y \mid \theta^{(i)})P(\theta^{(i)})}\} \quad (10)$$

According to the MCWM algorithm, the parameter estimate of $\theta^{(0)}, \theta^{(1)}, \cdots, \theta^{(M)}$ is obtained, and the average value of the parameter estimation result of $M$ is taken as the estimate of the parameter $\theta$ of the fractional stochastic SIR model by the MCWM algorithm.

## IV. CASEANALYSIS

**The Case Of Influenza In British Boarding Schools**

Statistics on influenza patients, published in the British Medical Journal in 1978, counted the outbreak and epidemic of influenza in boarding schools for a total of 763 people from January 22 to February 4. The initial moment $S_0 = 762, I_0 = 1, R_0 = 0$, the parameters $\beta = 0.0022, \gamma = 0.4404$ [18]. In this paper, considering the influence of order on fractional SIR model, $\alpha$ gradually decreases from 1, and the second-order Adams-Bashforth method is used to obtain the numerical solution of the number of infected people by taking 1, 0.99, 0.98, 0.97, and 0.96, respectively, the software MATLAB was used to plot the trend of the number of infected people as shown in Figure 1. When $\alpha$ is 1, the fractional SIR model is equal to the integer SIR model.

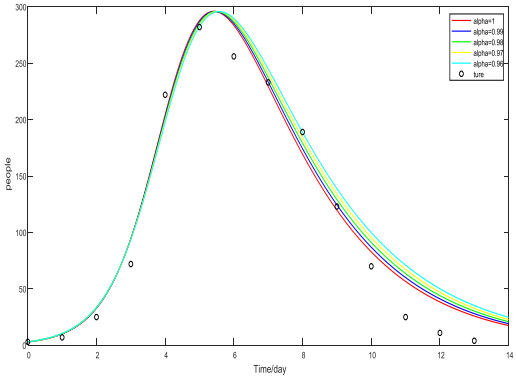


**Figure 1 Simulation diagram of fractional SIR model of British boarding school**

From Figure 1, it can be seen that the fractional SIR model can reasonably select a rate of change, that is, the fractional order of the model, To achieve a better fit of the real data.Table 1 shows the root mean square error(RMSE) between the simulated value and the original value to calculate the number of infected people. It can be found that when $\alpha = 0.91$, the RMSE of the fractional SIR model reaches the minimum value, and when $\alpha \in [0.83, 0.99]$ decreases to 0.82, the RMSE of the fractional SIR model exceeds the root mean square error of the integer SIR model.

| $\alpha$ | 1 | 0.97 | 0.94 | 0.91 | 0.88 | 0.85 | 0.83 | 0.82 |
|---|---|---|---|---|---|---|---|---|
| RMSE | 53.0903 | 48.8246 | 45.9251 | 44.9691 | 46.1776 | 49.5212 | 52.7604 | 54.6336 |

**Table 1 Root mean square error table of the number of infected persons in fractional SIR Model**

Considering that stochastic models are more realistic, according to the Gillespie stochastic simulation algorithm, the simulation data of the infected population of the stochastic SIR model and the fractional stochastic SIR model are respectively made to obtain Figure 2.

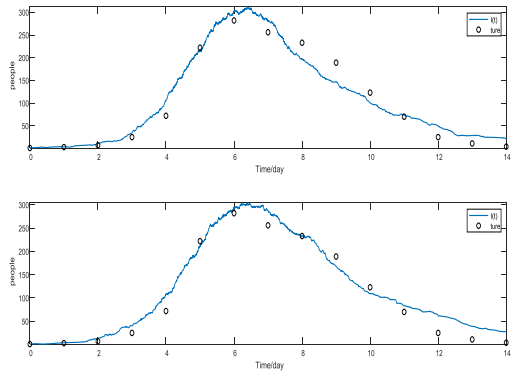


**Figure 2 Simulation diagram of fractional stochastic SIR model of British boarding school**

The upper figure of Figure 2 is the simulation diagram of the integerstochastic SIR model, and the figure below is the fractional stochastic SIR model, and the fractional order is 0.91. Comparing the above two figures, it can be seen that the integer stochastic SIR model is higher than the real data on days 1 to 6. On days 7

to 11, the simulated value is lower than the true value, and the overall fitting of the fractional stochastic SIR model is better than the integer order, which is relatively close to the true value, so the fractional stochastic SIR model fits better than the integer stochastic SIR model.

Considering the influence of parameters on the model, maximum likelihood estimation was used to estimate parameters $\beta$ and $\gamma$ of the stochastic SIR model and the fractional stochastic SIR model, respectively, generate a sample value of 5000 parameter estimates and use their mean as the final result of parameter estimation, and the results and RMSE pairs are shown in Table 2. Due to space limitations, some of the results are listed for comparison. It can be seen from Table 2 that when $\alpha \in [0.83, 0.99]$, the estimation result of the fractional stochastic SIR model is better than that of the integer stochastic SIR model.

| $\alpha$ | 1 | 0.97 | 0.94 | 0.91 | 0.88 | 0.85 | 0.82 |
|---|---|---|---|---|---|---|---|
| $\hat{\beta}$ | 0.0023 | 0.0022 | 0.0022 | 0.0022 | 0.0022 | 0.0022 | 0.0023 |
| $\hat{\gamma}$ | 0.4217 | 0.4278 | 0.4488 | 0.4563 | 0.4344 | 0.4267 | 0.4170 |
| RMSE | 24.9161 | 23.9433 | 20.6447 | 19.7083 | 21.1926 | 24.0995 | 25.0661 |

**Table2 Comparison table of maximum likelihood parameter estimates**

The MCWM algorithm was used to estimate the parameters of the fractional stochastic SIR model, a total of 10,000 iterations were performed, the burn-in period was set to 2000 periods, and the average of the parameter estimates in the next 8000 periods was taken as the final estimation result, and the parameter estimation results were shown in Table 3. Observation data $Y_k$ follows a normal distribution with a mean $I_{t_k}$ variance of $\sigma^2$, which $I_{t_k}$ is obtained by the Gillespie stochastic simulation algorithm and $\sigma^2$ is calculated from the infected population data obtained by the Gillespie stochastic simulation algorithm.

| $\alpha$ | 1 | 0.97 | 0.94 | 0.91 | 0.88 | 0.85 | 0.82 |
|---|---|---|---|---|---|---|---|
| $\hat{\beta}$ | 0.0020 | 0.0020 | 0.0021 | 0.0022 | 0.0021 | 0.0020 | 0.0020 |
| $\hat{\gamma}$ | 0.4181 | 0.4384 | 0.4341 | 0.4370 | 0.4426 | 0.4374 | 0.4147 |
| RMSE | 26.7194 | 23.9210 | 23.6085 | 22.1827 | 23.4231 | 24.0134 | 26.8195 |

**Table 3 Estimation of fractional stochastic SIR model by MCWM algorithm**

It can be seen that when $\alpha \in [0.83, 0.99]$, the MCWM algorithm has a better effect on the parameter estimation effect of the fractional stochastic SIR model than that of the integer stochastic SIR model, and the parameter estimation effect is best when $\alpha = 0.91$.

**SARS Case In Hong Kong**

The SARS epidemic in Hong Kong from March 31 to June 11, 2003, was counted given the isolation and control of the second phase of the epidemic, which was more in line with the setting of the model in this paper, initial moment $S_0 = 1290, I_0 = 497, R_0 = 33$, parameter $\beta = 1.12 \times 10^{-4}, \gamma = 0.046$ [23]. The numerical solution of the number of infected people was obtained by using the second-order Adams-Bashforth method when $\alpha$ was 1, 0.99, and 0.98, respectively, and the trend of the number of infected people was plotted by software MATLAB as shown in Figure 3.

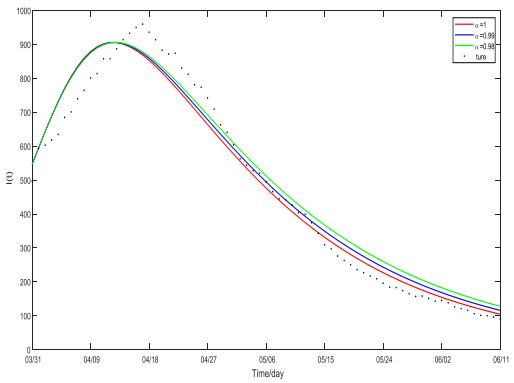


**Figure 3 Simulation diagram of fractional SIR model of Hong Kong SARS**

According to the simulation results, the RMSE between the simulated value of the infected number and the original data is calculated, and the RMSE of the integer SIR model is 49.3977. The RMSE of the fractional SIR model is 49.1924 ( $\alpha = 0.99$ ) and 52.7421 ( $\alpha = 0.98$ ), respectively, so when $\alpha = 0.99$ , the fractional SIR model fits better than the integer SIR model.

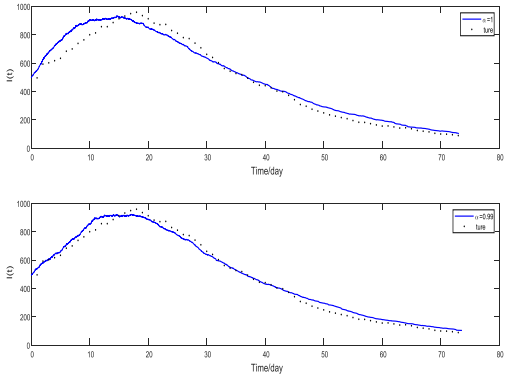


**Figure 4 Simulation diagram of fractional random SIR model of Hong Kong SARS**

Gillespie stochastic simulation algorithm was used to make the simulation data figure of the stochastic SIR model and fractional stochastic SIR model ( $\alpha = 0.99$ ) infected population, respectively. The upper figure of Figure 4 is the integer stochastic SIR model simulation diagram, and the following figure is the fractional stochastic SIR model simulation diagram. It can be seen that the stochastic SIR model fits the original data more closely than the determined SIR model, and the fitting effect of the integer stochastic SIR model in the first 40 days is worse than that of the fractional stochastic SIR model, and the fitting effect in the later stage is not much different. So the fractional stochastic SIR model fits better than the integer stochastic SIR model.

| | $\hat{\beta}$ | $\hat{\gamma}$ | RMSE |
|---|---|---|---|
| $\alpha = 1$ | $1.0365 \times 10^{-4}$ | 0.0389 | 42.3668 |
| $\alpha = 0.99$ | $1.0400 \times 10^{-4}$ | 0.0381 | 41.8384 |
| $\alpha = 0.98$ | $1.0269 \times 10^{-4}$ | 0.0373 | 44.3958 |

**Table 4 Comparison table of maximum likelihood parameter estimates**

Using maximum likelihood estimation to estimate the parameters $\beta$ and $\gamma$ of the stochastic SIR model and the fractional stochastic SIR model, respectively, the results of the parameters and the RMSE between the simulated value of the number of infected people and the original value are shown in Table 4, and when $\alpha = 0.99$ can be obtained from Table 4, the fractional stochastic SIR model has a better effect than the integer stochastic SIR model.

| | $\hat{\beta}$ | $\hat{\gamma}$ | RMSE |
|---|---|---|---|
| $\alpha = 1$ | $1.1929 \times 10^{-4}$ | 0.0466 | 51.6645 |
| $\alpha = 0.99$ | $1.1150 \times 10^{-4}$ | 0.0454 | 49.5413 |
| $\alpha = 0.98$ | $1.1109 \times 10^{-4}$ | 0.0451 | 52.2503 |

**Table 5 Estimation of fractional stochastic SIR model by MCWM algorithm**

The MCWM algorithm was used to estimate the parameters of the fractional stochastic SIR model, a total of 10,000 iterations were performed, the burn-in period was set to 2000 periods, and the average of the parameter estimates in the next 8000 periods was taken as the final estimation result, and the parameter estimation results were shown in Table 5. It can be seen that when $\alpha = 0.99$ , the MCWM algorithm has a better effect on the fractional stochastic SIR model than the integer stochastic SIR model parameter estimation effect, indicating that the algorithm is more applicable to the fractional stochastic SIR model.

This section analyzes the impact of different fractional orders on the model, which reflects the rate at which the number of infected people changes. At the same time, the parameter estimation of the integer stochastic SIR model and fractional stochastic SIR model using maximum likelihood estimation and MCWM algorithm were compared and analyzed. The results show that when $\alpha$ taking a value within a certain range, the

estimation error of the fractional stochastic SIR model is smaller than that of the integer stochastic SIR model, indicating that these two estimation methods have a better estimation effect on fractional stochastic SIR model than integer stochastic SIR model, and also indicates that the fractional stochastic SIR model is more suitable for real situations.

## V. CONCLUSION

In this paper, the Conformable fractional stochastic SIR model is proposed, the simulation plot of the integer stochastic SIR model and fractional stochastic SIR model is compared, and the ability to fit the original data is greatly improved by adjusting the order. At the same time, by using maximum likelihood estimation and the MCWM algorithm, the parameter estimation results of integer and fractional stochastic SIR models are compared. It is found that the value of the fractional order within a certain range can reduce the error of parameter estimation, and the estimation error is less than the result of the integer stochastic SIR model. It shows that the fractional stochastic SIR model can reasonably select the fractional order, to correctly understand and estimate the parameters of the infectious disease model, which is conducive to the prediction and prevention, and control of infectious diseases.

With the deepening of infectious disease model research in recent years, the research of fractional infectious disease models has become more and more popular. In the next research, consider the influence of more uncertain factors, establish a more complex fractional infectious disease model, such as the fractional infectious disease model with time-varying parameters, and analyze the model. At the same time, the parameter estimation method is optimized to predict the development direction of infectious diseases more accurately.

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