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Estimating the effective reproduction number of the 2019-nCoV in China

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1 **Article Summary Line:** This modeling study indicates that 2019-nCoV has a higher
2 effective reproduction number than SARS with a comparable fatality rate.

3 **Running Title:** Effective reproduction number of 2019-nCoV

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6 **Estimating the effective reproduction number of the 2019-nCoV in China**

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NOTE: This preprint reports new research that has not been certified by peer review and should not be used to guide clinical practice.

25 **Abstract—35 words**

26 We estimate the effective reproduction number for 2019-nCoV based on the daily reported
27 cases from China CDC. The results indicate that 2019-nCoV has a higher effective
28 reproduction number than SARS with a comparable fatality rate.

29 **Text—799 words**

30 As of 01/26/2020, the 2019 novel coronavirus (2019-nCoV), originated in Wuhan
31 China, has spread to 29 mainland provinces, Hong Kong, Macau, Taiwan, as well as 11 other
32 countries (1, 2). Early genome sequence and clinical studies of 2019-nCoV provided the
33 evidence of human-to-human transmission and revealed its similarity to as well as differences
34 from SARS (3-5). However, epidemiological investigations of 2019-nCoV are just
35 beginning, and data-driven studies are critically needed to develop insights into this ongoing
36 outbreak and evaluate the effectiveness of public health strategies, such as the currently
37 implemented lockdown of Wuhan.

38 An important epidemiological understanding of 2019-nCoV is concerned with its
39 transmissibility, quantified by the basic reproduction number R_0 and the effective
40 reproduction number R . R_0 is the expected number of secondary infectious cases generated
41 by an infectious case in a susceptible population. R is the expected number of secondary
42 cases generated by an infectious case once an epidemic is underway (6). $R = R_0x$, where $x \in$
43 $(0, 1)$ is the proportion of the population susceptible. Following (7), R is calculated as
44 follows:

45
$$R = K^2(L \times D) + K(L + D) + 1,$$

46 where L is the average latent period, D the average latent infectious period, K the logarithmic
47 growth rate of the case counts as reported by China CDC. This form of R is appropriate
48 because 2019-nCoV is still at its early growth stage. According to China CDC, we set $L = 7$
49 days and $D = 9$ days. Experiments with varying L and D values were also conducted.

50 Let t denote the number of days since the start of the outbreak and $Y(t)$ the number of
51 cases. K is estimated based on $Y(t)$ at six time points. (Time-1) 12/31/2019, when the
52 authorities reported the first 27 cases with the infection dated as early as 12/16/2019. As
53 such, $t = 15$, $Y(15) = 27$. (Time-2) 01/04/2020, $t = 19$, $Y(19) = 41$; (c) 01/21/2020, $t = 36$,
54 $Y(36) = 375$; (Time-3) 01/22/2020, $t = 37$, $Y(37) = 437$; (Time-4) 01/23/2020, $t = 38$, Y
55 $(38) = 507$; (Time-5) 01/24/2020, $t = 39$, $Y(39) = 572$; (Time-6) 01/25/2020, $t = 40$, $Y(40)$
56 $= 618$. Note that the case data between 01/05/2020-01/20/2020 were discarded due to
57 significant changes experienced in this time period in the case reporting requirements and
58 practice.

59 Using the data described above, R is estimated to be 4.08, indicating that an infected
60 patient infects more than four susceptible people during the outbreak. This value substantially
61 exceeds WHO's estimate of R_0 (supposed to be smaller than R) between 1.4 and 2.5, and is
62 also higher than a recent R_0 estimate between 3.6 and 4.0 (8). Compared against the 2003
63 SARS epidemic, R of 2019-nCoV is higher than that of SARS in both Beijing (2.76) and
64 Guangzhou (3.01) (calculated using the same method). To test the robustness of findings, we
65 performed sensitivity analyses by adopting varying values of L and D , generated from a
66 Gaussian distribution with $L \sim N(7,1)$ and $D \sim N(9,1)$. The resulting mean of R estimates is
67 4.08, as expected, with $SD=0.36$ (95% CI 3.37~4.77).

68 To predict the future outbreak profile, we developed a model based on the
69 deterministic Susceptible-Exposed-Infectious-Recovered-Death-Cumulative (SEIRDC)
70 structure (9). Overall, our model appears to explain the reported case counts very well during
71 the current early stage of the outbreak. An interesting finding is that by setting the start date
72 to a time earlier than 12/16/2020 (the experimented range is from 12/01/2019—12/15/2019),
73 the SEIRDC model is able to provide a better fit for the case counts. This indicates that
74 human-to-human transmission may have started earlier than what the current prevailing

75 viewpoint suggests. Obviously, further molecular and epidemiological studies are needed to
76 draw any conclusions in this regard.

77 The SEIRDC model estimates the fatality rate for 2019-nCoV is 6.50%. As a base of
78 comparison, the fatality rate for 2003 SARS was 7.66% and 3.61% for Beijing and
79 Guangzhou, respectively. We used the model to predict the confirmed case counts and death
80 counts in the first 80 days of the ongoing 2019-nCoV outbreak. We simulated these counts
81 for the 2003 SARS outbreaks in Beijing and Guangzhou as well, using the case counts as
82 input. The basic assumption is the absence of any control measures in all these scenarios. At
83 the end of this 80-day period, according to our simulations, the 2019-nCoV case counts
84 (35,454) is close to that of SARS in Guangzhou (37,663) and much higher than that of SARS
85 in Beijing (17,594). The 2019-nCoV death count (1,089) is much higher than that of SARS in
86 Guangzhou (725) and Beijing (690).

87 Our study also suggests that by reducing the average infectious period to <2.3 days,
88 the resulting R will decrease to a value less than 1, meaning the epidemic can be effectively
89 controlled.

90 In conclusion, considering transmissibility and fatality rate, 2019-nCoV poses a major
91 public health threat, at least at the level of 2003 SARS. Epidemiological studies are critically
92 called for to evaluate the effectiveness of stringent measures such as lockdown and help the
93 design of refinements and development of potential alternative strategies for the next phase of
94 the 2019-nCoV outbreak.

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100 **Disclaimers**

101 Nil.

102 **Author Bio**

103 Dr. Zhidong Cao is a researcher in the State Key Laboratory of Management and
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105 primary research interests are infectious disease informatics, spatio-temporal data processing,
106 and social computing.

107 **Footnotes**

108 ¹ These first authors contributed equally to this article.

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141 Figure. SEIRDC model predictions for (A) cumulative numbers of infected persons and (B)
142 deaths of 2019-nCoV, 2003-SARS in Beijing, and 2003 SARS in Guangzhou in the first 80
143 days after the outbreak.

