

# Impact of COVID-19 Pandemic on the Epidemiology of STDs in China: Based on the GM (1,1) Model

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## Research Article

**Keywords:** COVID-19, HIV infection, Syphilis, Gonorrhea, Epidemiology, GM (1,1)

**Posted Date:** February 23rd, 2022

**DOI:** <https://doi.org/10.21203/rs.3.rs-994599/v1>

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1 **Impact of COVID-19 pandemic on the epidemiology of STDs in China: based on**  
2 **the GM (1,1) model**

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1 **Abstract**

2 **Background:** It has been reported that COVID-19 pandemic has greatly impacted on  
3 the epidemiological trend of Sexually Transmitted Diseases (STDs) in many countries.  
4 However, relevant researches are limited in China. We aimed to analyze the extent of  
5 COVID-19 pandemic impact on STDs in China.

6 **Methods:** The incidence of HIV infection, syphilis and gonorrhea in China from 2008  
7 to 2020 was collected. But only data of these three STDs from 2013 to 2018 were used  
8 to establish the Grey Model (1,1) considering about the impact of policies of China.  
9 Then we calculated the predictive incidence of each STD in 2019, 2020 and 2021 by  
10 the established Model. And then we estimated the extent of the impact of COVID-19  
11 on the epidemiological changes of STDs by analyzing the difference between  
12 the absolute percentage error (APE) of the predictive incidence and actual rate in  
13 2019 and 2020.

14 **Results:** The incidence of HIV infection and syphilis showed an increasing trend from  
15 2008 to 2019 in China, but that for gonorrhea was fluctuant. Of note, the incidence of  
16 these three STDs decreased significantly in 2020 compared with that in 2019. The APE  
17 of HIV infection, syphilis and gonorrhea in 2020 (20.54%, 15.45% and 60.88%) were  
18 about 7 times, 4 times and 2 times of that in 2019 (2.94%, 4.07% and 30.41%). The  
19 incidence of HIV infection, syphilis and gonorrhea would be 5.77/100,000,  
20 39.64/100,000 and 13.19/100,000 in 2021 based on our model.

21 **Conclusions:** Our analysis revealed that the epidemiological trend of STDs in China  
22 was significant influenced by COVID-19 pandemic. The result highlights the critical

1 need for transformative strategies in STDs control in the context of the long-term effects  
2 of COVID-19 pandemic in the future.

3

4 **Keywords** COVID-19, HIV infection, Syphilis, Gonorrhoea, Epidemiology, GM (1,1)

5

## 6 **Introduction**

7 War, natural disaster, epidemic of infectious diseases and other social events would  
8 affect people's life and health [1]. Known as a catastrophe in global infectious disease  
9 history, the outbreak of Coronavirus Disease 2019 (COVID-19) pandemic has affected  
10 people's daily life, medical behavior and many other aspects [2, 3]. Researches have  
11 shown that the COVID-19 pandemic has influenced individual's sexual health, sexual  
12 behavior, and the diagnosis and treatment process of Sexually Transmitted Diseases  
13 (STDs), which in turn changed the epidemiological trend of STDs [4-7]. It reported that  
14 except Denmark [8], the incidence or reported cases of STDs in Spain, Greece, Cuba,  
15 and the US significantly decreased in 2020 compared with the corresponding period in  
16 2019 [5, 9-11].

17 As we know the prevalence of COVID-19 pandemic is different from country to  
18 country, and each country has introduced its own strategies to prevent and control the  
19 spread of COVID-19 [11, 12]. The research in Cuba found that when strict social  
20 restrictions are taken, the incidence of syphilis and gonorrhoea continued to decline,  
21 while following social measures subsequently relaxed, the incidence of syphilis was  
22 increased [10]. As a country with a sustained rise in STDs incidence in recent years [13,  
23 14], however, relevant researches are limited about the influence of this pandemic on

1 the STDs in China. HIV infection, syphilis and gonorrhea are national statutory  
2 infectious diseases in China, so in this study we aim to analyze the extent of the COVID-  
3 19 pandemic impact on these three STDs in China by using the Grey Model (1,1) (GM  
4 (1,1)).

5 The grey prediction in the grey system theory (GST), is used to investigate a large  
6 amount of unknown information using a small amount of information in a system  
7 containing incomplete data, which was firstly proposed by Professor Julong Deng in  
8 the 1980s [15]. In the grey prediction model GM (n,m), 'n' and 'm' represents the order  
9 of the differential equation and the number of variables respectively. The GM (1,1)  
10 model is the classical primary time-series predictive model, representing the first-order  
11 model with a single variable, was most commonly used in grey system theory due to its  
12 virtue of "strong adaptability, simple model, easy parameter changes" [16, 17]. It is  
13 widely used to predict in the industries of energy [18], environment [19], medical and  
14 health institutions [16, 20]. Therefore, in the present study we used the GM (1,1) model  
15 to analyze the influence of COVID-19 pandemic on the epidemiological changes of  
16 STDs in China. Hopefully this study can provide predictive information for the  
17 allocation of medical resources and policy formulation during the COVID-19 pandemic.

18

## 19 **Methods**

### 20 **Data collection**

21 HIV infection, syphilis and gonorrhea are national statutory infectious diseases in China,  
22 therefor the reported data of the incidence of these three STDs were collected in this

1 study. The incidence of each STD from 2008 to 2020 was collected from the website of  
2 Administration for Disease Control and Prevention of China [21], shown in Additional  
3 file 1: Table S1.

#### 4 **The establishment of the GM (1,1) model**

5 As we know China revised *the Law of the People's Republic of China on Prevention*  
6 *and Control of Infectious Diseases* for the second time in 2013 [22], which further  
7 strengthened the prevention and control of infectious diseases. Therefore only data of  
8 the actual incidence of each STD from 2013 to 2018 were used to establish the GM (1,1)  
9 model considering about the impact of policies. Then we calculated the predictive  
10 incidence of each STD in 2019, 2020 and 2021, which approximately represented the  
11 incidence value without influence of COVID-19 pandemic. We further calculated the  
12 absolute percentage error (APE) between actual incidence and predictive value in 2019  
13 and 2020. And then we estimated the extent of impact of the COVID-19 pandemic on  
14 the epidemiological changes of STDs in China, according to the difference between the  
15 APE in 2019 and 2020.

16 The grey prediction has three basic operations: Cumulative Generation Operator  
17 (AGO), Inverse Accumulated Generating Operation (IAGO) and Grey Model (GM)  
18 [23]. The steps of the GM (1,1) is as follows:

19 Step 1. Suppose the original data sequence  $X^{(0)}$  with n sample showed in Eq.(1).

$$20 \quad X^{(0)} = (x^{(0)}(1), x^{(0)}(2), x^{(0)}(3), \dots, x^{(0)}(n)) \quad n \geq 4 \quad (1)$$

21 Where  $x^{(0)}(i) > 0, i = 1, 2, 3 \dots n$ . Then transforming the  $X^{(0)}$  to the monotonically  
22 increasing series  $X^{(1)}$  using a first time AGO (1-AGO) showed in Eq.(2). This aims to

1 weaken the random factors of the original time series data, strengthen its regularity.  
 2 Then establish the differential equation of the generated number from which the data  
 3 can be predicted and estimated.

$$4 \quad X^{(1)} = (x^{(1)}(1), x^{(1)}(2), x^{(1)}(3), \dots, x^{(1)}(n)) \quad (2)$$

5 where,

$$6 \quad x^{(1)}(k) = \sum_{i=1}^k x^{(0)}(i) \quad k = 1, 2, 3, \dots, n \quad (3)$$

7 Step 2. A first-order grey differential equation is formed to obtain GM (1,1) model  
 8 shown in Eq.(4).

$$9 \quad x^{(0)}(k) + aZ^{(1)}(k) = b \quad k = 2, 3, 4, \dots, n \quad (4)$$

10 where,

$$11 \quad Z^{(1)}(k) = \frac{1}{2} [x^{(1)}(k) + x^{(1)}(k-1)] \quad k = 2, 3, 4, \dots, n \quad (5)$$

12 Where 'a' represent the developing coefficient and 'b' represent the driving  
 13 coefficient.  $Z^{(1)}(k)$  is the background value of  $x^{(0)}(k)$ . The two parameters 'a' and 'b'  
 14 can be estimated by the least square method  $[a, b]^T$  shown in Eq.(6).

$$15 \quad \begin{bmatrix} a \\ b \end{bmatrix} = [B^T \quad B]^{-1} B^T Y \quad (6)$$

16 Where 'Y' is the constant vector, and 'B' is the accumulated matrix showed in Eq.(7)  
 17 and Eq.(8).

$$18 \quad Y = \begin{bmatrix} x^0(2) \\ x^0(3) \\ x^0(4) \\ M \\ M \\ x^0(n) \end{bmatrix} \quad (7)$$

$$B = \begin{bmatrix} -Z^{(1)}(2) & 1 \\ -Z^{(1)}(3) & 1 \\ -Z^{(1)}(4) & 1 \\ M & M \\ M & M \\ -Z^{(1)}(n) & 1 \end{bmatrix} \quad (8)$$

Step 3. The approximate differential equation (whitening equation) model is established by using the discrete data sequence as Eq.(9).

$$\frac{dX^{(1)}}{dk} + aX^{(1)} = b \quad (9)$$

The predicted value,  $\hat{x}^{(1)}(k+1)$ , can be obtained by solving the differential equation with initial condition  $x^{(1)}(1) = x^{(0)}(1)$ .

$$\hat{x}^{(1)}(k+1) = \left[ x^{(0)}(1) - \frac{b}{a} \right] e^{-ak} + \frac{b}{a} \quad k = 1, 2, 3, \dots, n \quad (10)$$

Finally, by means of the IAGO, the predicted value,  $\hat{x}^{(0)}(k+1)$ , can be calculated as follows:

$$\hat{x}^{(0)}(k+1) = \hat{x}^{(1)}(k+1) - \hat{x}^{(1)}(k) \quad k = 1, 2, 3, \dots, n \quad (11)$$

therefore,

$$\hat{x}^{(0)}(k+1) = (1 - e^a) \left( x^{(0)}(1) - \frac{b}{a} \right) e^{-ak} \quad k = 1, 2, 3, \dots, n \quad (12)$$

Note that  $\hat{x}^{(1)}(1) = \hat{x}^{(0)}(1)$  holds.

### 14 The accuracy evaluation metrics of the GM (1, 1) Model

Prediction accuracy is an important criterion for evaluating the performance of a forecasting model. In this study, two ways were used to estimate the accuracy of the GM (1, 1) model: the absolute error size test and the posterior deviation test [24].

1 (1) *The Absolute Error Size Test*. It is used to observe whether the absolute error  
 2 meets the requirements by comparing the predicted incidence and the actual value of  
 3 STDs in this study. The APE is showed as Eq.(13).

$$4 \quad \text{APE} = \left| \frac{x^{(0)}(i) - \hat{x}^{(0)}(i)}{x^{(0)}(i)} \right| \times 100\% \quad (13)$$

5 The mean absolute percentage error (MAPE) of GM (1,1) is used to measure the  
 6 prediction performance with respect to  $x^{(0)}(k)$  ( $k = 2,3,4 \dots, n$ ) can be calculated as  
 7 Eq.(14).

$$8 \quad \text{MAPE} = \frac{1}{n} \left( \sum_{i=2}^n \left| \frac{x^{(0)}(i) - \hat{x}^{(0)}(i)}{x^{(0)}(i)} \right| \right) \times 100\% \quad (14)$$

9 Meanwhile, Lewis' criterion shown in Table 1 is used to illustrate the prediction  
 10 ability of the model [25]. According to that the established GM (1.1) model can be  
 11 graded four levels "Excellent, Good, Reasonable and Incorrect", respectively. The  
 12 better the grading, the better the predictive effectiveness of the model.

13 **Table 1** Lewis' criterion for model evaluation. Reproduced with permission from Ref.  
 14 [25]. Copyright 2021 Elsevier.

MAPE (%)	Prediction performance
<10	Excellent
10-20	Good
20-50	Reasonable
>50	Incorrect

15 The accuracy of GM (1, 1) model is  $P^o$  showed as Eq.(15).

$$16 \quad P^o = (1 - \text{MAPE}) \times 100\% \quad (15)$$

17 General requirement is  $P^o > 80\%$ .

1 (2) *The Posterior Deviation Test*. It is tested according to the probability distribution  
 2 of residual. The posterior variance ratio  $C$  and the posterior probability  $P$  are two main  
 3 indicators used to evaluate the accuracy of the model.

4 Calculate the a posteriori variance ratio  $C$  as Eq.(16).

$$5 \quad C = \frac{S_2}{S_1} \quad (16)$$

6 where,

$$7 \quad S_1 = \sqrt{\frac{1}{n} \sum_{k=1}^n [x^{(0)}(k) - \bar{x}]^2} \quad (17)$$

8 and,

$$9 \quad S_2 = \sqrt{\frac{1}{n} \sum_{k=1}^n [\varepsilon(k) - \bar{\varepsilon}]^2} \quad (18)$$

10 Calculate the posterior probability  $P$  as Eq.(19).

$$11 \quad P = P\{|\varepsilon(k) - \bar{\varepsilon}| < 0.6745S_1\} \quad (19)$$

12 where,

$$13 \quad \bar{x} = \frac{1}{n} \sum_{k=1}^n x^{(0)}(k) \quad (20)$$

$$14 \quad \bar{\varepsilon} = \frac{1}{n} \sum_{k=1}^n \varepsilon(k) \quad (21)$$

$$15 \quad \varepsilon(k) = x(k) - \hat{x}(k) \quad (22)$$

16 The smaller the  $C$  value, the more concentrated the difference between the model  
 17 predicted value and the actual value. Meanwhile, the larger the  $P$  value, the less  
 18 difference between the residual and the residual mean, and the higher fitting accuracy  
 19 of the GM (1,1) model. According to the size of the value of  $C$  and  $P$ , the predictive

1 accuracy rating of the established GM (1,1) model can be graded into four levels

2 “Superior, Qualified, Marginal and Disqualified” [13], as shown in Table 2.

3 **Table 2** The Posterior Deviation criterion of predictive accuracy for the GM (1,1).

4 Reproduced with permission from Ref. [13]. Copyright 2019 Medical science monitor

5 (CC BY-NC-ND 4.0).

Predictive accuracy	posterior variance	posterior probability	
class	ratio (C)	(P)	
Superior	$\leq 0.35$	$\geq 0.95$	7
Qualified	$0.35 < C \leq 0.50$	$0.80 \leq P < 0.95$	8
Marginal	$0.50 < C \leq 0.65$	$0.70 \leq P < 0.80$	9
Disqualified	$> 0.65$	$< 0.70$	10

## 11 Statistical analysis

12 All data were analyzed using SPSS 26.0 software, and the trend chi-square test was

13 adopted to conduct statistical analysis of the data trends which are described as  $\chi^2$ trend.

14 Finally,  $p < 0.05$  were considered as statistically significant. The construction, operation

15 and verification of the GM (1,1) model was done by using Python software.

16

## 17 Results

### 18 The epidemiological status of STDs in China.

19 The results showed that the incidence of HIV infection ( $\chi^2$ trend=10.588,  $p = 0.001$ ) and

20 syphilis ( $\chi^2$ trend=9.893,  $p = 0.002$ ) presented an increasing trend from 2008 to 2019,

21 with an annual growth rate of 18.89% and 6.35%, respectively (Fig. 1). While for

22 gonorrhoea, it was constantly fluctuating in recent years ( $\chi^2$ trend=0.159,  $p = 0.69$ ) (Fig.

1) The incidence of HIV infection, syphilis and gonorrhea declined by 13.1%, 13.8% and 11.4% in 2020 (4.43/100,000, 33.08/100,000, 7.49/100,000, respectively), compared with that in 2019 (5.1/100,000, 38.37/100,000, 8.45/100,000, respectively) (Fig. 1), respectively. Therefore, we further used the GM (1,1) model to analyze the extent of COVID-19 pandemic impact on STDs in China.

### 6 The established GM (1,1) model of HIV infection, syphilis and gonorrhea

The GM (1,1) model was established based on the original data of the incidence of HIV infection, syphilis and gonorrhea from 2013 to 2018, respectively. The fixed values of parameters ‘a’, ‘b’, and the formula of predictive incidence was shown in Table 3.

10 **Table 3** The GM (1,1) model of each STD

	a	b	b/a	GM (1,1) model
HIV infection	-0.077	2.998	-39.026	$\hat{x}^{(0)}(k + 1) = 3.117e^{0.077k}$
Syphilis	-0.037	28.922	-785.691	$\hat{x}^{(0)}(k + 1) = 29.482e^{0.037k}$
Gonorrhea	-0.090	6.050	-67.028	$\hat{x}^{(0)}(k + 1) = 6.420e^{0.090k}$

11

As our results shown, for HIV infection the model test indexes MAPE = 1.37%,  $P^o = 98.63\%$ , and  $C = 0.012$ ,  $P = 1$  (Table 4), for syphilis the MAPE = 1.16%,  $P^o = 98.84\%$ , and  $C = 0.052$ ,  $P = 1$  (Table 4), for gonorrhea the MAPE = 3.74%,  $P^o = 96.26\%$ , and  $C = 0.132$ ,  $P = 1$  (Table 4). According to Lewis’ criterion (Table 1) and the Posterior Deviation criterion (Table 2), the model of HIV infection, syphilis and gonorrhea were all graded “Excellent” and “Superior”. The comprehensive evaluation showed that the established GM (1,1) model can be best used to popularize and forecast the incidence

1 of each STD. The predictive value and actual incidence of each STD was shown in  
 2 Table 4.

3 **Table 4** Forecasting results of the GM (1,1) model in each STD

Years	HIV infection			Syphilis			Gonorrhoea		
	Actual incidence (1/100000)	Predictive incidence (1/100000)	APE(%)	Actual incidence (1/100000)	Predictive incidence (1/100000)	APE(%)	Actual incidence (1/100000)	Predictive incidence (1/100000)	APE(%)
2013	3.12	-	-	30.04	-	-	7.36	-	-
2014	3.33	3.37	1.20	30.93	30.59	1.10	7.05	7.02	0.43
2015	3.69	3.64	1.36	31.85	31.75	0.31	7.36	7.69	4.48
2016	3.97	3.93	1.01	31.97	32.94	3.03	8.39	8.41	0.24
2017	4.14	4.24	2.42	34.49	34.18	0.90	10.06	9.20	8.55
2018	4.62	4.58	0.87	35.63	35.47	0.45	9.59	10.07	5.01
<b>MAPE(%)</b>		1.37			1.16			3.74	
<b>P<sup>o</sup>(%)</b>		98.63			98.84			96.26	
<b>C</b>		0.012			0.052			0.132	
<b>P</b>		1			1			1	
2019	5.1	4.95	2.94	38.37	36.81	4.07	8.45	11.02	30.41
2020	4.43	5.34	20.54	33.08	38.19	15.45	7.49	12.05	60.88
2021	-	5.77	-	-	39.64	-	-	13.19	-

4

5 **For HIV infection**

6 The predictive incidence of HIV infection in 2019 and 2020 were 4.95/100,000,  
 7 5.34/100,000 (Table 4), respectively. And the APE between the predictive incidence and  
 8 actual value in 2020 (20.54%) was about 7 times of that in 2019 (2.94%) (Table 4). The  
 9 error value between predictive and actual incidence of HIV infection in 2020 was about  
 10 0.91/100,000. The result showed a striking difference between the predictive incidence  
 11 and the actual value of HIV infection in 2020, indicating that the actual incidence  
 12 significantly influenced by COVID-19 pandemic.

13 **For syphilis**

1 In syphilis, the predicted incidence was 36.81/100,000, 38.19/100,000 in 2019 and 2020  
2 (Table 4), respectively. The value of APE in 2020 (15.45%) was about 4 times of that  
3 in 2019 (4.07%), which showed a significant difference between predictive and actual  
4 incidence of syphilis in 2020. The result indicated that COVID-19 has impacted on the  
5 actual incidence of syphilis similarly to HIV infection in 2020. And the error value was  
6 about 5.11/100,000 between the predictive incidence and the actual value of syphilis in  
7 2020.

#### 8 **For gonorrhea**

9 As shown in Table 4, the predictive incidence of gonorrhea was 11.02/100,000 and  
10 12.05/100,000 in 2019 and 2020, respectively. The APE in 2020 (60.88%) was about 2  
11 times of that in 2019 (30.41%). The difference between the predictive incidence and the  
12 actual value in 2020 is a result of the influence of COVID-19 pandemic. And the error  
13 value between predictive and actual incidence was about 4.56/100,000.

14 From the analysis of the three kinds of STDs above, we found that the  
15 epidemiological feature of STDs in China was significantly changed during COVID-  
16 19 pandemic and was dramatically decreased in 2020.

#### 17 **Forecasting results of each STD in 2021**

18 The incidence of HIV infection, syphilis and gonorrhea would be 5.77/100,000,  
19 39.64/100,000 and 13.19/100,000 in 2021 based on our model (Table 4), respectively.  
20 It reflects a continuously increasing trend of the incidence of STDs in the following  
21 year.

22

## 1 **Discussion**

2 STDs remain the most common contagious diseases worldwide. According to  
3 WHO, the estimated new infections of syphilis and gonorrhea were about 6 million and  
4 78 million globally in 2016 [26]. By 2020, about 77.5 million people have been infected  
5 with HIV worldwide, and approximately 34.7 million people have died from AIDS-  
6 related diseases since the first case of HIV infection was reported [27].

7 In China, HIV infection, syphilis and gonorrhea are national statutory infectious  
8 diseases, and the incidence of these three reported STDs showed an increasing trend in  
9 recent twenty years [13, 14]. According to the latest reports from the *Administration for*  
10 *Disease Control and Prevention of China* [21], there were 62,167, 464,435 and 105,160  
11 people had been infected with HIV, syphilis and gonorrhea in 2020, respectively, which  
12 were dramatically decreased by 12.7% (71,204), 13.3% (535,819) and 10.8% (117,938)  
13 compared with that in 2019. As our results shown (Fig. 1), the incidence of HIV  
14 infection and syphilis presented an increasing trend in recent years, while the incidence  
15 of gonorrhea presented a form of fluctuation. However, this increasing trend was broken  
16 in 2020. The incidence of HIV infection, syphilis and gonorrhea all dramatically  
17 declined by 13.1%, 13.8% and 11.4% in 2020 compared with that in 2019, respectively,  
18 as shown in our results (Fig. 1).

19 China experienced the COVID-19 pandemic at the beginning of 2020. Though the  
20 COVID-19 pandemic happened in Wuhan at that time, the run on medical resources  
21 caused panic across the country [28]. At the same time, the country has also taken a  
22 number of prevention measures, such as city closure, home-staying, keep social

1 distance, advocating wearing masks and hands hygiene, emergency medical assistance  
2 for COVID-19, which effectively contained the spread of COVID-19 [12, 29, 30].  
3 However, all those measures have had a profound impact on sexual health and behavior  
4 of individual [4]. As reported by Bonett, Stephen et al. [31] the disruptions in sexually  
5 transmitted infection (STI) testing infrastructure during the COVID-19 pandemic  
6 threaten to impact STI service. The STI test counts decreased and test positivity  
7 increased during the pandemic period. According to the report from Greece, Cuba and  
8 other countries, the epidemiology of STDs has been widely affected by the COVID-19  
9 pandemic, and presented a dramatically decreased trend [5, 8-10]. The same situation  
10 could happen in China, in our unpublished data at the STD clinic in Shanghai Skin  
11 Disease Hospital, we found that patients with STDs interrupted follow-up at the  
12 beginning of the COVID-19 outbreak, and the first visit patients sharply declined. Our  
13 observed reduction of hospital visits in patients with STDs during COVID-19 pandemic,  
14 similar to those with non-COVID-19 related disease which has been reported elsewhere  
15 [32]. Two out of the three STD clinics of our hospital which located in the center  
16 Shanghai were closed meanwhile. Based on a survey in our hospital (unpublished data),  
17 people reduced their high-risk sexual behavior because of fear of being infected with  
18 the COVID-19. In this study, we analyzed the extent of COVID-19 pandemic's impact  
19 on the epidemiological trend of STDs in China. We found that the APE of HIV infection,  
20 syphilis and gonorrhoea in 2020 was about 7 times, 4 times and 2 times of that in 2019,  
21 which revealed a significant change of the epidemiology of STDs in 2020, especially  
22 HIV infection and syphilis. Though it is not clear whether the sharp decline in the

1 incidence of STDs in 2020 was due to the fact that the STDs was hidden by the COVID-  
2 19 pandemic, or that STDs had been controlled because of the policy of “city closure,  
3 home-staying, keep social distance, lockout, postponed the opening of school, and so  
4 on ”, or people reduced their high-risk sexual behavior during COVID-19 pandemic,  
5 due to the fear and anxiety of people about the highly contagious characteristics of  
6 COVID-19, we suspect that both might contribute to the STDs incidence decline in  
7 China.

8 The management of STDs should focus on early detection, early treatment, and  
9 prevention. However, in 2020, under the influence of COVID-19, the prevention and  
10 treatment of STDs may somewhat be hindered. The research shown by Patrícia M.  
11 Pascoal, et al. highlighted the role of mental health in the impact of COVID-19 on  
12 sexual health [4]. Due to the increasing difficulty in the supervision of STDs during  
13 COVID-19, the real situation of the epidemiology of STDs may be underestimated, and  
14 STDs incidence might rebound after a long-term development, resulting in a more  
15 serious disease burden of society. Therefore, except for emphasizing those well-known  
16 policies to prevent STDs, such as education on sexual healthy, condom use, partner  
17 notification, et al. [33] it is very important that in the event of major pandemics, medical  
18 resources should be reasonably allocated. When managers strengthening pandemic  
19 control, the medical aid resources for STDs should be protected from damage, to  
20 prevent increasing heavier burden of social diseases in the long-term process. In the  
21 event of major pandemics, people's mental health should be guided in a timely manner.  
22 The official notice should play a positive role in guiding the real-time reporting of the

1 pandemic, guiding the public to prevent diseases with scientific means, to reduce the  
2 fear and anxiety of people caused by the pandemic.

3 This study also predicted the burden of STDs in 2021, which showed an increasing  
4 incidence trend, warning that we should always keep an eye on the transmission of  
5 STDs seriously in China. And with the pandemic is well controlled in China for that  
6 time, a much little difference between predictive and real infection rate would be strong  
7 evidence to prove our findings.

8 There are some limitations in our study. As we know the GM(1,1) model is a time-  
9 series model [15], “Simplicity and efficiency” are the advantages of it. However, using  
10 a time-series model to predict the trend of STDs has its inevitable limitations, because  
11 the time-series predictive model mainly emphasizes the influence of time factor, which  
12 cannot comprehensively show the influence of various factors. While for STDs, the  
13 sexual behavior of the population dictates the incidence and trend of the pandemic. As  
14 mentioned, the pandemic of COVID-19 could have impacted the epidemiology of STDs  
15 in a number of ways. Positively, it could reduce the chance of high-risk sexual behaviors.  
16 Because of social-distancing and lockdown, casual and commercial sex would decline  
17 and reduce the incidence of STDs. Negatively, COVID-19 might disrupt healthcare  
18 services, such as HIV testing, following and distribution of antiretroviral therapy (ART)  
19 drugs, and all these increases the risk of STDs transmission. Further, the number of  
20 diagnoses during COVID-19 also drops might because less testing has been conducted.  
21 Therefore the GM(1,1) model in this study might not reflect the actual transmission of  
22 the three diseases.

1

## 2 **Conclusions**

3 Despite the potential limitation, our research showed the significant impact of COVID-  
4 19 pandemic on the epidemiological trend of STDs in China. During the period of  
5 COVID-19 pandemic, the incidence of STDs reduced accordingly. Above all, our  
6 findings highlight that transformative strategies in STDs control is highly needed under  
7 the context of the long-term effects of COVID-19 pandemic in the future.

8

## 9 **Abbreviations**

10 COVID-19: Coronavirus Disease 2019; STD: Sexually Transmitted Disease; APE:  
11 Absolute Percentage Error; MAPE: Mean Absolute Percentage Error; *C*: posterior  
12 variance ratio; *P*: posterior probability.

13

## 14 **Supplementary information**

15

16 **Additional file 1: Table S1.** The actual incidence of each STD from 2008 to 2020 in  
17 China (1/100000).

18

19 **Acknowledgments** We greatly appreciate Professor Lei Zhang for his valuable  
20 suggestions of the manuscript. A/Prof Zhang is the head of Artificial Intelligence and  
21 Modelling in Epidemiology Program, Central Clinical School, Monash University,  
22 Australia.

23

## 24 **Declarations**

25

1 **Authors' contributions** PZ and JY designed the study. JY collected the data. JY and  
2 YL analyzed the data. JY wrote the first draft of the manuscript. All authors contributed  
3 to the interpretation of the results and critical revision of the manuscript for important  
4 intellectual content. All authors have read and approved the final version. PZ is the  
5 guarantor of this study.

6

7 **Funding** This work was supported by grants from National Natural Science Foundation  
8 of China (grant number: 81572039), Shanghai Science and Technology Commission  
9 (grant number: 16411961300, 17DZ2293300, YDZX20193100002868), Clinical  
10 Research Plan of SHDC (grant number: 16CR3111B, 16CR1029B), National  
11 megaproject on key infectious diseases (grant number: 2017ZX10202102-001-007).

12

13 **Competing interests** The authors declare that they have no competing interests.

14

15 **Ethics approval and consent to participate** Not applicable.

16

17 **Consent for publication** Not applicable.

18

19 **Availability of data and materials** All data generated or analysed during this study are  
20 included in this published article and its supplementary information files. The original  
21 data was obtained from the website of Administration for Disease Control and  
22 Prevention of China, publicly available at

23 [http://www.nhc.gov.cn/jkj/new\\_index.shtml](http://www.nhc.gov.cn/jkj/new_index.shtml).<sup>[21]</sup>

24

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5

6 **Figure Legend:**

7 Fig. 1 The incidence of each STD from 2008 to 2020 in China.

8

9

# Figures

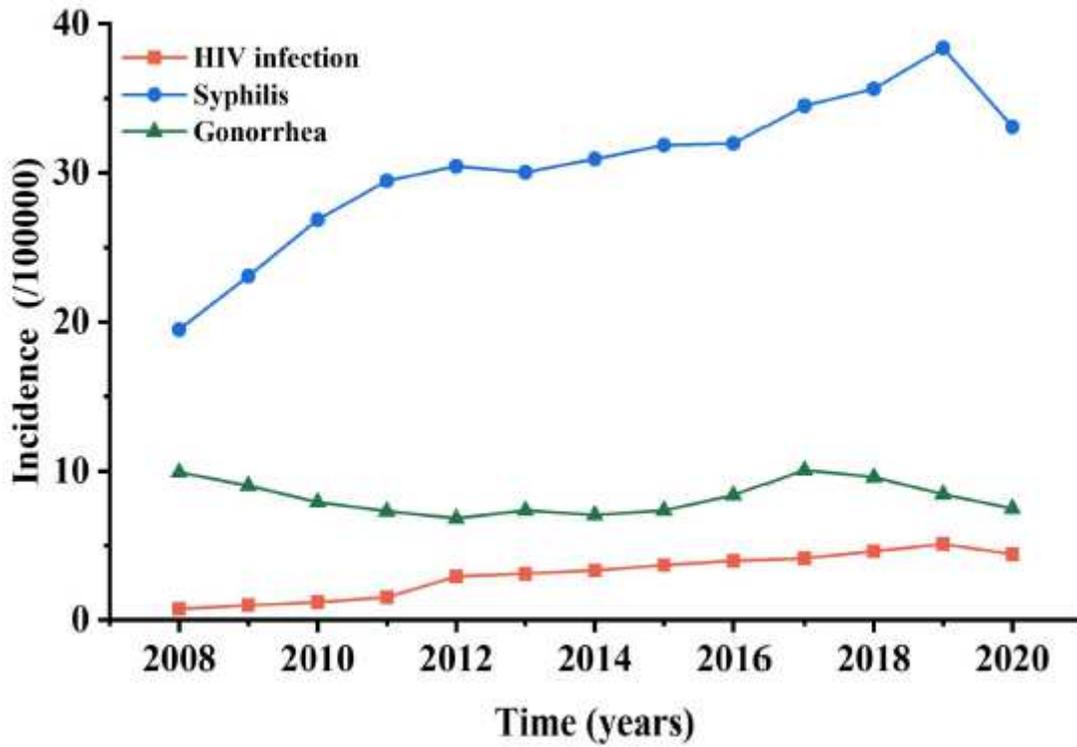


Figure 1

The incidence of each STD from 2008 to 2020 in China.

## Supplementary Files

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