Supplementary material:

Mathematical models for devising the optimal SARS-CoV-2 eradication in China, South Korea, and Italy

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1. Supplemental Methods

1.1. Model 1: *SIR* model.

Basic Considerations. Parameters obtained from market performance: (1) it takes an average of 7 days from Susceptible to Infected, so $\sigma=1/7$; (2) it takes an average of 14 days from Infected to Removed, so $\gamma=1/14$. Estimated of the β parameter sensitivity (the probability of transfer from the cultivated state to the resistant state): At the beginning, the number of infected persons was 1. We used the early stage of the pneumonia outbreak data to estimate the parameters.

1.2. Model 2: *SEIR* model.

Basic Considerations. In this study, we divided the total population into four groups (1) Susceptible group (*S*): People who have no immunity against the disease. They are very likely to be infected by coming in direct contact with infected people (see below). Let *S* denote the number of people in the susceptible group. (2) Incubation group (*E*): People who have been infected but have not displayed any explicit symptoms. They do not transmit the virus to susceptible people. Let *E* denote the number of people in the incubation group. (3) Infected group (*I*): People in the infected group show explicit symptoms of SARS-CoV-2, and they can transmit the virus to susceptible people. Let *I* denote the number of people in the infected group. (4) Removed group (*R*): The removed group includes people who have died of the disease or who have survived the disease. People who have survived the disease will obtain complete immunity against it. Let *R* denote the number of people in the removed group.

Assumptions: (1) There is currently no vaccine, so no one is naturally resistant to the virus; (2) the virus does not mutate; once a person is cured by his or her own immune system, the person will not get re-infected.

1.3. Model 3: Advanced Model 1: Considering hospital isolation.

Basic Considerations. We incorporated the hospital isolation factor in this model to fit the actual situation. The function of hospital isolation is to decrease the chances of contact between susceptible and infected people; therefore, the spread of the virus can be controlled down to a lower level. We needed to add one more group on the basis of the basic model and define some parameters for the new group. Hospital isolation group: People in this group are isolated from susceptible people. We define α as the isolation rate, which is the rate of people moving from the infected group to the hospital isolated group. The larger α is, the higher the medical condition and the spread of SARS-CoV-2 can be expected to be at a lower level. We also define ω as the outflow rate of this group; thus, $1/\omega$ denotes the period that one person stays in this group. Let H be the number of people in this group.

Assumptions: (1) People in the incubation group are treated as susceptible people and will not be moved into hospital isolation; (2) People in the hospital isolation group have absolutely no chance to infect susceptible people; (3) People in the hospital isolation group will also die after a $1/\omega$ period of time since there is no medication in this model. We assume that $1/\omega=1/\gamma$, that is, isolated people, will die with the same rate of infected people.

1.4. Model 4: Advanced Model 2: Considering medicine and vaccine.

Basic Considerations. We further incorporated drugs and vaccines into this advanced

model. We first made some changes about the grouping of people based on advanced model one. **Immunity group:** People in this group gain complete immunity against SARS-CoV-2 virus. They can either obtain immunity through a vaccination or recover from the disease. Let M denote the number of people in this group, and θ denote the vaccination rate; that is, the percentage of susceptible people who receive a vaccination each day. **Infected group:** These people should be further divided into two sub-groups in this model. **Early infected group:** People who have displayed explicit symptoms of COVID-19 and can transmit the virus to susceptible people. In addition, they can be cured with COVID-19 drugs. We assume this phase lasts 3 days. Let I_E denote the number of people in this group and $1/\gamma_E$ denote the period of this phase. **Advanced infected group:** People who also have displayed explicit symptoms of COVID-19 and can transmit the virus to susceptible people. However, they cannot be cured by the COVID-19 drugs. We assume this phase lasts 2.6 days. Let I_L denote the number of people in this group and $1/\gamma_L$ denote the period of this phase.

Assumptions: (1) Medications, including vaccines and drugs, have been used since February 1, 2020. In addition, we set this day as t = 0; (2) Vaccines have no effect on people in the incubation group, i.e., vaccines can either provide immunity or cure the disease for them; (3) Infected people are only moved to hospital isolation during the early infected phase. Advanced infected people will not enjoy the same treatment; (4) Drugs are only for people in hospital isolation; (5) Each person in the hospital isolation group will be provided with enough medications so that they will all recover from the disease. The drug production quantity is sufficient.

2. Supplemental Tables.

2.1. Table S1 Reports in the different mathematical model published in COVID-19.

Models	Methods	Parameters and results	References
GLEAM	BCA	T_g: 7.5 days; R_0: 2.57 (90% CI 2.37 - 2.78); T_d: 4.2 days (90% CI 3.8 - 4.7)	(1)
SEIR model	MCMC method	R_0: 2.68 (95% CrI 2.47-2.86); The epidemic doubling time: 6.4 days (95% CrI 5.8-7.1)	(2)
A branching process model	A negative binomial distribution	R_0: 1.5, 2.5, 3.5	(3)
Stochastic simulations model	A negative-binomial offspring distribution	R_0 was 2.2 (90% high density interval: 1.4 - 3.8); k: median: 0.54, 90% high density interval: 0.014-6.95	(4)
SEIR model	---	R_0 was 3.11 (95% CI, 2.39 - 4.13)	(5)
GAM	The lagged probability distribution	R_0 of nationwide and Wuhan: 4.5, 4.4; The doubling time: 2.4 days	(6)
Simple non-linear growth models	The NLS framework	R_0: 2.24 (95% CI: 1.96 - 2.55) to 3.58 (95% CI: 2.89 - 4.39); g was 8- and 2-fold	(7)
A dynamic compartmental model (Eq. (1)-(2))	NLS method; MCMC methods; M-H algorithm	Basic R_0: 4.71 (4.50 - 4.92); Effective R_0: 2.08 (1.99 - 2.18); The epidemic peak time: peak in early March 2020 (80 days since initiation)	(8)
IDEA model	---	R_0 varied from 2.0 to 3.1	(9)
BDSS model	The Bayesian MCMC algorithm	The median estimate of Re shifted from 1.6 to 1.1 on around January 1, 2020.	(10)
SEIR and SEIHR models	The least square method; MCMC; Likelihood function method	R_0 was 6.47 (95% CI: 5.71 - 7.23)	(11)
Modified SIR model	---	The actual number of infected cases: 88,075 cases (Jan 31, 2020); Isolation wards and ICU were 34,786 and 9,346, respectively	(12)

Notes: GLEAM: The Global Epidemic and Mobility Model; Bayesian Computation approach: BCA; T_g: A generation time; R_0: reproductive number; T_d: a doubling time; MCMC: Markov Chain Monte Carlo; k: Dispersion parameter; GAM: generalized additive model; NLS: nonlinear least square; g: Intrinsic growth rate; MH: Metropolis-Hastings; IDEA: Incidence Decay and Exponential Adjustment; EG: Exponential Growth; ML: maximum likelihood; BDSS: birth-death skyline serial; Re: effective reproductive number

3. References

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