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Effects of test timing and isolation length to reduce the risk of COVID-19 infection associated with airplane travel, as determined by infectious disease dynamics modeling

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ABSTRACT
Effective measures to reduce the risk of coronavirus disease 2019 (COVID-19) infection in overseas travelers are urgently needed. However, the effectiveness of current testing and isolation protocols is not yet fully understood. Here, we examined how the timing of testing and the number of tests conducted affect the spread of COVID-19 infection associated with airplane travel. We used two mathematical models of infectious disease dynamics to examine how different test protocols changed the density of infected individuals traveling by airplane and entering another country. We found that the timing of testing markedly affected the spread of COVID-19 infection. A single test conducted on the day before departure was the most effective at reducing the density of infected individuals travelling; this effectiveness decreased with increasing time before departure. After arrival, immediate testing was found to overlook individuals infected on the airplane. With respect to preventing infected individuals from entering the destination country, isolation with a single test on day 7 or 8 after arrival was comparable with isolation only for 11 or 14 days, respectively, depending on the model used, indicating that isolation length can be shortened with appropriately timed testing.

1. Introduction
During the coronavirus disease 2019 (COVID-19) pandemic, restrictions on travel and mass gatherings have been imposed due to concerns about the spread of infection. Although it is important to assess the risk of infection due to mass gatherings (Murakami et al., 2021), the risk assessment of travel is also important because such mass gatherings increase overseas travel including airplane travel, but the risk from such travel is rarely discussed. Although there are studies examining the effectiveness of current infection prevention measures (Clifford et al., 2020; Quilty et al., 2020), little is currently known about how different testing and isolation protocols affect the spread of COVID-19 infection associated with airplane travel.

In Japan, the Ministry of Foreign Affairs (2021) requires that all overseas travelers entering the country obtain a certificate of negative COVID-19 test result prior to departure from their country of origin, and then upon arrival in Japan that they undergo additional testing followed by isolation for 14 days. However, it is unclear how close to departure the pre-flight test should be conducted, or how effective the combination of testing upon arrival followed by 14-day isolation is at preventing infected individuals from entering the country. Although it is obvious that repeated testing (polymerase chain reaction and antigen testing) will reduce the spread of infection, testing is costly in terms of time and money. In addition, delays caused by testing at the airport and the long isolation period upon arrival can increase the stress of travel. Therefore, measures to reduce the spread of infection that are less costly, easier and quicker to implement, and have at least the same effectiveness as current measures are needed. Here, by using two mathematical models of infectious disease dynamics, we examined how the timing of testing and the number of tests conducted affect the spread of COVID-19 infection associated with airplane travel.
both models, each individual was considered to be in one of five major model, were used to guarantee the robustness of the results (Fig. 1). In infectious disease dynamics, a discrete time model and a continuous time states: susceptible to infection (S), exposed (E), presymptomatic (P), infected (I), and recovered from infection (R). State I was further divided into individuals in an asymptomatic state (Ia) or a symptomatic state (Is).

In the continuous time model, epidemic parameters $\sigma$, $\rho$, and $\gamma$ were the rate of transition from state E to P, from P to Ia or Is, and from Ia or Is to R, respectively. The average duration (in days) for each state was taken from He et al. (2020a) and rounded to the nearest integer (Fig. 1), resulting in state E lasting an average of 3 days ($=1/\sigma$), state P lasting an average of 2 days ($=1/\rho$), and states Ia and Is each lasting an average of 7 days ($=1/\gamma$). In the discrete time model, state E was split into three sub-states (E1, E2, and E3) with exposed individuals progressing at a rate of one sub-state per day, for a total of three days in state E as in the continuous time model. Similarly, state P was split into two sub-states (P1 and P2), and states Ia and Is were each split into seven sub-states (Ia1-7 and Is1-7) with the same daily sub-state progression.

We assumed that the proportion of infected individuals (prevalence, $\rho$) in the country of origin was constant through the time period of concern (up to 7 days), and the rate of transmission ($\beta$) was determined for the proportion of infected individuals that remained at $\rho$. Because an infected individual was considered to have recovered at 12 days after infection (sum of the durations of E, P, and Ia or Is), on average, $\beta/12$ infected individuals were lost every day, and hence the rate of transmission ($\beta$) was $\rho/12$.

The partition coefficient ($\eta$) of Ia and Is was estimated in He et al. (2020b) and found to be 0.54 (i.e., $Ia = 0.54Ia$). We assumed that once an individual had developed symptoms, the individual did not become asymptomatic before recovery (i.e., there was no transition between states Ia and Is).

The flight was assumed to take 1 day because the unit of time in the continuous time model was 1 day. Further details of the models are provided in the Appendix.

The infectious disease dynamics were divided into three domains (see details in Appendix):

1. **In the country of origin**: Infection was assumed to occur by contact between individuals in state S and infected individuals in the general population at a rate of $\rho/12$, where $\rho$ is the proportion of infected individuals in the country of origin (prevalence) in the population.

2. **In the airplane**: During travel, infection was assumed to occur between individuals in state S and individuals in state P or I. We assume that the density of newly infected individuals in the airplane proportional to the density of infected individuals in the airplane, and the proportionality constant is denoted by $\lambda$. Previous studies have shown that $\lambda$ ranges from almost 0 to 15 (Pombal et al., 2020; Khan et al., 2020). Powell (2020) summarized the 11 studies and found that 41 secondary infectors were occurred from 154 primary infectors in the air travels, and hence $\lambda$ was estimated as 41/154 $\approx 0.27$. We set $\lambda$ as 0.5 based on a slightly pessimistic scenario.

3. **In the destination country**: Travelers entering the destination country were isolated for 14 days. During isolation, we assumed that there were no new infections ($\mu = 0$). The risk of infected individuals entering the destination country was defined as the density of infected individuals leaving isolation (i.e., the density of infected individuals at day 14).

Infected individuals were removed in one of two ways. The first was by what we call "self-exit", which is the event where an individual recognized the symptoms of infection themself. These individuals were removed from the Is state. Russell et al. (2020) reported that 40–80% of individuals with symptoms of infection isolated themselves. We assumed a removal probability per day ($\delta$) of 0.12. Since the Is state lasted 7 days, total removal probability was $1 - (1 - 0.12)^7 = 0.59$, which was at about the center of the range reported by Russell et al. The

### Table 1

Densities of infected individuals arriving at a destination country under various pre-travel testing scenarios, as estimated by two models of infectious disease dynamics. All values shown have been multiplied by 1000 for ease of presentation. Daily self-exit is assumed unless otherwise stated. The prevalence in the country of origin ($\rho$) was 0.001. Test sensitivity was 0.7, $\lambda$ is the proportionality constant for the secondary infection while on the airplane. See Appendix (A2) for the derivation of these values.

| Scenario | Continuous time model | Discrete time model |
|----------|-----------------------|---------------------|
|          | Number of infected individuals | Difference from baseline scenario ($\lambda = 0.5$) | Number of infected individuals | Difference from baseline scenario ($\lambda = 0.5$) |
| Test at 3 days before departure (baseline scenario) | 0.56 ± 0.36 | 0 | 0.60 ± 0.38 | 0 |
| No test, no self-exit | 0.92 ± 0.75 | 0.56 | 0.92 ± 0.75 | 0.51 |
| No test | 0.88 ± 0.75 | 0.52 | 0.88 ± 0.75 | 0.47 |
| Test at 3 days before departure, no self-exit | 0.60 ± 0.39 | 0.055 | 0.62 ± 0.40 | 0.030 |
| Tests at 7 and 3 days before departure | 0.51 ± 0.30 | −0.080 | 0.58 ± 0.35 | −0.035 |
| Tests at 4 and 3 days before departure | 0.49 ± 0.28 | −0.11 | 0.54 ± 0.30 | −0.10 |
| Test at 4 days before departure | 0.59 ± 0.39 | 0.045 | 0.64 ± 0.43 | 0.065 |
| Test at 2 days before departure | 0.53 ± 0.32 | −0.050 | 0.54 ± 0.32 | −0.090 |
| Test at 1 day before departure | 0.48 ± 0.27 | −0.13 | 0.49 ± 0.27 | −0.17 |

### 2. Methods

We considered individuals who left their country of origin and traveled on an airplane to a destination country. Two models of infectious disease dynamics, a discrete time model and a continuous time model, were used to guarantee the robustness of the results (Fig. 1). In both models, each individual was considered to be in one of five major...
country of origin was 0.7 and the prevalence of infection in the country of origin was 0.001.

second way for the removal of infected individuals was by testing. The removal probability (test sensitivity, \(a\)) was assumed to be 0.7 (baseline value) for individuals in the P, Ia, and Is states, and 1 − 0.999 (test specificity, \(b\)) for individuals in the S, E, and R states, based on the reported sensitivity of polymerase chain reaction tests in individuals in these states (Boger et al., 2020). The effects of assuming values of test sensitivity other than 0.7 are discussed in the sensitivity analysis section; however, it should be noted that we only consider differences in test sensitivity and do not distinguish between polymerase chain reaction and antigen testing. The test sensitivity may differ for individuals in the P, Ia, and Is states; however, we used the same values for test sensitivity irrespective of the state.

3. Results

3.1. Risk of infected individuals arriving at the destination country

First, the most pessimistic scenario with no testing and no self-exit was considered. The number of infected individuals arriving at the destination country was calculated by using the following equation:

\[
np(0.92 + 0.75i),
\]

where \(n\) is the number of travelers and \(p\) is the prevalence of infection in the country of origin; the derivation of the values 0.92 and 0.75 used in Eq. (1) can be found in Appendix (A3). When \(n = 1000, p = 1/1000, and \(\lambda = 0.5\), the density of infected individuals arriving at the destination country is 1.295 per 1000 travelers.

Next, we examined the density of infected individuals arriving at the destination country under various test timing scenarios. The models showed comparable results for each scenario (Table 1).

The density of infected individuals arriving at the destination country decreases with increasing test sensitivity in the country of origin. The effect of test sensitivity on the density of infected individuals arriving at the destination country is discussed in the Appendix (A. 2.6).

3.2. Risk of infected individuals entering the destination country

The dynamics of the two models under a scenario of 2-week isolation with no testing after arrival (baseline dynamics) are shown in Fig. 2a. The initial condition was the density of infected individuals arriving at the destination country after being tested 3 days before departure with a test sensitivity of 0.7. The models provided slightly different dynamics, with the most obvious difference being that in the discrete time model the density of infected individuals reached zero at day 12, whereas in the continuous time model it never reached zero, even at day 14 after entry.

We then examined whether the current standard 14-day isolation period could be shortened by adding additional testing during the isolation period without increasing the risk of admitting an infected person. We denote the density of individuals at state \(x = E, P, Ia\), or Is) as \(x(t)\) in the continuous time model as a function of time. The risk at the end of isolation without any testing (density of infected individuals at day 14) is

\[
\varphi^c_{r}(14) = E(14) + P(14) + Ia(14) + Is(14),
\]

where \(\varphi^c_{r}(14)\) represents the risk without testing. If we carry out a test on day \(T\) and cease isolation, the risk is

\[
\varphi^c_{r}(T) = bE(T) + (1 - a)P(T) + Ia(T) + Is(T)).
\]

The value of \(T\) leading to the same risk can be found by equating the two equations:

![Fig. 2](image-url) Infectious disease dynamics after arrival at the destination country. (a) Baseline dynamics obtained with the continuous (solid line) and discrete (dots) time models under the scenario of isolation for 14 days with no testing after arrival. (b) Finding the risk-equivalent isolation period (\(T\)) for the discrete time model (Eq. (2)). Black dots show the density of infected individuals without testing, and gray dots show the density of individuals after testing. The horizontal dashed line is the risk-equivalent line. The gray dots become lower than the risk-equivalent line at day 7, meaning that 7-day isolation followed by testing and then stopping isolation has the same risk as 11-day isolation without testing. A sharp reduction (indicated by two arrows and an asterisk) occurred as all E state individuals became state P. In all simulations, the test sensitivity in the
The density of infected individuals arriving at the destination country were compared for several pre-travel test-timing scenarios (Table 1). Compared with the baseline scenario (test at 3 days before departure and daily self-exit of a defined proportion of symptomatic individuals; $\lambda = 0.5$), adding an additional test at 7 days before departure reduced the density of infected individuals by less than $0.080 \times 10^{-3}$ (continuous time model) and $0.035 \times 10^{-3}$ (discrete time model) individuals. An additional test at 4 days before departure reduced the density of infected individuals by about $0.11 \times 10^{-3}$ (continuous time model) and $0.10 \times 10^{-3}$ (discrete time model) individuals. The results of the scenarios for just one test before departure show that the timing of the testing before departure markedly affects the density of infected individuals arriving at the destination country. When we examined the use of a single test at 1, 2, or 4 days before departure, the change of the risk compared to the baseline scenario (3 days before departure) were $-0.13 \times 10^{-3}$, $-0.050 \times 10^{-3}$, $0.045 \times 10^{-3}$, respectively, and hence the best scenario was testing at 1 day before departure, which we attributed to the likelihood of new infections increasing with increasing time between the test and departure days. Until now, we have not specified the type of test. The current major testing methods are antigen test and PCR test; it would be difficult to do the test 1 day before departure since the PCR test takes 1 to several days to have the test results. Therefore, it is important to note that, the results of the PCR test one day before departure cannot be used in reality. It is effective to take the test as close to the departure date as possible, within the time frame for which the test results are available.

**Effect of test intervention strategies after arrival**

The infectious disease dynamics after arrival at the destination country are shown in Fig. 2. Based on the dynamics from the continuous time model, the risk level by isolation alone was equal to $7.54$ days of isolation plus testing (risk-equivalent isolation period). These findings are consistent with a report that isolation for 8 days plus testing is comparable to isolation for 14 days without testing (Clifford et al., preprint). Similar results were obtained with the discrete time model: with a test-sensitivity of 0.7, isolation for 11 days was equivalent to isolation for 7 days plus testing.

In the dynamics obtained with the discrete time model, there was a sharp reduction in the density of infected individuals between days 1 and 2 (asterisk in Fig. 2b). This reduction was because all individuals in state E (state undetectable by testing) had transitioned to state P (state detectable by testing) at 2 days after arrival (i.e., 1 day in the airplane + 2 days in the destination country). The individuals in state E arriving at the destination country were infected individuals newly infected between their negative test 3 days before departure and their disembarking the airplane. Testing at the airport immediately upon arrival overlooks the risk of new infections. Waiting a few days after arrival before testing is likely a more effective approach.

The sensitivity analysis showed that the sensitivity of parameters except for $\lambda$ and $b$ were positive. This implies that increases of these parameters reduce the risk-equivalent isolation period. Indeed, increasing the parameters related to transition between states ($\gamma$, $I_a$, $I_p$, $\gamma$) would lead to faster recovery (lower $R_0$), and increasing $\eta / (I_a I_p$ partition rate) would lead to the detection of a greater density of infected individuals. Among these parameters, the sensitivity of $\gamma$ is the largest, indicating that the uncertainty of this parameter plays the largest role in determining the risk-equivalent isolation period, and therefore, this parameter should be estimated most carefully.

The risk of infected individuals entering a destination country depends on the timing of testing. Before departure, waiting until just before departure is the most effective approach to prevent infected individuals from traveling. After departure, waiting for infected individuals to enter the presymptomatic period is the most effective approach to identify infected individuals before they enter the country. The typical isolation length of 14 days after arrival in the destination country can be shortened to 7 days by combining isolation and testing.
The establishment of tests with greater sensitivities will contribute to shortening the isolation period even more. This study provides quantitative findings on the effectiveness of testing and isolation strategies to reduce the risk of infection during air travel and of infected individuals entering destination countries.

Author statement

Masashi Kamo analyzed models; Seiya Imoto and Michio Murakami conceptualized the study framework and literature survey.

Appendices

In this study, we considered travelers who left their country of origin and traveled on an airplane to a destination country. Two models of infectious disease dynamics, a discrete time model and a continuous time model, were used to guarantee the robustness of the results. In both models, each individual was considered to be in one of six states: susceptible to infection (S), exposed (E), presymptomatic (P), infected but asymptomatic (Ia), infected and symptomatic (Is), or recovered from infection (R). Individuals in state S transition to state E at a rate of $\beta p$, where $\beta$ is the rate of infection and $p$ is the prevalence of infection in the country of origin. Since we considered a short period of time for the infectious dynamics, $p$ was assumed to be a constant. Individuals transition from state E to P, and from state P to either Ia or Is. The proportion of individuals in state P that transitions to Is is $\eta$, and the proportion that transitions to Ia is $1-\eta$. These variables were scaled by the total number of travelers ($n$) such that the sum of the variables equaled 1:

$$1 = S + E + P + Ia + Is + R.$$  

(A1)

Numbers of individuals were calculated by multiplying by the total number of travelers (e.g., number of individuals in state E is $nE$). In both models, the infectious disease dynamics were considered in three discrete domains: dynamics in the country of origin, those in the airplane, and those in the destination country.

A1. Discrete time model

A1.1. Infectious disease dynamics in the country of origin

The discrete time model had a unit of time of 1 day. A newly infected individual at time $t$ was considered to stay in state E for 3 days, and this was implemented by dividing state E into three sub-states [$E_1(t)$, $E_2(t)$, and $E_3(t)$], where exposed individuals transitioned at a rate of one sub-state per day. Similarly, state P was divided into two sub-states [$P_1(t)$ and $P_2(t)$] and states Ia and Is were each divided into seven sub-states [$Ia_1(t)$ and $Ia_2(t)$ and $Ia_3(t)$] and states Is and Is were each divided into seven sub-states [$Is_1(t)$ and $Is_2(t)$ and $Is_3(t)$]. Thus, a newly infected individual remained infectious for 12 days in total, which afforded a turnover rate of 1/12.

Infected individuals were removed by testing (polymerase chain reaction or antigen testing) or by recognizing symptoms in themselves (self-exit). Removal by testing occurred for infected individuals in states E [as false-positives with a probability (1-$b$), where $b$ is the test specificity], P, Ia, and Is with a sensitivity (a). The rate of self-exit was $q$, and individuals in state Is were removed with probability $q$ every day.

New infections could occur by contact between the travelers and infected individuals in the general population in the country of origin. The proportion of infected individuals in the country of origin (prevalence) is $p$. If travelers are randomly selected from the population in the country of origin, the probability that a traveler is infected is $p$. In the short time periods considered in the present study (3–7 days), $p$ in the country of origin is unlikely to change much, so it can be treated as a constant (estimating the dynamics of $p$ in the country of origin was outside the scope of the present study). Because density of $p/12$ individuals (where 12 is the infection period in days) are removed daily due to recovery, the rate of new infection ($\beta$) required to keep the proportion of infected individuals ($p$) constant is also $p/12$; hence

$$\beta = p/12.$$  

A constant force of infection is approximately true for a population in which the density of infected individuals does not drastically change.

A1.2. Initial densities and definition of day

The density of infected individuals in the country of origin is $p$ (prevalence), and there are a total of 12 sub-states (three for E, two for P, and seven for Ia or Is states) in the discrete time model. Densities were allocated equally to each state; hence, the initial condition for states E and P is $p/12$, for state Ia is $(1-\eta)p/12$, and for state Is is $\eta p/12$. The initial densities of recovered individuals were assumed to be 0 [$R(0) = 0$], and hence the initial density of susceptible individuals is $S(0)=1-p$. These densities are defined as densities on day 0. In the discrete time model, for example, the densities for state $E_2(1)$ on day 1 were obtained as

$$E_2(1) = E_1(0) = p/12.$$  

when there is no measure of risk (testing or self-exit) removing the infected individuals. If a test is conducted on day 0, individuals in state E are removed as false-positives (because state E is not detectable by testing), and the density of $E_2(1)$ is

$$E_2(1) = bE_1(0) = bp/12.$$  

where $b$ is the test specificity. By applying these rules for all states, we have a discrete time model for population densities.

Declaration of Competing Interest

The authors declare no competing interests.

Data Availability

No data was used for the research described in the article.

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A1.3. Dynamics before departure

The model in the country of origin is described by

\[ S(t + 1) = S(t) - bE(t), \]
\[ E_i(t + 1) = S(t) - bE(t) \text{ for } i = 2, 3, \]
\[ P_i(t + 1) = bE_i(t) + bE_{i-1}(t) \text{ for } i = 2, 3, \]
\[ R(t + 1) = bE(t) + bE_{i-1}(t) \text{ for } i = 2, 3, \]
\[ I_{a1}(t + 1) = (1 - \eta)(1 - a)P_2(t), \]
\[ I_{a2}(t + 1) = (1 - \eta)(1 - a)P_2(t) + (1 - a)(1 - q)I_{a1}(t), \]
\[ I_{s1}(t + 1) = (1 - a)I_{a2}(t) \text{ for } i = 2, ..., 7, \]
\[ I_{s2}(t + 1) = (1 - a)(1 - q)I_{a2}(t) \text{ for } i = 2, ..., 7, \]
\[ R(t + 1) = R(t) + (1 - a)I_{a2}(t) + (1 - a)(1 - q)I_{s1}(t). \]

(A2)

It was assumed that self-exit occurs each day with a probability of \( q \) and that tests were conducted at 1, 3, 4, or 7 days before departure. On a day with no testing, \( a \) was set at 0 and \( b \) was set at 1.

A1.4. Infectious disease dynamics on the airplane

While on the airplane, it was assumed that infection occurred among travelers and that the rate of infection was proportional to the total density of infected individuals in the infective states (P, Ia, and Is), with the proportionality constant of increase denoted by \( \lambda \):

\[ \lambda \left( \sum_{i=1}^{7} P_i(t) + \sum_{i=1}^{7} (I_{a_i}(t) + I_{s_i}(t)) \right) \]

when the density of infected individuals is low. Hence, the dynamics are represented by

\[ S(t + 1) = S(t) - \lambda \left( \sum_{i=1}^{7} P_i(t) + \sum_{i=1}^{7} (I_{a_i}(t) + I_{s_i}(t)) \right), \]
\[ E(t + 1) = E(t) - \lambda \left( \sum_{i=1}^{7} P_i(t) + \sum_{i=1}^{7} (I_{a_i}(t) + I_{s_i}(t)) \right). \]

The other equations are the same as in Eq. (A2) (note that no tests were carried out in the airplane). The densities of E, P, Ia, and Is states at time \( t + 1 \) were considered as the initial values of the dynamics in the destination country (densities at day 0 in the destination country), and the sum of these are shown in Table 1.

A1.5. Infectious disease dynamics in the destination country

After arrival at the destination country, complete isolation was assumed, so new infection did not occur (\( \beta = 0 \)). Therefore, the equations are the same as Eq. (A2) but with \( \beta = 0 \).

A2. Continuous time model

In the continuous time model, the model variables were defined in the same manner as in the discrete time model. Parameters \( \sigma, p, \) and \( \gamma \) were the rates of transition from state E to P, from state P to state Ia or Is, and from state Ia or Is, respectively. The partition rates for Ia and Is were \( (1 - \eta) \) and \( \eta \), respectively. The rate of new infection \( \beta \) was \( p/12 \), as discussed for the discrete time model (see Section A1.2).

A2.1. Infectious disease dynamics in the country of origin

The densities before departure changed over time as follows:

\[ \frac{dS}{dt} = -\beta S, \]
\[ \frac{dE}{dt} = \beta S - \sigma E, \]
\[ \frac{dE}{dt} = \sigma E - \rho P, \]
\[ \frac{dI_a}{dt} = (1 - \eta)\rho P - \gamma I_a, \]
\[ \frac{dI_s}{dt} = \eta \rho P - (q + \gamma) I_s, \]
\[ \frac{dR}{dt} = \gamma (I_a + I_s), \]

(A3)

where \( q \) is the rate of self-exit (see Table A1 for other definitions). Testing was treated as a discrete event, and once testing was conducted the densities were replaced immediately with
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Following were obtained: the assumption that \( p \) is constant. By setting the dynamics for the infected states (E, P, Ia, and Is) in Eq. A3 equal to zero and solving the equations, the

\[
\begin{align*}
S(t) &= bS(t), \\
E(t) &= bE(t), \\
P(t) &= (1-a)P(t), \\
Ia(t) &= (1-a)Ia(t), \\
Is(t) &= (1-a)Is(t),
\end{align*}
\]

where \( a \) is the sensitivity and \( b \) is the specificity of the test.

A2.2. Infectious disease dynamics on the airplane

New infections on the airplane were also treated as discrete events. New infections were assumed to occur just after the travelers had boarded the airplane, and the densities were replaced with

\[
\begin{align*}
S(t) &= S(t) - \lambda(P(t) + Ia(t) + Is(t)), \\
E(t) &= E(t) + \lambda(P(t) + Ia(t) + Is(t)),
\end{align*}
\]

where \( \lambda \) is the proportionality constant for the secondary infection while on the airplane. No other contact was considered, and in this domain, \( \beta \) in Eq. (A3) was set at 0. The flight time was assumed to be 1 day for consistency with the discrete time model (time unit in the discrete time model was 1 day). Solving Eq. (A3) for 1 day afforded densities for entry into the destination country (Table 1 in the main text).

A2.3. Infectious disease dynamics in the destination country

After the travelers had entered the destination country, the dynamics were the same as in Eq. (A3) with \( \beta = 0 \). In the scenarios with isolation plus testing and release, the densities of released infected individuals were calculated as

\[
bE(t) + (1-a)(Ia(t) + Is(t)),
\]

where \( t \) is the time at which the test was conducted.

A2.4. Initial densities

The initial conditions for Eq. (A3) were determined by assuming that the infectious disease dynamics were stable in the country of origin (based on the assumption that \( p \) is constant). By setting the dynamics for the infected states (E, P, Ia, and Is) in Eq. A3, equal to zero and solving the equations, the following were obtained:

\[
\begin{align*}
E(0) &= (\beta/\sigma)S(0), \\
P(0) &= (\sigma/\rho)E(0) = (\beta/\rho)S(0), \\
Ia(0) &= (1-\eta)(\beta/\gamma)P(0) = (1-\eta)\beta/\gamma S(0), \\
Is(0) &= (\eta/\gamma)P(0) = (\eta/\gamma)S(0).
\end{align*}
\]

We assumed that there were no recovered individuals in the group at time 0 [i.e., \( R(0)=0 \); therefore, \( S(0)=1 - E(0) - P(0) - Ia(0) - Is(0) \). Table A1 shows a summary of the parameters used in the continuous model.

A2.5. Solution of Eq. (A3)

Eqs. A3 form a linear model, and we can solve them. The solutions are

\[
\begin{align*}
S(t) &= S(0)e^{-\beta t}, \\
E(t) &= \frac{-\beta S(0)e^{-\beta t} + [\beta S(0) + (\beta - \sigma)E(0)]e^{-\sigma t}}{\beta - \sigma}, \\
P(t) &= \frac{A1e^{-\beta t} + A2e^{-\rho t} + A3e^{-\eta t}}{\beta - \sigma/(\beta - \rho)(\gamma - \sigma)/(\rho - \sigma)}, \\
Ia(t) &= \frac{B1e^{-\beta t} + B2e^{-\rho t} + B3e^{-\eta t} + B4e^{-\sigma t}}{\beta - \gamma/(\beta - \sigma)(\beta - \rho)(\gamma - \sigma)/(\rho - \sigma)}, \\
Is(t) &= \frac{C1e^{-\beta t} + C2e^{-\rho t} + C3e^{-\eta t} + C4e^{-\sigma t}}{\beta - \sigma/(\beta - \rho)(\gamma - \sigma)/(q + \gamma - \rho)/(q + \gamma - \sigma)},
\end{align*}
\]

where \( A1, A2, A3, B1, B2, B3, B4, C1, C2, C3 \) and \( C4 \) are constants and are

\[
\begin{align*}
A1 &= (\beta - \rho)/(\beta - \sigma)E(0), \\
A2 &= (\beta - \rho)/(\beta - \sigma)S(0), \\
A3 &= (\beta - \rho)/(\beta - \sigma)S(0) + (\beta - \rho)/(\beta - \sigma)P(0), \\
B1 &= \sigma(1-\eta)(\beta - \gamma)(\beta - \rho)/(\gamma - \sigma)/(\rho - \sigma)E(0), \\
B2 &= \sigma(1-\eta)(\beta - \gamma)(\beta - \rho)/(\gamma - \sigma)/(\rho - \sigma)S(0), \\
B3 &= \rho(1-\eta)(\beta - \gamma)/(\beta - \sigma)/(\gamma - \sigma)/(\rho - \sigma)E(0), \\
B4 &= (\beta - \rho)/(\beta - \sigma)/(\gamma - \sigma)/(\rho - \sigma)/a0 \\
-\rho(1-\eta)[(\beta - \gamma)/(\beta - \sigma)E(0) - (\beta - \sigma)/(\beta - \gamma)E(0)],
\end{align*}
\]
\[ C_1 = \rho \sigma (q + \gamma - \beta)(\beta - \rho)(q + \gamma - \rho)(q + \gamma - \sigma)E(0), \]
\[ C_2 = \beta \sigma (q + \gamma - \rho)(q + \gamma - \sigma)S(0), \]
\[ C_3 = \nu (q + \gamma - \beta)(q + \gamma - \rho)(q + \gamma - \sigma) \times \rho \beta \rho P(0) - \beta \rho E(0) + \rho P(0), \]
\[ C_4 = (\beta - \rho)(q + \gamma - \sigma) \times (q + \gamma - \rho)(q + \gamma - \sigma) \times \nu \rho (q + \gamma - \beta)(q + \gamma - \rho)E(0) - \nu \rho E(0) - \nu \rho (q + \gamma - \beta)(q + \gamma - \rho)P(0)). \]

A2.6. Densities of infected individuals leaving the country of origin and arriving at the destination country

The densities of infected individuals (Table 1 in the main text) for the continuous time model were computed as follows (for the scenario with testing three days before departure):

1. Obtain initial densities (time 0 at the country of origin) using Eq.A7.
2. Obtain densities after testing using Eq. (A4) with \( t = 0 \).
3. Obtain densities before departure using Eq. (A8) by setting \( t = 3 \) (dynamics for 3 days).
4. Determine initial densities in the airplane using Eq. A3.
5. Obtain densities arriving at destination country using Eq. (A8) by setting \( t = 1 \). In the dynamics in the airplane, \( \beta = 0 \) because new infection is regulated by \( \lambda \).

The total density arriving at the destination country is the sum of the densities of states E, P, Ia, and Is. We can write down these densities explicitly, but these are very complicated and hard to understand. If we were to substitute parameters other than \( \lambda \) and \( a \) [prevalence (p) in the destination country is 0.001 and the others are shown in Fig. 1], we have the density as

\[ P(0) = 0.000821906 - (0.000375056 + 0.004426123) a + 0.000667669. \]

Substituting \( a = 0.7 \) yields the value in Table 1 for this scenario. When \( \lambda = 0.5 \), it becomes

\[ 0.00129827 - 0.000680335a \]

and this implies that an increase in a by 1 indicates a decrease in the density of infected individuals by 0.00068033, and therefore the amount of risk reduction by testing.

A3. Density of infected individuals arriving at the destination country

The densities of infected individuals with no self-exit and no testing was 0.92 + 0.75\( i \) in both models (Table 1 in the main text). The densities are explicitly derived by

\[ p(0.92 + 0.75\lambda(1 - p)), \]

where \( p \) is the prevalence in the country of origin and \( \lambda \) is the proportionality constant for the secondary infection while on the airplane.

Considering an infected individual taking a 1-day flight from the country of origin to the destination country, during the flight the individual may recover. Because the total duration of infection is 12 days in our parameterization, the probability that the individual recovers is 1/12, and hence the probability that the individual is still infected at arrival is 1 - 1/12 ≈ 0.92, and this is the density in the first term in the brackets in Eq. A9 representing the probability that an individual infected in the country of origin is still infected at the time of arrival at the destination country.

Susceptible individuals in the airplane may be infected by an infected individual with infectivity (i.e., states P, Ia, and I) by \( \lambda \). Since state E lasts 3 days and the total duration of infection is 12 days, the probability that the infected individual is in one of those states is 9/12 = 0.75. The \( (1 - p) \) in the second term in the brackets in Eq. A9 is the density of susceptible individuals. Hence, the density of individuals infected while on the airplane is 0.75\( \lambda \) \( (1 - p) \). The sum of the first term and the second term is the density of infected individuals arriving at the destination country.

If the prevalence in the country of origin is \( p \), then the probability that an individual is infected is \( p \). Multiplication all these yields Eq. A9

When the prevalence \( p \) is low enough, the squared term of \( p \) can be approximated to be 0, and then we have

\[ p(0.92 + 0.75\lambda). \]

This is the density of infected individuals, and if there are \( n \) travelers, we have Eq. (1) in the main text as the number of infected individuals.

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