Optimal Border Control during the Re-opening Phase of the COVID-19 Pandemic

Zhen Zhu¹, Enzo Weber², Till Strohsal³, and Duaa Serhan⁴

¹one world Management Company
²IAB Nürnberg and University of Regensburg
³German Federal Ministry for Economic Affairs and Energy and School of Business & Economics, Freie Universität Berlin
⁴American Airlines *

Abstract

Most of the existing literature on the current pandemic focuses on approaches to model the outbreak and spreading of COVID-19. This paper proposes a generalized Markov-Switching approach, the SUIHR model, designed to study border control policies and contact tracing against COVID-19 in a period where countries start to re-open. We offer the following contributions. First, the SUIHR model can include multiple entities, reflecting different government bodies with different containment measures. Second, constraints as, for example, new case targets and medical resource limits can be imposed in a linear programming framework. Third, in contrast to most SIR models, we focus on the spreading of infectious people without symptoms instead of the spreading of people who are already showing symptoms. We find that even if a country has closed its borders completely, domestic contact tracing is not enough to go back to normal life. Countries having successfully controlled the virus can keep it under check as long as imported risk is not growing, meaning they can lift travel restrictions with similar countries. However, opening borders towards countries with less controlled infection dynamics would require a mandatory quarantine or a strict test on arrival.

Despite the initial panic and chaos, most countries of the world have withstood the first wave of COVID-19. To “bend the curve” of the virus spreading, authorities closed their borders, put stay-at-home orders in place and introduced several measures of social distancing. Recently, authorities in many countries and territories have started the phase of reopening to recover their economy. After opening restaurants and retail stores again, when and how to reopen the borders has become a heated topic. While there is little doubt that travel and tourism contribute greatly to the economy (Manzo, 2019), reopening the border in an unstructured manner is likely to result in a spike of cases and new lockdown orders.

This paper proposes a new approach to study border control policies against COVID-19, or any other pandemic, during the re-opening phase. This is especially important in view of the new increases of infection numbers currently appearing worldwide. Our model can be seen as a generalization and extension to the SIR model that was first proposed by Kermack and McKendrick (1927). SIR

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and SEIR models are Markov transition models that have long been used to model epidemic spreading and controls such as lockdowns and vaccines; see Hethcote (2000); or, for recent applications Peng et al. (2020), Prem et al. (2020) or Maier and Brockmann (2020). The approach we introduce is in discrete time and can be described as $S$(usceptible) $U$(nidentified infectious) $I$(dentified infectious) $H$(ospitalized) $R$(ecovered) model.

The model extensions have several dimensions. First, the SUIHR model can include multiple entities, reflecting different government bodies with different containment measures. We explicitly model the importation of infected individuals from one entity to another so that the effect of border control policies can be studied. Second, in contrast to most SIR models, we focus on the spreading of infectious people without symptoms instead of the spreading of people who are already showing symptoms. This is to account for the new characteristics of the re-opening phase compared to the initial outbreak control phase. The danger of COVID-19 is now well known and people have the awareness to avoid spreading once they are identified as infected. Testing is largely available, most people who show symptoms can get a diagnose quickly and will be isolated. Third, contact tracing, a promising technology that many countries have recently introduced, is built into our model. During the re-opening phase, “trace & isolate” should be the main method to reduce the spreading of the virus - again, with the focus on avoiding spreading through potentially infected individuals which are not yet showing symptoms. Fourth, unlike the outbreak control phase, in which swift lockdown actions needed to be taken at all costs to prevent overwhelming the healthcare systems, the re-opening phase is likely to be more strategic. Therefore, constraints such as new case targets and medical resources are incorporated into the model framework as part of the policy optimization process. Solutions to our model can be obtained via linear programming.

For our empirical analysis, a central element is that strategies against corona vary strongly across countries. Therefore, we classify government entities in the world into three major groups based on their control strategies. Group 1 entities were able to completely eliminate domestic new cases and then started to re-open. Examples of Group 1 entities are mainland China, Hongkong and New Zealand. Group 2 entities are those which have successfully controlled the virus (i.e., the new cases are steadily decreasing for a long time and only a small portion of the total population has been infected) and have started to re-open before the virus was completely eliminated. Most of the Europe Union countries belong to this group. Group 2 countries need to keep COVID-19 under control, as long as the imported risk is not growing over time. For group 2 countries to open to group 3 countries, a strict test at border is needed to sufficiently limit the imported risk, i.e. to prevent imported cases from growing over time. In absence of such a test, a mandatory quarantine on arrival is needed.

The literature on mathematical and statistical models for COVID-19 is growing fast. Several extensions to the standard SIR model have been proposed. Optimal policies facing the trade-off between health and economic damage have been studied in Eichenbaum et al. (2020), Alvarez et al.
It has been confirmed that social distancing and lockdowns were successful in bringing down the number of new infections, see e.g. Prem et al. (2020), Radulescu and Cavanagh (2020), Dehning et al. (2020), Jüni et al. (2020) and Weber (2020). The effectiveness of “smarter”, economically less harmful, measures has been studied as well; for example, face masks are analyzed in Lyu and Wehby (2020) and Mitze et al. (2020), group specific approaches (e.g. stricter social distancing rules for vulnerable groups) and contact tracing are investigated in Acemoglu et al. (2020) and Grimm et al. (2020). Models with group specific parameters and policies are most closely related to our approach. However, we propose a model to optimize a multi-entity problem where each country applies uniform policies. A border between countries that effectively separates one uniform policy from another is what we have observed during the last six months of the world-wide corona pandemic.

The effectiveness of border closures and controls is supported by the academic literature, particularly with respect to reducing the number of imported individuals, which are infected but asymptomatic; see Wells et al. (2020) and Lee et al. (2020). In this regard, the effectiveness of border closures can also depend on further containment measures considered in combination (see e.g. Deb et al., 2020, Weber, 2020, Chinazzi et al., 2020 and Nussbaumer-Streit et al., 2020). Chinazzi et al. (2020) used the global epidemic and mobility model (GLEaM) to confirm that international travel restrictions helped to slow down the spreading of COVID-19. The GLEaM, a combination of the SIR model and a network model, is particularly designed to simulate the outbreak and global spreading of an epidemic through airline traffic.

Similarly, the effectiveness of contact tracing is generally supported, too, see e.g. Fraser et al. (2004). Grimm et al. (2020) show that a combination of targeted policies with contact tracing can be very effective in preventing a high death toll. According to Ferretti et al. (2020), it is crucial that contact tracing is digital to be fast enough to break infection chains. Recently, many countries (for example France and Germany) have introduced a corona tracing app. What is still unclear to decision makers, however, is how much can exactly be gained by contact tracing. For example, how helpful can a tracing app be in allowing to relax conventional measures like border closures.

The paper is organized as follows. In Section 2 we introduce the SUIHR model and show analytical results. In the third section we present the simulation results. Section 4 solves a border control problem using linear programming. Section 5 concludes.

2 The SUIHR Model: A Generalized Markov-Switching Framework with Border Controls and Contact Tracing

2.1 Markov States, Discrete Time Scale and Fundamental COVID-19 Dynamics

We define the following health states, summarized in Table 1 and graphically illustrated in Figure 1:

- **Susceptible**: An individual has not been infected by the virus and is susceptible to infection.
- **Unidentified Infectious**: An individual is infected already, but not yet identified. Also, the individual is not aware of the infection and hence does not adjust its behavior. This state includes people who are exposed, pre-symptomatic, and asymptomatic. In the re-opening phase, we assume people who have symptoms can immediately get a test by which they will be identified.
- **Identified Infectious**: A person is identified as infectious. For the re-opening phase, we assume anyone who is showing symptoms will be identified quickly.
- **Hospitalized**: Some fraction of the infected people need to be hospitalized.
- **Recovered:** Individuals which are recovered from the virus infection and, at least for some time, are immune to re-infection.

- **Death:** People who have died from the infection.

On top of the health states, we define two mobility states:

- **Free:** The person can move freely and hence can interact with anyone.

- **Quarantined:** No free movement is permitted and no spreading of virus to others is possible.

### Table 1: Model States

| State | Descriptions                                          |
|-------|-------------------------------------------------------|
| S     | Susceptible                                           |
| $I_1$ | Unidentified Infectious Free                          |
| $I_2$ | Unidentified Infectious Quarantined                   |
| $I_1$ | Identified Infectious, Stage 1 (first week only)      |
| $I_2$ | Identified Infectious, Stage 2 (week 2 and later)     |
| $H_1$ | Hospitalization, Stage 1 (first week only)            |
| $H_2$ | Hospitalization Infectious, Stage 2 (week 2 and later)|
| R     | Recovered                                             |
| D     | Death                                                  |
In general, everyone in susceptible. Unidentified and identified infectious, and recovered individuals can either be free or quarantined. However, in the re-opening phase, we assume that anyone who has been identified as infectious will be quarantined immediately to avoid virus spreading. Hospitalized people are also automatically quarantined in our model. In contrast to the initial outbreak control phase, we do not consider block quarantine on healthy (susceptible and recovered) people. Only a very small portion of the susceptible population are put into quarantine with contact tracing. We will ignore the (marginal) positive effect on reducing the virus spreading from quarantining healthy people. Instead, we focus on quarantining the unidentified infectious individuals. We further split the unidentified infectious group into \( U_F \) (unidentified infectious free) and \( U_Q \) (unidentified infectious quarantined).

The model we propose is in discrete time. Without loss of generality, we define each time epoch to be one week. This is mainly motivated by the fact that any policy that lasts less than one week is too short and unstable to be executed in practice. Also 7-day averages are commonly used to measure COVID-19 statistics. SIR and SEIR models are Markov models, in which a fix percentage of the cohort from each state transits to another state in each time epoch. The transition is assumed to be memoryless and for a given cohort in any state, the time of staying in that state before leaving it follows an exponential distribution (or a geometric distribution for discrete time models). Hence, the percentage of a cohort leaving a state is decreasing over time. However, the existing evidence on COVID-19, as summarized in Figure 2, is in contrast to the decreasing transition probabilities, see Lechien et al. (2020); Zhou et al. (2020); To et al. (2020). For example, it has been clinically observed that only 25% of the hospitalized patients are discharged within the first week, while 50% are discharged during the second week (Zhou et al., 2020). Therefore, a different distributional assumption is made.

As shown in Figure 3, for some states, the time needed to transition out of that state follows a distribution whose peak comes at time epoch \( t = m > 1 \), i.e. the probability of leaving a state is increasing for some time and only decreasing after the \( m - th \) epoch. For the "head" part before the \( m - th \) epoch, we build exactly \( m - 1 \) transient sub-states, which all belong to the same physical state. Agents in those sub-states must transit to a different state or to the next sub-state at each time epoch. For the "tail" part (i.e. \( t \geq m \)), we introduce a single sub-state, which can be represented using a geometric distribution. Overall, a total of \( m \) sub-states from the same state are created. Using the previous example of COVID-19 hospitalization time. Most of the patients are discharged in the second week, hence for state \( H \), \( m = 2 \), two sub-states \( H_1 \) and \( H_2 \) are created, in which \( H_1 \) is a transient state for week 1 only. \( H_2 \) represents hospital stays from week 2 and after.

In the SUIHR model, we have two transient sub-states of Identified Infectious (i.e., \( I_1 \) and \( I_2 \)) and two sub-states of Hospitalization (i.e., \( H_1 \) and \( H_2 \)). \( I_1 \) and \( H_1 \) correspond to weekly new cases and weekly new hospital admission, respectively. The new case number is the most closely monitored statistic that decision makers rely on.

### 2.2 Model Parameters

We denote \( t \in [t_0, t_1, ..., T] \) to be the time epochs in which we consider implementing a policy strategy. We assume at time epoch \( T \), vaccine will be available and broadly used.

The entity has a population of \( C \), assuming no net immigration, the entity has \( x_t \) people traveling into the entity at time \( t \) and the same amount of people leaving the entity. We use \( N_S, N_U, \ldots \) to denote the number of people in each states. We denote \( \phi \in \Phi \) to be a specific control policy combination in a set of all possible controls. An example of a control policy \( \phi \) is no gathering of more
Figure 1: Transitional Diagram
than 5 people and the requirement of face masks in public areas. We assume under policy $\phi$ every infectious person in the $U_F$ state on average has close contact to $\sigma_\phi$ people in a time epoch given the social distance practice. We refer to the probability of infection with close contact by $\gamma_\phi$. Given that $N_S/C$ percent of the population is susceptible, $\sigma_\phi \cdot \gamma_\phi \cdot N_S/C$ will become infected. Factors that impact $\sigma$ are, for example, population density, social distancing and stay home orders. Factors that impact $\gamma$ are, for example, wearing face masks and proper disinfection such as hand washing.

Naturally, $\sigma$ and $\gamma$ are difficult to observe in practice. The parameter $r = \sigma \cdot \gamma$ stands for the expected number of people an infectious person can spread the virus to in a time epoch given a life style, i.e. given a specific containment policy. Note that here $r$ is slightly different from the base reproduction number (commonly denoted by $R_0$) or effective reproduction number $R_t$ popular in literature. For each entity, base reproduction number $R_0$ is a constant that only depends on the nature of the virus. Effective reproduction number $R_t$, is calculated as ratio of the new cases in time epoch $t$ versus the previous time epoch. $R_t$ is an observed outcome which depends on the domestic containment policy, represented by $r$, and other control mechanism such as contact tracing.

$P_{ij}^t$ is the probability that an individual transits from health state $i$ into state $j$ at each time epoch, where $i, j \in \{S, U, I_1, I_2, H_1, H_2, R, D\}$. Note the transition of health state is independent of the mobility state. Therefore, $U_F$ and $U_Q$ share the same transitional probability.

We summarize the parameters in Table 2.
Table 2: Parameter Definition

| Parameter | Definition |
|-----------|------------|
| $t$       | Index for time epoch |
| $\phi$    | A given control policy, $\phi \in \Phi$ |
| $C$       | Population of the entity of interest |
| $x_t$     | Directional traffic that enter/leave the entity at time $t$ |
| $c_\phi$  | Average number of people a person have close contact with under policy $\phi$ |
| $\gamma_\phi$ | Probability of spreading the virus after close contact under policy $\phi$ |
| $r_\phi$  | $r_\phi = c_\phi \cdot \gamma_\phi$ |
| $\theta$  | Percentage of close contacts that can be traced and quarantined |
| $\beta$   | Percentage of incoming travelers that will go through 14-day quarantine |
| $N_i$     | Number of people in State $i$ |
| $P_{ij}$  | Probability of transition from state $i$ to $j$ |

2.3 Imported Risk

Consider an entity controls the traffic into its own territory, assuming a screening policy can effectively stop all the symptomatic individuals. Therefore, only people in state $U_F$ (i.e., unidentified infectious and free to move) can travel, and no identified infectious people (i.e., people in $U_I$) should be allowed to enter without being quarantined. We do not take into account people that commute daily across the border to work, since daily commuters should not be considered as external. We assume people who travel outside the entity and return later would bare the same risk of being infectious as people with foreign origins.

Due to the screening, only a small percentage $\alpha$ of travelers are infectious. We assume all of those people are still $U_F$ upon arrival and hence can potentially spread the virus into the population of the entity of arrival. Also, people could potentially get infected during the trip and hence some may depart as $S$ from the origin entity but arrive as $U_F$.

We denote $x^k_t$ to be the traffic coming in from origin $k$ at time epoch $t$, and we use $\alpha_k$ to denote the percentage of unidentified infectious people from origin $k$. Note that $k$ can be from any other entity with any means of transportation. For example, people coming into Germany from France by air and by land can be modeled as separate origins with a different risk level $\alpha_k$. By $x^0$ it is referred to the number of people leaving the entity of interest, and $\alpha_0$ is the percentage of people in $U_I$ who are leaving.

It is assumed that there is a quarantine policy after travel and a certain percentage of travelers $\beta$ will actually be sent to quarantine while the rest will enter the free state. A very strict mandatory quarantine will have $\beta = 1$. A stay home quarantine would be less effective with $\beta < 1$. A no quarantine policy would be represented by $\beta = 0$.

2.4 Contact Tracing

We explicitly model contact tracing. When someone is identified as infectious, contact tracing will reveal a percentage of the people the newly identified person has contacted. Those people will be quarantined. Formally, if someone is identified, $\theta$ percent of the $\sigma$ people who had close contact with the identified $I_1$ person will be put into quarantine. The newly infected individuals are given by $\sigma \cdot \gamma \cdot \theta \cdot N^S / C = r \cdot \theta \cdot N^S / C$.

2.5 SUIHR Model Equations and Analytical Results

With the parameter defined, we can formally write down the dynamic equations in our model. We first consider only domestic cases only and assume there are no imported cases. We start assuming
the control policy is given.

\[
N_{t+1}^i = N_t^i - N_t^{IF} \cdot r \cdot N_t^S / C \\
N_{t+1}^{IF} = \frac{P_{Ut}^i}{N_t^i} \cdot N_t^{IF} + N_t^{IF} \cdot r \cdot N_t^S / C - \frac{P_{Ut}^i}{N_t^i} \cdot N_t^{IF} \cdot r \cdot N_t^S / C \cdot \theta + \sum_k a_k \cdot x_k^i \cdot (1 - \beta) - a_0 \cdot x_0^i \\
N_{t+1}^{U0} = \frac{P_{Ut}^i}{N_t^i} \cdot N_t^{U0} + P_{Ht}^i \cdot N_t^{IF} \cdot r \cdot N_t^S / C \cdot \theta + \sum_k a_k \cdot x_k^i \cdot \beta \\
N_{t+1}^{H1} = P_{Ht}^i \cdot N_t^{IF} + P_{Ht}^i \cdot N_t^{IF} \\
N_{t+1}^{H2} = P_{Ht}^i \cdot N_t^{IF} + P_{Ht}^i \cdot N_t^{IF} \\
N_{t+1}^{R1} = N_t^{R1} + P_{Rt}^i \cdot (N_t^{IF} + N_t^{U0}) + P_{Rt}^i \cdot N_t^{IF} + P_{Rt}^i \cdot N_t^{IF} + P_{Rt}^i \cdot N_t^{IF} + P_{Rt}^i \cdot N_t^{IF} \\
N_{t+1}^{U0} = N_t^{U0} + P_{Ht}^i \cdot N_t^{H1} + P_{Ht}^i \cdot N_t^{H2} \\
\]

Note the term \( P_{Ut}^i \cdot N_t^{IF} \cdot r \cdot N_t^S / C \cdot \theta \) in Equation (2) and (3) represent the infected people sent to quarantine by contact tracing. Here \( P_{Ut}^i \cdot N_t^{IF} \) are the newly discovered cases in time \( t + 1 \). As soon as the new cases are discovered, \( P_{Ut}^i \cdot N_t^{IF} \cdot \sigma \cdot \theta \) people are quarantined, among which \( \gamma \cdot N_t^S / C \) are actually infected.

We denote \( y_t = \sum_k a_k \cdot x_k^i \cdot (1 - \beta) - a_0 \cdot x_0^i \) to be the total net imported infectious cases. Technically \( y \) can be negative as more infectious people are leaving the entity than entering. However, any rational policy maker should not rely on exporting their problems to others, rather they should manage the imported risk as in the worst case scenario where they only have imported cases and export no infectious to other entities. Therefore we can assume \( y_t \geq 0 \).

As mentioned earlier, in the re-opening phase, only people in \( U_F \) can spread the virus. Therefore, when \( N_t^{IF} \) is non-increasing over time, the virus spreading is under control.

\[
N_{t+1}^{IF} = \frac{P_{Ut}^i}{N_t^i} \cdot N_t^{IF} + N_t^{IF} \cdot r \cdot N_t^S / C - \frac{P_{Ut}^i}{N_t^i} \cdot N_t^{IF} \cdot r \cdot N_t^S / C \cdot \theta + y_t \\
= \left\{ \frac{P_{Ut}^i}{N_t^i} + (1 - \frac{P_{Ut}^i}{N_t^i} \cdot \theta) \cdot r \cdot N_t^S / C \right\} \cdot N_t^{IF} + y_t \\
\]

Let \( R_t = \frac{P_{Ut}^i}{N_t^i} + (1 - \frac{P_{Ut}^i}{N_t^i} \cdot \theta) \cdot r \cdot N_t^S / C \), this is the effective domestic reproduction rate at time epoch \( t \) without any imported cases. When \( R_t \leq 1 \), the spread is contained domestically when the border is closed or anyone coming in are subject to mandatory quarantine.

It is easy to see that \( \frac{\partial R_t}{\partial \theta} = -\frac{P_{Ut}^i}{N_t^i} \cdot r \cdot N_t^S / C < 0 \). This means the reproduction rate is decreasing as the effectiveness of contact tracing \( \theta \) increases. Hence, any level of contact tracing is beneficial in terms of containing the virus spreading.

It is also easy to see that \( \frac{\partial R_t}{\partial \theta} > 0 \). This means if the infectious incubation period is long, it makes containing the virus more difficult, which makes perfect sense in reality.

Another thing worth mentioning is that the term \( N_t^i / C \) here in general represents the effect of herd immunity. When evaluating policies, we need to consider the worst case scenario that \( N_t^i / C \approx 1 \). Therefore, we denote \( \hat{R} = \frac{P_{Ut}^i}{N_t^i} + (1 - \frac{P_{Ut}^i}{N_t^i} \cdot \theta) \cdot r \), when \( \hat{R} \leq 1 \), we consider the control policy working without the need to rely on herd immunity over time.
Grouping Countries Strategies against corona vary strongly across countries. Decision makers need to decide if risk associated with opening up the borders to other countries is consistent with domestic policy targets. For example, government entities will need to evaluate the need for a 14 days mandatory quarantine upon arrival, which will eliminate imported risk but at the same time eliminate almost all travel demand. Less aggressive alternatives such as semi-mandatory stay home quarantine upon arrival and contact tracing to contain the imported risk must be evaluated as well. Also, if an entity decides to open up, how much traffic from different sources should it take as time progresses before the vaccine is available? We classify government entities in the world into three major groups based on their control strategies. Mathematically, Group 1 entities have $N_0^{UI} = 0$ and $\hat{R} > 1$; Group 2 entities have $N_0^{UI} > 0$ and $\hat{R} < 1$, and Group 3 entities have $N_0^{UI} > 0$ and $\hat{R} > 1$. Less formally, Group 1 entities were able to completely eliminate domestic new cases and then started to re-open. Examples of Group 1 entities are mainland China, Hongkong and New Zealand. These countries are currently opening-up and push back domestic life to the pre-pandemic “normal”. Group 2 entities are those which have successfully “bent” the curve and have started to re-open before the virus was completely eliminated. Most of the Europe Union countries belong to this group. Group 2 countries need to keep a relatively tight control (e.g., no large crowd gathering for sport events, limited number of customers in shops) to keep COVID-19 under check until effective vaccines are developed. Group 3 entities are those aiming for herd immunity either strategically or involuntarily. Examples are Sweden, Brazil and the US.

Analytical Results

Lemma 2.1. There exists some $r$, above which even perfect contact tracing (i.e., $\theta = 1$) alone is not enough to contain the spreading, i.e., $\hat{R} > 1$.

Proof. By definition we have $\hat{R} = P_{IU}^{\hat{R}} + (1 - P_{IU}^{\hat{R}} \cdot \theta) \cdot r$. Because $P_{IU}^{\hat{R}} < 1$ and $\theta \leq 1$, we have $1 - P_{IU}^{\hat{R}} \cdot \theta > 0$. That means when

$$r > \frac{1 - P_{IU}^{\hat{R}}}{1 - P_{IU}^{\hat{R}} \cdot \theta} \quad (10)$$

$\hat{R} > 1$, and when $r > \frac{1 - P_{IU}^{\hat{R}}}{1 - P_{IU}^{\hat{R}} \cdot \theta}$, $\hat{R} > 1$ for any $\theta$. $\square$

In reality, $P_{IU}^{\hat{R}}$ is estimated to be around 0.25 and $P_{IU}^{\hat{R}}$ about 0.6. This means if $r > 1.875$, then $\hat{R} > 1$ even with perfect contact tracing. Consistent with existing estimates, we assume that when the virus first broke out, $R_0 \approx 2.8$, which is equivalent to $r = 2.1$ without any interventions. This means even perfect contact tracing cannot contain the virus outbreak by itself. Lemma 2.1 also means, Group 1 countries won’t be able to control the imported case from spreading domestically with contact tracing alone. Hence, mandatory quarantine upon arrival is needed for people in Group 1 countries to enjoy normal life.

Lemma 2.2. If the total net imported cases are non-increasing, and the entity has employed a control policy that the domestic reproduction rate is less than 1 (i.e., $\hat{R} < 1$) without the imported cases. Then the total new cases will eventually decrease at some point even without the help of herd immunity.

Proof. We know that $N_{i+1}^{UI} = \hat{R} \cdot N_i^{UI} + y_i$ without considering herd immunity overt time, therefore we have $N_{i+1}^{UI} - N_i^{UI} = \hat{R} \cdot (N_i^{UI} - N_{i-1}^{UI}) + (y_i - y_{i-1})$. Since $y_i$ is non-increasing, we have $y_i - y_{i-1} \leq 0$. Therefore we have

$$N_{i+1}^{UI} - N_i^{UI} \leq \hat{R} \cdot (N_i^{UI} - N_{i-1}^{UI}) \leq (\hat{R})^{t_i} \cdot (N_{i+1}^{UI} - N_i^{UI}) \quad (11)$$

10
If there exists a \( t_s \) such that \( N_{t_s}^{UF} \leq N_{t_s}^{IF} \), then \( N_{t+1}^{IF} \leq N_{t}^{IF} \) holds for all \( t > t_s \). On the other hand,
\[
N_{t+1}^{IF} - N_{t}^{IF} = y_t - (1 - \hat{R}) \cdot N_{t}^{IF} 
\]
We know \( \hat{R} < 1 \), therefore when \( N_{t}^{IF} \geq \frac{y_t}{(1 - \hat{R})} \), \( N_{t+1}^{IF} \leq N_{t}^{IF} \). Since \( \frac{y_t}{(1 - \hat{R})} \) is a finite positive number, this means the spreading will be contained even without the herd immunity.

Lemma 2 shows that Group 2 countries, with their relative strict internal control, are able to keep the curve flattened without the need of herd immunity, so long as the imported risk is not growing over time. Assume that \( x_t^i \) grows proportionally to the number of infectious free people from the origin entities, it is possible for Group 2 entities to open borders towards Group 1 (i.e., \( x_t = 0 \) because no infectious people in the Group 1 entities) and other Group 2 countries (i.e., \( x_t \) decrease over time due to the decreasing of infectious cohort in the origin entities) without a mandatory quarantine and to keep the virus spreading in check. For Group 2 countries to open to Group 3 countries, since the total number of infectious people in Group 3 countries are increasing over time (before herd immunity is achieved), the imported risk from Group 3 countries is also increasing over time. This means either there exists a strict test at border, which can limit the number of \( UF \) people that sneak in under the radar at any \( t \) to a constant, or a mandatory quarantine on arrival is then needed to prevent virus spreading growing out of control.

3 Data Characteristics and Simulation Results

After explaining our parameter calibration, we address a baseline for a single entity and border control for group 2 entities.

3.1 Parameter Description

In this section, we will demonstrate some important results using simulation. We acknowledge that the literature regarding COVID-19 is constantly developing and hence the parameters used in this paper are subject to change as better knowledge regarding the virus is available. However, the qualitative interpretation of the results in this paper would be applicable even the parameters differ.

We calibrate the model based on parameter values taken from the existing literature. For the transitional probability matrix, we use the following parameter set.

- \( P_{II}^{U} = 0.25 \), \( P_{II}^{I_1} = 0.6 \) and \( P_{II}^{R} = 0.15 \). This set of parameter means that 80% of the infected people will eventually show symptom with 60% of them showing the symptom in the first week (Lauer et al., 2020). Also 20% of the infected will be asymptomatic throughout the course of infection, this is in line with the findings in Streeck et al. (2020).

- \( P_{I_2}^{I_1} = 0.718 \), \( P_{I_2}^{H_1} = 0.095 \) and \( P_{I_2}^{R} = 0.187 \); \( P_{I_2}^{I_2} = 0.270 \), \( P_{I_2}^{H_1} = 0.096 \) and \( P_{I_2}^{R} = 0.634 \). According to Lechien et al. (2020), the mean duration of COVID-19 symptoms of mild-to-moderate cured patients was 11.5 ± 5.7 days. Assuming normal distribution, we estimate 21% of the symptomatic cases can recover with in 7 days. Among patients who developed severe disease, the medium time to dyspnoea from the onset of illness or symptoms ranged from 5 to 8 days (of Disease Control and Prevention, 2020). Zhou et al. (2020) also reported the median time from illness onset to dyspnoea is 7 days with the first quarter quantile to be 4 days and third quantile to be 9 days (i.e., IQR being 4 to 9 days). Furthermore, 19% of the total symptomatic cases are severe to critical and would require hospitalization (Li et al., 2020).
\* \( P_{H1}^H = 0.700, P_{H1}^R = 0.250 \) and \( P_{H1}^D = 0.050; P_{H2}^H = 0.130, P_{H2}^R = 0.770 \) and \( P_{H2}^D = 0.100. \)

The median hospital length of stay is 11 days with IQR being 7 to 14 (Zhou et al., 2020). The overall fatality rate here is 2.5\% for symptomatic cases, which is well within the range of various studies (To et al., 2020).

Without loss of generality, we choose our entity in simulation to have a population of 80 million people. This is similar in population size as the country of Germany. We warm start the system so that the states at time epoch 0 \( N_{UF} = 3600 \) and \( N_{I1} = 2543 \). This can be interpreted as an average of 363 new cases are observed everyday in the entity with a total of 3600 unidentified cases in the starting week.

3.2 Simulation Results For Domestic Controls

3.2.1 Single Entity Baseline

To set the baseline for understanding the simulation result, first we take a look at a single entity that has been completely shut its border. The entity just came out of lock down and starts to relax its internal control. As mentioned in the previous section, \( r \) being the average number of people a free infected person can spread the virus to, can be used to measure the tightness of the domestic control. As shown in Figure 4, the higher \( r \) is, the more relax the domestic control policy is. Figure 5 demonstrates the relationship between \( r \) and the effective reproduction rate \( R_t \). When no contact tracing is employed, \( r > 0.75 \) will result in the effective reproduction rate \( R_t > 1 \), hence the situation will go out of control again. Millions of people will be infected in a single week at peak and hospital beds will run out easily.

During the lockdown, many entities, such as Germany, were able to achieve effective reproduction rate around 0.8 (i.e., \( r = 0.6 \) during the lockdown). In a normal life, \( r \) is likely to be between 2 and 3. Therefore, to avoid another outbreak, people must endure a restrained lifestyle. However, with contact tracing, it is possible to alleviate the restrictions. As shown in Figure 6 and 7, with good tracing, we can allow life going back to \( r = 1.4 \) whereas without it, the situation will be out of control very quickly.

Given countries value domestic life higher than trans-border traveling, entities should first find the suitable domestic control policy with the level of contact tracing to achieve a steady state that
keeps the virus contained. Only after that, should travel restriction be relaxed. Here, we simulate three different quarantine policies. As stated in the previous section, when a mandatory centralized quarantine is imposed, $\beta = 1$. In the other two cases, $\beta = 0$ means no quarantine upon arrival, while $\beta = 0.6$ represents a stay home quarantine policy that is not strictly enforced. For this simulation, we assume the entity can achieve 50% effectiveness in contact tracing (i.e., $\theta = 0.5$) and in order to avoid another lockdown, the domestic control is relaxed to $r = 1$. We further assume an average of 1000 unidentified cases (based on 1 million weekly incoming travelers, and 0.1% being infected) can pass the border undetected every week.

As shown in Figure 8, without mandatory quarantine upon arrival, both new cases and hospitalized patients will increase overtime. However, as shown in Lemma 2, despite the increase, the
number of new cases will stabilize over time and total number of hospitalized patients are less than 5000, which is a manageable cohort size. This shows that when good internal control is present, opening the border brings in controllable risk as long as the imported cases are not increasing over time.

### 3.2.2 Border Control for Group 2 Entities

As stated earlier, for Group 1 countries, strict mandatory quarantine is necessary to avoid another lockdown. Therefore, travel demand to Group 1 countries would be suppressed mostly due to the quarantine requirement. Also cross border travel would be limited by the available quarantine facilities. We are more interested in the options of Group 2 entities here. First, we study the exchange between two Group 2 entities. In this simulation, Entity 1 has the same population size and starting profile as the entity used in the previous single entity simulation. We keep \( r^{Ent_1} = 1.4 \) and \( \theta^{Ent_1} = 0.8 \) for Entity 1. The effective reproduction rate \( \hat{R}^{Ent_1} < 1 \), but very close to 1. The initial starting value for this simulation has been warmed up assuming contact tracing has been implemented for at least a month before the border opening. A second entity (i.e. Entity 2) is added to the simulation. Entity 2 has 50 million population, and \( r^{Ent_2} = 1.1 \) and \( \theta^{Ent_2} = 0.6 \), so Entity 2 is also a Group 2 entity with \( \hat{R}^{Ent_2} < 1 \). We assume 2% of the unidentified infectious people (i.e., 3280 for Entity 1 and 4885 for Entity 2 initially) would travel at each time epoch. This would provide somewhere between 10 to 20 daily imported cases to each entity initially. We further acknowledge the possibility of infection on the trip, hence in one of the settings, we double the infectious people during the trip to test the effect of infection during trip (i.e., for every infectious person leaving one entity, there will be 2 infectious people arriving at the other entity). Moreover, we assume no quarantine upon arrival is needed. Due to the lack of credible data sources, in this simulation setting, both the percentage of infectious people traveling and the doubling of the number of infectious people on the road may not truly reflect
Figure 8: Effectiveness of Quarantine on Arrival

reality. However, such setting would serve the purpose of demonstrating the qualitative results.

As shown in Figure 9, despite being worse than the case of having a travel ban, both Entity 1 and Entity 2 keep the new cases under control and decrease together. This is the case, even when there is infection happening during the trip and the infectious cases would double. It is worth noting that, when there is no infection during the trip, one of the entities could be a net exporter of infectious people, while the other one would be a net importer. For the net exporter (i.e., Entity 1 in our simulation at the beginning and Entity 2 towards the end), the situation would improve compared to closing borders. However, when there is infection on the road, both entities can end up being net importer of infectious cases.

We have shown that it is possible to allow travel between two Group 2 entities without quarantine requirement and still maintain decreasing new cases in both entities over time. We cannot, however, make the same conclusion for a Group 2 entity to open its border to a Group 3 entity. To illustrate this, we assume Entity 2 now does not have contact tracing. Therefore, with $r = 1.1$, $\hat{R}_{Ent2} = 1.35$, and Entity 2 is in Group 3. We further assume no additional infection happen during travel. Even then, as shown in Figure 10, without strict border control, Entity 1 would experience another outbreak from imported cases. The number of patients in hospital at peak time would be over 100 thousand, which will overwhelm the health system.

We further examine if quarantine upon arrival is enough for Entity 1 (Group 2), to accept travelers from Entity 2 (Group 3), without overwhelming its own system. From Figure 11 we can see that a less strict stay home quarantine upon arrival policy may not be enough to contain the situation. Mandatory quarantine is needed for travelers from Group 3 entities. Even with mandatory quarantine, the weekly new cases would increase 10 folds at peak for Entity 2 comparing with its initial weekly new cases. An alternative to mandatory quarantine would be having screening at the border. That might be given by showing proofs of RNA/anti-body test result before embarking on flights or trains. While such screening would have a small failure rate, this would cap the potential number of imported cases at a constant level.
(a) Weekly New Cases for Entity 1

(b) Weekly Hospitalization for Entity 1

(c) Weekly New Cases for Entity 2

(d) Weekly Hospitalization for Entity 2

Figure 9: Interaction between two Group 2 Entities

(a) Weekly New Cases

(b) Weekly Hospitalization

Figure 10: Interaction between Group 2 and Group 3 Entities
4 Solving Optimal Border Control Problem for Group 2 entities using Linear Programming

We now consider a risk management problem for the policy maker in a Group 2 entity of interest. We are not going to consider the herd immunity approach in the re-opening and allowing imported risk. Therefore, the number of sick people is a small portion of the population. In that case we assume \( N_S/C \approx 1 \). (If 10% of the population is immune from the first wave, we can assume \( N_S/C \approx 0.9 \). However, as policy maker, a more conservative estimation is preferred, hence we will assume everyone in the entity are still susceptible). Under that assumption we can further assume the net traffic of susceptible people from traveling is 0. Hence, we are only focusing on the imported unidentified infectious people into the system.

Practically, opening border should only be considered after the entity’s internal control policy has been established for the re-opening phase. In other words, the entity has found its optimal re-opening policy with \( \hat{R} < 1 \) and plans to hold it until vaccine is found (and any further relaxation on internal control will result in \( \hat{R} > 1 \)).

Based on the practical assumptions above, we are now trying to determine the optimal level of incoming traffic \( x_j \) so that the entity’s internal control targets are met. These control targets can be, but not limited to, the number of new cases staying under certain level, number of patients hospitalized not exceeding certain capacity limit, and etc.

4.1 The Linear Programming Model

With the assumptions above, we can rewrite the dynamic equations (1) - (9) using the following linear dynamic system equations.
For simplicity, the equations above can be written as:

\[ N_{t+1} = AN_t + Bx_t \]  

and we have

\[ N_t = (A)^t N_0 + (A)^{t-1} B x_0 + (A)^{t-2} B x_1 + \cdots + B x_{t-1} \]  

For the objective function, it is common to use economic measures. For example,

\[ G^t = \sum_j w_j x_j^t \]  

Here \( G^t \) is the total economic gain of bringing in \( x_j \) traveler from source \( j \) at time epoch \( t \). \( w_j \) is the marginal economical value of one traveler from source \( j \).
Also consider the cost of treating one person in \( U_I \) to be \( c_I \) and person in hospital to be \( c_H \). where

\[
c = \begin{pmatrix}
0 \\
0 \\
c_I \\
c_I \\
c_H \\
c_H \\
0 \\
0
\end{pmatrix}
\]  

(17)

The objective function can be written as

\[
\min_{x_t} \sum_t (c'N_t - w'x_t)
\]  

(18)

The objective function above can be turned into a linear programming problem with respect to \( x_t \).

This is because

\[
c'N_t - w'x_t = c'(1 + A + A^2 + \cdots + A^t)N_0
+ [c'(1 + A + A^2 + \cdots + A^{t-1})B - w']x_0
+ [c'(1 + A + A^2 + \cdots + A^{t-2})B - w']x_1
+ \cdots + (c'B - w')x_{t-1} - w'x_t
\]  

(19)

Constraints can be

\[
N_{I_1}^t \leq L
\]

(20)

\[
N_{H_1}^t + N_{H_2}^t \leq M
\]

(21)

for all \( t \). The first constraint is to contain the new cases under a target level \( L \), and the second is to make sure the hospitalized patients are under the medical capacity \( M \). The major benefit is that this is an easily solvable linear problem - not a complex combinatorial problem.

4.2 Numerical Result for LP model

For this numerical study, we assume the entity of interest has \( r = 1.4 \) and good contact tracing (\( \theta = 0.8 \)). We consider only two sources of imported cases in this numerical study for illustration purposes. Both sources have weekly maximum travel demand of 1 million people. Origin 1 is of lower risk. On average 0.1% of the traveler from Origin 1 can enter the border undetected. Origin 2 is of higher risk, with 0.3% of the travelers may enter undetected. Assume the entity government wants to keep the weekly new cases under 5000 and the number of hospitalized patients under 1500 in any time epoch. Due to the lack of real cost information and GDP impact coefficient (i.e., \( c \) and \( w \)) in the objective function (19), we are simply going to maximize the total number of travelers allowed. Note this simplification provides the same solution (i.e., \( x_t \)) as the original problem when the cost of treating corona patients are smaller than the economic impact of shutting down the border.
As shown in Figure 12 (d), our travel capacity is limited by the hospital resources. We can see when the capacity is constrained, Origin 1 with lower imported risk is preferred over the higher risk Origin 2. Another interesting observation is that the optimal policy is “zig-zaging” as shown in Figure 12 (a). This means the optimal policy would actually be a series of open-close cycles until the hospital constraint is reached. Such open-close cycle will re-appear before the vaccine is available at time epoch $T$. Note that the increase in travel allowance at the end of the time period is due to vaccine being available at time epoch $T$.

The open-close policy is problematic in implementation and confusing for travelers who usually plan ahead. Therefore, we introduce a set of smoothing constraints:

$$x_t \leq x_{t+1}$$  \hspace{1cm} (22)

for all $t < T$. This smoothing constraint forces a gradual re-opening.

As shown in Figure 13 and 14, with the smooth constraints, the optimal policy is no longer zig-zaging. However, this policy is less optimal in terms of maximizing the total travel capacities.

Figure 15 shows that stricter quarantine on arrival policies (i.e., larger $\beta$) will allow more travel capacity into the entity.

Thus, there is a trade-off between general openness to travelers and quarantine restrictions for those actually traveling. Practical policies will have to take into account that travel demand is likely to be reduced by stricter quarantine requirements.
Figure 13: Solution from the LP model for Border Control with Smoothing Constraints

Figure 14: With Smooth Constraints vs No Smooth Constraints

Figure 15: Quarantine Policy on the Travel Capacity
5 Conclusion

A new approach is proposed in this paper to study border control policies against COVID-19, or any other epidemic, during the re-opening phase in an on-going pandemic. For this purpose, we develop several model extensions, e.g. regarding border control and contact tracing. We calibrate the model to the current COVID pandemics.

Our main findings are as follows. We formally proof and illustrate by simulation that even perfectly efficient contact tracing does not allow to go back to normal life. Assuming a base reproduction ($R_0$) rate of 2.8, the theoretically highest gain from contact tracing would be to achieve a realized reproduction rate of 1.27. Even much smaller gains might be very helpful in relaxing alternative containment measures. Economically, this is of crucial importance because large parts of the observed labor market slump can be traced back to these measures (e.g. Bauer and Weber, 2020). In line with the intuition, the effects of opening up the borders to other countries depend on the foreign policies. In a steady state situation, when the imported risk stays non-increasing, for countries with $\hat{R} < 1$ opening up to other countries with $\hat{R} < 1$, the virus stays in check. Opening the borders to countries with $\hat{R} > 1$ requires either border controls with strict testing at the border or mandatory quarantine on arrival. Countries which have completely eliminated the virus ($R_t \approx 0$ due to no domestic cases, but $\hat{R} > 1$) should impose mandatory quarantine to any country that have not eliminated domestic spreading of the virus. Finally, the model provides a general framework, where model parameters can also be estimated empirically.

While the present paper employs simulations based on parameter combinations from the existing literature to analyze future pandemic scenarios, future research can easily fit the model to realized corona data. Extending the model to have even more refined states is another possibility, e.g. if policy makers are interested in differentiating between “normal” hospitalization and treatment in intensive care units, combined with appropriate capacity restrictions.
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