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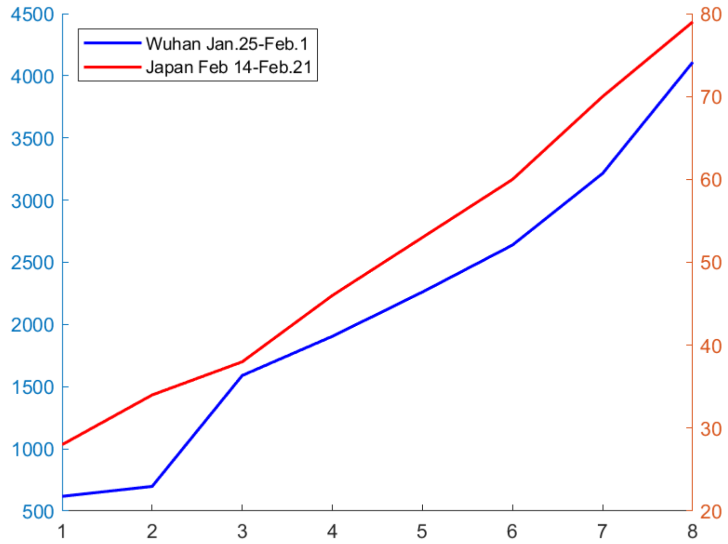
COVID-19 in Japan: What could happen in the future?



上海市现代应用数学重点实验室
Shanghai Key Laboratory of Contemporary Applied Mathematics

COVID-19 in Japan: What could happen in the future?

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COVID-19 has been impacting on the whole world critically and constantly Since December 2019. We have independently developed a novel statistical time delay dynamic model on the basis of the distribution models from CCDC.

Only based on the numbers of confirmed cases in different regions in China, the model can clearly reveal that the containment of the epidemic highly depends on early and effective isolation. We apply the model on the epidemic in Japan and conclude that there could be a rapid outbreak in Japan if no effective quarantine measures are carried out immediately as soon as possible.

Is it just similar?

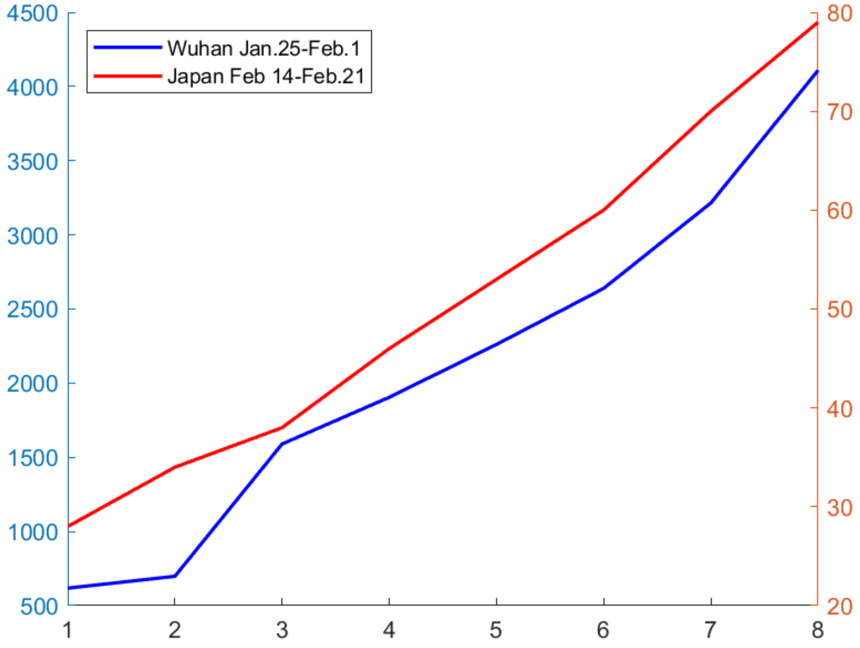

Figure 1: Cumulative number of confirmed cases in Wuhan, China (in blue) and Japan (in red).

Figure 1 shows the cumulative number of confirmed cases in Wuhan, China (Jan.25th–Feb.1st, in blue) and Japan (Feb14th–Feb21st, in red). We find that the epidemic development of the early stage of COVID-19 in Japan is very similar to that in Wuhan, China in one similiar linear growth. We suspect that there may be similarities in future trend. Therefore, we forecast that the situation in Japan is hardly optimistic, if the current isolation rate of Wuhan is used for Japan. We should concern that there could be a possible severe outbreak in Japan if no strong quarantine strategy are carried out as early as possible.

Background

In December 2019, a pneumonia of unknown cause broke out in Wuhan, Hubei Province. The atypical pneumonia was caused by 2019 novel coronavirus, later named as COVID-19 by World Health Organization. As of Feb 20, 2020, there have been 74675 confirmed cases in mainland China and spread to 26 countries (20). Given that Wuhan is the major transportation hub in central China, the epidemic also spread domestically to other major Chinese cities such as Beijing, Shanghai, Chongqing, Guangzhou and Shenzhen (1). COVID-19 is a group of SARS-like coronaviruses (2) and closely related to SARS-CoV and MERS-CoV. All of them are zoonotic viruses and epidemiologically similar. It is reported that human-to-human transmission has occurred among close contacts since the middle of December 2019 on the basis of evidence from early transmission dynamics (3). Cases found outside Wuhan also indicate independent self-sustaining human-to-human spread in multiple Chinese major cities (20). Thus the risk of epidemic outbreak cannot be neglected outside Wuhan.

COVID-19 raised intense attention not only within China but internationally, people concerned about the spread of epidemic and its development trend. Many researchers devoted to the modelling of the epidemic. Specifically, there are some works focused on the effect of migration and transportation on the spread of epidemic. In (4), they estimated the probability of transportation of COVID-19 from Wuhan to 369 cities in China before the quarantine of Wuhan with the expected risk greater than 50% in 130

(95% CI 89-190) cities and greater than 99% in the 4 largest metropolitan areas of China. In (5), they conducted the research of feasibility of controlling COVID-19 outbreaks by isolation of cases and contacts. Their results showed it can hardly work with a high value of R_0 and a large initial number of cases when less than 1% of transmission occurred before symptom onset. Similarly, $(1, 6)$ also suggested proper transmissibility reduction to avoid the outbreak of epidemic. Case numbers are rising exponentially in multiple cities due to human-to-human transmission. To possibly secure containment of the spread of infection, substantial public health interventions should be considered and carried out immediately. Multiple provinces including Hubei have adopted measures such as metropolitan-wide quarantine and reduction of inter-city mobility. Isolation of patients and trace and quarantine contacts as early as possible are still crucial because asymptomatic infection appears possible (7).

On the other hand, many researchers devoted to more details about the quantitative analysis of the spread of epidemic with some novel models. For instance, (8) adopted a novel statistical time delay dynamic system to estimate the reproductive number R_0 of COVID-19 based on Wallinga and Lipsitch framework (9) with distribution of the generation interval of the infection obtained. The growth rate of COVID-19 almost in $[0.30, 0.32]$ is larger than that estimated by CCDC (3), also the reproductive number R_0 estimated in $[3.25, 3.4]$ of COVID-19 is bigger than that of SARS. Some paralleled results also have been shown based on different models, see $(1, 5, 10–14)$.

In our study, we simulate and predict the outbreak trend of COVID-19 in multiple cities in China, as well as the growth rate and basic reproductive number of the epidemic with a novel statistical time delay dynamic model. Our model appears to be consistent with the current situation in several cities including Wuhan, and the epidemic situation in Japan is quite similar to that in Wuhan. Thus, we apply the model to track and predict the spread of COVID-19 in Japan. Our findings could provide potent evidence for enhancing public health interventions to avoid severe outbreaks.

Model

The data employed in this paper are the cumulative confirmed cases from Jan 16, 2020 to Feb 21, 2020 (for mainland China), and from to (for Japan) acquired from the National Health Commission of China (http://www.nhc.gov.cn), and Ministry of Health, Labour, and Welfare, Japan (https://www.mhlw.go.jp/index.html). All the data can be accessed publicly. No other data are used in this paper.

As the data are announced daily, we apply the following discrete version of the FUDAN-CCDC model proposed recently (8):

$$\begin{aligned} I(t+1) &= I(t) + rI_0(t), \\ J(t+1) &= J(t) + r\sum_{s\le t} f_4(t-s)I_0(s), \\ G(t+1) &= G(t) + \ell(t)\sum_{s\le t} f_2(t-s)I_0(s) - \ell(t)\sum_{s\le t} f_4(t-s)I_0(s). \end{aligned}$$

A sketch map of the model is displayed in Figure 2. Here $I(t)$ represents the cumulative number of cases in the infected stage at time t; $J(t)$ represents the cumulative ones in hospitalization stage; $G(t)$ represents the instant (not cumulative) number of infected and isolated but yet confirmed cases. They are infected in fact, but are not confirmed by the hospital, then not appeared in the infected list of CCDC; $I_0(t) := I(t) - J(t) - G(t)$ is the number of infected people neither confirmed nor isolated, i.e., the ones who are potentially infectious to healthy ones. The two important parameters r and ℓ are the growth rate and the isolation rate respectively. $f_2(t)$ and $f_4(t)$ are the transition probabilities from infection to illness onset, and from infection to hospitalization, respectively. We have reconstructed them from one important paper by CCDC, see Fig 2 in (3).

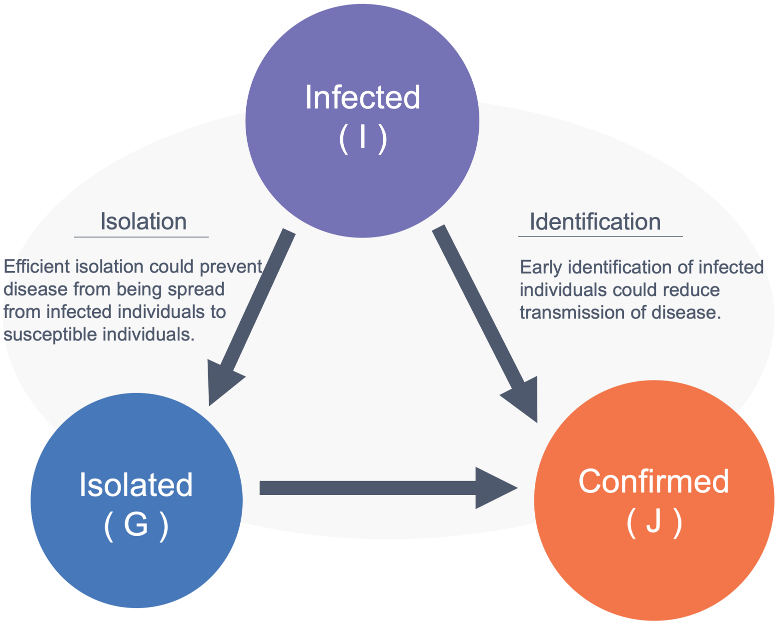

Figure 2: Sketch map of the model.

We make some interpretations for the model: from date t to $t+1$,

1. The newly infected people comes from a proportion (expressed as a growth rate r) of the potential infectious ones who might transmit the coronavirus to others.
2. The newly confirmed people comes from the newly infected people in history.
3. The infected ones are put into isolation (with isolation rate ℓ) once they show symptoms. And the newly confirmed people should be removed from the isolation group.

Quarantine strategy. We use a piecewise constant isolation rate ℓ to model the quarantine strategy:

$$\ell = \begin{cases} \ell_1 & \text{if } t < t_\ell \\ \ell_2 & \text{otherwise,} \end{cases} \tag{1}$$

which means that at the day t_ℓ, the quarantine strategy is changed to control the spread of the epidemic, leading to a change in the isolation rate.

Initial date t_0 Given $I(t_0)$, our model is able to track the initial date of the epidemic t_0. It is REALLY important to find the initial starting date statistically correct in different regions. We fit the real data to identify the parameters, listed in Table 1. As the growth rate r is identified, we can determine the reproductive number R_0 of COVID-19 in (8).

	r	ℓ_1	ℓ_2	t_0	t_ℓ	$t_\ell - t_0$
Shanghai	0.3137	0.1713	0.6149	Dec.27	Jan.16	20
Beijing	0.3125	0.1824	0.5880	Dec.27	Jan.17	21
Hunan	0.3098	0.0444	0.8421	Dec.26	Jan.19	24
Zhejiang	0.3129	0.1072	0.5950	Dec.22	Jan.15	24
Henan	0.3121	0.0592	0.5912	Dec.25	Jan.17	23
Guangdong	0.3118	0.1004	0.5679	Dec.23	Jan.16	24
China without Hubei	0.3072	0.1482	0.5973	Dec.18	Jan.18	31
Hubei without Wuhan	0.3135	0.1789	0.5084	Dec.17	Jan.17	31
Wuhan	0.3019	0.1142	0.4567	Dec.17	Jan.17	31

Table 1: Parameters.

	estimated infected cases	Population(million)	
Shanghai	335	24.23	1.38e-5
Beijing	401	21.54	1.86e-5
Hunan	1030	68.99	1.49e-5
Zhejiang	1220	57.37	2.13e-5
Henan	1286	96.05	1.34e-5
Guangdong	1360	113.46	1.20e-5
China without Hubei	12854	1226.21	9.62e-6
Hubei without Wuhan	18013	48.09	3.75e-4
Wuhan	48891	11.08	4.41e-3

COVID-19 in mainland China

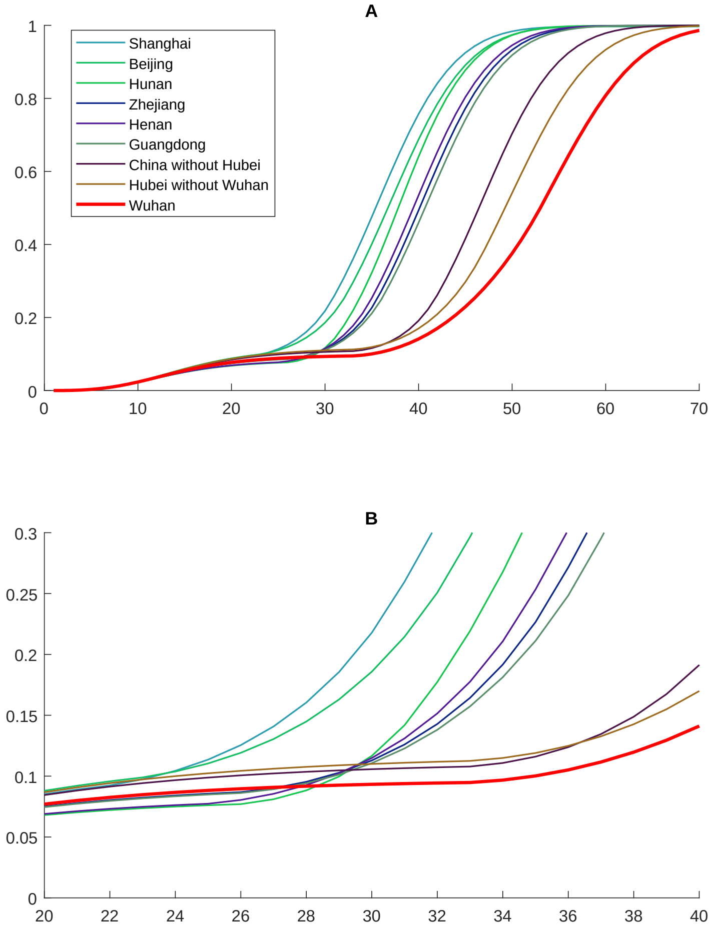

Figure 3: Fitting results of J/I for several regions in mainland China. (A) The whole time interval from the first infection date to the 70th day. (B) The local zoom from the 20th day to the 40th day since the first infection date t_0 estimated by Fudan-CCDC model.

In Figure 3, we plot the evolutions of J/I in several regions in mainland China. The x-axis represents dates started from the first infection date. From this figure we see that the curve for Beijing and Shanghai are ahead of Wuhan and Hubei, implying that earlier restrictive measures make the epidemic more controllable.

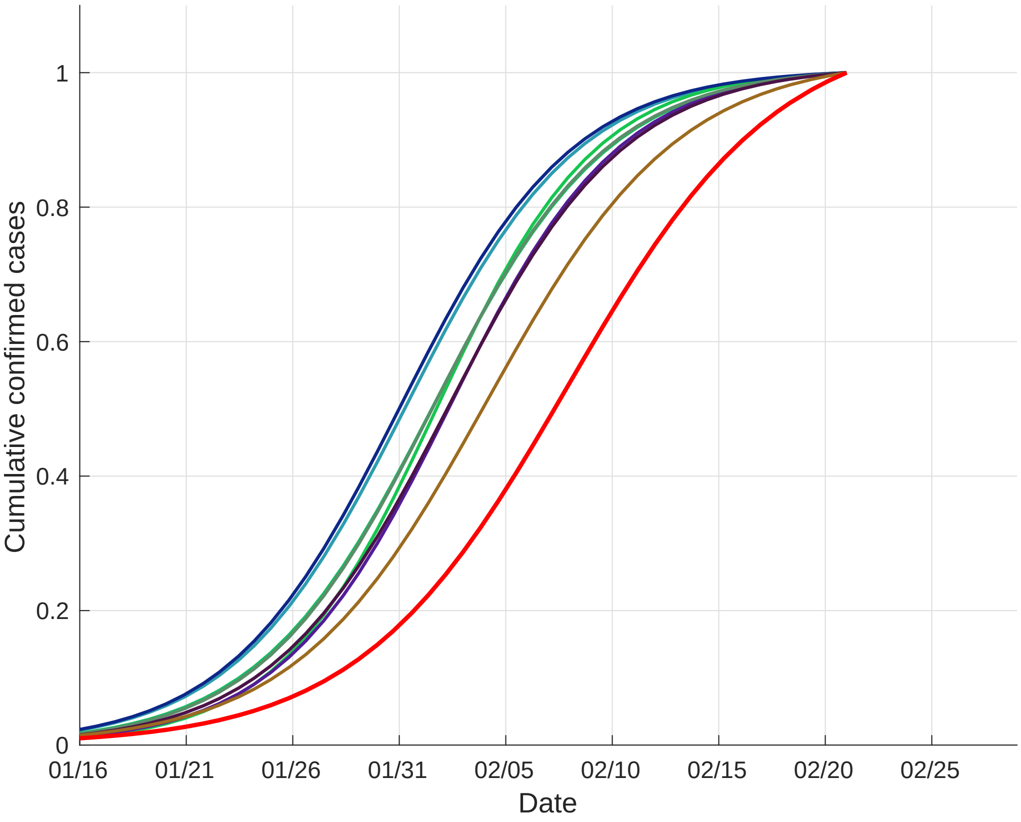

Figure 4: Fitting results of the cumulative number of confirmed cases in several districts in mainland China.

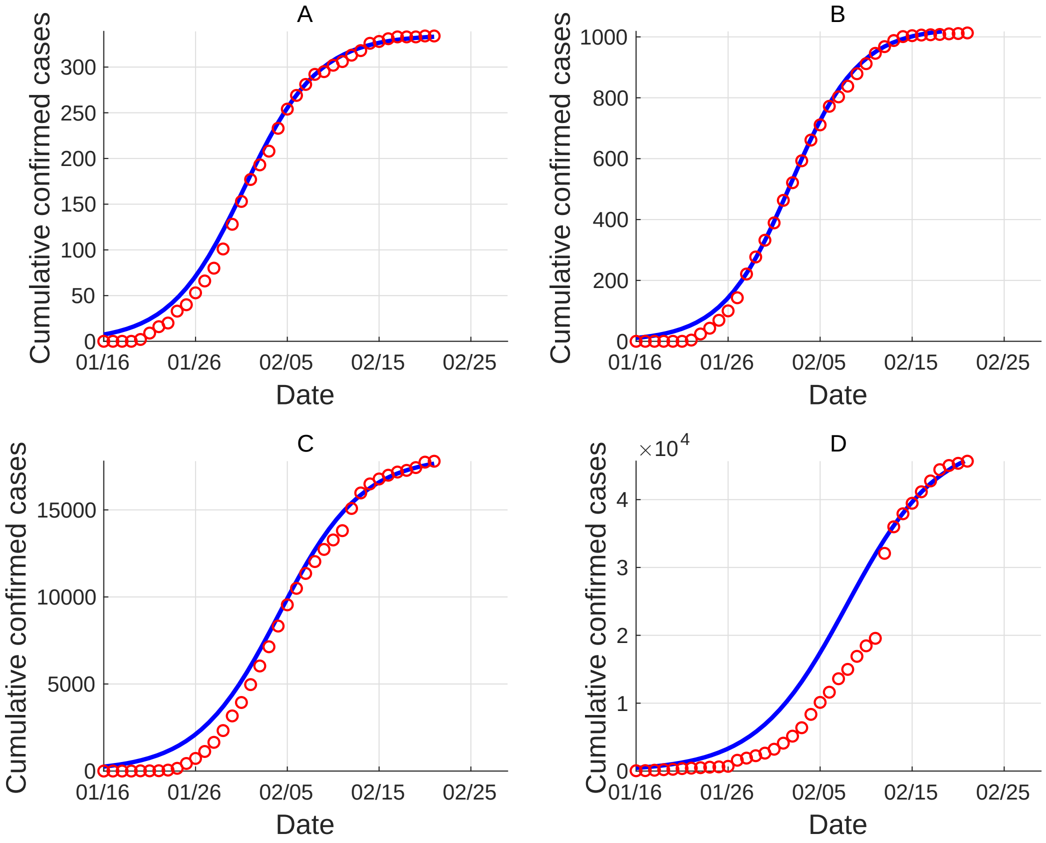

Figure 5: Fitting results of the cumulative number of confirmed cases in (A) Shanghai, (B) Hunan, (C) Hubei Province (without Wuhan), (D) Wuhan.

We show in Figure 4-Figure 5 the fitting results of the cumulative number of confirmed cases in several regions in mainland China. Data are presented in scattered red circles; the blue solid line is the fitting results of the data and its prediction, to which we applied Logistic regression $\frac{a}{b+e^{-cx}}$. Our model is consistent with the published data from multiple cities outside Wuhan such as Shanghai. The discrepancy between the model and data from Wuhan could be explained by insufficient isolation and quarantine measures at the early stage of the epidemic. In other words, individuals with close contacts and suspicious exposure to confirmed cases were not isolated for a 14-day health observation period as later advised. Besides, the capacity of pathogenic diagnosis couldn¡¯t meet the need of viral nucleic acid test for suspected cases at the nascent stage. Therefore, our estimation of infected cases is higher than the published data.

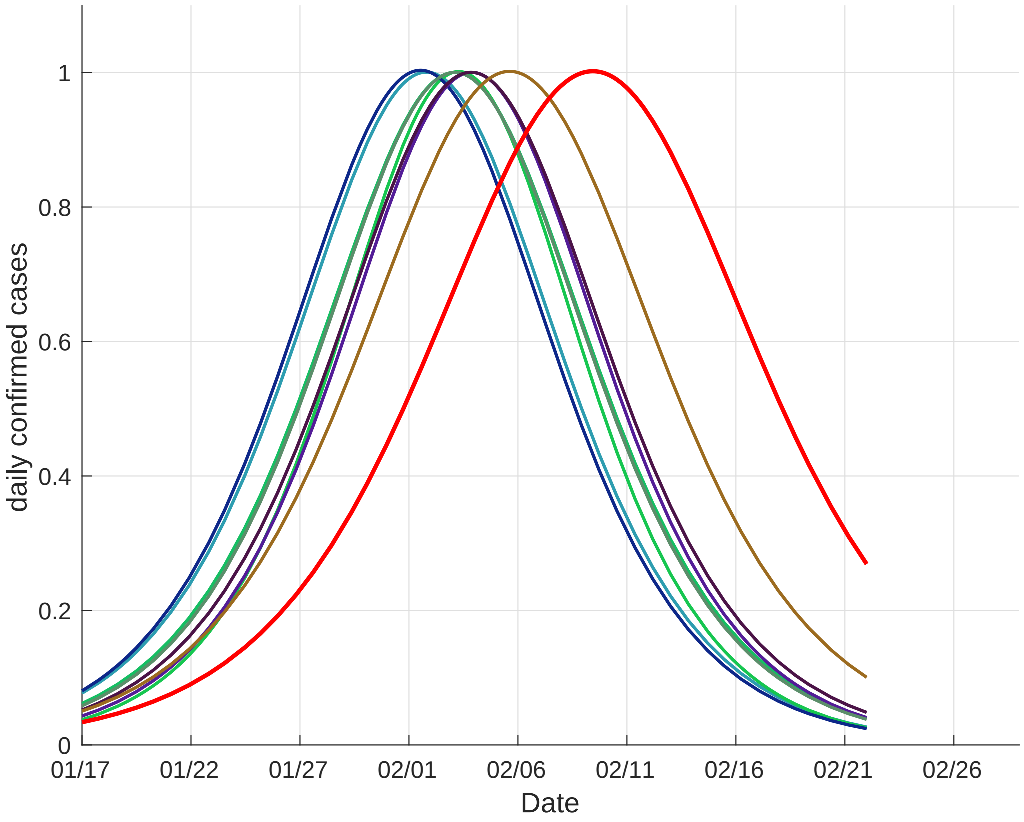

Figure 6: Fitting results of the daily confirmed cases in several districts in mainland China.

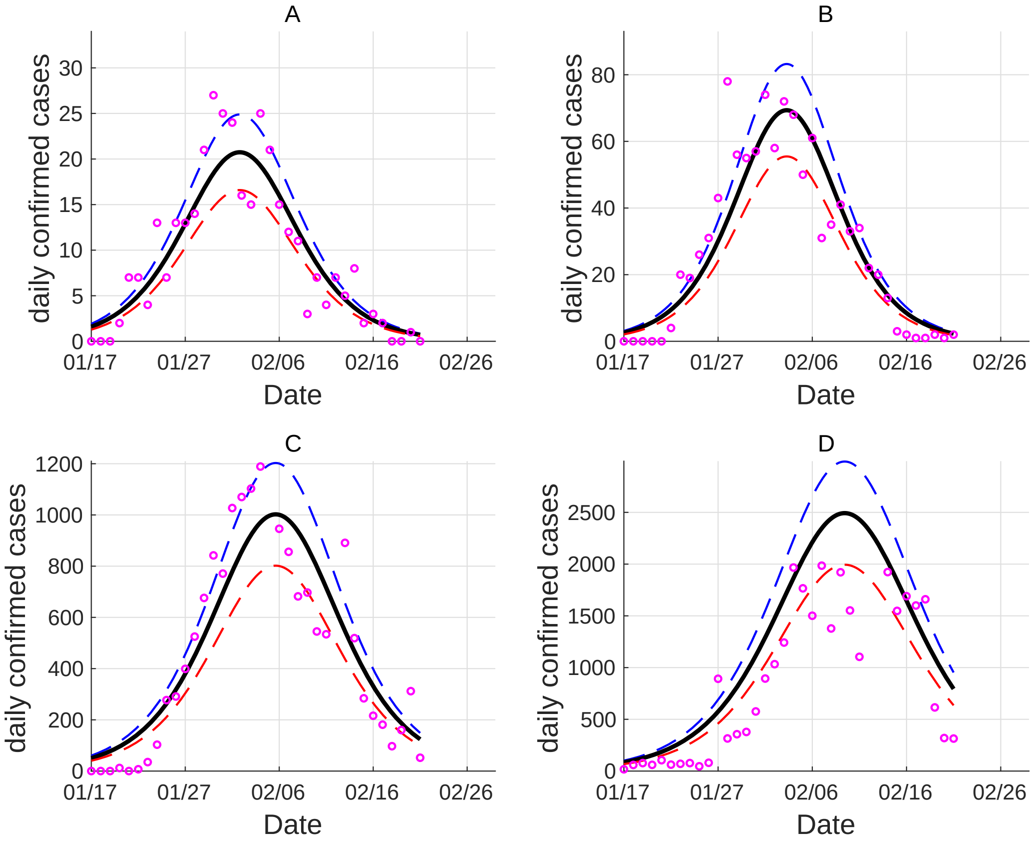

Figure 7: Fitting results of the daily confirmed cases in (A) Shanghai, (B) Hunan, (C) Hubei Province (without Wuhan), (D) Wuhan.

We show in Figure 6-Figure 7 the fitting results of the daily confirmed cases in several regions in mainland China. The black line represents the fitting results obtained from the derivatives of Logistic regressions.

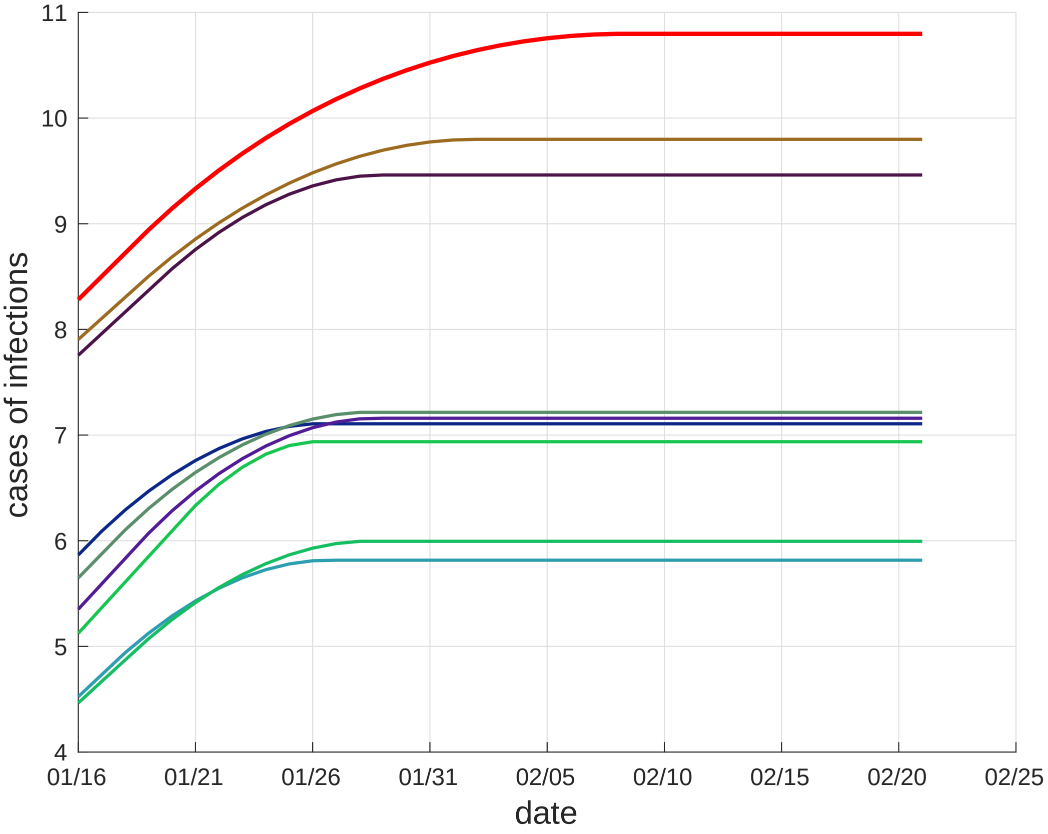

Figure 8: Fitting results of the cumulative infection number $(log(I(t)))$ in several districts in mainland China.

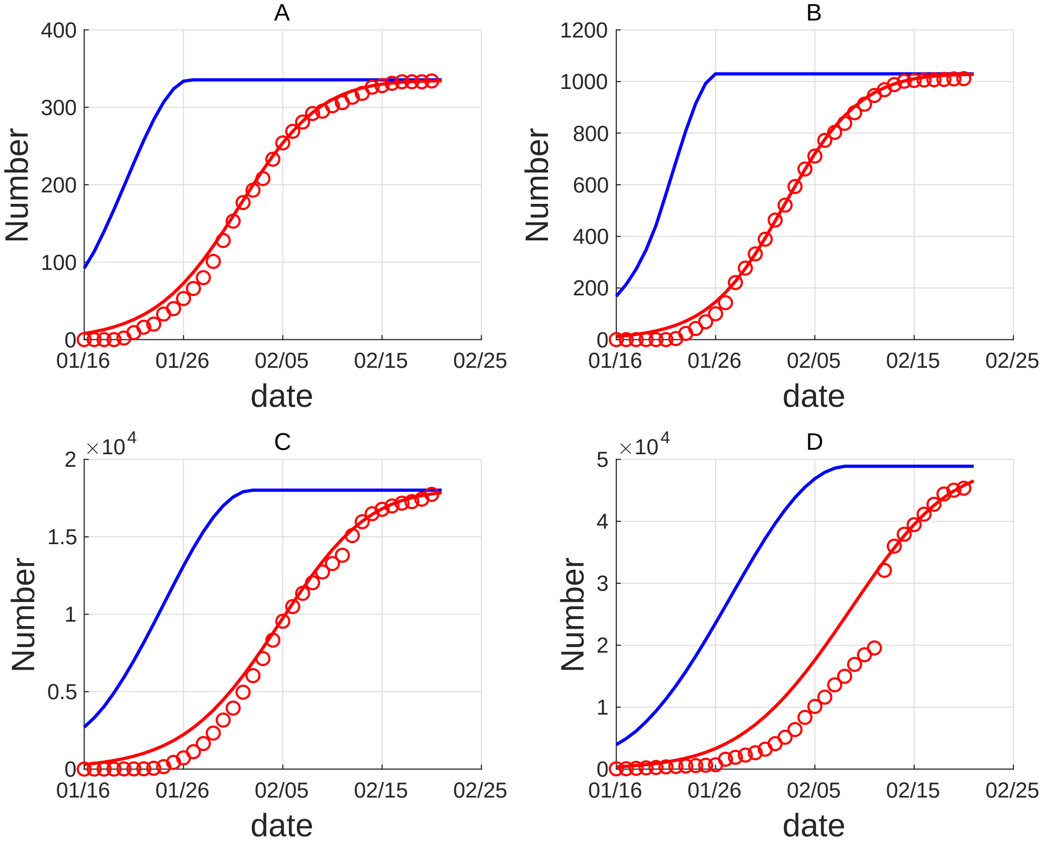

Figure 9: Fitting results of the epidemic situation in (A) Shanghai, (B) Hunan, (C) Hubei Province (without Wuhan), (D) Wuhan.

We show in Figure 9 the fitting results of the cumulative infection number (in blue) and the cumulative number of confirmed cases (in red) in four districts.

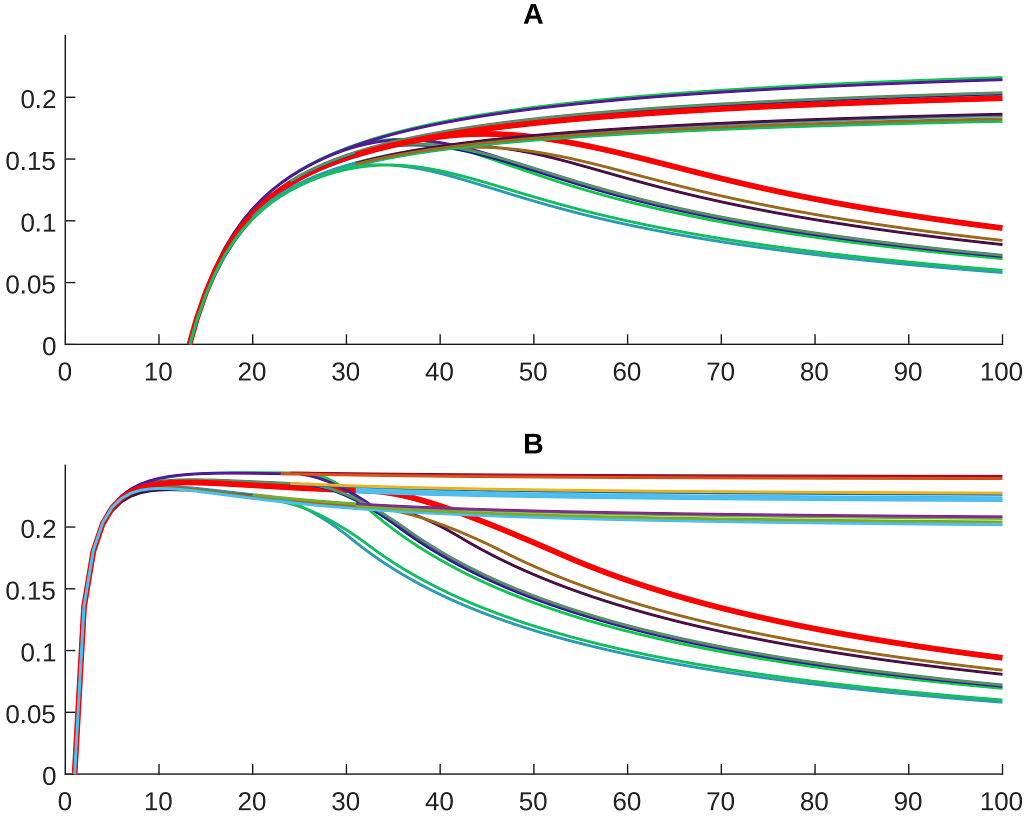

Figure 10: Fitting results of the epidemic evolution in several regions in mainland China, of which the legend is the same as in Figure 3. (A) The evolution of $\frac{1}{t}\ln\left(\frac{J(t)}{J(t_0)}\right)$ with respect to dates started from the first infection date. (B) The evolution of $\frac{1}{t}\ln\left(\frac{I(t)}{I(t_0)}\right)$ with respect to dates started from the first infection date.

Parameters used to generate Figure 10 are listed in Table 1, in which we used the public data from Jan. 16th to Feb. 21st. As can be seen from the sub-figure A in Figure 10, the nine districts can be divided into three groups based on number of confirmed cases. For Beijing and Shanghai, they are the first to take effective quarantine measures, and receive the best control effects. The second group consists of Hunan, Zhejiang, Henan and Shangdong, of which the isolation rate is lower and thus have a fast confirm rate. Specially, in a later stage, Hunan started taking strong quarantine measures and received better control effects, compared to the rest three districts in this group. Lastly, the third group is made up of China (without Hubei), Hubei (without Wuhan) and Wuhan, which were the last to take quarantine measures. In particular, the average administrative strength of China (without Hubei) is stronger than that of Hubei (without Wuhan), therefore, the average final control effects in China (without Hubei) is better than that of Hubei (without Wuhan).

As for the sub-figure B in Figure 10, there is no public data of infection number, we generate the data implicitly. It can be seen that the trend of the infection number has a high similarity with that of the confirmed number. Districts with poorer early stage management, such as Hunan and Henan, have a faster disease spread rate. After the time all plotted districts took effective quarantine measures, the curves evidently move downwards, which show that the epidemic is under control. Therefore, it's crucial to take effective quarantine measuers as soon as possible, and to increase the isolation rate ℓ.

Possible future scenarios for COVID-19 in Japan

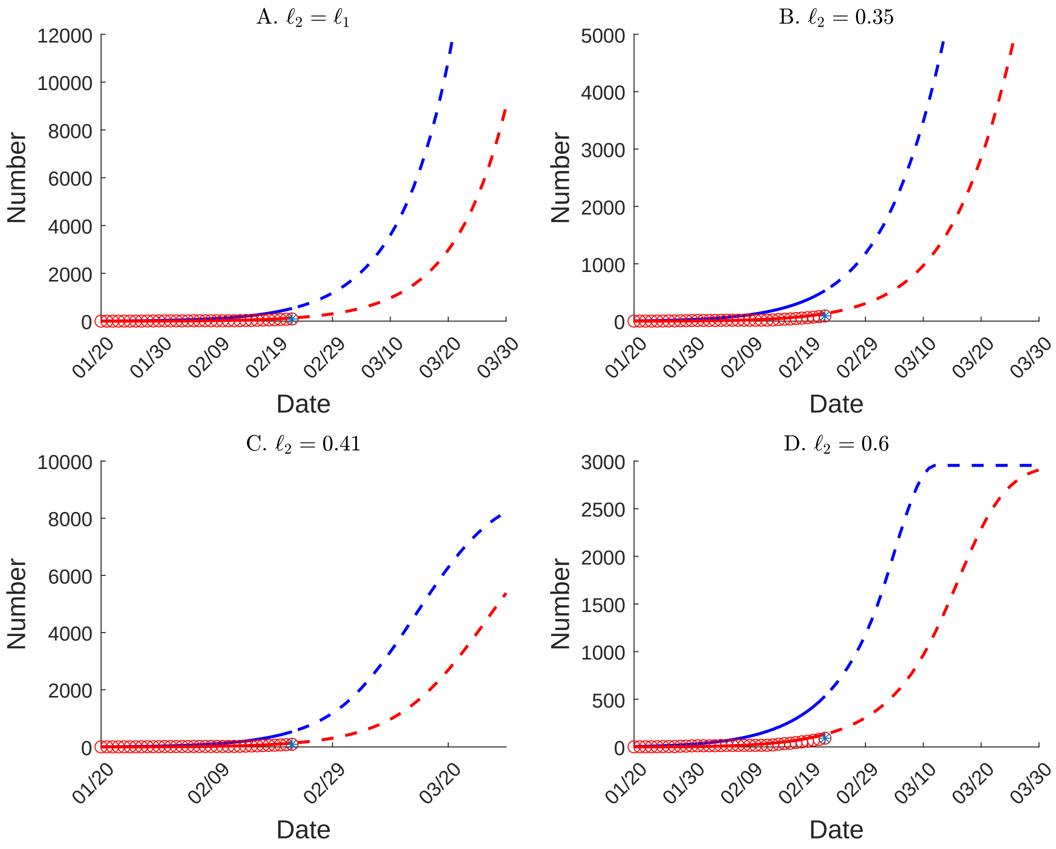

Figure 11: Fitting results of the epidemic evolution in Japan under 4 choices of ℓ_2 started from March 1st, 2020. (A) $\ell_2 = \ell_1 = 0.3051$. (B)$\ell_2 = 0.35$. (C)$\ell_2 = 0.41$.(D)$\ell_2 = 0.6$.

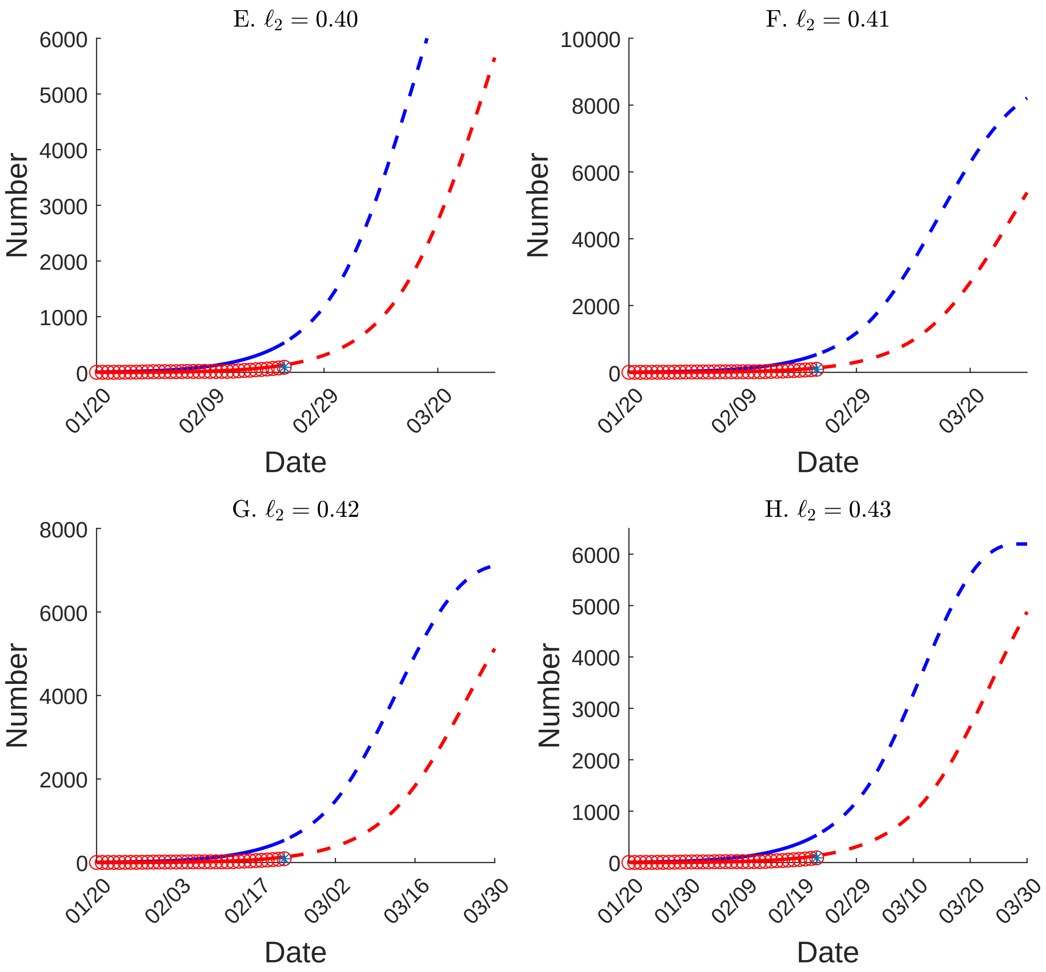

Figure 12: Fitting results of the epidemic evolution in Japan under 4 choices of ℓ_2 around 0.4 started from March 1st, 2020.(A) $\ell_2 = 0.4$. (B)$\ell_2 = 0.41$. (C)$\ell_2 = 0.42$.(D)$\ell_2 = 0.44$.

In Figure 11-Figure 12, we present the estimated results of the epidemic situation in Japan generated by FUDAN-CCDC model, as in Figure9. It can be clearly seen that when $\ell_2 = \ell_1$ or $\ell_2 = 0.35$, namely when the quarantine strategy taken is not effective enough, the infected/confirmed number will grow exponentially. When $\ell_2 = 0.40$, the growth rate fluctuates yet remains non-negative.

On the other hand, if $\ell_2 = 0.41$, the isolation rate reaches the threshold that the infection number is under control, though the final cumulative infection number is quite large. The estimated scale is about 3000. When $\ell_2 = 0.42$, the estimated final cumulative number of infection is about 2000. Lastly, when $\ell_2 = 0.6$, the estimated scale of final cumulative infection is smaller, which is about 3000.

Discussion

Our findings suggest that effective isolation measures as early as possible are crucial for affected regions. Based on our model, the future trend of the epidemic highly depends on when and how the measures will be adopted. Effective interventions include limiting population mobility (e.g. cancellation of mass gathering, school closures and work-from-home arrangements) and public education (e.g. use of face masks and improved personal hygiene) (1). Given that the effects of public health interventions will usually lag by a period of time, it is important to make adjustment on corresponding measures as soon as the epidemic changes. In order to establish effective measures, the data of confirmed and suspected cases should be as accurate as possible. The accuracy depends on the potency of diagnosis. Guidelines on diagnosis and therapy need to fit current situation. For example, on Feb 12, 2020, National Health Commission of China recommended to make clinical diagnosis besides pathogenic diagnosis when there were not enough kits and facilities to perform viral nucleic acid tests. We hope that suggestions from Chinese doctors and researchers could be seriously considered worldwide and that the situation in Wuhan could be discussed carefully. Just as the saying goes, things are always like this: COVID-19 is not likely to come once everything is in a state of preparedness, whereas an outbreak could hardly be avoided.

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Supplementary materials

Materials and Methods

Figs. S1 to S3

Tables S1 to S4

References (4-10)