Dynamic Modeling COVID-19 for Comparing Containment Strategies in a Pandemic Scenario

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Abstract

Since instances of coronavirus disease 2019 (COVID-19) community spread emerged in the United States, federal and local governments have implemented multiple containment measures. However, in order to satisfy the needs of its citizens, the strictest containment measures can be only executed for short period. This article compares two types of containment strategies: a constant containment strategy that could satisfy the needs of citizens for a long period and an adaptive containment strategy whose strict level changes across time. When to implement the strictest measure is also of interest. A dynamic prediction model is proposed and a simple tool is developed for policy makers to compare different containment strategies. As an example, a region with population 2.8 million and 200 initial infectious cases is considered assuming a 4% mortality rate. We found that compared with a constant containment strategy, adaptive containment strategies shorten the outbreak length and executing the strictest measures early will cause less mortality.

Keywords: Statistical analysis, pandemic, adaptive containment measures, period of communicability, infectious period
1 Introduction

To prevent the spread of a new respiratory disease – coronavirus disease 2019 (COVID-19), policy makers rely on prediction models to foresee the number of infectious cases and to prepare for adopting containment measures including patient quarantine, active monitoring of contacts, border controls, and community education and precautions (1–4). There are many prediction models available for this kind of modeling (5–14). In predicting local COVID-19 spread, there are two major challenges. Firstly, number of actual infected cases is usually unconfirmed and could be far larger than confirmed cases because there are significant number of infected cases in incubation period and test kits may be insufficient. Secondly, regions that experienced earlier outbreaks can provide valuable information, such as the distribution of cure time, death time, and mortality rate (15), but it is not easy to integrate these dynamic parameters into many current models.

This article provides a simple and robust model framework whose parameters are dynamically adjustable and generally interpretable for policy makers. Statistical analysis is integrated in it to borrow information from regions that experienced earlier outbreaks. Moreover, the model enables containment measures to change over time (16) through introducing a novel reproduction number which incorporates containment measures and the basic reproduction number ($R_0$).

2 The model

Assume the disease of interest has a $M$-day period of communicability so that infected people are either cured or dead within $M$ days. Denote the mortality rate within an infectious period as $m_{\text{death}}$ and the cure rate will be $1 - m_{\text{death}}$. On day $t$, denote the number of people that have been infected for $d$ days as $p_{t,d}$. The total number of infectious cases at time $t$ is $P_t = \sum_{d=1}^{M} p_{t,d}$, where $p_{t,d}$ is determined by the following factors:

- Mortality rate for people that have been infected for $d$ days, denoted as $m_d$,
- Cure rate for people that have been infected for $d$ days, denoted as $c_d$,.
• Average number of people an infectious person can communicate on day \( t \), denoted as \( R_t \).

• Number of travelers from other areas who have been infected for \( d \) days, denoted as \( p_{t,d}^{imp} \).

When moving forward from day \( t \) to \( t + 1 \), the number of infectious cases, \( P_{t+1} \), is the sum of these three terms: (a) the number of survived but uncured cases from day \( t \); (b) the number of newly infected cases; and (c) the number of imported cases, denoted as

\[
P_{t+1} = \sum_{d=1}^{M} p_{t+1,d} = \sum_{d=1}^{M-1} p_{t,d}(1 - m_d - c_d) + P_t R_t + P_{t+1}^{imp}.
\]

Note that the people who have been infected for \( M \) days on day \( t \) \( (p_{t,M}) \) will not affect \( P_{t+1} \) since their period of communicability will be over and they will be either dead or cured on day \( t + 1 \). Also observe \( p_{t+1,1} = P_t R_t \), which counts newly infected cases, and for \( d = 1, \ldots, M - 1 \), we have \( p_{t+1,d+1} = p_{t,d}(1 - m_d - c_d) \).

3 Parameter specification

To specify mortality rate \( m_d \), a cumulative distribution function \( F_{death}(t) = \mathbb{P}(T_d \leq t) \) is defined in interval \([0, M]\) for death time \( T_d \) and \( F_{death}(M) = m_{death} \). A lognormal distribution function is used as

\[
F_{death}(t) = \frac{1}{2} + \frac{1}{2} \text{erf} \left[ \frac{\ln t - \mu}{\sqrt{2} \sigma} \right],
\]

where \( \text{erf}(x) = \frac{2}{\sqrt{\pi}} \int_0^x e^{-t^2} dt \). Here, parameters are set as \( \sigma = 0.8 \) and \( \mu = \ln(M) - \sqrt{2} \sigma \text{erf}^{-1}(2m_{death} - 1) \), where \( \text{erf}^{-1}(x) \) denotes the inverse function of \( \text{erf}(x) \). A patient has the probability of dying from day \( d \) to \( d + 1 \) as

\[
m_d = \mathbb{P}(d < T > d + 1) = F_{death}(d + 1) - F_{death}(d).
\]

Similarly, cure rate \( c_d \) is modeled as \( c_d = F_{cure}(d + 1) - F_{cure}(d) \), where \( F_{cure}(t) = \mathbb{P}(T_c \leq t) \) is defined in interval \([0, M]\) for cure time \( T_c \) and \( F_{cure}(M) = 1 - m_{death} \). After specifying \( F_{cure}(t) = \frac{1}{2} + \frac{1}{2} \text{erf} \left[ \frac{\ln t - \mu_c}{\sqrt{2} \sigma_c} \right] \), we set \( \sigma_c = 0.4 \) and \( \mu_c = \ln(M) - \sqrt{2} \sigma_c \text{erf}^{-1}(1 - 2m_{death}) \).

For initial time, set \( F_{death}(0) = F_{cure}(0) = 0 \).

The reproductive number \( R_t \) is determined by the basic reproduction number \( R_0 \), the containment measures on day \( t \) and the percentage of uninfected people. It is assumed that cured cases
will not get infected again since they are immune to the disease. Since $R_0$ is a constant, we only need to set 

$$R_t = r_t \times \frac{P_{\text{pop}} - P_t - \sum_{i=1}^{t}(D_i + C_i)}{P_{\text{pop}}}.$$ 

where $D_i = \sum_{d=2}^{M} p_{i-1,d} m_d$ is the number of deaths on day $t = i$, $C_i = \sum_{d=2}^{M} p_{i-1,d} c_d$ is the number of cured patients on day $t = i$, and $P_{\text{pop}}$ denotes the total population. The crucial parameter is $r_t$ which is used to specify the containment scenario.

For initialization, infected durations are generated from Poisson distribution to mimic the individual variation (20), where $p_{1,d} = \sum_{i=1}^{P_1} 1_{X_i=d}$ and $p_{\text{imp},d} = \sum_{j=1}^{P_{\text{imp}}} 1_{X_j=d}$. $X_i$s and $X_j$s are identically and independently distributed from a Poisson distribution with mean $\lambda$. When the generated value is zero or larger than $M$, it is set as 1 or $M$.

## 4 Results and conclusion

To compare different containment strategies, suppose a region will experience a COVID-19 outbreak in the scenario illustrated in Table 1. The first set of parameters are disease related and include parameters used for the distributions of cure time and death time. The second set of parameters are population related. The third parameter is $r_t$ which defines the containment strategy. For example $r_t = 0.21$ from strategy A, implies every 100 infectious cases will communicate to 21 individuals per day on average. Strategy A is a constant containment strategy. Strategies B and C on the other hand are adaptive and allowed to change weekly: strategy B is the same as C but applied two weeks earlier. The averages of $r_t$ for strategies A, B and C are all 0.21; thus all strategies have the same overall strict level.

Results are displayed in Figure 1. After monitoring 100 simulations, the dynamic of number of infectious cases does not change much from random initialization. In total, numbers of deaths from strategies A, B and C are $5.01 \times 10^3$, $3.71 \times 10^3$ and $4.96 \times 10^3$; numbers of infected cases are $1.75 \times 10^5$, $1.30 \times 10^5$ and $1.74 \times 10^5$. The number of infectious cases, $P_t$, reaches its peak on the 47th, 39th and 40th day and the number of deaths, $D_t$, reaches its peak on the 70th, 61th and 63th day for strategies A, B and C. After the peak of $P_t$, containment strategy does not make
Table 1: Necessary inputs for policy makers to compare different containment strategies.

| Domain | Value | Description |
|--------|-------|-------------|
| Disease | $M = 40$ | Infected cases will be either cured or dead within $M$ days. |
|        | $m_{\text{death}} = 4\%$ | Within $M$ days, $m_{\text{death}}$ of infected cases will be dead. |
|        | $\sigma = 0.8$ | Parameter to shape the distribution function of death time. |
|        | $\sigma_c = 0.8$ | Parameter to shape the distribution function of cure time. |
| People | $P_{\text{pop}} = 2.8 \times 10^6$ | On day 1, $P_{\text{pop}}$ individuals are not infected within the region. |
|        | $P_1 = 200$ | On day 1, $P_1$ individuals are infectious. |
|        | $P_{15}^{\text{imp}} = P_{48}^{\text{imp}} = 2$ | On day 15, 29, 48 and 63, there are two, four, two and four infectious people who travel into the region. |
|        | $P_{29}^{\text{imp}} = P_{63}^{\text{imp}} = 4$ | |
|        | $\lambda = 10$ | Initial infectious cases, counted in $P_1$ and $P_t^{\text{imp}}$, have been infected for $\lambda$ days on average. |
| Policy | $r_t$ described in Figure 1(c) | Smaller value represents stricter containment measures*. |

* $r_t$ can be interpreted as the average number of newly infected case communicated per infectious person per day on day $t$, if nearly all the population are uninfected. The model will adjust these inputs with percentage of infected cases across time, which produces $R_t$. 

5
Figure 1: Containment strategy comparison using inputs of Table 1. Cumulative distribution functions of death time and cure time with 4% mortality rate within 40 days are plotted in sub-figures (a) and (b). Sub-figure (c) demonstrates three different containment strategies across time. Strategy A (black) has a constant strict level while strict level is allowed to change weekly from strategies B (blue) and C (red). Strategy B is similar to strategy C but implements the strictest measures two weeks earlier. The averages of $r_t$ for strategies A, B and C are all 0.21, which means that they have the same overall strict level. From sub-figure (d) and (e), we observe that strategy B results in the smallest number of infected patients and deaths. Overall, the adaptive containment strategies, B and C, end the outbreak faster.
much difference on the trend of $P_t$ or $D_t$.

In conclusion, compared with a constant containment strategy, adaptive containment strategies shorten the outbreak length. Adaptive strategies are less strict at the beginning, which results in more severe spread. However, the stricter measures that are enforced after this have the effect of shortening the outbreak length. Fine tuning these stricter adaptive measures is critical to achieving a minimum death rate and/or reducing maximum daily number of cases.

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Supplement

An online prediction tool is provided at [https://minlu.shinyapps.io/killCOVID19/](https://minlu.shinyapps.io/killCOVID19/).

References

1. F. M. Shearer, R. Moss, J. McVernon, J. V. Ross, J. M. McCaw, *PLoS Medicine* 17 (2020).

2. Y. Ng, *et al.* (2020).

3. D. J. Hunter, *New England Journal of Medicine* (2020).

4. K. Kupferschmidt, J. Cohen, Will novel virus go pandemic or be contained? (2020).

5. C. Dye, N. Gay, *Science* 300, 1884 (2003).

6. C. T. Bauch, J. O. Lloyd-Smith, M. P. Coffee, A. P. Galvani, *Epidemiology* pp. 791–801 (2005).
7. C.-Y. Huang, C.-T. Sun, J.-L. Hsieh, H. Lin, *Journal of Artificial Societies and Social Simulation* **7** (2004).

8. V. Colizza, A. Barrat, M. Barthelemy, A.-J. Valleron, A. Vespignani, *PLoS medicine* **4** (2007).

9. H. Rahmandad, J. Sterman, *Management Science* **54**, 998 (2008).

10. A. Gray, D. Greenhalgh, L. Hu, X. Mao, J. Pan, *SIAM Journal on Applied Mathematics* **71**, 876 (2011).

11. V. Capasso, G. Serio, *Mathematical Biosciences* **42**, 43 (1978).

12. V. Capasso, *Mathematical structures of epidemic systems*, vol. 97 (Springer Science & Business Media, 2008).

13. W.-m. Liu, S. A. Levin, Y. Iwasa, *Journal of mathematical biology* **23**, 187 (1986).

14. J. Zhang, J. Lou, Z. Ma, J. Wu, *Applied Mathematics and Computation* **162**, 909 (2005).

15. D. L. Wilson, *Mechanisms of ageing and development* **74**, 15 (1994).

16. J. Cohen, K. Kupferschmidt, Strategies shift as coronavirus pandemic looms (2020).

17. M. Chinazzi, *et al.*, *Science* (2020).

18. S. P. Layne, J. M. Hyman, D. M. Morens, J. K. Taubenberger, New coronavirus outbreak: Framing questions for pandemic prevention (2020).

19. G. Pacheco, J. Bustamante-Castañeda, J.-G. Caputo, M. Jiménez-Corona, S. Ponce-De-León (2020).

20. J. O. Lloyd-Smith, S. J. Schreiber, P. E. Kopp, W. M. Getz, *Nature* **438**, 355 (2005).