

Supplementary Materials: Framework for Assessing and Easing Global COVID-19 Travel Restrictions

Thien-Minh Le^{1*}, Louis Raynal¹, Octavious Talbot¹, Hali Hambridge¹, Christopher Drovandi³, Antonietta Mira², Kerrie Mengersen³, and Jukka-Pekka Onnela^{1*}

¹Harvard T.H. Chan School of Public Health, Department of Biostatistics, Boston, Massachusetts, U.S.A.

²Università della Svizzera Italiana, Lugano, Switzerland

³Queensland University Technology, School of Mathematical Sciences, Faculty of Science, Brisbane, Australia

*Corresponding authors: thle@hsph.harvard.edu & onnela@hsph.harvard.edu

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1 Models and methods

1.1 Local epidemiological model

We first consider a local epidemiological model as in Warne et al. (2020)¹. In this local model, for each country, at a given time, its population's status is divided into 6 mutually exclusive compartments: susceptible (S), undetected infected (I), active confirmed (A), confirmed recovered (R), confirmed deceased (D) and unconfirmed removed (Z). Its dynamic states evolve as in Figure S1, where α is the transmission rate, γ is the identification rate, β is the recovery rate, and δ is the death rate.

Suppose that for a given country the status of its population at time t is $\mathbf{X}(t) = [S(t), I(t), A(t), R(t), D(t), Z(t)]$, and $\theta = (\alpha, \beta, \delta, \gamma)$ represents the parameter of the statistical model for the country. Using the tau leaping method by Gillespie (2001)², the status of its population at time $(t + \tau)$ evolves as $\mathbf{X}(t + \tau) = \mathbf{X}(t) + \sum_{j=1}^5 Y_j(h_j(\mathbf{X}(t))\tau) \mathbf{v}_j$. In the above formula, $\mathbf{v}_j$, $j = 1, \dots, 5$, are the transition vectors, $\mathbf{v}_1 = [-1, 1, 0, 0, 0, 0]^T$, $\mathbf{v}_2 = [0, -1, 1, 0, 0, 0]^T$, $\mathbf{v}_3 = [0, 0, -1, 1, 0, 0]^T$, $\mathbf{v}_4 = [0, 0, -1, 0, 1, 0]^T$, and $\mathbf{v}_5 = [0, -1, 0, 0, 0, 1]^T$. Let the random variables $Y_j(h_j(\mathbf{X}(t))\tau)$ be Poisson distributed with rates $h_j(\mathbf{X}(t))\tau$, for $j \in \{1, \dots, 5\}$. More specifically, $h_1(\mathbf{X}(t))\tau = \alpha\tau \frac{S(t)I(t)}{P}$, $h_2(\mathbf{X}(t)) = \gamma\tau I(t)$, $h_3(\mathbf{X}(t)) = \beta\tau A(t)$, $h_4(\mathbf{X}(t)) = \delta\tau A(t)$, $h_5(\mathbf{X}(t)) = \beta\tau I(t)$, and P is the country's population.

We choose $\tau = 1$, which represents the change in population status after each day. Then the dynamic evolution of the epidemic in the country can be elaborated further as follows. After each day, the state of the model evolves from

$\mathbf{X}(t) = [S(t), I(t), A(t), R(t), D(t), Z(t)]$ to $\mathbf{X}(t+1) = [S(t+1), I(t+1), A(t+1), R(t+1), D(t+1), Z(t+1)]$ by the transformation $\mathbf{X}(t+1) = \mathbf{X}(t) + \sum_{j=1}^5 Y_j(h_j(\mathbf{X}(t))) \mathbf{v}_j$. In particular, $S(t+1) = S(t) - Y_1(t)$, $I(t+1) = I(t) + Y_1(t) - Y_2(t) - Y_5(t)$, $A(t+1) = A(t) + Y_2(t) - Y_3(t) - Y_4(t)$, $R(t+1) = R(t) + Y_3(t)$, $D(t+1) = D(t) + Y_4(t)$, $Z(t+1) = Z(t) + Y_5(t)$, where $Y_j(t)$ are Poisson distributed with rates $h_j(\mathbf{X}(t))$, $j = 1, \dots, 5$, $h_1(\mathbf{X}(t)) = \alpha \frac{S(t)I(t)}{P}$, $h_2(\mathbf{X}(t)) = \gamma I(t)$, $h_3(\mathbf{X}(t)) = \beta A(t)$, $h_4(\mathbf{X}(t)) = \delta A(t)$, $h_5(\mathbf{X}(t)) = \beta I(t)$.

The local model can be made more flexible by letting the transmission rate α change over time, i.e., setting $\alpha = \alpha_1 \mathcal{I}_{0,T(1)}(t) + \alpha_2 \mathcal{I}_{T(1),T(2)}(t) + \dots + \alpha_m \mathcal{I}_{T(m-1),T(m)}(t)$, where $0 = T(0) < T(1) < \dots < T(m) = T$, and the indicator function $\mathcal{I}_{T(i),T(i+1)}(t) = 1$ if $T(i) < t \leq T(i+1)$, and 0 otherwise.

1.2 Global travel model

Our global epidemiological model is built based on the local model by utilizing travel flow data as follows. For a given country i , suppose the status of its population at the end of day $(t-1)$ is $\mathbf{X}_i(t-1) = [S_i(t-1), I_i(t-1), A_i(t-1), R_i(t-1), D_i(t-1), Z_i(t-1)]$, and the parameter of the statistical model for this country is $\theta_i = (\alpha_i, \beta_i, \delta_i, \gamma_i)$. On day t , the epidemic state in country i is updated via two steps. First, the state evolves based on country i 's internal population. Second, the state evolves based on external factors, here the inflow of airline travelers from other countries and the outflow of airline travelers to other countries.

We consider changes due to internal effects first. For country i , the transition from $t-1$ to t is characterized by the shift

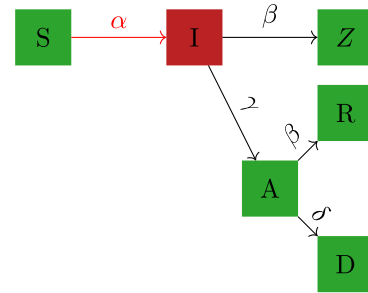


Figure S1. Schematic of the local epidemiological compartmental model which describes the state of the country at any given time. The population of each country is divided into six mutually exclusive compartments: susceptible (S), undetected infected (I), active confirmed (A), confirmed recovered (R), confirmed deceased (D), and unconfirmed removed (Z). The basic reproductive number in this model is given by $R_0 = \alpha/(\gamma + \beta)$.

from $\mathbf{X}_i(t-1)$ to $\mathbf{X}_i(t) = [S_i(t), I_i(t), A_i(t), R_i(t), D_i(t), Z_i(t)]$ where

$$\begin{aligned} S_i(t) &= S_i(t-1) - Y_{1,i}(t-1), \\ R_i(t) &= R_i(t-1) + Y_{3,i}(t-1), \\ I_i(t) &= I_i(t-1) + Y_{1,i}(t-1) - Y_{2,i}(t-1) - Y_{5,i}(t-1), \\ D_i(t) &= D_i(t-1) + Y_{4,i}(t-1), \\ A_i(t) &= A_i(t-1) + Y_{2,i}(t-1) - Y_{3,i}(t-1) - Y_{4,i}(t-1), \\ Z_i(t) &= Z_i(t-1) + Y_{5,i}(t-1) \end{aligned}$$

and $Y_{j,i}(t-1)$, $j = 1, \dots, 5$, are Poisson distributed with rates

$$\begin{aligned} h_{1,i}(\mathbf{X}_i(t-1)) &= \alpha_i \frac{S_i(t-1)I_i(t-1)}{P_i(t-1)}, \\ h_2(\mathbf{X}_i(t-1)) &= \gamma I_i(t-1), \\ h_3(\mathbf{X}_i(t-1)) &= \beta_i A_i(t-1), \\ h_4(\mathbf{X}_i(t-1)) &= \delta_i A_i(t-1), \\ h_5(\mathbf{X}_i(t-1)) &= \beta_i I_i(t-1) \end{aligned}$$

and $P_i(t-1)$ is the size of the population in country i on day $(t-1)$.

The travel data specify how many new individuals enter the country on day t from each of the disease states. The current state is updated as $\mathbf{X}_i^+(t) = [S_i^+(t), I_i^+(t), A_i^+(t), R_i^+(t), D_i^+(t), Z_i^+(t)]$, where $\mathbf{X}_i^+(t) = \mathbf{X}_i(t) + \mathbf{f}_i^{\text{in}}(t) - \mathbf{f}_i^{\text{out}}(t)$, where $\mathbf{f}_i^{\text{in}}(t)$ represents the six compartments of people entering the country on day t and $\mathbf{f}_i^{\text{out}}(t)$ represents the six compartments of people leaving the country on day t . Due to temperature checks and other approaches for screening travelers, we assume that all active confirmed cases are unable to travel. We also assume that deceased individuals do not travel between countries. Consequently, the compartments in $\mathbf{f}_i^{\text{in}}(t)$ and $\mathbf{f}_i^{\text{out}}(t)$ only include non-zero elements in four of the six disease states: susceptible (S), undetected infected (I), recovered confirmed (R), and unconfirmed removed (Z). Travelers in the recovered confirmed (R) and unconfirmed removed (Z) states do not impact the epidemiological state of destination population. However, data on all four categories is not readily available. While each country keeps track of the total number of confirmed recovered each day, they do not necessarily keep track of how many of them leave the country. Therefore, we take a conservative approach and assume that each traveler either belongs to the S category or the I category, meaning travelers bring some potential risk when they arrive in a new country as undetected infected can spread the disease and susceptible individuals reduce population immunity and can proliferate disease spread. In other words, we impose $\mathbf{f}_i^{\text{in}}(t) = [S_i^{\text{in}}(t), I_i^{\text{in}}(t), 0, 0, 0, 0]$ and $\mathbf{f}_i^{\text{out}}(t) = [S_i^{\text{out}}(t), I_i^{\text{out}}(t), 0, 0, 0, 0]$, where $I_i^{\text{in}}(t)$ and $I_i^{\text{out}}(t)$ are the number of undetected infected that enter and leave country i on day t , respectively. $S_i^{\text{in}}(t)$ and $S_i^{\text{out}}(t)$ are the total numbers of susceptible individuals who enter and leave country i on day t , respectively. $S_i^{\text{in}}(t) + I_i^{\text{in}}(t) = T_i^{\text{in}}(t)$ gives the total number of travelers that enter country i on day t , and $S_i^{\text{out}}(t) + I_i^{\text{out}}(t) = T_i^{\text{out}}(t)$ gives the total number of individuals who leave the country i on day t . As such, $\mathbf{X}_i(t)$ and $\mathbf{X}_i^+(t)$ only differ in the first two categories, where $\mathbf{X}_i^+(t) = [S_i^+(t), I_i^+(t), A_i(t), R_i(t), D_i(t), R_i^u(t)]$, $S_i^+(t) = S_i(t) + S_i^{\text{in}}(t) - S_i^{\text{out}}(t)$, and $I_i^+(t) = I_i(t) + I_i^{\text{in}}(t) - I_i^{\text{out}}(t)$. On day $(t+1)$, the internal model will be updated based on $\mathbf{X}_i^+(t)$. The compartmental quantities are updated as follows

$$\begin{aligned}
S_i(t+1) &= S_i^+(t) - Y_{1,i}(t), \\
R_i(t+1) &= R_i(t) + Y_{3,i}(t), \\
I_i(t+1) &= I_i^+(t) + Y_{1,i}(t) - Y_{2,i}(t) - Y_{5,i}(t), \\
D_i(t+1) &= D_i(t) + Y_{4,i}(t), \\
A_i(t+1) &= A_i(t) + Y_{2,i}(t) - Y_{3,i}(t) - Y_{4,i}(t), \\
Z_i(t+1) &= Z_i(t) + Y_{5,i}(t).
\end{aligned}$$

and $Y_{j,i}(t)$, $j = 1, \dots, 5$, are Poisson distributed with rates

$$\begin{aligned}
h_{1,i}(\mathbf{X}_i(t)) &= \alpha_i \frac{S_i^+(t) I_i^+(t)}{P_i(t)}, \\
h_2(\mathbf{X}_i(t)) &= \gamma_i I_i^+(t), \\
h_3(\mathbf{X}_i(t-1)) &= \beta_i A_i(t), \\
h_4(\mathbf{X}_i(t)) &= \delta_i A_i(t), \\
h_5(\mathbf{X}_i(t)) &= \beta_i I_i^+(t).
\end{aligned}$$

Our model assumes that active confirmed cases do not spread the disease due to self-isolation or hospitalization. Therefore, undetected infected cases are the only ones to spread the disease. Moreover, when $I = 0$, the pandemic in the country will cease if we stop admitting undetected infected cases from other countries. Each day, among the people that travel from country i to other countries, there may be some undetected infected cases. If an undetected infected individual enters a country with zero undetected infectious cases, they will seed a new outbreak in this country. Suppose that on day t , there are $I_{ij}^{\text{out}}(t)$ undetected infected people departing from country i for country j , $j \neq i$. Then $I_i^{\text{out}}(t) = \sum_{j=1, j \neq i}^n I_{ij}^{\text{out}}(t)$, where $I_{ij}^{\text{out}}(t)$ is the number of undetected infected moving from country i to country j on day t , and n is the total number of countries. We model the number of undetected infected people who leave country i for country j on day t using a multinomial distribution with probabilities based on travel network data. In other words, $\{I_{ij}^{\text{out}}(t)\}_{1 \leq j \neq i \leq n} \sim M(I_i^{\text{out}}(t), \{p_{ij}(t)\}_{1 \leq j \neq i \leq n})$, where $p_{ij}(t) = \frac{T_{ij}^{\text{out}}(t)}{T_i^{\text{out}}(t)}$ and $T_i^{\text{out}}(t)$ is the total number of travelers leaving country i for j on day t . Let us denote $S_{ij}^{\text{out}}(t)$ as the number of susceptible people who travel from country i to country j at day t . Then $T_{ij}^{\text{out}}(t) = S_{ij}^{\text{out}}(t) + I_{ij}^{\text{out}}(t)$. Therefore, at the end of day t , the six states for country i are updated as $\mathbf{X}_i^+(t) = [S_i^+(t), I_i^+(t), A_i(t), R_i(t), D_i(t), R_i^u(t)]$, where

$$\begin{aligned}
S_i^+(t) &= S_i(t) + S_i^{\text{in}}(t) - S_i^{\text{out}}(t) = S_i(t) + \sum_{1 \leq j \neq i \leq n} S_{ji}^{\text{out}}(t) - S_i^{\text{out}}(t) \\
I_i^+(t) &= I_i(t) + I_i^{\text{in}}(t) - I_i^{\text{out}}(t) = I_i(t) + \sum_{1 \leq j \neq i \leq n} I_{ji}^{\text{out}}(t) - I_i^{\text{out}}(t).
\end{aligned}$$

1.3 Travel regulation policies

Our goal is to find a value p so that the number of undetected infected $I^+(1), I^+(2), \dots, I^+(T)$ stay below a given threshold c . We consider two types of regulation: average control policy and probability control policy.

1. Regulation in terms of **average control**. We find a proportion p such that the average number of undetected cases each day in the next T days stays below a threshold c : $E(I^+(1)) < c, E(I^+(2)) < c \dots, E(I^+(T)) < c$, where E denotes the expectation.
2. Regulation in terms of **probability control**. We find a proportion p such that the probability of undetected cases each day in the next T days being lower than a threshold c is at least at π : $P(I^+(1) < c, I^+(2) < c, \dots, I^+(T) < c) \geq \pi$.

The following lemmas gives us the proportion p that satisfies the above requirements.

Lemma 1. Under the assumptions of our model, for a given country with population size P , initial state $\mathbf{X}(0) = [S(0), I(0), A(0), R(0), D(0), Z(0)]$, and the parameter of the statistical model $\theta = (\alpha, \beta, \delta, \gamma)$, let us denote $\psi = 1 + \alpha \frac{S(0)}{P} - \gamma - \beta$.

1. The average control requirement is satisfied if

$$p = \min_{k=1, \dots, T} \left(\frac{(c/I(0))^{1/k}}{\psi} - 1 \right). \quad (1)$$

2. The probability control requirement is satisfied if

$$p = \min_{k=1, \dots, T} \left(\frac{(c(1-\pi)/I(0))^{1/k}}{\psi} - 1 \right). \quad (2)$$

Proof:

1. *Average control.* With an initial number $I(0)$ of undetected infected cases, from the internal evolution process, we have $I(1) = I(0) + Y_{1,0} - Y_{2,0} - Y_{5,0}$, and at the end of this day we have $I^+(1) = I(1)(1+p)$, where $Y_{1,0} \sim \text{Poisson}(\alpha \frac{S(0)I(0)}{P})$, $Y_{2,0} \sim \text{Poisson}(\gamma I(0))$, and $Y_{5,0} \sim \text{Poisson}(\beta I(0))$. Therefore, we have $E(I^+(1)) = E(E(I^+(1)/I(0))) = I(0)(1 + \alpha \frac{S(0)}{P} - \gamma - \beta)(1+p) = I(0)\psi(1+p)$. Similarly, we have $E(I^+(2)) = E(E(I^+(2)/I^+(1))) = E(I^+(1)(1 + \alpha \frac{S(1)}{P} - \gamma - \beta)(1+p)) < (1+p)\psi E(I^+(1)) = (1+p)^2\psi^2 I(0)$. Repeating this argument until reaching day T results in $E(I(T)^+) < (1+p)^T \psi^T I_0$. For average control, therefore, we want to find a p such that $(1+p)\psi I(0), (1+p)^2\psi^2 I(0), \dots, (1+p)^T \psi^T I(0) < c$. By solving the above inequality, the p that satisfies the requirements is

$$p = \min_{k=1, \dots, T} \left(\frac{(c/I(0))^{1/k}}{\psi} - 1 \right) \quad \blacksquare$$

2. *Probability control.* Here we have

$$\begin{aligned} E(I^+(1)/I(0)) &= \psi(1+p)I(0), E(I^+(2)/I^+(1)) < \psi(1+p)I^+(1), \\ E(I^+(3)/I^+(2)) &< \psi(1+p)I^+(2), \dots, E(I^+(T)/I^+(T-1)) < \psi(1+p)I^+(T-1). \end{aligned}$$

Let us denote $\frac{I^+(1)}{\psi(1+p)} = I^*(1), \frac{I^+(2)}{\psi^2(1+p)^2} = I^*(2), \dots, \frac{I^+(T)}{\psi^T(1+p)^T} = I^*(T)$. The sequence $I^*(1), I^*(2), \dots, I^*(T)$ forms a non-negative supermartingale sequence since

$$\begin{aligned} E(I^*(1)/I(0)) &= I(0), E(I^*(2)/I^*(1)) < I^*(1), \\ E(I^*(3)/I^*(2)) &< I^*(2), \dots, E(I^*(T)/I^*(T-1)) < I^*(T-1). \end{aligned}$$

Applying the maximal inequality for a non-negative supermartingale we have $P(\cup_{i \geq 1} (I^*(i) \geq m)) \leq \frac{E(I^*(1))}{m}$ for a given $m > 0$. This gives $1 - P(\cup_{i \geq 1} (I^*(i) \geq m)) \geq 1 - \frac{E(I^*(1))}{m}$. In other words, $P(I^*(1) < m, I^*(2) < m, \dots, I^*(T) < m) \geq 1 - \frac{E(I^*(1))}{m} = 1 - \frac{I(0)}{m}$. If we want $P(I^*(1) < m, I^*(2) < m, \dots, I^*(T) < m) \geq \pi$, then the smallest value of m must satisfy the relation $1 - \frac{I(0)}{m} = \pi$. We choose $m = \frac{I(0)}{1-\pi}$. We have: $P(I^*(1) < m, I^*(2) < m, \dots, I^*(T) < m) = P(I^+(1) < m\psi(1+p), I^+(2) < m\psi^2(1+p)^2, \dots, I^+(T) < m\psi^T(1+p)^T)$. So, if we want $I^+(1), I^+(2), \dots, I^+(T) < c$, then we need to find a p such that $m\psi(1+p) < c, m\psi^2(1+p)^2 < c, \dots, m\psi^T(1+p)^T < c$. In other words, we need a p that satisfies: $p < \frac{(c/m)^{1/k}}{\psi} - 1, \forall k = 1, \dots, T$, or $p < \frac{(c(1-\pi)/I(0))^{1/k}}{\psi} - 1, \forall k = 1, \dots, T$. In conclusion, for a probability

control level π and a threshold c in the next T days, the required p is

$$p = \min \left(\frac{(c(1-\pi)/I(0))^{1/k}}{\psi} - 1 \right)_{k=1, \dots, T} . \blacksquare$$

Remark: The probability control policy is more conservative than the average control policy. Under the same threshold c , the difference between the two policies is the factor $(1-\pi)$ in the numerator of the probability control policy. If we want the probability to be at least $\pi = 0.9$, the factor $(1-\pi) = 0.1$. As a result, the proportion p in probability control is much smaller than the proportion p in average control. If we want to use the probability control with a probability of at least 0.9, we need to set the threshold c higher in probability control than the threshold c in average control to make sure that p is non-negative.

Note that in the above Lemma, we identify imported cases to the local cases. Why is this justifiable? There are two sets of factors to consider here: properties of the pathogen and properties of the host. On the former, there are multiple viral variants at this point as is to be expected, but the pathogen does not know whether it was imported or local. On the latter, hosts who end up importing a case to a target country (i.e., travelers who are positive) at large will use the same health care services as local residents, therefore the identification rate parameter γ , recovery rate parameter β , and death rate parameter δ should be, at least to a good approximation, the same. The travelers are also exposed to the same social and behavioral and built environment as the locals, ranging from basic demographic factors, such as population density, to various cultural factors, such as acceptability of mask wearing. For these reasons, at least as a first order approximation, we use the same transmission rate α for everyone within the given (target) country.

Example 1. Here we give one example of using the average control policy to regulate travel. For simplicity, we consider a small world with only three countries, with the following initial states and true parameter values:

$$\mathbf{X}_1(0) = [S_1(0), I_1(0), A_1(0), R_1(0), D_1(0), Z_1(0)] = (28718795, 68, 167, 259, 149, 101)$$

$$\theta_1 = (\alpha_1, \beta_1, \delta_1, \gamma_1) = (0.82, 0.18, 0.09, 0.68)$$

$$\mathbf{X}_2(0) = (6358016, 40356, 1573, 454, 55, 320)$$

$$\theta_2 = (0.74, 0.15, 0.02, 0.06)$$

$$\mathbf{X}_3(0) = (28507087, 206, 764, 619, 72, 188)$$

$$\theta_3 = (0.92, 0.13, 0.02, 0.76).$$

We wish to regulate the incoming travel in the first country (Country 1). The above choices of initial conditions and parameter values are based on our simulations where the benefits of travel restriction can be seen clearly. We now need to find regulation sequences $\{p_{21}(t)\}_{t=1, \dots, 7}$ and $\{p_{31}(t)\}_{t=1, \dots, 7}$ that can regulate airline travel from Country 2 to Country 1 and from Country 3 to Country 1, respectively, such that for the next $T = 7$ days, the expected number of undetected infected cases in the arriving country will not exceed $c = 70$ cases any day.

Applying Lemma 1.1, we can find the value of p for Country 1 as $p = \min((c/I_0)^{1/k}/\psi - 1)_{k=1, \dots, 7} = 0.035$. The sequence of the number of undetected infected imported cases Country 1 can accept each day is $\left(((1+p)\psi)^k I(0)\right)_{k=1, \dots, 7} = (2, 2, 2, 2, 2, 2, 2)$. Because Country 1 has two “neighbors”, so Country 1 can accept about 1 undetected infected from each neighbor during each day of the regulation period.

The next step is to predict, for each day, the number of undetected infected travelers from countries 2 and 3 that would enter Country 1 in the next 7 days if full travel were allowed. We obtain these numbers by simulating data given the true parameters under the fully open scenario. We first simulate 10000 stochastic realizations under this scenario and use the 97.5th percentile of the simulated sequence of undetected infected in countries 2 and 3 in the next 7 days as proxies for the number of undetected infected cases in these countries. We then simulate a deterministic realization under the fully open scenario

during the regulation period and use the values from the deterministic realization to calculate the percentage of undetected infected people in countries 2 and 3. Based on these percentages and the travel data, we estimate how many undetected infected individuals enter Country 1 from Country 2 and Country 3 daily during the regulation period if full travel is allowed. The final step is obtaining the regulation sequence that Country 1 can allow for passengers from Country 2 and Country 3 to enter. The regulation sequence $\{p_{21}(t)\}_{t=1,\dots,7}$ that Country 1 can allow from Country 2 during the regulation period is obtained by dividing the number of daily undetected infected cases that Country 1 can tolerate from Country 2 by the daily estimated number of imported undetected infected cases from Country 2 if full travel is allowed. Notice that if the daily proportion is greater or equal to 1, we set it to 1. Repeating the same procedure, we find the regulation sequence from Country 3 to Country 1.

Following the above steps, we find that in the next 7 days, the regulation sequence of proportions of people who can travel from Country 2 to Country 1 is (0.103, 0.076, 0.051, 0.035, 0.022, 0.014, 0.009), and the sequence of proportions of people who can travel from Country 3 to Country 1 is (1, 1, 1, 1, 1, 1, 1). Compared to the fully open scenario, using the average control approach with the threshold of 70 cases during the 7-day regulation period, about 6% of travelers from Country 2 are allowed enter the Country 1, and all travelers from Country 3 are allowed to enter Country 1. Overall, the volume of inbound travelers in Country 1 is about 89% of the normal level.

In practice, the value of the transmission rate α varies over time, and we therefore provide an additional lemma that generalizes Lemma 1 to address the aspect of varying α .

Lemma 2. *Under the assumptions of our model, for a given country with population size P , initial status*

$\mathbf{X}(0) = [S(0), I(0), A(0), R(0), D(0), Z(0)]$ *and the parameter of the statistical model for this country over the time period from $0 = T(0)$ to $T = T(m)$ is $\theta = (\alpha, \beta, \delta, \gamma)$, where $\alpha = \alpha_1 \mathcal{I}_{0,T(1)}(t) + \alpha_2 \mathcal{I}_{T(1),T(2)}(t) + \dots + \alpha_m \mathcal{I}_{T(m-1),T(m)}(t)$. Let us denote $\psi_{\max} = \max_{i=1,\dots,m} \left(1 + \alpha_i \frac{S(0)}{P} - \gamma - \beta\right)$.*

1. *The average control requirement is satisfied if*

$$p = \min_{k=1,\dots,T} \left(\frac{(c/I_0)^{1/k}}{\psi_{\max}} - 1 \right). \quad (3)$$

2. *The probability control requirement is satisfied if*

$$p = \min_{k=1,\dots,T} \left(\frac{(c(1-\pi)/I_0)^{1/k}}{\psi_{\max}} - 1 \right). \quad (4)$$

Proof:

1. *Average control.* Follow the same argument as in the proof of Lemma 1, we have $E(I^+(1) = E(E(I^+(1)/I(0))) = I(0)(1 + \alpha \frac{S(0)}{P} - \gamma - \beta)(1 + p) = I(0)(1 + \alpha_1 \frac{S(0)}{P} - \gamma - \beta)(1 + p) < I(0)\psi_{\max}(1 + p)$. Repeating the argument until we reach day T yields $E(I(T)^+) < (1 + p)^T \psi_{\max}^T I(0)$. Therefore, we want to find a p such that $(1 + p)\psi_{\max} I(0), (1 + p)^2 \psi_{\max}^2 I(0), \dots, (1 + p)^T \psi_{\max}^T I(0) < c$. Hence the value p that satisfies the requirements for average control is

$$p = \min_{k=1,\dots,T} \left(\frac{(c/I(0))^{1/k}}{\psi_{\max}} - 1 \right) \quad \blacksquare$$

2. *Probability control. Here we have*

$$\begin{aligned} E(I^+(1)/I(0)) &< \psi_{\max}(1+p)I(0), E(I^+(2)/I^+(1)) < \psi_{\max}(1+p)I^+(1), \\ E(I^+(3)/I^+(2)) &< \psi_{\max}(1+p)I^+(2), \dots, E(I^+(T)/I^+(T-1)) < \psi_{\max}(1+p)I^+(T-1). \end{aligned}$$

Let us denote $\frac{I^+(1)}{\psi_{\max}(1+p)} = I^*(1), \frac{I^+(2)}{\psi_{\max}^2(1+p)^2} = I^*(2), \dots, \frac{I^+(T)}{\psi_{\max}^T(1+p)^T} = I^*(T)$. Similar to Lemma 1, the sequence of $I^*(1), I^*(2), \dots, I^*(T)$ forms a non-negative supermartingale sequence. Hence, following the same arguments as in Lemma 1, for a probability control level π and a threshold c in the next T days, the required p is

$$p = \min_{k=1, \dots, T} \left(\frac{(c(1-\pi)/I(0))^{1/k}}{\psi_{\max}} - 1 \right) \quad \blacksquare$$

1.4 Choosing distance and summary statistics in Approximate Bayesian Computation

There are many variants of ABC, but they are all based on a comparison of observed and simulated data, which in most cases requires specification of data summary statistics, a distance measure, and a scalar distance threshold ε . The most basic ABC algorithm, the so-called accept-reject method, starts by simulating a parameter value from a prior distribution and then uses the model, given this parameter value, to generate one realization of data. If the distance between the summary statistics for the observed data and the summary statistics for the simulated data is less than or equal to ε , the sampled parameter value is retained; otherwise, it is discarded. The collection of accepted parameter values constitutes a sample from an approximation of the posterior distribution. The approximation generally improves with smaller values of ε , but at the same time it becomes more computationally expensive to obtain acceptances.

This basic ABC algorithm is computationally inefficient when working with a small threshold ε as a vast majority of sampled parameter values are rejected. To address this inefficiency, some sequential variants of ABC have been proposed, such as the ABC Markov chain Monte Carlo algorithm (ABC-MCMC) by Marjoram, et al. (2003) and the ABC Sequential Monte Carlo algorithm (ABC-SMC) by Sisson et al. (2007), Toni, et al. (2009), and Drovandi and Pettitt (2011)³⁻⁶. In this paper, we use the variant from Drovandi and Pettitt (2011)⁶, called replenishment ABC (RABC). For its implementation, we use the R package protoABC from Ebert (2020)⁷. This package is very flexible as the users can employ any priors, generative models, and distance functions.

A commonly used distance is the Euclidean distance due to its simple form. Let $\text{Data}^{(i)}$ refer to the observed data, $\text{Data}^{(i)}$ to the i^{th} simulated dataset, and S to a function that maps data to data summaries. In our problem setting, the Euclidean distance $L(S(\text{Data}^{(i)}), S(\text{Data}))$ can be written as

$$\left(\frac{1}{T} \sum_{t=1}^T \left[\left(A^{(i)}(t) - A(t) \right)^2 + \left(R^{(i)}(t) - R(t) \right)^2 + \left(D^{(i)}(t) - D(t) \right)^2 \right] \right)^{1/2},$$

where $(A^{(i)}(t), R^{(i)}(t), D^{(i)}(t))$ and $(A(t), R(t), D(t))$ are cumulative active confirmed cases, cumulative recovered confirmed cases, and cumulative confirmed deaths on day t of the simulated data and the observed empirical data, respectively, and T is the number of observations in the time series. However, simply using the Euclidean distance may not be the best choice since it does not account for the scale of different quantities, and may need to be standardized (see for example Beaumont et al. (2002), Csilléry et al. (2012), or Prangle (2017)⁸⁻¹⁰). This is why we also consider the following weighted Euclidean distance, with weights given by the inverse standard deviations:

$$\left(\frac{1}{T} \sum_{t=1}^T \left[\left(\frac{A^{(i)}(t) - A(t)}{\sigma_A(t)} \right)^2 + \left(\frac{R^{(i)}(t) - R(t)}{\sigma_R(t)} \right)^2 + \left(\frac{D^{(i)}(t) - D(t)}{\sigma_D(t)} \right)^2 \right] \right)^{1/2},$$

where $\sigma_A(t)$, $\sigma_R(t)$, and $\sigma_D(t)$ for $t = 1, \dots, T$ are the prior predictive standard deviations of $A(t), R(t), D(t)$ at each time step. They are obtained by first generating N (N being large) parameters values $\theta = (\alpha, \beta, \delta, \gamma)$ from the prior $\pi(\theta)$, and then generating one realization of simulated data for each. The standard deviation at each time step is then calculated based on these N simulated data giving $\sigma_A(t)$, $\sigma_R(t)$, and $\sigma_D(t)$ for $t = 1, \dots, T$. In our simulation study, we chose $N = 5000$.

To improve the predictive quality of ABC algorithms, we can also use additional information about parameter estimates as summary statistics. For simplicity, we first limit our discussion to the local model, where each country is considered separately. The choice of the distance for the global model will be discussed in Section 1.5.

Under our model assumptions we have $R(t) = R(t-1) + \text{Poisson}(\beta A(t-1))$, where $t = 1, \dots, T$. For a given $A(t-1)$, the expected value $E(R(t) - R(t-1)) = \beta A(t-1)$ which yields $E\left(\frac{R(t) - R(t-1)}{A(t-1)}\right) = \beta$. For a given sequence of known $\{A(t)\}_{t=1, \dots, T}$, the sequence of independent variables $\left\{\frac{R(t) - R(t-1)}{A(t-1)}\right\}_{t=1, \dots, T}$ has β as the common mean value. Therefore, we can use its median value to estimate β . If our algorithm generated a reasonable $\theta^{(i)}$, then the data generated by $\theta^{(i)}$ should give us a sequence $\left\{\frac{R^{(i)}(t) - R^{(i)}(t-1)}{A^{(i)}(t-1)}\right\}_{t=1, \dots, T}$ with median value close to the corresponding median value of $\left\{\frac{R(t) - R(t-1)}{A(t-1)}\right\}_{t=1, \dots, T}$. Therefore under our model assumptions, adding the term $\left|\text{median}\left\{\frac{R(t) - R(t-1)}{A(t-1)}\right\}_{t=1, \dots, T} - \text{median}\left\{\frac{R^{(i)}(t) - R^{(i)}(t-1)}{A^{(i)}(t-1)}\right\}_{t=1, \dots, T}\right|$ when calculating $L(S(\text{Data}^{(i)}), S(\text{Data}))$ should help improve estimation of β . Similarly, the median of the sequence $\left\{\frac{D(t) - D(t-1)}{A(t-1)}\right\}_{t=1, \dots, T}$ can be used to estimate the death rate δ , and we can improve estimation of δ by adding the term $\left|\text{median}\left\{\frac{D(t) - D(t-1)}{A(t-1)}\right\}_{t=1, \dots, T} - \text{median}\left\{\frac{D^{(i)}(t) - D^{(i)}(t-1)}{A^{(i)}(t-1)}\right\}_{t=1, \dots, T}\right|$.

We now try to learn the transmission rate α under our model assumptions. We have $S(t) = S(t-1) + \text{Poisson}\left(\alpha \frac{S(t-1)I(t-1)}{P}\right)$, $t = 1, \dots, T$, where P is the total population size of the country. So for a given $S(t-1), I(t-1)$, we have $E(S(t) - S(t-1)) = \alpha \frac{S(t-1)I(t-1)}{P}$. This yields $E\left(\frac{S(t) - S(t-1)}{S(t-1)I(t-1)} P\right) = \alpha$. Unfortunately, $S(t-1)$ and $I(t-1)$ are hidden states and not available in our data. To use the above strategy to improve the estimation of α , we need to reconstruct these hidden states based on the available data $\{A(t), R(t), D(t)\}_{t=1, \dots, T}$. Because our model is stochastic, all values change each time we rerun the model. However, based on the available data $\{A(t), R(t), D(t)\}_{t=1, \dots, T}$ we can reconstruct the mean realization of the hidden states.

We start with reconstruction of the mean realization of $I(t)$. Let $U(t)$ denote the total number of confirmed cases at time t , $\Delta U(t-1)$ the number of new confirmed cases at time t , and $\Delta Z(t-1)$ the number of new undocumented recovered cases on day t . Note that $U(t) = A(t) + R(t) + D(t)$, $\Delta U(t-1) = U(t) - U(t-1)$, and $\Delta Z(t-1) = Z(t) - Z(t-1)$.

From the local model we have:

$$\begin{aligned} U(t) &= A(t) + R(t) + D(t) \\ &= A(t-1) + Y_2(t-1) - Y_3(t-1) - Y_4(t-1) \\ &\quad + R(t-1) + Y_3(t-1) + D(t-1) + Y_4(t-1) \\ &= A(t-1) + R(t-1) + D(t-1) + Y_2(t-1) \\ &= U(t-1) + Y_2(t-1) \end{aligned}$$

From this we obtain $Y_2(t-1) = U(t) - U(t-1) = \Delta U(t-1)$. Moreover, since $Y_2(t-1) \sim \text{Poisson}(\gamma I(t-1))$, we have

$$E(I(t-1)) = E\left(\frac{\Delta U(t-1)}{\gamma}\right). \quad (5)$$

Equation (5) tells us that given the observed data $\{A(t), R(t), D(t)\}_{t=1, \dots, T}$, if the identification rate γ is known, the average realization of $I(t)$ can be reconstructed up to time $T-1$.

We can similarly reconstruct the mean realization of $Z(t)$. Since $Z(t) = Z(t-1) + Y_5(t-1)$, where $Y_5(t-1) \sim \text{Poisson}(\beta I(t-1))$,

we have

$$E(\Delta Z(t-1)) = E(\beta I(t-1)).$$

Using (5), we obtain

$$E(\Delta Z(t-1)) = E\left(\frac{\beta \Delta U(t-1)}{\gamma}\right). \quad (6)$$

Moreover, using $Z(t) = Z(0) + \sum_{i=1}^{t-1} \Delta Z(i)$ and (6), the average value of $Z(t)$ can be reconstructed as

$$\begin{aligned} E(Z(t)) &= E(Z(0)) + \sum_{i=1}^{t-1} E(\Delta Z(i)) \\ &= E(Z(0)) + \sum_{i=1}^{t-1} E(\beta I(i)) \\ &= E(Z(0)) + \sum_{i=1}^{t-1} E\left(\frac{\beta \Delta U(i)}{\gamma}\right) \end{aligned} \quad (7)$$

Equations (5) and (7) tell us that based on the available data $\{A(t), R(t), D(t)\}_{t=1, \dots, T}$, if the identification rate γ and the recovery rate β are available to us, then we can reconstruct the average realization of $I(t)$ and $Z(t)$, $t = 1, \dots, T-1$. The average realization of $S(t)$ can also be reconstructed as $P - E(I(t) - A(t) - R(t) - D(t) - Z(t)) = P - U(t) - \frac{\Delta U(t)}{\gamma} - \sum_{i=0}^{t-1} \frac{\beta}{\gamma} \Delta U(i)$, where P is the population size of the country.

Overall, based on the observed data $\{A(t), R(t), D(t)\}_{t=1, \dots, T}$, suppose that the identification rate γ and the recovery rate β are available to us. The average realization can be reconstructed up to time $T-1$ as

$$\begin{aligned} &\{S(t), I(t), A(t), R(t), D(t), Z(t)\}_{t=1, \dots, T-1} \\ &= \{P(t) - U(t) - \frac{\Delta U(t)}{\gamma} - \sum_{i=0}^{t-1} \frac{\beta}{\gamma} \Delta U(i), \frac{\Delta U(t)}{\gamma}, A(t), R(t), D(t), \sum_{i=0}^{t-1} \frac{\beta}{\gamma} \Delta U(i)\}_{t=1, \dots, T-1}. \end{aligned}$$

Therefore α can be estimated as the median of the sequence $\left\{ \frac{S(t-1) - S(t)}{S(t-1)I(t-1)} P \right\}_{1, \dots, T-1}$.

Since β and γ are not known in advance, they need to be estimated. In step 1 of the ABC algorithm, a parameter value $\theta^{(i)} = (\alpha^{(i)}, \beta^{(i)}, \delta^{(i)}, \gamma^{(i)})$ is generated and available to us. If $\gamma^{(i)}$ and $\beta^{(i)}$ are correctly specified as γ and β of the underlying true parameter $\theta = (\alpha, \beta, \delta, \gamma)$, we would expect the median value of the sequence $\left\{ \frac{S(t-1) - S(t)}{S(t-1)I(t-1)} P \right\}_{1, \dots, T-1}$, constructed using $\gamma^{(i)}$ and $\beta^{(i)}$ and the available data $\{A(t), R(t), D(t)\}_{t=1, \dots, T}$, to give us a good estimator for the underlying true α value. Similarly, the median value of the sequence $\left\{ \frac{S^{(i)}(t-1) - S^{(i)}(t)}{S^{(i)}(t-1)I^{(i)}(t-1)} P \right\}_{1, \dots, T-1}$, constructed using $\gamma^{(i)}$ and $\beta^{(i)}$ and the available data $\{A^{(i)}(t), R^{(i)}(t), D^{(i)}(t)\}_{t=1, \dots, T}$, should give us a good estimator for the underlying true α value. Therefore the distance $|\text{median} \left\{ \frac{S(t-1) - S(t)}{S(t-1)I(t-1)} P \right\}_{t=1, \dots, T-1} - \text{median} \left\{ \frac{S^{(i)}(t-1) - S^{(i)}(t)}{S^{(i)}(t-1)I^{(i)}(t-1)} P \right\}_{t=1, \dots, T-1}|$ in $L(S(\text{Data}^{(i)}), S(\text{Data}))$ should be close to 0. On the other hand, if the generated parameters $\gamma^{(i)}$ and $\beta^{(i)}$ are far away from the true parameter values, then $|\text{median} \left\{ \frac{S^{(i)}(t) - S^{(i)}(t-1)}{S^{(i)}(t-1)I^{(i)}(t-1)} P \right\}_{t=1, \dots, T-1} - \text{median} \left\{ \frac{S(t) - S(t-1)}{S(t-1)I(t-1)} P \right\}_{t=1, \dots, T-1}|$ should not be close to 0.

Based on this observation, we then add the term

$$\left| \text{median} \left\{ \frac{S^{(i)}(t) - S^{(i)}(t-1)}{S^{(i)}(t-1)I^{(i)}(t-1)} P \right\}_{t=1, \dots, T-1} - \text{median} \left\{ \frac{S(t) - S(t-1)}{S(t-1)I(t-1)} P \right\}_{t=1, \dots, T-1} \right|$$

in $L(S(\text{Data}^{(i)}), S(\text{Data}))$ to improve the estimation for α .

Our final proposed distance for the model is as follows:

$$\sqrt{\frac{1}{T} \sum_{t=1}^T \left[\left(\frac{A^{(i)}(t) - A(t)}{\sigma_A(t)} \right)^2 + \left(\frac{R^{(i)}(t) - R(t)}{\sigma_R(t)} \right)^2 + \left(\frac{D^{(i)}(t) - D(t)}{\sigma_D(t)} \right)^2 \right]} + \sqrt{d},$$

where

$$\begin{aligned} d = & \left| \text{median} \left\{ \frac{R(t) - R(t-1)}{A(t-1)} \right\}_{t=1, \dots, T} - \text{median} \left\{ \frac{R^{(i)}(t) - R^{(i)}(t-1)}{A^{(i)}(t-1)} \right\}_{t=1, \dots, T} \right| \\ & + \left| \text{median} \left\{ \frac{D(t) - D(t-1)}{A(t-1)} \right\}_{t=1, \dots, T} - \text{median} \left\{ \frac{D^{(i)}(t) - D^{(i)}(t-1)}{A^{(i)}(t-1)} \right\}_{t=1, \dots, T} \right| \\ & + \left| \text{median} \left\{ \frac{S(t-1) - S(t)}{S(t-1)I(t-1)} P \right\}_{t=1, \dots, T-1} - \text{median} \left\{ \frac{S^{(i)}(t-1) - S^{(i)}(t)}{S^{(i)}(t-1)I^{(i)}(t-1)} P \right\}_{t=1, \dots, T-1} \right|. \end{aligned}$$

1.5 Marginal approach to parameter estimation

In the following, we will discuss how to use ABC to estimate parameters in each country for our global model. The challenge of using ABC to estimate the global model parameters is that many parameters need to be estimated. Therefore directly using ABC to estimate all the parameters for all countries at once may result in unstable parameter estimation and is computationally expensive. We propose a marginal estimation approach to estimate each country's parameters for the global model separately while still taking into account the travel data.

For simplicity, let us first consider a given Country m with the parameter $\theta_m = (\alpha_m, \beta_m, \delta_m, \gamma_m)$. Let $A_k(t), R_k(t), D_k(t)$ denote the number of cumulative active confirmed cases, cumulative recovered confirmed cases, and cumulative confirmed deaths in Country k on day t , respectively. Let $T(t) = [T_{ij}(t)]_{i,j=1, \dots, n}$ denote the global travel matrix on day t , where $T_{ij}(t)$ is the number of travelers from Country i to Country j at day t . Notice that $T_{ij}(t) = 0$ if $i = j, \forall t \in 1, \dots, T$. With the available data from the global model $\{A_k(t), R_k(t), D_k(t)\}_{k=1, \dots, n; t=1, \dots, T}$ and the travel data $\{T(t)\}_{t=1, \dots, T}$, we need to estimate θ_m .

Before introducing our estimation procedure, we rewrite how our global model evolves for country m on day t and $(t+1)$:

Step 1a *The internal pandemic evolves on day t :* The internal epidemiological situation in the country evolves from $\mathbf{X}_m(t-1)$ to $\mathbf{X}_m(t) = [S_m(t), I_m(t), A_m(t), R_m(t), D_m(t), Z_m(t)]$, where $S_m(t) = S_m(t-1) - Y_{1,m}(t-1)$, $I_m(t) = I_m(t-1) + Y_{1,m}(t-1) - Y_{2,m}(t-1) - Y_{5,m}(t-1)$, $A_m(t) = A_m(t-1) + Y_{2,m}(t-1) - Y_{3,m}(t-1) - Y_{4,m}(t-1)$, $R_m(t) = R_m(t-1) + Y_{3,m}(t-1)$, $D_m(t) = D_m(t-1) + Y_{4,m}(t-1)$, $Z_m(t) = Z_m(t-1) + Y_{5,m}(t-1)$. Here $Y_{j,m}(t-1), j = 1, \dots, 5$ are Poisson distributed with rates $(h_{j,i}(\mathbf{X}_m(t-1)))$: $h_{1,m}(\mathbf{X}_m(t-1)) = \alpha_m \frac{S_m(t-1)I_i(t-1)}{P_m(t-1)}$, $h_2(\mathbf{X}_m(t-1)) = \gamma_m I_m(t-1)$, $h_3(\mathbf{X}_m(t-1)) = \beta_m A_m(t-1)$, $h_4(\mathbf{X}_m(t-1)) = \delta_m A_m(t-1)$, and $h_5(\mathbf{X}_m(t-1)) = \beta_m I_m(t-1)$.

Step 1b *The external pandemic added on day t :* From the travel data, $\mathbf{X}_m(t)$ is updated to $\mathbf{X}_m^+(t) = [S_m^+(t), I_m^+(t), A_m(t), R_m(t), D_m(t), Z_m(t)]$, where $S_m^+(t) = S_m(t) + S_m^{\text{in}}(t) - S_m^{\text{out}}(t)$, and $I_m^+(t) = I_m(t) + I_m^{\text{in}}(t) - I_m^{\text{out}}(t)$.

Step 2a *The internal pandemic evolves on day $(t+1)$:* The internal epidemiological situation in the country evolves from $\mathbf{X}_m^+(t)$ to $\mathbf{X}_m(t+1) = [S_m(t+1), I_m(t+1), A_m(t+1), R_m(t+1), D_m(t+1), Z_m(t+1)]$, where $S_m(t+1) = S_m^+(t) - Y_{1,m}(t)$, $I_m(t+1) = I_m^+(t) + Y_{1,m}(t) - Y_{2,m}(t) - Y_{5,m}(t)$, $A_m(t+1) = A_m(t) + Y_{2,m}(t) - Y_{3,m}(t) - Y_{4,m}(t)$, $R_m(t+1) = R_m(t) + Y_{3,m}(t)$, $D_m(t+1) = D_m(t) + Y_{4,m}(t)$, $Z_m(t+1) = Z_m(t) + Y_{5,m}(t)$. Here $Y_{j,m}(t), j = 1, \dots, 5$ are Poisson distributed with rates $h_{j,m}(\mathbf{X}_m(t))$: $h_{1,m}(\mathbf{X}_m(t)) = \alpha_m \frac{S_m^+(t)I_m^+(t)}{P_m(t)}$, $h_2(\mathbf{X}_m(t)) = \gamma_m I_m^+(t)$, $h_3(\mathbf{X}_m(t)) = \beta_i A_i(t)$, $h_4(\mathbf{X}_i(t)) = \delta_i A_i(t)$, and $h_5(\mathbf{X}_m(t)) = \beta_m I_m^+(t)$.

Step 2b *The external pandemic added on day $(t+1)$:* From the travel data, $\mathbf{X}_m(t+1)$ is updated to $\mathbf{X}_m^+(t+1) = [S_m^+(t+1), I_m^+(t+1), A_m(t+1), R_m(t+1), D_m(t+1), Z_m(t+1)]$.

1), $I_m^+(t+1), A_m(t+1), R_m(t+1), D_m(t+1), Z_m(t+1)$], where $S_m^+(t+1) = S_m(t+1) + S_m^{\text{in}}(t+1) - S_m^{\text{out}}(t+1)$, and $I_m^+(t+1) = I_m(t+1) + I_m^{\text{in}}(t+1) - I_m^{\text{out}}(t)$.

As shown above, Step 1b and Step 2b make the global model behave differently from the local model. Therefore, if we can estimate quantities $S_m^{\text{in}}(t), I_m^{\text{in}}(t), S_m^{\text{out}}(t), I_m^{\text{out}}(t)$ for each day t , then we can use a marginal approach to estimate each country's parameters separately. The two quantities $S_m^{\text{out}}(t), I_m^{\text{out}}(t)$ can be calculated during the data generation process of the ABC algorithm. Our main task now is estimating $S_m^{\text{in}}(t)$ and $I_m^{\text{in}}(t)$.

We have $S_m^{\text{in}}(t) = \sum_{1 \leq j \neq m \leq n} S_{jm}^{\text{out}}(t), I_m^{\text{in}}(t) = \sum_{1 \leq j \neq m \leq n} I_{jm}^{\text{out}}(t)$, where $S_{jm}^{\text{out}}(t)$ and $I_{jm}^{\text{out}}(t)$ are the number of susceptible and undetected infected people moving from Country j to Country m on day t , respectively. Under our model assumptions, the sum of $S_{jm}^{\text{out}}(t)$ and $I_{jm}^{\text{out}}(t)$ gives us the total number of people traveling from Country j to Country m on day t : $S_{jm}^{\text{out}}(t) + I_{jm}^{\text{out}}(t) = T_{jm}(t)$. So if we can estimate $\{I_{jm}^{\text{out}}(t)\}_{1 \leq j \neq m \leq n, t=1, \dots, T}$, with the travel data we can estimate $\{S_{jm}^{\text{out}}(t)\}_{1 \leq j \neq m \leq n, t=1, \dots, T}$. As a result, we can estimate $S_m^{\text{in}}(t)$ and $I_m^{\text{in}}(t)$.

To estimate $I_{jm}^{\text{out}}(t)$, we need to estimate the epidemiological situation in Country j on day t : $\mathbf{X}_j^+(t) = [S_j^+(t), I_j^+(t), A_j(t), R_j(t), D_j(t), Z_j(t)]$. Based on these compartments and the travel data $T_{jm}(t)$, we can estimate $I_{jm}^{\text{out}}(t)$ as $T_{jm}(t) = \frac{T_{jm}(t)I_j^+(t)}{S_j^+(t)+I_j^+(t)}$.

From the global model we have:

$$\begin{aligned} U_j(t+1) &= A_j(t+1) + R_j(t+1) + D_j(t+1) \\ &= A_j(t) + Y_{2,j}(t) - Y_{3,j}(t) - Y_{4,j}(t) + R_j(t) + Y_{3,j}(t) + D_j(t) + Y_{4,j}(t) \\ &= A_j(t) + R_j(t) + D_j(t) + Y_{2,j}(t) = U_j(t) + Y_{2,j}(t), \end{aligned}$$

so $Y_{2,j}(t) = U_j(t+1) - U_j(t) = \Delta U_j(t)$. Since $Y_{2,j}(t) \sim \text{Poisson}(\gamma_j I_j^+(t-1))$, we have

$$E(I_j^+(t-1)) = E\left(\frac{\Delta U_j(t)}{\gamma_j}\right). \quad (8)$$

Similarly, we also have

$$E(I_j^+(t-2)) = E\left(\frac{\Delta U_j(t-1)}{\gamma_j}\right). \quad (9)$$

From (8) and (9), we have

$$\frac{E(I_j^+(t-1))}{E(I_j^+(t-2))} = \frac{E\left(\frac{\Delta U_j(t)}{\gamma_j}\right)}{E\left(\frac{\Delta U_j(t-1)}{\gamma_j}\right)} = \frac{E(\Delta U_j(t))}{E(\Delta U_j(t-1))}. \quad (10)$$

Applying (10) for $t = 1, \dots, T-1$, we have the sequence of relationships: $\frac{E(I_j^+(1))}{E(I_j(0))} = \frac{E(\Delta U_j(2))}{E(\Delta U_j(1))}, \frac{E(I_j^+(2))}{E(I_j^+(1))} = \frac{E(\Delta U_j(3))}{E(\Delta U_j(2))}, \dots, \frac{E(I_j^+(T-1))}{E(I_j^+(T-2))} = \frac{E(\Delta U_j(T))}{E(\Delta U_j(T-1))}$. Therefore, based on the available data for Country j , $\{A_j(t), R_j(t), D_j(t)\}_{t=1, \dots, T}$, we can approximate the average realization of the sequence of undetected infected people in Country j up to time $(T-1)$ by $I_j(0)$, $I_j^+(1) = I_j(0) \frac{\Delta U_j(2)}{\Delta U_j(1)}, I_j^+(2) = I_j^+(1) \frac{\Delta U_j(3)}{\Delta U_j(2)}, \dots, I_j^+(T-1) = I_j^+(T-2) \frac{\Delta U_j(T)}{\Delta U_j(T-1)}$.

In addition, we also have $Z_j(t) = Z_j(t-1) + Y_{5,j}(t-1)$, where $Y_{5,j}(t-1) \sim \text{Poisson}(\beta I_j^+(t-1))$. Therefore,

$$E(\Delta Z_j(t-1)) = E(\beta I_j^+(t-1)). \quad (11)$$

We have $R_j(t) = R_j(t-1) + Y_{3,j}(t-1)$, where $Y_{3,j}(t-1) \sim \text{Poisson}(\beta A_j(t-1)), \forall t = 1, \dots, T$. Therefore, the median value of the sequence $\left\{\frac{R_j(t)-R_j(t-1)}{A_j(t-1)}\right\}_{t=1, \dots, T}$ can be used to approximate β . We denote this median value as $\hat{\beta}$.

The fact that $Z_j(t) = Z_j(0) + \sum_{i=1}^{t-1} \Delta Z_j(i)$ and (11) tells us that the average value of $Z(t)$ in Country j can be reconstructed as

$$\begin{aligned} E(Z_j(t)) &= E(Z_j(0)) + \sum_{i=1}^{t-1} E(\Delta Z_j(i)) \\ &= E(Z_j(0)) + \sum_{i=1}^{t-1} \beta E(I_j^+(i)), \end{aligned} \quad (12)$$

where the sequence $\{E(I_j^+(i))\}_{j=1,\dots,T-1}$ and β are estimated as above.

The average realization of the pandemic in Country j can be reconstructed up to time $T-1$ as

$$\{S_j^+(t), I_j^+(t), A(t), R(t), D(t), Z(t)\}_{t=1,\dots,T-1} = \{P_j(t) - U_j(t) - I_j^+(t) - Z_j(t), I_j^+(t), A(t), R(t), D(t), Z_j(t)\}_{t=1,\dots,T-1}.$$

We can now estimate the average realization of a given Country j based on the available data $\{(A_j(t), R_j(t), D_j(t))\}_{t=1,\dots,T}$, which gives us estimates of $S_{jm}^{\text{out}}(t)$ and $I_{jm}^{\text{out}}(t)$. This means we can estimate $S_m^{\text{in}}(t)$ and $I_m^{\text{in}}(t)$. Therefore, the underlying true parameter θ_m in a given Country m can be approximated marginally by using this estimating procedure.

We now discuss the proposed distance when estimating θ_m marginally in a given Country m by ABC. Following the same argument as in Section 1.4, instead of using the Euclidean distance to estimate θ_m , we first need to standardize each sequence and then we try to learn each parameter under our model assumptions. From the available data $\{(A_m(t), R_m(t), D_m(t))\}_{t=1,\dots,T}$ of Country m , following the same argument as in Section 1.4, we can add the term

$$\left| \text{median} \left\{ \frac{R_m(t) - R_m(t-1)}{A_m(t-1)} \right\}_{t=1,\dots,T} - \text{median} \left\{ \frac{R_m^{(i)}(t) - R_m^{(i)}(t-1)}{A_m^{(i)}(t-1)} \right\}_{t=1,\dots,T} \right| \text{ to improve estimation of the recovery rate } \beta_m, \text{ and}$$

$$\text{adding the term } \left| \text{median} \left\{ \frac{D_m(t) - D_m(t-1)}{A_m(t-1)} \right\}_{t=1,\dots,T} - \text{median} \left\{ \frac{D_m^{(i)}(t) - D_m^{(i)}(t-1)}{A_m^{(i)}(t-1)} \right\}_{t=1,\dots,T} \right| \text{ to improve estimation of the death rate}$$

δ_m . For the transmission rate α_m at time $t+1$, we have $S_m(t+1) = S_m^+(t) - Y_{1,m}(t)$, where $Y_{1,m}(\mathbf{X}_m(t)) \sim \text{Poisson}(\alpha_m \frac{S_m^+(t) I_m^+(t)}{P_m(t)})$. Therefore, $\alpha_m = P_m(t) E(\frac{S_m^+(t) - S_m(t+1)}{S_m^+(t) I_m^+(t)})$. Notice that $S_m(t+1) = S_m^+(t+1) - S_m^{\text{in}}(t+1) + S_m^{\text{out}}(t+1)$.

The hidden states $S_m^+(t)$ and $I_m^+(t)$ can also be reconstructed. From (8) we have $E(I_m^+(t-1)) = E(\frac{\Delta U_m(t)}{\gamma_m})$. Therefore the average realization of $\{I_m^+(t)\}_{t=1,\dots,T}$ can be reconstructed as $\{\frac{\Delta U_m(t)}{\gamma_m}\}_{t=1,\dots,T}$. Using (12), we have $E(Z_m(t)) = E(Z_m(0)) + \sum_{i=1}^{t-1} \beta_m E(I_m^+(i))$. Therefore the average realization of $\{Z_m(t)\}_{t=1,\dots,T}$ can be reconstructed as $\{Z_m(0) + \sum_{i=1}^{t-1} \frac{\beta_m \Delta U_m(t)}{\gamma_m}\}_{t=1,\dots,T}$.

The average realization of the pandemic in country m can be reconstructed up to time $T-1$ as

$$\begin{aligned} \{S_m^+(t), I_m^+(t), A_m(t), R_m(t), D_m(t), Z_m(t)\}_{t=1,\dots,T-1} = \\ \left\{ P_m(t) - U_m(t) - \frac{\Delta U_m(t)}{\gamma_m} - (Z_m(0) + \sum_{i=1}^{t-1} \frac{\beta_m \Delta U_m(t)}{\gamma_m}), \frac{\Delta U_m(t)}{\gamma_m}, A_m(t), R_m(t), D_m(t), Z_m(0) + \sum_{i=1}^{t-1} \frac{\beta_m \Delta U_m(t)}{\gamma_m} \right\}_{t=1,\dots,T-1}. \end{aligned}$$

Similarly as above, in Step 1 of the ABC algorithm, the parameter $\theta_m^{(i)} = (\alpha_m^{(i)}, \beta_m^{(i)}, \delta_m^{(i)}, \gamma_m^{(i)})$ is generated and available to us. If $\gamma_m^{(i)}, \beta_m^{(i)}$ are correctly specified as γ_m, β_m of the underlying true parameter $\theta_m = (\alpha_m, \beta_m, \delta_m, \gamma_m)$, we would expect the distance

$\left| \text{median} \left\{ P_m(t) \frac{S_m^+(t) - S_m(t+1)}{S_m^+(t) I_m^+(t)} \right\}_{1,\dots,T-1} - \text{median} \left\{ P_m^{(i)}(t) \frac{S_m^{(i)+}(t) - S_m^{(i)}(t+1)}{S_m^{(i)+}(t) I_m^{(i)+}(t)} \right\}_{1,\dots,T-1} \right|$ to be close to 0. The values of the sequence $\left\{ P_m(t) \frac{S_m^+(t) - S_m(t+1)}{S_m^+(t) I_m^+(t)} \right\}_{1,\dots,T-1}$ are constructed based on $\gamma_m^{(i)}, \beta_m^{(i)}$ and the available data $\{(A_m(t), R_m(t), D_m(t))\}_{t=1,\dots,T}$, and values of the sequence $\left\{ P_m^{(i)}(t) \frac{S_m^{(i)+}(t) - S_m^{(i)}(t+1)}{S_m^{(i)+}(t) I_m^{(i)+}(t)} \right\}_{1,\dots,T-1}$ are constructed based on $\gamma_m^{(i)}, \beta_m^{(i)}$ and the simulated data $\{A_m^{(i)}(t), R_m^{(i)}(t), D_m^{(i)}(t)\}_{t=1,\dots,T}$. So adding the term:

$$\left| \text{median} \left\{ P_m(t) \frac{S_m^+(t) - S_m(t+1)}{S_m^+(t) I_m^+(t)} \right\}_{1,\dots,T-1} - \text{median} \left\{ P_m^{(i)}(t) \frac{S_m^{(i)+}(t) - S_m^{(i)}(t+1)}{S_m^{(i)+}(t) I_m^{(i)+}(t)} \right\}_{1,\dots,T-1} \right| \text{ is expected to help improve the estimation of } \alpha_m.$$

Finally, the proposed global distance in the calibrating step of the ABC algorithm is designed as follow:

$$\sqrt{\frac{1}{T} \sum_{t=1}^T \left[\left(\frac{A_m^{(i)}(t) - A_m(t)}{\sigma_{A_m}(t)} \right)^2 + \left(\frac{R_m^{(i)}(t) - R_m(t)}{\sigma_{R_m}(t)} \right)^2 + \left(\frac{D_m^{(i)}(t) - D_m(t)}{\sigma_{D_m}(t)} \right)^2 \right] + \sqrt{d_m}},$$

where $\sigma_{A_m}(t)$, $\sigma_{R_m}(t)$, and $\sigma_{D_m}(t)$ for $t = 1, \dots, T$ are the prior predictive standard deviations of $A_m(t), R_m(t), D_m(t)$ at

each time step and

$$d_m = \left| \text{median} \left\{ \frac{R_m(t) - R_m(t-1)}{A_m(t-1)} \right\}_{t=1, \dots, T} - \text{median} \left\{ \frac{R_m^{(i)}(t) - R_m^{(i)}(t-1)}{A_m^{(i)}(t-1)} \right\}_{t=1, \dots, T} \right| \\ + \left| \text{median} \left\{ \frac{D_m(t) - D_m(t-1)}{A_m(t-1)} \right\}_{t=1, \dots, T} - \text{median} \left\{ \frac{D_m^{(i)}(t) - D_m^{(i)}(t-1)}{A_m^{(i)}(t-1)} \right\}_{t=1, \dots, T} \right| \\ + \left| \text{median} \left\{ P_m(t) \frac{S_m^+(t) - S_m(t+1)}{S_m^+(t) I_m^+(t)} \right\}_{t=1, \dots, T-1} - \text{median} \left\{ P_m^{(i)}(t) \frac{S_m^{(i)+}(t) - S_m^{(i)}(t+1)}{S_m^{(i)+}(t) I_m^{(i)+}(t)} \right\}_{t=1, \dots, T-1} \right|.$$

2 Simulation studies

2.1 Simulation 1: Performance of different RABC distance metrics for a single country

For our first simulation study, we limit our model to the analysis of only one country, i.e., we only use the internal model. We here demonstrate the impact of the choice of the distance in ABC algorithms and which one to choose in our epidemiological framework.

We simulate $N = 200$ sets of parameters and data, in an ABC fashion, by first simulating a parameter value from the prior and using it to generate data according to the model. We treat these N simulations as our test data set to assess how accurately the true parameters are recovered by ABC using various distance functions. The simulation proceeds as follows.

Step 1. Generating data and parameters: For $i \in \{1, \dots, N\}$ (N large), we generate the parameter $\theta^{(i)} = (\alpha^{(i)}, \beta^{(i)}, \delta^{(i)}, \gamma^{(i)})$ from uniform priors $\alpha^{(i)} \sim U(0, 2)$, $\beta^{(i)} \sim U(0, 1)$, $\delta^{(i)} \sim U(0, 1)$, and $\gamma^{(i)} \sim U(0, 1)$. Based on the parameters and the stochastic model, we generate a data set $\text{Data}^{(i)}$ corresponding to $\theta^{(i)}$. If the generated data set $\text{Data}^{(i)}$ satisfies certain conditions making it sufficiently real-world like (having the number of confirmed accumulated deaths greater than 1%, lower than 30% of total confirmed cases, and having the number of accumulated recovered cases at least twice the number of accumulated deaths), then we keep $\theta^{(i)}$ as a true parameter value to be estimated and treat the generated data $\{A_t^{(i)}, R_t^{(i)}, D_t^{(i)}\}$ as observed data. We repeat the process until we obtain 200 underlying true parameter values $\theta^{(i)}$ and the corresponding 200 datasets $\{A_t^{(i)}, R_t^{(i)}, D_t^{(i)}\}$. For simplicity, we fix the initial condition of the six compartments in the model as $\mathbf{X}_1(0) = [S_1(0), I_1(0), A_1(0), R_1(0), D_1(0), Z_1(0)] = (9999972, 15, 13, 0, 0, 0)$ and set the simulation time period $T = 84$ days for all i .

Step 2. Estimating parameters: For each iteration i , $i \in \{1, \dots, 200\}$, based on the sequence of $\{A_t^{(i)}, R_t^{(i)}, D_t^{(i)}\}$, we use RABC with different distance metrics to estimate the underlying true parameter value $\theta^{(i)}$. In this estimation step, we choose the acceptance rate 0.01 and sample 1000 particles to form the posterior. From the posterior distribution for each i , we calculate the median values of each parameter: $\hat{\alpha}^{(i)}, \hat{\beta}^{(i)}, \hat{\delta}^{(i)}, \hat{\gamma}^{(i)}$. Then $\hat{\theta}^{(i)} = (\hat{\alpha}^{(i)}, \hat{\beta}^{(i)}, \hat{\delta}^{(i)}, \hat{\gamma}^{(i)})$ is used as the best candidate for estimating the underlying true $\theta^{(i)}$.

Step 3. Evaluating parameter estimates: For each iteration i , $i \in \{1, \dots, 200\}$, we evaluate estimation accuracy in terms of the absolute bias, absolute relative bias, interquartile range, and coverage rate of the interquartile for each parameter $\alpha^{(i)}, \beta^{(i)}, \delta^{(i)}, \gamma^{(i)}$ and its average. These accuracy measurements are defined as follows. For a given parameter $\alpha^{(i)}$ the absolute bias is defined as $|\hat{\alpha}^{(i)} - \alpha^{(i)}|$, and the absolute relative bias is defined as $|\frac{\hat{\alpha}^{(i)} - \alpha^{(i)}}{\alpha^{(i)}}|$. Similarly for $\beta^{(i)}, \gamma^{(i)}$, and $\delta^{(i)}$. Average absolute bias for all parameters is defined as $(|\hat{\alpha}^{(i)} - \alpha^{(i)}| + |\hat{\beta}^{(i)} - \beta^{(i)}| + |\hat{\delta}^{(i)} - \delta^{(i)}| + |\hat{\gamma}^{(i)} - \gamma^{(i)}|)/4$ and average absolute relative bias for all parameters is defined as $(|\frac{\hat{\alpha}^{(i)} - \alpha^{(i)}}{\alpha^{(i)}}| + |\frac{\hat{\beta}^{(i)} - \beta^{(i)}}{\beta^{(i)}}| + |\frac{\hat{\delta}^{(i)} - \delta^{(i)}}{\delta^{(i)}}| + |\frac{\hat{\gamma}^{(i)} - \gamma^{(i)}}{\gamma^{(i)}}|)/4$. For each parameter, we also calculate the interquartile range (IQR) of the posterior, denoted $\text{IQR}^{(i)}$, which is the difference between the third and the first quartile of the resulting ABC posterior distribution. Furthermore, we check whether the IQR of the posterior covers the underlying true parameter value, which we use to calculate the coverage rate $\text{CR}^{(i)}$. Finally, the average over the 200 iterations of these accuracy metrics is calculated, which we use as our overall accuracy metrics for comparing the performance of the two RABC distance metrics.

Table S1 summarizes the different estimation accuracy measures for the two RABC distances. This table shows that the

proposed distance improves estimation accuracy in terms of relative bias. The two types of bias are much smaller compared to using Euclidean distance. We also observe that the IQR for the proposed distance is smaller than the IQR for the Euclidean distance. Figure S1 shows boxplots of the IQR for the two distance metrics.

Table S1. Estimation accuracy of Euclidean distance and our proposed distance when using RABC to estimate the four parameters of the local model.

Accuracy	Distances	Average	alpha	beta	delta	gamma
Absolute bias	Euclidean	0.071	0.125	0.046	0.012	0.101
	Proposed	0.028	0.054	0.004	0.002	0.052
Absolute relative bias	Euclidean	0.148	0.107	0.089	0.093	0.303
	Proposed	0.077	0.039	0.007	0.022	0.241
IQR	Euclidean	0.153	0.264	0.094	0.031	0.222
	Proposed	0.060	0.107	0.014	0.012	0.109
IQ coverage	Euclidean	0.677	0.620	0.675	0.770	0.645
	Proposed	0.777	0.635	0.880	0.960	0.635

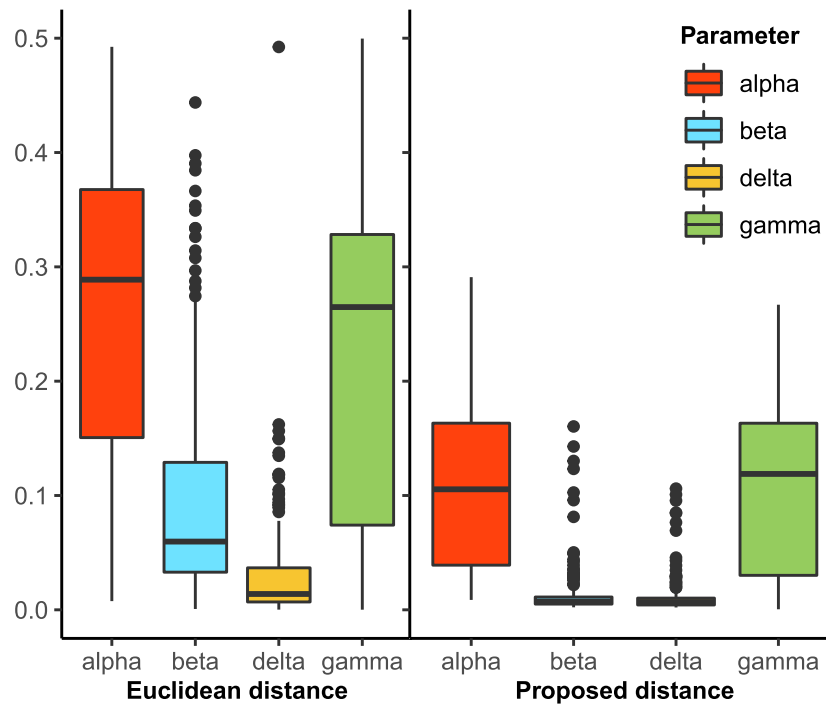


Figure S2. Box plot of the interquartile range (IQR) using Euclidean distance and the proposed distance for the local model for one country over 200 iterations.

2.2 Simulation 2: Performance of local and global estimation for three countries

In this simulation study, we investigate the accuracy of three different estimation procedures for the global travel model consisting of three countries. We limit this investigation to three countries for simplicity. The population sizes of the three countries are the following: $p_1 = 10 \times 10^6$, $p_2 = 3 \times 10^6$, and $p_3 = 2 \times 10^6$. The first procedure uses a local approach with the Euclidean distance to estimate each country's parameters independently and ignores the travel between the countries. We call this estimation procedure Euclidean local, and we use it as a benchmark to be compared with the other two approaches. Then we consider global estimation procedures as discussed in Section 1.5 to estimate each country's parameters. Here we use two distance metrics, Euclidean distance and the distance proposed in Section 1.5. We call these estimation procedures Euclidean global and Proposed global, respectively. The simulation is set up as follows.

Step 1. Generating data and parameters: For $i \in \{1, \dots, 500\}$, we generate the parameter $\theta^{(i)} = (\theta_1^{(i)}, \theta_2^{(i)}, \theta_3^{(i)})$, where for each $j \in \{1, 2, 3\}$, $\theta_j^{(i)} = (\alpha_j^{(i)}, \beta_j^{(i)}, \delta_j^{(i)}, \gamma_j^{(i)})$ from uniform priors as $\alpha_j^{(i)} \sim U(0, 2)$, $\beta_j^{(i)} \sim U(0, 1)$, $\delta_j^{(i)} \sim U(0, 1)$, and $\gamma_j^{(i)} \sim U(0, 1)$. Based on the parameters and the stochastic model, we generate a data set $\text{Data}^{(i)}$ corresponding to $\theta^{(i)}$. If the generated data set $\text{Data}^{(i)}$ satisfies the conditions described above for Simulation 1, we retain $\theta^{(i)}$ and treat it as the underlying true parameter value; we also retain the data $\{A_{(t,j)}^{(i)}, R_{(t,j)}^{(i)}, D_{(t,j)}^{(i)}\}$ and treat them as the observed data from these three countries. We repeat the procedure until we have 500 parameter values and their corresponding data sets $\{A_{(t,j)}^{(i)}, R_{(t,j)}^{(i)}, D_{(t,j)}^{(i)}\}_{j=1,2,3}$.

For simplicity, we fix the initial condition of the six compartments in the model as

$$\mathbf{X}_1(0) = [S_1(0), I_1(0), A_1(0), R_1(0), D_1(0), Z_1(0)] = (9999720, 150, 130, 0, 0, 0),$$

$$\mathbf{X}_2(0) = [S_2(0), I_2(0), A_2(0), R_2(0), D_2(0), Z_2(0)] = (2999970, 20, 10, 0, 0, 0),$$

$$\mathbf{X}_3(0) = [S_3(0), I_3(0), A_3(0), R_3(0), D_3(0), Z_3(0)] = (1999970, 15, 15, 0, 0, 0),$$

and set the simulation period $T = 84$ days for all i . Each day, the number of outbound travelers from Country j is drawn from a normal distribution with mean $\mu_j = P_j * 0.0003$ and standard deviation $\text{sd}_j = 0.05 * \mu_j$, where P_j is the size of the population of Country j . Those outbound travelers will enter one of the neighboring countries with proportions that are proportional to the populations of the target countries. For example, the number of people leaving Country 1 for Country 2 is $\frac{n_1 P_2}{P_2 + P_3}$, and the number of people entering Country 3 is $\frac{n_1 P_3}{P_2 + P_3}$.

Step 2. Estimating parameters: For each iteration i , $i \in \{1, \dots, 500\}$, based on the sequence of $\{A_{(t,j)}^{(i)}, R_{(t,j)}^{(i)}, D_{(t,j)}^{(i)}\}_{j=1,2,3}$, we first naively use RABC with the local estimation approach and Euclidean distance to estimate $\theta^{(i)}$. Then we use RABC with the global estimation approach with the two distance metrics to estimate $\theta^{(i)}$. Then $\hat{\theta}_j^{(i)} = (\hat{\alpha}_j^{(i)}, \hat{\beta}_j^{(i)}, \hat{\delta}_j^{(i)}, \hat{\gamma}_j^{(i)})$ is obtained as the median of the RABC posterior samples for $j = 1, 2, 3$.

Step 3. Evaluating parameter estimates: For each iteration i , $i \in \{1, \dots, 500\}$, for each country, we evaluate the accuracy of our parameter estimates based on the absolute bias, absolute relative bias, interquartile range (IQR), and coverage rate of IQR for each parameter $\alpha^{(i)}, \beta^{(i)}, \delta^{(i)}, \gamma^{(i)}$ and its average as in Simulation 1. The final accuracy measurements are calculated by averaging the accuracy measurements across all three countries. When averaging accuracy measures over multiple countries, we consider two weighted averages, one having equal weights for all countries regardless of their population sizes and the other weighted based on relative population sizes. In the latter, the weights are $\frac{P_1}{P_1 + P_2 + P_3}$ for country 1, $\frac{P_2}{P_1 + P_2 + P_3}$ for country 2, and $\frac{P_3}{P_1 + P_2 + P_3}$ for country 3.

Tables S2 and S3 show the overall accuracy of different estimation procedures using equal weights for each country (Table S2) and using population-based weights for each country (Table S3). The two tables convey the same message: using a local approach to estimate the parameters in the travel model is not appropriate. As shown in these tables, the Euclidean local estimation procedure yields the highest bias, largest interquartile range, largest 95 % percentile range, and lowest coverage. The performance is better for the Euclidean global procedure. As expected, the proposed distance, which takes into account the travel model, performs best of the three.

Table S2. Estimation accuracy using three distance metrics with RABC to estimate the four parameters of the global travel model. For simplicity, we consider a small world of just three countries with different population sizes. Here each country has the same weight when computing the overall accuracy.

Accuracy	Estimation procedure	Average	alpha	beta	delta	gamma
Absolute bias	Euclidean local	0.496	1.328	0.108	0.058	0.490
	Euclidean global	0.236	0.448	0.070	0.030	0.397
	Proposed global	0.205	0.497	0.023	0.054	0.248
Absolute relative bias	Euclidean local	0.928	1.611	0.176	0.591	1.332
	Euclidean global	0.502	0.534	0.109	0.280	1.085
	Proposed global	0.494	0.629	0.034	0.545	0.769
IQR range	Euclidean local	0.171	0.263	0.179	0.060	0.180
	Euclidean global	0.149	0.218	0.129	0.040	0.210
	Proposed global	0.091	0.135	0.041	0.038	0.151
IQ coverage	Euclidean local	0.528	0.463	0.577	0.690	0.381
	Euclidean global	0.610	0.539	0.649	0.714	0.540
	Proposed global	0.631	0.543	0.647	0.761	0.574
95% range	Euclidean local	0.410	0.646	0.406	0.157	0.430
	Euclidean global	0.361	0.542	0.309	0.107	0.486
	Proposed global	0.247	0.378	0.116	0.115	0.380
95% coverage	Euclidean local	0.866	0.819	0.956	0.978	0.712
	Euclidean global	0.935	0.893	0.957	0.980	0.911
	Proposed global	0.958	0.923	0.972	0.989	0.949

Table S3. Estimation accuracy using three distance metrics. See Table S2 caption for more details.

Accuracy	Estimation procedure	Average	alpha	beta	delta	gamma
Absolute bias	Euclidean local	0.380	0.939	0.095	0.048	0.438
	Euclidean global	0.194	0.338	0.064	0.025	0.351
	Proposed global	0.155	0.372	0.019	0.043	0.186
Absolute relative bias	Euclidean local	0.862	1.277	0.162	0.636	1.371
	Euclidean global	0.512	0.459	0.101	0.304	1.185
	Proposed global	0.414	0.583	0.028	0.564	0.480
IQR range	Euclidean local	0.147	0.228	0.156	0.048	0.154
	Euclidean global	0.131	0.191	0.118	0.035	0.182
	Proposed global	0.073	0.111	0.033	0.030	0.120
IQR coverage	Euclidean local	0.526	0.468	0.575	0.661	0.400
	Euclidean global	0.610	0.548	0.641	0.701	0.550
	Proposed global	0.613	0.536	0.595	0.733	0.586
95% range	Euclidean local	0.360	0.571	0.361	0.128	0.380
	Euclidean global	0.325	0.488	0.284	0.094	0.433
	Proposed global	0.201	0.310	0.094	0.090	0.309
95% coverage	Euclidean local	0.860	0.812	0.950	0.973	0.704
	Euclidean global	0.928	0.887	0.954	0.976	0.898
	Proposed global	0.948	0.905	0.962	0.985	0.941

2.3 Simulation 3: Effectiveness of travel regulation

In this simulation study, we study the effectiveness of different travel regulation policies. We compare the percentages of people allowed to travel under each policy and the epidemiological situation in the country adopting the policy. The simulation encompasses four countries and proceeds as follows.

Step 1. Generating data and parameters: For $i \in \{1, \dots, N\}$ (N large), we generate the parameter $\theta^{(i)} = (\theta_1^{(i)}, \theta_2^{(i)}, \theta_3^{(i)}, \theta_4^{(i)})$, where $\theta_j^{(i)} = (\alpha_j^{(i)}, \beta_j^{(i)}, \delta_j^{(i)}, \gamma_j^{(i)})$, from uniform priors as $\alpha_j^{(i)} \sim U(\varepsilon, 1 - \varepsilon)$, $\beta_j^{(i)} \sim U(\varepsilon, 0.25 - \varepsilon)$, $\delta_j^{(i)} \sim U(\varepsilon, 0.25 - \varepsilon)$, and $\gamma_j^{(i)} \sim U(\varepsilon, 1 - \varepsilon)$. We chose $\varepsilon = 0.001$ to make sure that the generated parameters do not fall at the boundaries of the parameter space and generate atypical data. We also added some constraints to ensure the parameter values are reasonable by only keeping parameters with the basic reproduction number $R_0 = \frac{\alpha_j^{(i)}}{\beta_j^{(i)} + \gamma_j^{(i)}}$ between 0.47 and 6.47 as reported for different regions around the world¹¹. To investigate the effectiveness of travel regulations, we use one more constraint to set the reproduction number R_0 in these 4 countries in 4 different zones, where Country 1 has R_0 between 0.47 and 0.9, Country 2 has R_0 between 0.9 and 1, Country 3 has R_0 between 1 and 1.1, and Country 4 has R_0 between 1.1 and 6.47. The initial conditions of each country are generated randomly as $(S_j^{(i)}(0), I_j^{(i)}(0), A_j^{(i)}(0), R_j^{(i)}(0), D_j^{(i)}(0), Z_j^{(i)}(0)) = (P_j - (I_j^{(i)}(0) + A_j^{(i)}(0)), I_j^{(i)}(0), A_j^{(i)}(0), 0, 0, 0)$, where $P_i \sim U(50 * 10^4, 100 * 10^6)$, $I_j^{(i)}(0) \sim U(0, 200)$, $A_j^{(i)}(0) \sim U(0, 10)$. Based on the parameters and the stochastic model, we generate a data set $\text{Data}^{(i)}$ corresponding to $\theta^{(i)}$. If the generated data set $\text{Data}^{(i)}$ satisfies the conditions described for Simulation 1 above, we keep $\theta^{(i)}$ and treat it as the underlying true value of the parameter; we also retain the data $\{A_{(t,j)}^{(i)}, R_{(t,j)}^{(i)}, D_{(t,j)}^{(i)}\}$ for $j = 1, 2, 3, 4$, which we treat as the observed data collected from each country. We keep generating data till we get 200 underlying true parameters $\theta^{(i)}$ and the corresponding 200 data sets $\{A_{(t,j)}^{(i)}, R_{(t,j)}^{(i)}, D_{(t,j)}^{(i)}\}_{j=1,2,3,4}$. We fix the duration of the simulation to $T = 42$ days for all i . Each day, the total number of outbound travelers from country j is drawn from a normal distribution with mean $\mu_j^{(i)} = P_j^{(i)} * 0.0003$ and standard deviation $\text{sd}_j^{(i)} = 0.05 * \mu_j^{(i)}$, where $P_j^{(i)}$ is the size of the population of country j . The outbound travelers enter other countries in proportion to sizes of their populations.

Step 2. Estimation step: For each iteration i , $i \in \{1, \dots, 200\}$, based on the sequence of $\{A_{(t,j)}^{(i)}, R_{(t,j)}^{(i)}, D_{(t,j)}^{(i)}\}_{j=1,2,3,4}$, we use the proposed global approach to estimate the underlying true $\theta^{(i)}$. Then $\hat{\theta}_j^{(i)} = (\hat{\alpha}_j^{(i)}, \hat{\beta}_j^{(i)}, \hat{\delta}_j^{(i)}, \hat{\gamma}_j^{(i)})$ are obtained as the median values of the RABC posterior samples and are used to estimate the underlying true $\theta_j^{(i)}$ for $j = 1, 2, 3, 4$.

Step 3. Prediction step: For each iteration i , $i \in \{1, \dots, 200\}$, based on the estimated parameter $\hat{\theta}_j^{(i)}$, we simulate data for the following two weeks under eight different travel regulation policies. The first two are the most extreme, where all countries are either fully open or fully closed. The third and the fourth are currently used policies, where a 14-day quarantine is required for all arrivals or arrivals from high-risk countries only. The remaining 4 policies are our proposed travel regulation policies. We describe each policy in detail below.

P1 All countries are fully open and allow all airline travel as usual.

P2 All countries are fully closed and no airline travel is allowed across their borders.

P3 The country requires a 14-day quarantine for all arrivals. This policy is currently used by countries such as Korea or India. The other countries are fully open.

P4 The country requires a 14-day quarantine for travelers from high-risk countries only, i.e., countries with the average number of active confirmed daily cases greater than 20 in 100000 people during the last 2 weeks, and no quarantine for arrivals from other countries. This policy currently used by some European countries such as the U.K., Switzerland, and Portugal. The other countries are fully open.

P5 The country adopts the simplified average control policy: we regulate travel such that the expected number of daily undetected infected cases is at most 10% higher than the maximum number of daily cases under P2. The other countries are fully open.

P6 The country adopts the simplified probability control policy: we regulate travel such that the expected number of daily undetected infected cases is at most 10% higher than the maximum number of daily cases under P2 with probability at least 90%. The other countries are fully open.

P7 Policy 7 is similar to P5 but we use the full version of the proposed average control policy as in Example 1 of Section 1.3. The other countries are fully open.

P8 Policy 8 is similar to P6 but we use the full version of the proposed probability control policy as in Example 1 of Section 1.3. The other countries are fully open.

Policy effectiveness is evaluated based on two factors: the percentage of people allowed to travel and the epidemiological situation in the country once the policy is adopted.

1. The percentage of people allowed to enter the country under each policy is denoted T_c . This number is calculated using the number of people allowed to travel inbound to the country divided by the total number of people traveling to the country under normal circumstances.
2. The percentage of people that will travel due to each policy is denoted T_e . This number is an adjusted version T_c . If a 14-day quarantine is applied to a country, we assume that only 5% of the normal number of travelers from this country are willing to travel under this policy. The choice of 5% is based on the data provided by Korea Tourism Organization. (Korea is one of the countries that require a 14-day quarantine for all arrivals.) This adjustment gives us more insights into the effect of the 14-day quarantine requirement. T_e is obtained by using the number of expected inbound travelers divided by the normal number of inbound travelers.

The effectiveness of policies on the epidemic in the adopting country is evaluated based on 7 factors.

1. Percentage of active confirmed imported cases that enter the country due to each policy, denoted as IA . This number is calculated using the total number of inbound traveling active confirmed cases that eventually become active confirmed cases, divided by the total number of inbound travelers during the regulation period.
2. Percentage of undetected infected imported cases entering the country due to each policy, denoted as II . This number is obtained using the total number of undetected infected cases traveling inbound divided by the total number of inbound travelers during the regulation period.
3. Percentage of undetected infected imported cases when quarantining after entering the country, denoted as IIQ . A policy that does not require quarantine is equivalent to a 0-day quarantine. This number is obtained by taking the total number of undetected infected inbound travelers after quarantine divided by the total number of inbound travelers during the regulation period.
4. Relative change in total new cases (detected and undetected), denoted as RU . This number is calculated as the difference in the total number of cases at the end of the regulation period and the beginning of the regulation period, divided by the total number of cases at the beginning of the regulation period.
5. Relative change in total new active confirmed cases, denoted as RA . This number is calculated similarly to RU above but instead of using the number of cases, all counts are based on the number of active confirmed cases.
6. Percent change in total new cases, denoted as PU . This number is calculated as the difference in the total number of cases at the end of the regulation period and the beginning of the regulation period, divided by the population of the country.
7. Percent change in total confirmed cases, denoted as PA . This number is calculated as the difference in the total number of confirmed cases at the end of the regulation period and the beginning of the regulation period, divided by the population of the country.

We generate 1000 stochastic realizations conditional on the estimated parameters and initial conditions at the beginning of the regulation period. For each realization, we calculate the above metrics and we report 2.5th and 97.5th percentiles values of each based on the 1000 realizations. To assess the impact of these policies on different countries, we stratify the countries into three different groups: Group 1 corresponds to countries with an effective reproduction number R_t lower than 0.9, Group 2 corresponds to countries with R_t between 0.9 and 1.1, and Group 3 for countries with an R_t greater than 1.1. In our model, following Diekmann et al. (2009)¹², the effective reproduction number of a given country i is $R_{t,i} = \frac{S_i^{(t)+} \alpha_i}{P_i(t)(\beta_i + \gamma_i)}$. We computed the overall average across the 200 iterations of the above metrics for each group of countries to compare the effectiveness of different policies.

Table S4. Summary of effectiveness of travel regulation policies. We show (2.5, 97.5) percentiles of pandemic changes for different scenarios. For a given policy, the upper value and lower value of each measurement are the 2.5th percentile value and the 97.5th percentile value, respectively. G1, G2, and G3 denote countries in Group 1, 2, and 3, respectively. RU is the relative change in number of cases (including detected and undetected), RA is the relative change in number of confirmed cases, PU is the percent change in total number of new cases, and PA is the percent change in total number of new confirmed cases.

		P1	P2	P3	P4	P5	P6	P7	P8
G1	RU	2.53	0.06	0.64	0.88	0.06	0.06	0.11	0.06
		3.20	0.27	0.92	1.26	0.27	0.26	0.35	0.26
	RA	1.58	0.08	0.86	0.99	0.08	0.08	0.12	0.08
		2.14	0.27	1.15	1.36	0.27	0.27	0.34	0.27
	PU (%)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	PA (%)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
G2	RU	1.50	0.45	0.63	0.86	0.46	0.45	0.48	0.45
		2.05	0.84	1.02	1.32	0.84	0.84	0.88	0.84
	RA	0.99	0.36	0.60	0.71	0.37	0.36	0.39	0.36
		1.37	0.64	0.90	1.04	0.64	0.64	0.67	0.64
	PU (%)	0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01
		0.02	0.02	0.02	0.02	0.02	0.02	0.02	0.02
	PA (%)	0.01	0.01	0.01	0.01	0.01	0.01	0.01	0.01
		0.02	0.01	0.01	0.01	0.01	0.01	0.01	0.01
G3	RU	6.28	6.30	6.28	6.28	6.28	6.28	6.28	6.28
		6.65	6.67	6.65	6.65	6.65	6.65	6.65	6.65
	RA	5.32	5.33	5.32	5.32	5.32	5.32	5.32	5.32
		5.56	5.57	5.56	5.56	5.56	5.56	5.56	5.56
	PU (%)	5.39	5.40	5.38	5.39	5.38	5.38	5.38	5.38
		5.50	5.52	5.50	5.50	5.50	5.50	5.50	5.50
	PA (%)	2.39	2.40	2.39	2.39	2.39	2.39	2.39	2.39
		2.45	2.46	2.45	2.45	2.45	2.45	2.45	2.45

In Table S5, we see that under P4 the number of expected inbound travelers, T_e , is higher than under P5, the simplified average control policy. However, under P4, the percentage of undetected infected after quarantine, IIQ , entering Group 1 countries is (0.03%, 0.03%) and Group 2 countries is (0.03%, 0.04%). These values are high compared to (0.00%, 0.00%) for both groups under P5. This is because the average number of increased cases each day in the last 14 days is used to decide whether a country belongs to green zone or red zone. However, the number of undetected infectious cases may grow very fast in the green zone countries, and in the absence of quarantine, undetected infectious cases from green zone countries may spread the disease fast in the arrival country.

Table S5. Summary of effectiveness of travel regulation policies. We show (2.5, 97.5) percentiles of travel effects for different policies. For a given policy, the upper value and lower value of each measurement are the 2.5th percentile value and the 97.5th percentile value, respectively. IA is the percent of incoming travellers that will eventually become active confirmed after arrival, II is the percent of incoming travellers that are undetected infectious, IIQ is the percent of incoming travellers who are undetected infectious after the quarantine if the destination country requires a 14-day quarantine, Tc is the percent of inbound travel capacity, and Te is the percent of expected of inbound travel.

		P1	P2	P3	P4	P5	P6	P7	P8
G1	IA (%)	0.09	0.00	0.09	0.09	0.00	0.00	0.00	0.00
		0.11	0.00	0.11	0.11	0.00	0.00	0.01	0.00
	II (%)	0.17	0.00	0.17	0.17	0.00	0.00	0.00	0.00
		0.19	0.00	0.19	0.19	0.00	0.00	0.01	0.00
	IIQ (%)	0.17	0.00	0.00	0.03	0.00	0.00	0.00	0.00
		0.19	0.00	0.00	0.03	0.00	0.00	0.01	0.00
	Tc	100%	0%	100%	100%	34%	0%	37%	0%
	Te	100%	0%	5%	89%	34%	0%	37%	0%
G2	IA (%)	0.09	0.00	0.09	0.09	0.00	0.00	0.00	0.00
		0.11	0.00	0.11	0.11	0.00	0.00	0.01	0.00
	II (%)	0.18	0.00	0.18	0.18	0.00	0.00	0.01	0.00
		0.20	0.00	0.20	0.20	0.00	0.00	0.02	0.00
	IIQ (%)	0.18	0.00	0.00	0.03	0.00	0.00	0.01	0.00
		0.20	0.00	0.00	0.04	0.00	0.00	0.02	0.00
	Tc	100%	0%	100%	100%	60%	0%	63%	0%
	Te	100%	0%	5%	89%	60%	0%	63%	0%
G3	IA (%)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	II (%)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	IIQ (%)	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
		0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
	Tc	100%	0%	100%	100%	34%	0%	34%	0%
	Te	100%	0%	5%	100%	34%	0%	34%	0%

2.4 Simulation 4. Effectiveness of policy coordination

In this simulation study, we study the effectiveness of policy coordination on the pandemic in terms of the percent of people allowed to travel and the overall worldwide epidemiological situation. Simulations are set up similarly to those in Section 2.3 but here we consider a world of 8 countries: Countries 1 and 2 with R_0 between 1.1 and 6.47, Countries 3 and 4 with R_0 between 1 and 1.1, Countries 5 and 6 with R_0 between 0.9 and 1, and Countries 7 and 8 with R_0 between 0.47 and 0.9.

We consider 8 different policy coordination scenarios:

- S1 All countries are fully open and allow all travel.
- S2 All countries are fully closed and do not allow any international airline travel.
- S3 All countries require a 14-day quarantine for all arrivals.
- S4 All countries use the simplified average control policy.
- S5 Countries 1, 3, 5, 7 require a 14-day quarantine for all arrivals, and countries 2, 4, 6, 8 allow no inbound travel.
- S6 Countries 1, 3, 5, 7 use the simplified average control policy, and countries 2, 4, 6, 8 allow no inbound travel.
- S7 Countries 1, 3, 5, 7 require a 14-day quarantine for all arrivals, and countries 2, 4, 6, 8 are fully open.

S8 Countries 1, 3, 5, 7 use the simplified version of the proposed average control policy, and countries 2, 4, 6, 8 are fully open.

The coordination effectiveness is evaluated based on the overall change in the global pandemic and for each group of countries as in the simulation studies of Section 2.3.

Table S6. Summary of global travel policy coordination. See Table S4 caption for more information.

		S1	S2	S3	S4	S5	S6	S7	S8
G	RU	10.68	2.65	4.02	2.66	3.45	2.65	6.79	6.01
		11.56	3.06	4.51	3.07	3.92	3.07	7.46	6.61
	RA	8.13	2.77	4.92	2.77	4.08	2.77	6.34	5.04
		8.89	3.13	5.43	3.14	4.55	3.13	6.97	5.56
	PU (%)	8.35	8.31	8.28	8.31	8.29	8.31	8.31	8.33
		8.39	8.35	8.32	8.35	8.33	8.35	8.35	8.37
	PA (%)	4.40	4.38	4.37	4.38	4.37	4.38	4.38	4.39
		4.42	4.40	4.39	4.40	4.39	4.40	4.41	4.41
G1	RU	11.16	0.59	3.17	0.60	1.84	0.59	7.24	6.01
		12.23	0.93	3.61	0.94	2.21	0.93	7.99	6.70
	RA	9.01	0.74	4.42	0.75	2.52	0.74	6.62	4.85
		9.95	1.06	4.90	1.07	2.91	1.07	7.33	5.48
	PU (%)	0.05	0.01	0.02	0.01	0.01	0.01	0.03	0.03
		0.05	0.01	0.02	0.01	0.01	0.01	0.04	0.03
	PA (%)	0.03	0.00	0.01	0.00	0.01	0.00	0.02	0.02
		0.03	0.00	0.02	0.00	0.01	0.00	0.02	0.02
G2	RU	12.13	1.54	2.98	1.54	2.50	1.54	6.43	5.47
		13.29	2.13	3.68	2.13	3.19	2.13	7.32	6.27
	RA	8.14	1.62	4.08	1.62	3.33	1.62	5.79	4.08
		9.14	2.13	4.81	2.13	4.04	2.13	6.64	4.74
	PU (%)	0.11	0.04	0.05	0.04	0.05	0.04	0.08	0.08
		0.13	0.05	0.06	0.05	0.06	0.05	0.10	0.09
	PA (%)	0.07	0.03	0.04	0.03	0.03	0.03	0.05	0.05
		0.08	0.04	0.05	0.04	0.04	0.04	0.06	0.06
G3	RU	7.31	6.94	6.94	6.94	6.94	6.94	7.07	7.07
		7.45	7.08	7.07	7.08	7.08	7.08	7.21	7.21
	RA	7.25	7.10	7.12	7.09	7.11	7.10	7.18	7.17
		7.35	7.20	7.22	7.20	7.21	7.20	7.29	7.27
	PU (%)	33.11	33.14	32.99	33.14	33.06	33.14	33.05	33.12
		33.24	33.27	33.12	33.27	33.19	33.27	33.18	33.25
	PA (%)	17.43	17.44	17.39	17.44	17.42	17.44	17.41	17.44
		17.50	17.52	17.46	17.52	17.49	17.52	17.48	17.51

3 Real data analysis

List of 92 countries and its corresponding Alpha3 codes (in the parenthesis) with more than 500 cases by April 15, 2020 includes: Afghanistan (AFG), Albania (ALB), United Arab Emirates (ARE), Argentina (ARG), Armenia (ARM), Australia (AUS), Austria (AUT), Azerbaijan (AZE), Belgium (BEL), Burkina Faso (BFA), Bangladesh (BGD), Bulgaria (BGR), Bahrain (BHR), Bosnia and Herzegovina (BIH), Belarus (BLR), Brazil (BRA), Canada (CAN), Switzerland (CHE), Chile (CHL), China (CHN), Ivory Coast (CIV), Cameroon (CMR), Columbia (COL), Costa Rica (CRI), Cuba (CUB), Cyprus (CYP), Czech Republic (CZE), Germany (DEU), Djibouti (DJI), Denmark (DNK), Dominican Republic (DOM), Algeria (DZA), Ecuador (ECU), Egypt (EGY), Espanol (ESP), Estonia (EST), Finland (FIN), France (FRA), United Kingdom (GBR), Ghana (GHA), Greece (GRC), Croatia (HRV), Hungary (HUN), Indonesia (IDN), India (IND), Ireland (IRL), Iran (IRN), Iraq (IRQ), Iceland

Table S7. Summary of global travel policy coordination. See Table S5 caption for more information.

		S1	S2	S3	S4	S5	S6	S7	S8
G	IA (%)	1.57	0.00	1.57	0.00	0.80	0.00	1.57	0.78
		1.67	0.00	1.68	0.00	0.85	0.00	1.68	0.83
	II (%)	2.68	0.00	2.68	0.01	1.36	0.00	2.68	1.32
		2.81	0.00	2.81	0.01	1.42	0.00	2.81	1.38
	IIQ (%)	2.68	0.00	0.00	0.01	0.00	0.00	1.32	1.32
		2.81	0.00	0.00	0.01	0.00	0.00	1.38	1.38
	Tc	100%	0%	100%	50%	50%	25%	100%	75%
	Te	100%	0%	5%	50%	3%	25%	52%	75%
G1	IA (%)	1.98	0.00	1.98	0.00	0.99	0.00	1.98	0.99
		2.09	0.00	2.09	0.01	1.04	0.00	2.10	1.05
	II (%)	3.10	0.00	3.10	0.01	1.57	0.00	3.10	1.54
		3.24	0.00	3.24	0.01	1.63	0.00	3.24	1.61
	IIQ (%)	3.10	0.00	0.00	0.01	0.00	0.00	1.53	1.54
		3.24	0.00	0.00	0.01	0.00	0.00	1.60	1.61
	Tc	100%	0%	100%	64%	50%	32%	100%	82%
	Te	100%	0%	5%	64%	3%	32%	52%	82%
G2	IA (%)	1.77	0.00	1.77	0.00	0.89	0.00	1.77	0.89
		1.89	0.00	1.89	0.01	0.95	0.00	1.90	0.95
	II (%)	3.02	0.00	3.02	0.01	1.52	0.00	3.02	1.51
		3.17	0.00	3.17	0.01	1.59	0.00	3.17	1.59
	IIQ (%)	3.02	0.00	0.00	0.01	0.00	0.00	1.51	1.51
		3.17	0.00	0.00	0.01	0.00	0.00	1.58	1.59
	Tc	100%	0%	100%	64%	50%	32%	100%	82%
	Te	100%	0%	5%	64%	3%	32%	52%	82%
G3	IA (%)	0.77	0.00	0.77	0.00	0.42	0.00	0.77	0.35
		0.82	0.00	0.82	0.00	0.45	0.00	0.82	0.37
	II (%)	1.57	0.00	1.57	0.01	0.85	0.00	1.57	0.72
		1.64	0.00	1.64	0.01	0.88	0.00	1.64	0.76
	IIQ (%)	1.57	0.00	0.00	0.01	0.00	0.00	0.72	0.72
		1.64	0.00	0.00	0.01	0.00	0.00	0.76	0.76
	Tc	100%	0%	100%	7%	50%	3%	100%	53%
	Te	100%	0%	5%	7%	3%	3%	52%	53%

(ISL), Israel (ISR), Italy (ITA), Japan (JPN), Kazakhstan (KAZ), Korea (KOR), Kuwait (KWT), Lebanon (LBN), Lithuania (LTU), Luxembourg (LUX), Latvia (LVA), Morocco (MAR), Moldova (MDA), Mexico (MEX), Macedonia (MKD), Malaysia (MYS), Niger (NER), Netherlands (NLD), Norway (NOR), New Zealand (NZL), Oman (OMN), Pakistan (PAK), Panama (PAN), Peru (PER), Philippines (PHL), Poland (POL), Portugal (PRT), Qatar (QAT), Romania (ROU), Russia (RUS), Saudi Arabia (SAU), Singapore (SGP), Serbia (SRB), Slovakia (SVK), Slovenia (SVN), Sweden (SWE), Thailand (THA), Tunisia (TUN), Turkey (TUR), Ukraine (UKR), Uruguay (URY), United States(USA), Uzbekistan (UZB), and South Africa (ZAF).

The remaining countries are combined to make an artificial country, called "Others."

4 Choice of the local epidemiological model

In this study, we use the SIR-type local epidemiological model as described in Warne *et al.* (2020)¹, but other local models can also be easily accommodated within our modeling architecture. Some of the model assumptions may of course be violated in practice. For example, the assumption about the population of each country being fully-mixed does not hold as the individual-level contact networks vary from person to person. Further, our model specification leads to exponentially distributed recovery times, which is not realistic for COVID-19. However, despite these and other violations of the assumptions of the local epidemiological model, our meta-population framework remains valid. As Figure 2 in the main text shows, the meta-population

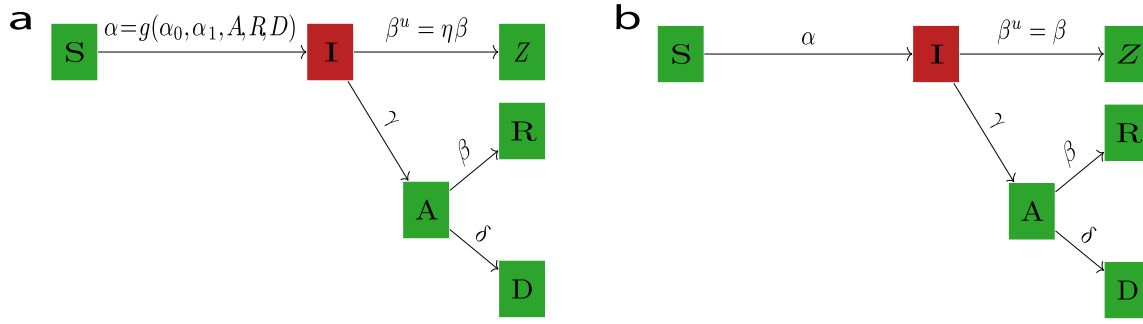


Figure S3. Two variants of the local model: **(a)** original model by Warne *et al.* (2020) and **(b)** our version of the model.

model fits the empirical data well.

Figure S3 shows the main differences between the original model of Warne *et al.* (2020)¹ and our model. In the original model, the transmission rate is an investigator-specified function g which depends on α_0 , α_1 , $A(t)$, $R(t)$ and $D(t)$. The removal rate β^u is modeled as $\eta\beta$ for some non-negative constant η . In our model, we specified the transmission rate function g in two different ways: it is either a constant function $g(t) = \alpha$ for all t or, alternatively, it is a piecewise constant function $g(t) = \alpha_1 \mathcal{I}_{0,T(1)}(t) + \alpha_2 \mathcal{I}_{T(1),T(2)}(t) + \dots + \alpha_m \mathcal{I}_{T(m-1),T(m)}(t)$. The unconfirmed removal rate β^u is modeled as β .

Consider the following two pathways in our model. First, individuals who are undetected infected (I) and change their status to unconfirmed removed (Z) do so at rate β^u . Individuals who are active confirmed (A) and then become either confirmed recovered (R) or confirmed deceased (D) have an average removal rate of $1/(1/\gamma + 1/(\beta + \delta))$, which lies within the interval $[1/(1/\gamma + 1/\beta), \beta + \delta]$. If we believe that individuals in these two pathways have similar removal rates, it is reasonable to model the recovery rate β^u as belonging to the interval $[1/(1/\gamma + 1/\beta), \beta + \delta]$. Since β belongs to the interval $[1/(1/\gamma + 1/\beta), \beta + \delta]$, we simply model β^u as β . As both states I and Z in our model are unobserved, this modeling choice will help obtain a robust estimate of β^u and avoids increasing the model complexity unnecessarily.

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