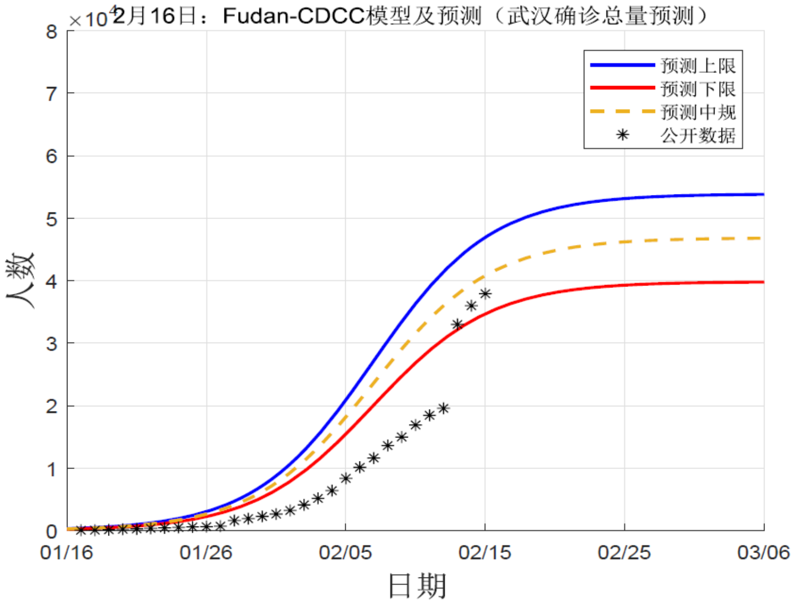
上海市现代应用数学重点实验室研究报告
Research Report Series of SKLCAM

(2020 年第四期)

The reproductive number R_0 of COVID-19 Based on estimate of a statistical time delay dynamical system



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

The reproductive number R_0 of COVID-19 based on estimate of a statistical time delay dynamical system

Nian Shao*, Jin Cheng†, Wenbin Chen‡

Abstract. In this paper, we estimate the reproductive number R_0 of COVID-19 based on Walling and Lipsitch framework [2] and a novel statistical time delay dynamic system.We use the observed data reported in CCDC's paper to estimate distribution of the generation interval of the infection and apply the simulation results from the time delay dynamic system as well as released data from CCDC to fit the growth rate. The conclusion: , which is similar to that of SARS.

1 One formula for the distribution of generation interval

The serial interval distribution presented in the paper "Early transmission dynamics in Wuhan, China, of novel coronavirus-infected peneumonia" [1] by the group of Chinese Center for Disease Control and Prevention(CCDC) et al, which is defined as the duration between symptom onset insuccessive cases in the transmission chain in Fig.2B of [1]. We assume that the distribution is Gamma distribution, i.e., the corresponding probability density function is

$$P(t)=\frac{b^n}{\Gamma(n)}t^{n-1}e^{-bt}=\frac{\left(\frac{2}{3}\right)^5}{\Gamma(5)}t^4e^{-\frac{2t}{3}}. \tag{1.1}$$

the parameters are $n = 5$ and $b = \frac{2}{3}$. So the mean of the distribution is $\frac{n}{b} = 7.5$ which is exact equal to the number announced in [1], where they claimed that the mean serial interval of COVID-19 is 7.5 days (95% CI, 5.3 to 19). The formula is so beautiful, that **we believe it must be true**. The other distributions are also given in our recent report [3].

We think this distribution just as the one of generation interval mentioned in [2]. Now we can determine the reproductive numbers R_0 of COVID-19 if we know the growth rate r of COVID-19 by

$$R_c = 1 + rT_c, \tag{1.2}$$

where $T_c = 7.5$ can be obtained form (1.1). Before we discuss how to get the estimate of the growth rate r of COVID-19, let us review the elegant framework by Wallinga and Lipsitch [2].

---

*School of Mathematical Sciences, Fudan University, 220 Handan Road, Yangpu District, Shanghai, 200433, China, P. R. China. (`16307130024@fudan.edu.cn`).

†School of Mathematical Sciences and SKLCAM, Fudan University, 220 Handan Road, Yangpu District, Shanghai, 200433, China, P. R. China. (`jcheng@fudan.edu.cn`).

‡School of Mathematical Sciences and SKLCAM, Fudan University, 220 Handan Road, Yangpu District, Shanghai, 200433, China, P. R. China. (Corresponding author. `wbchen@fudan.edu.cn`).

2 Wallinga and Lipsitch's framework

According to the framework of Wallinga and Lipsitch [2], in order to obtain the reproductive numbers R_0, some variables and distributions should be known based on the data before we use their uniform framework:

- the growth rate of the epidemic r;
- the mean generation interval of the infection T_c;
- or the generation interval distribution of the infection $g(t)$.

We just mention that the mean generation interval T_c is the first moment of the generation interval distribution $g(t)$:

$$T_c = \int_0^\infty t g(t) dt. \tag{2.1}$$

If r and T_c are computed, the value of the reproductive number R_0 can be simply estimated through a linear equation([2, 6, 7, 8, 9]):

$$R_c = 1 + rT_c. \tag{2.2}$$

And if r and $g(t)$ are estimated, R_0 can be computed as

$$R_g = \frac{1}{M(-r)}, \tag{2.3}$$

where $M(z)$ is the moment generating function of the distribution $g(t)$:

$$M(z) = \int_0^\infty e^{zt} g(t) dt. \tag{2.4}$$

Wallinga and Lipstch's processes are simple but powerful, where clearly demonstrate how generation intervals shape the relationship between growth rate and reproductive numbers. Specially, if $g(t)$ is Gamma distribution with parameters (b, n) as in [2], then we can have two estimates of R_0, one is by (2.2)

$$R_{\Gamma,c} = 1 + \frac{nr}{b}, \tag{2.5}$$

and the another is by (2.3)

$$R_{\Gamma,g} = \left(1 + \frac{r}{b}\right)^n. \tag{2.6}$$

Based on the formula of the generation interval, we know that $b = \frac{2}{3}$ and n,

We will use (1.2) to obtain R_0, and our main focus is to get an accurate estimate for the growth rate r.

In [2], Wallinga and Lipsitch point out that if the epidemic model is assumed to be susceptible-exposed-infectious-recovered(SEIR) model, then the generation interval distribution is Gamma distribution.

So we can obtain our conjecture:

Conjecture 2.1. *The epidemic model for COVID-19 is SEIR if CCDC's data are correct.*

Now we introduce how we can estimate the growth rate r.

3 Fudan-CCDC model

Our group has developed some models for the growth rate of COVID-19 (TDD-NCP models [5, 4] and Fudan-CCDC models[3]). Because of the outstanding agreement with data from CCDC, we decide to use the following model.

Firstly, Let us introduce some variables:

- $I(t)$: (the distribution of) cumulative ones in infection stage at time t;
- $J(t)$: (the distribution of) cumulative ones in hospitalization stage at time t;
- $G(t)$: (the distribution of) cumulative isolated ones who are in one stage at time t: are infected in fact, but are not confirmed by the hospital, then not appeared in the infected list of CCDC;
- $I_0(t)$: $I_0(t) = I(t) - J(t) - G(t)$.

We also make some assumptions on the transition probability functions $f_2(t)$, $f_3(t)$ and $f_4(t)$:

- $f_2(t)$: the transition probability of from infection to illness onset;
- $f_3(t)$: : the transition probability of from illness onset to hospitalization;
- $f_4(t)$: the transition probability of from infection to hospitalization, which can be obtain the convolution of $f_2(t)$ and $f_3(t)$.

We use the log-noraml for $f_2(t)$ and the Weibull for $f_3(t)$[3], and the parameters can be estimated form CCDC by fitting the figures in [1]. Finally two important parameters are used:

- β: is exactly same as the growth rate, i.e., $\beta = r$.
- ℓ: is to reflect the quarantine strategy, for example, specially, we consider this parameter which depends on the isolation rate. Large ℓ means the government more likes to control the spreading of COVID-19.

Now we can introduce our Fudan-CCDC model: $I(t)$, $J(t)$ and $G(t)$ can be approximated by the following (statistical) dynamical system:

$$\frac{\mathrm{d}I}{\mathrm{d}t} = rI_0(t), \tag{3.1}$$

$$\frac{\mathrm{d}J}{\mathrm{d}t} = r\int_{-\infty}^{t} f_4(t-s)I_0(s)\mathrm{d}s, \tag{3.2}$$

$$\frac{\mathrm{d}G}{\mathrm{d}t} = \ell\int_{-\infty}^{t} f_2(t-s)I_0(s)ds - \ell\int_{-\infty}^{t} f_4(t-s)I_0(s)\mathrm{d}s. \tag{3.3}$$

Or one may use the discrete system with each step representing one day:

$$I(t+1) = I(t) + rI_0(t), \tag{3.4}$$

$$J(t+1) = J(t) + r\sum_{s\le t} f_4(t-s)I_0(s), \tag{3.5}$$

$$G(t+1) = G(t) + \ell\sum_{s\le t} f_2(t-s)I_0(s) - \ell\sum_{s\le t} f_4(t-s)I_0(s). \tag{3.6}$$

We will fit and estimate suitable β and ℓ based on the cumulative infections from CCDC.

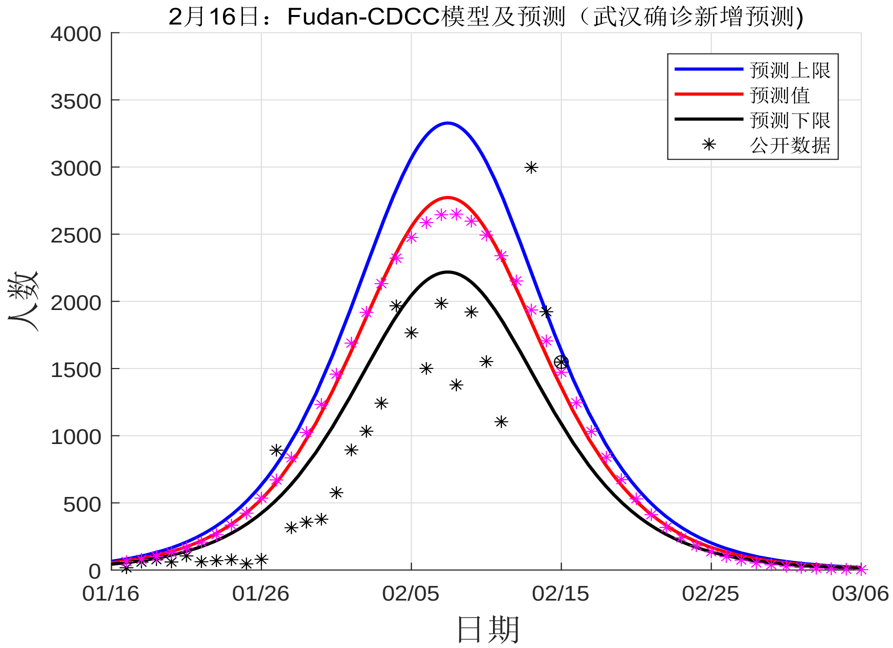
The simulation is implemented via Matlab, and some constrains are imposed in the real code. And after many subtle adjusted, we can summarize the results here, the data is updated to Feb. 16, 2020. We are surprised that our code can get uniform estimators on the growth rate r and the reproductive numbers R_0.

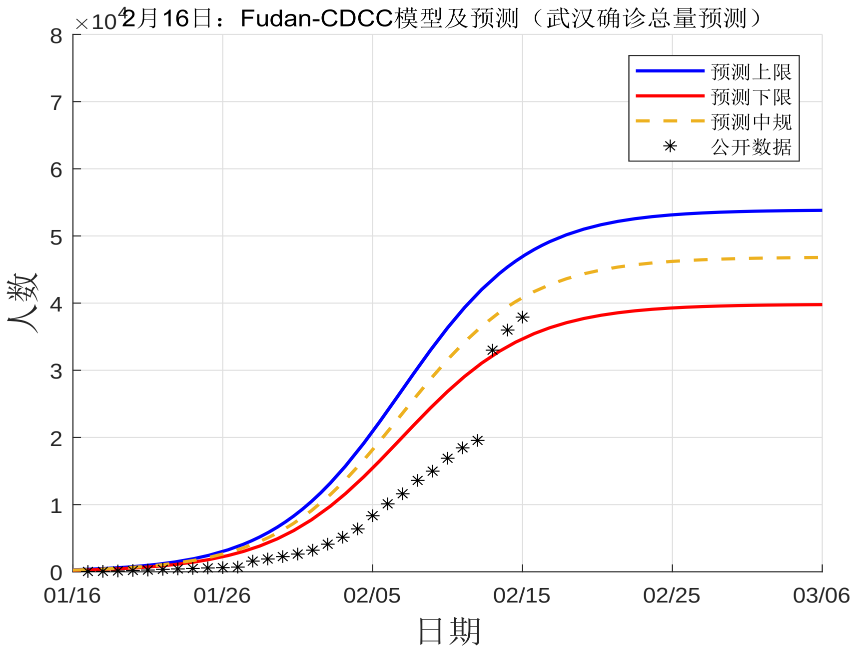
Table 1: The growth rate r and the reproductive numbers R_0

	the growth rate	the reproductive number
Wuhan	0.2858	3.1435
Hubei(without Wuhan)	0.2731	3.04825
China(without Hubei)	0.27	3.025

4 Prediction of Wuhan

We just list two figures on the prediction of Wuhan on cumulative incidence of diagnosed case and new cases that developed in a given period, which we concern the most in China , and the figures and some other results are submitted to CCDC, Wuhan.





5 Acknowledgements

We should truly thank Prof. Daqian Li and Prof. Guanhong Ding for their leading work on the SARS models, we are also sincerely grateful to every member in our group, special to Dr. Yu Jiang, Dr. Yue Ye, Dr. Boxi Xu, Dr. Yu Chen, Dr. Keji Liu, Miss Xinyue Luo, Dr. Ming Zhong, Dr. Xiang Xu and Prof. Shuai Lu and other group members. We also thank Yongzhen Wang in our school, Dr. Zhihua Shen(fusionfintrade.com), Prof. Xingjie Li(University of North Carolina at Charlotte), our friends Ling Ye(China CDC in Daishan, Zhejiang) and Xinkang Chao(Mathworks Company). Wenbin Chen specially thank our colleague Prof. Rongmin Li who mentioned us to use the Gamma distribution. Wenbin Chen was supported in part by the National Science Foundation of China (11671098, 91630309) and 111 project(B08018), Jin Cheng was supported in part by the National Science Foundation of China (11971121). Wenbin Chen thanks the Winning's group(winning.com.cn), who always believe and support us, he also thanks his wife Dr. Jie Xu, hers hometown is Wuhan.

We should thanks everyone who are fighting for Wuhan, specially we present our deep respects to Doctor Wenliang Li and Prof. Nanshan Zhong.[1].

References

[1] Li Qun, Guan Xuhua, Wu Peng, Wang Xiaoye, Zhou Lei, Tong Yeqing, Ren Ruiqi, Leung Kathy S.M., Lau Eric H.Y., Wong Jessica Y., Xing Xuesen, Xiang Nijuan, Wu Yang, Li

---

[1] There must exists lots of typos and many references are note cited, since the paper is finished in one night and now is Feb. 17, 5:25am, 2020, after Xingjie Li helps me to modify the notes. Please let us know if you have any question and suggestions, please email us at wbchen@fudan.edu.cn. Moreover, we don't know where to publish our results without any proof in mathematics. We both are math people, we believe the proof. But now I do not care about the proof. Now we believe the model, and hope it can be useful for the people in Wuhan.

Chao, Chen Qi, Li Dan, Liu Tian, Zhao Jing, Liu Man, Tu Wenxiao, Chen Chuding, Jin Lianmei, Yang Rui, Wang Qi, Zhou Suhua, Wang Rui, Liu Hui, Luo Yinbo, Liu Yuan, Shao Ge, Li Huan, Tao Zhongfa, Yang Yang, Deng Zhiqiang, Liu Boxi, Ma Zhitao, Zhang Yanping, Shi Guoqing, Lam Tommy T.Y., Wu Joseph T., Gao George F., Cowling Benjamin J., Yang Bo, Leung Gabriel M., Feng Zijian. (2020) Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus–Infected Pneumonia. N Engl J Med DOI: 10.1056/NEJMoa2001316.

[2] J. Wallinga and M. Lipstch. How generation intervals shape the relatoinship between growth rates and reproductive numbers, Proc. R. Soc. B(2007) 274, 599-604.

[3] Nian Shao, Yu Chen,Jin Cheng and Wenbin Chen. Some novel statistical time delay dynamic model by statistics data from CCDC on Novel Coronavirus Pneumonia, submitted to Journal of Control Theory and Applications(in Chinese), 2020.

[4] Y. Yan, Y. Chen, K. Liu, X. Luo, B. Xu, Y. Jiang and J. Cheng. Modeling and prediction for the trend of outbreak of 2019-nCoV based on a time-delay dynamic system (in Chinese), *Sci. Sin. Math.*, **50**(3), 1-8, 2020. https://doi.org/10.1360/SSM-2020-0026.

[5] Y. Chen, J. Cheng, Y.Jiang and K. Liu. A time delay dynamical model for outbreak of 2019-nCov and the pramameter identification[EB/OL], arXiv:2002.00418,2020.

[6] R. M. Anderson, R. M. May. Infectious diseases of humans: dyanmics and control. Oxford, Uk: Oxford University Press.

[7] O. G. Pybus et al., The epidemic behaviour of hepatitis C virus. Science 22, 2323-2325.

[8] N. Ferguson, et al. Strategies for containing an emerging influenza pandemic in Southeast Asia. Nature 437, 209-214.

[9] N. Ferguson, et al. strategies for mitigating and influenza pandemic. Nature 442, 448-452.