Reproduction matrix for an epidemic and lockdowns in a city

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Abstract

We consider an epidemic spreading in a city which is divided geographically into different districts. We introduce the reproduction matrix $\mathcal{R} = \big(R(i,j)\big)$ between districts, where $R(i,j)$ is the mean number of individuals in district j infected by an individual from district i. We analyse policies of partial lockdowns of the city, that is of a set of districts, based on the study of matrix $\mathcal{R}$, where rows and columns corresponding to districts in lockdown are set to zero. This schema can also be applied to a country divided into regions or other appropriate units, provided the relevant information is available. We conclude by analyzing a matrix $\mathcal{R}$ which was constructed for the spread of COVID-19 in Santiago, Chile, with the aid of an agent-based simulator for generating surrogate district data.

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1 Introduction

We are interested in studying the spread of an epidemic in a city divided into districts. The city is assumed to be isolated. We require the population to have attained some stable equilibrium in terms of social behavior. We shall assume that the only policy decision that the city authority has at its disposal for confronting the epidemic is to impose a lockdown on a set of districts during some period of time. In practice, one would expect this set of districts to vary throughout the evolution of the epidemic.

In addition, we assume that during a lockdown, city inhabitants will modify their social behavior ideally in order to comply with the lockdown. Nevertheless, based on a number of partial lockdowns instituted by the government in Santiago, the capital of Chile, as well as the level of economic activity and daily commuting by public and private transport that typically prevails in this city, it is not certain that the population will achieve the necessary degree of compliance for a lockdown to be effective.

The motivation for this work is in reaction to the COVID-19 epidemic currently being suffered in Santiago, where the inhabitants throughout the city use masks and practise social distancing measures, and where schools, universities and other education facilities were closed and the teaching of classes moved on line where possible near the commencement of the outbreak. On the other hand, the Chilean authorities have decreed a series of partial dynamic lockdowns of various districts in Santiago. Our intent here is to try and provide a more theoretical basis for these kinds of decisions.

In the next section, we introduce the reproduction matrix $\mathcal{R}$ and explain the key role of its Perron-Frobenius eigenvalue for describing the behavior of $\mathcal{R}$ as it is iteratively applied to the evolution equation. This eigenvalue essentially constitutes the effective reproduction number which determines if the epidemic explodes, persists or becomes extinct.

In Section 3, we describe the spread of the epidemic in terms of the evolution of powers of the reproduction matrix. In order to do this, we make two simplifications of the epidemic evolution:

1. there exists some period of time such that once an individual is infected at, say, time t, he/she will only be contagious during the next period of time at $t+1$; and

2. the size of the population of susceptible individuals is on the order of the original population size.

The last assumption is realistic for Santiago because it is currently in the initial exponential-growth phase of the epidemic. The first assumption is less realistic as the period of time corresponds to the mean generational time-to-infection, which has been estimated to be around 4 or 5 days for COVID-19 [5].

In Section 4, we describe how lockdowns or sanitary cordons modify the structure of the matrix and the Perron-Frobenius eigenvalue.

The data necessary for estimating the matrix $\mathcal{R}$ is similar to the kind of data collected during contact tracing. However, contact tracing is labor intensive and more automated ways of collecting this kind of data, such as via smart phone apps and Bluetooth-enabled devices, come with a host of issues relating to privacy and use/misuse which many governments are currently wrestling with. At present, such data is generally not available, so we have elected to use a strategy whereby we obtain surrogate data by means of simulation in order to illustrate how $\mathcal{R}$ can be used to decide which districts to include in a lockdown. Section 5 describes the agent-based simulation model used to generate the surrogate data and obtain an estimation of the reproduction matrix $\mathcal{R}$ for the city of Santiago. In this model, agents represent people who can become infected by interacting with infected agents. They are placed in a grid so as to reproduce the real limits and densities of the city (and its districts) and to emulate daily commuter traffic-flow patterns based on real public transportation data. We explain how this model can be used to describe the propagation of the infection through the city and between the districts, and how the matrix $\mathcal{R}$ is estimated from a set of simulation replicates. We note that density, transportation and the spatial configuration of districts are the main characteristics determining the variability in the values of elements of the matrix $\mathcal{R}$.

Finally, the conclusions presented in Section 6 focus on the lockdowns that Santiago currently faces. In particular, by computing the spectral radius of the matrix $\mathcal{R}$, we can estimate the reproduction number for different scenarios: (a) When there is no district in lockdown; (b) when there is only a single district in lockdown (computed for each district under consideration), and (c) when there is a set of districts in lockdown.

2   The reproduction matrix

Let $I_m = \{1, 2, \ldots, m\}$ be the set of districts of a city, the population size of the city is denoted by N while N_i denotes the population of district i.

Define the matrix $\mathcal{R} = (R(i,j) : i, j = 1, \ldots, m)$ as follows: $R(i,j)$ is the mean number of individuals residing in district j that are infected by an individual from district i while the individual is contagious.

Hence $R_i = \sum_{j=1}^{m} R(i,j)$ is the overall mean number of people infected by an individual from district i, irrespective of the district they reside in. If R_i is the same for all districts, that is, $R_i = R$ for $i = 1, 2, \ldots, m$, then R is equivalent to the effective reproduction number R.

We note here that in order to have $R(i,j) > 0$ there must be contact between the populations of i and j, in which case one is highly likely to have $R(j,i) > 0$. There is no loss of generality in assuming the matrix $\mathcal{R} = (R(i,j) : i, j = 1, \ldots, m)$ is irreducible, which means that for any pair of districts i, j, there exists a path of infections (most likely passing through a number of districts) from an individual in i to some individual in j, that is $\mathcal{R}^t(i,j) > 0$ for some power $t > 0$. When there is no irreducibility, the components can be studied separately, but irreducibility is a very weak condition to assume in a city.

From the Perron-Frobenius theory [6, Chapter 1], there exists an eigenvalue $\rho(\mathcal{R}) > 0$ that satisfies the following conditions: It has unique (up to a constant multiple), strictly positive left and right eigenvectors $\ell = (\ell(i) : i \in I_m)$ and $h = (h(i) : i \in I_m)$ satisfying

$$\ell'\mathcal{R} = \rho(\mathcal{R})\ell' \text{ and } \mathcal{R}h = \rho(\mathcal{R})h.$$

Here the vectors are column vectors and $'$ signifies the transpose so that ℓ' is a row vector. Note that the vectors ℓ and h can be normalized such that $\sum_{i=1}^{m} \ell(i)h(i) = 1$. With this normalization, the matrix with elements

$$\rho^{-1}R(i,j)h(j)/h(i), \quad i,j \in I_m,$$

is stochastic with stationary distribution $(\ell(i)h(i) : i \in I_m)$. In the following discussion, we shall assume that the eigenvectors have been normalized in this way.

$\rho(\mathcal{R})$ is simple and it is the spectral radius of $\mathcal{R}$, so it satisfies

$$\rho(\mathcal{R}) = \lim_{t \to \infty} \|R^t\|^{\frac{1}{t}},$$

for any norm $\|\cdot\|$. It gives the geometric rate of the asymptotic behavior of iterative multiplication by $\mathcal{R}$, that is when it is successively multiplied by itself (powered up). One can specify the precise limit behavior of iterating the matrix $\mathcal{R}$:

$$\mathcal{R}^t = \rho(\mathcal{R})^t h\ell' + o\big((\rho(\mathcal{R}))^t\big),$$

where $o\big((\rho(\mathcal{R}))^t\big)$ is a matrix satisfying $\rho(\mathcal{R})^t o\big((\rho(\mathcal{R}))^t\big) \to 0$ as $t \to \infty$.

The matrix $A = h\ell'$, where $A(i,j) = h(i)\ell(j)$, is strictly positive for $i,j = 1, \ldots, m$. Therefore, as t becomes large, $\mathcal{R}^t$ has the following limit behavior:

$$\lim_{t \to \infty} R^t(i,j) = \begin{cases} \infty, & \text{if } \rho(\mathcal{R}) > 1, \\ h(i)\ell(j), & \text{if } \rho(\mathcal{R}) = 1, \\ 0 & \text{if } \rho(\mathcal{R}) < 1. \end{cases}$$

In particular one has

$$\lim_{t \to \infty} \mathcal{R}^t = 0 \;\Leftrightarrow\; \rho(\mathcal{R}) < 1. \tag{1}$$

Remark 1. *If R_i is the same for all districts, $R_i = R$ for $i = 1, 2, \ldots, m$, then $\rho(\mathcal{R}) = R$ is the effective reproduction number R. In fact, if $R = 1$, the matrix $\mathcal{R}$ must be stochastic and then $\rho(\mathcal{R}) = 1$ and the other cases follow easily (it suffices to argue that an iteration of a stochastic matrix is stochastic). Hence, our study extends the notion of an effective reproduction number to the introduction of an effective reproduction matrix $\mathcal{R}$.*

Remark 2. *Note that one can have $\rho(\mathcal{R}) < 1$ even if there exist some districts with $R_i > 1$ because the set of districts with $R_i < 1$ may compensate enough to obtain a spectral radius strictly smaller than one, ensuring the extinction of the epidemic. See Table 3 for an example of this.*

We note that the assumption of irreducibility implies that if all but one of the R_i's are constant, that is, for some i_0, $R_i = r$ for $i \neq i_0$, then one can check that $\rho(\mathcal{R})$ is less than, equal to or greater than r according as R_{i_0} is less than, equal to or greater than r respectively.

3   Evolution of total infected individuals

The matrix $\mathcal{R}$ captures the complex interaction between the different districts and the resulting effect on the spread of the disease. Due to this, it will be our primary tool for studying the evolution of the epidemic. We make the strong assumption that any infected individual will infect other individuals after some unitary period of time. That is, if individual i becomes infected at time t and i infects individual j, then j becomes infected exactly at time $t+1$. The unitary period of time could represent a fixed number of days, typically the mean time between a primary and secondary infection. For instance, this time is reported to be around 4 or 5 days for COVID-19 [5].

Let $J_i(s)$ be the total number of infected individuals at time s in district i and let $\mathcal{J}(s) = \big(J_i(s) : i \in I_m\big)$ be the vector of infected people in the city at time s. For stating the evolution equation, we assume we are

in the initial growth phase of the epidemic so that the number of susceptible individuals in district i will be on the order of N_i. Then, the evolution equation is

$$\mathcal{J}'(s+1) = \mathcal{J}'(s)\mathcal{R}, \text{ that is, } J_j(s+1) = \sum_{i=1}^{m} J_i(s)R(i,j), \quad s = 0, 1, \ldots.$$

Iterating the equation yields

$$\mathcal{J}'(s+t) = \mathcal{J}'(s)\mathcal{R}^t, \quad t = 1, 2, \ldots \text{ and } s = 0, 1, 2, \ldots. \tag{2}$$

Now, from (1) and (2), one has $\lim_{t \to \infty} \mathcal{J}(t) = 0$ if and only if the condition $\rho(\mathcal{R}) < 1$ holds. Consequently, the epidemic dies out if $\rho(\mathcal{R}) < 1$. In contrast, the infected population explodes geometrically when $\rho(\mathcal{R}) > 1$ while if $\rho(\mathcal{R}) = 1$, the epidemic continues to spread steadily at a constant rate. In the latter two cases, the viral epidemic eventually infects the entire population since the population size is finite.

Remark 3. *Let d_i be the probability that an infected individual from district i dies from the illness, so that with probability $1 - d_i$ an infected individual recovers. Further, since the population is finite, the epidemic is bound to die out. The spectral radius $\rho(\mathcal{R})$ merely determines the manner in which it spreads before the extinction time T has lapsed.*

- *For $\rho(\mathcal{R}) > 1$, irreducibility implies that the whole population of the city becomes infected geometrically fast (in time proportional to the logarithm of the population size N). Consequently, the number of people that die in district i is expected to be $d_i N_i$ and the total number of people that are expected to die during the course of the epidemic is $\sum_{i=1}^{m} d_i N_i$.*

- *If $\rho(\mathcal{R}) = 1$, the epidemic spreads at a constant rate, infecting the entire population in a time T proportional to the population size N. However, the total number of deaths expected to occur by the time the epidemic has run its course is once again $\sum_{i=1}^{m} d_i N_i$, the same as when $\rho(\mathcal{R}) > 1$.*

- *Finally, when $\rho(\mathcal{R}) < 1$ the epidemic becomes extinct geometrically fast. The total number of infected people in district i is $\sum_{s=0}^{T} J_i(s)$, and the expected number of deaths for the district is $d(i) \sum_{s=0}^{T} \mathcal{J}_i(s)$.*

  Thus, the total number of infected cases in the population during the epidemic is $\sum_{i=1}^{m} \sum_{s=0}^{T} J_i(s)$ and the total number of deaths is expected to be $\sum_{i=1}^{m} d(i) \sum_{s=0}^{T} \mathcal{J}_i(s)$.

4 Lockdown

When the authorities declare a lockdown for some districts, transmission of the infection between those districts and the districts not in lockdown theoretically halts. Community transmission continues to take place within the districts under lockdown, for instance, transmission among people sharing the same living space during the lockdown increases, but theoretically it should cease between people in the same district who do not live together. Infections in these locked-down districts is not due to the epidemic spreading within the district but caused by healthy and infected cohabitants being confined to shared (but disjoint) living spaces, so we will consider this separately.

Let $L \subset I_m$ be the set of districts that are put into lockdown. Then, the new matrix of the mean number of infections per contagious individual $\mathcal{R}_L = \big(R_L(i,j) : i, j \in I_m\big)$ becomes

$$R_L(i,j) = \begin{cases} R(i,j) & \text{if } i, j \notin L, \\ 0 & \text{if } i \in L \text{ or } j \in L. \end{cases}$$

This is no more than the truncation of $\mathcal{R}$ to the set of districts L^c, the complement of L. Since there are no interactions between the districts in L and L^c, the infection can only spread among districts in L^c which

are not subject to lockdown (as viral spread is essentially restricted to the shared living spaces of districts in L). So it is convenient to restrict the study of the evolution of the population to districts in L^c.

Note that the restriction of $\mathcal{R}$ and $\mathcal{R}_L$ to the states in L^c is the same. We set $\underline{\mathcal{R}} = \big(R(i,j) : i,j \in L^c\big)$ to be the matrix of mean infections for the districts that are not in lockdown. Let $\underline{\mathcal{J}}(s) = \big(\underline{J}_i(s) : i \in L^c\big)$ be the evolution of the infected individuals in districts in L^c. Note that the truncation is imposed from the moment the lockdown of L is decreed and so the initial point $\underline{J}_i(0)$ is the number of infected people in district $i \notin L$ when the lockdown starts. The evolution of the infected population vector during the lockdown is given by

$$\underline{\mathcal{J}}'(s+t) = \underline{\mathcal{J}}'(s)\underline{\mathcal{R}}^t.$$

We note that the spectrum of $\underline{\mathcal{R}}$ is the same as that for $\mathcal{R}_L$ and so the common spectral radius of $\underline{\mathcal{R}}$ and $\mathcal{R}_L$ will be denoted by $\rho(\mathcal{R}_L)$.

It is possible that the lockdown framework splits $\underline{\mathcal{R}}$ into a number of irreducible components because the infection from district i to i', both in L^c might only be due to agents in districts in L. When $\underline{\mathcal{R}}$ is irreducible, the analysis carried out on $\mathcal{R}$ remains valid on $\underline{\mathcal{R}}$. If not one must analyse the distinct irreducible components and the spectral radius $\rho(\mathcal{R}_L)$ of $\underline{\mathcal{R}}$ is the maximum of the spectral radii of the restrictions of $\underline{\mathcal{R}}$ to these components.

The choice of the set of districts L needs to ensure that the largest spectral radius $\rho(\mathcal{R}_L)$ is strictly smaller than 1 in order to bring the epidemic under control. Note that the minimum value of $\rho(\mathcal{R}_L) = 0$ is only obtained at $L = I_m$ when the whole city is in lockdown. However, choosing L to be the set of districts giving the biggest $\rho(\mathcal{R}_L)$ strictly smaller than 1 may not be the best strategy because $\rho(\mathcal{R}_L)$ may be too close to 1 to end the epidemic due to random fluctuations in incidence as well as uncertainty in the data used to compute $\rho(\mathcal{R}_L)$. The key point is that in reality, there are real-world constraints that need to be considered (such as the mean time that people are in lockdown) and this leads to a multi-objective optimization problem.

Remark 4. *Since we are choosing the districts L that are to be locked down so as to obtain a spectral radius of $\rho(\mathcal{R}_L) < 1$, it is the asymptotic behavior of the matrix $\mathcal{R}_L$ that will govern the evolution of the system during the period the lockdown is in force. Thus, the total number of infected people will decrease geometrically. In district $j \notin L$, the total number of infections that result will be $\sum_s \underline{J}_j(s)$ and so the final number of infections in the districts not under lockdown will be $\sum_{j \notin L} \sum_s \underline{J}_j(s)$. To obtain the total number of infections in the population from the time of imposing the lockdown it is necessary to add the quantity $\sum_{i \in L} \gamma_i M_i$, where M_i is the total number of healthy people cohabiting with infected individuals in district i during the lockdown and γ_i is the probability that a susceptible individual cohabiting with an infected individual becomes infected during the lockdown. The number of deaths expected to occur during the imposition of the total lockdown, provided the lockdown is in force long enough to bring the epidemic to extinction (or nearly to extinction) is:*

$$\sum_{j \notin L} d_j \sum_s \underline{J}_j(s) + \sum_{j \in L} d_j \gamma_j M_j.$$

Remark 5. *The policy of 'cordon sanitaire' or 'sanitary cordon' consists of disconnecting two geographic regions by preventing movement between them. In a city, this means selecting two groups of districts, both of which are internally connected so that individuals may move freely from district to district within each group, while the connections bridging them are suppressed. This is a weaker measure than the lockdown discussed above. If L and L^c are the two groups, the new matrix R^{cs} encapsulating the cordon sanitaire policy must preserve the values $R(i,j)$ for districts i and j inside the same group, but set $\mathcal{R}^{cs}(i,j) = 0$ when districts i and j belong to L and L^c or to L^c and L respectively. Thus, $R^{cs} = \big(\mathcal{R}^{cs}(i,j) : i,j \in I_m\big)$, where*

$$\mathcal{R}^{cs}(i,j) = \begin{cases} R(i,j), \textit{if } i,j \in L \textit{ or } i,j \in L^c, \\ 0, \textit{otherwise.} \end{cases}$$

The spectral radius $\rho(R^{cs})$ of this block diagonal matrix, which is given by the maximum of the spectral radii of the blocks, will be strictly smaller than $\rho(\mathcal{R})$ in general and in order for the cordon sanitaire policy to be effective, it must be strictly smaller than 1.

5 The simulator

To evaluate the effectiveness and applicability of the simple model proposed here, we computed a reproduction matrix $R(i,j)$ for the city of Santiago in Chile, at about one month into the outbreak by using the data obtained from a simulation of the epidemic's evolution in the city. As data detailing the chain of infection of individuals, together with their districts of residence was not available, it was necessary to obtain surrogate data to use in its stead.

We have developed an agent-based simulator which is capable of generating the chain of infection of each individual for a city. Within this simulator, the city of Santiago was represented considering the 40 most important districts of the greater Santiago area (part of the metropolitan region) with their corresponding population densities [4] and commuting flows [1]. A brief description of the simulator follows.

The simulator consists of a collection of agents representing a population of individuals that interact with each other following a set of rules:

- At each simulation step (representing a day), each agent has one of the following states: Susceptible, Latent (incubating the virus), Asymptomatic and contagious, Symptomatic and contagious, Hospitalized in a normal bed, Hospitalized in an ICU bed, Hospitalized in a normal bed but waiting for a ICU bed (there is a finite number of them), Recovered and Deceased.

- The area (or playground) inhabited by the agents and where they interact is modeled as a grid of cells onto which a map of Santiago is projected, together with the boundaries demarcating the districts.

- The position and age of each agent is assigned according to population densities and age distributions reported by district in census records [4].

- At each simulation step (representing a day), each agent moves from its starting position (home) to another cell in a designated destination district (representing work/school) according to a commuting matrix[1] indicating the flows between districts [1]. Then, each agent returns to their home cell where they have the opportunity to interact with neighbors in their vicinity.

- Each agent interacts with other nearby agents according to an interaction radius. A susceptible agent is infected by a contagious agent in their vicinity according to some fixed probability.

Agent states evolve day by day in response to interaction with other agents throughout the simulation timeline (where time is represented as a series of simulation steps). The agents' level of daily interaction is modeled by adjusting the size of their neighborhoods, their travel distance, and the probability of contact with neighboring agents. Recording the state transitions made by agents over the simulation time allows the evolution of the epidemic to be tracked and analyzed by means of different daily indicators such as incidence, prevalence, mortality, ICU occupancy.

In addition, the simulator implements a set of template rules that enable the behavior of agents to be changed at any step of the simulation according to various selection criteria such as the interaction and infection probabilities, mobility ranges (governing travel distances) and neighborhood sizes (which determine how close agents must be in order to interact). In this way, mitigation policies imposed by the health authority such as curfews, social isolation, total quarantine, school closures and isolation of the elderly or very young can be emulated directly as part of the simulation scenario.

This simulator integrates concepts from the simulation models used by Ferguson et al. [3] and Donsimoni et al. [2]. From the latter, we borrowed the basic idea of each agent interacting with different groups of individuals (home, work, school). The main difference is we restrict agents to move within a target community with a specified probability and randomly otherwise. Agents in Ferguson's model always interact within the same community. Similar to [3], we have modeled the evolution of the illness within an agent as a Markov chain, defining the series of states and state transitions that each agent must make according to specified probabilities before eventually either recovering or dying.

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[1]The commuting matrix was obtained from the public transportation operator Transantiago and is current as at 10 September, 2019.

The calibration of the scenario we simulated of Santiago was done in a two-fold procedure. On one hand, parameters were selected that allow the reproduction of epidemic and demographic characteristics such as the basic reproduction number R_0, the outbreak generation time, and the density and age distribution of the population, while on the other hand, interaction and infection rates were chosen in order to follow the progression of new symptomatic cases reported daily by the Chilean health authorities.

With the simulation appropriately fitted to the outbreak under study, the matrix $\mathcal{R}$ can be estimated by simulating the desired scenario multiple times using different random seeds to initialize the simulator in order to mimic the stochastic process governing the evolution of the epidemic. Note that matrix $\mathcal{R}$ depends on the number of susceptibles that each agent encounters during its contagious period, which varies during the course of the epidemic (at the beginning, this should generally be greater than it will be near the end).

Therefore, to obtain a matrix that describes the effective $\mathcal{R}$ at a given time (analogous to the well-known effective reproduction number R), we should consider only computing the number of infections transmitted by agents infected within a small interval prior to that time. Thus, $\mathcal{R}$ is estimated for a time t by considering the set of agents that contract the disease in a small window prior to and including t and calculating the mean number of infections they caused in each district during a single simulation execution (or simulation replicate). The set of matrices obtained from a number of simulation replicates is then averaged (elementwise) to provide an estimate of the reproduction matrix $\mathcal{R}$ for the city.

6   Application to Santiago

Simulations of a 1/9-scaled version of 40 districts within the Greater Santiago area were carried out using the simulator described in the preceding section. Parameters were calibrated to enable the simulator to mimic the overall trend in Chile during the first 30 days of the evolution of the epidemic (as reported daily by the Chilean health authority). The simulation was replicated 50 times and each such evolution of the epidemic was analyzed independently (in the time interval from day 20 through to day 30) in order to compute its reproduction matrix as at day 30. As described in the previous section, the 50 matrices were then averaged elementwise to obtain an estimate of the reproduction matrix $\mathcal{R}$ for Greater Santiago. Being 40×40, the matrix is too large to include here, but Table 1 displays summary statistics for each of its 40 rows, together with the row sums which yield the local reproduction number R_i for each district. The spectral radius of this matrix is 1.62.

Having obtained a spectral radius greater than one, we explored what happens if a single district is placed under lockdown. We computed the spectral radius of the matrix resulting from placing each of the 40 districts singly under lockdown. As described above, this is achieved by removing the row and column corresponding to the district in lockdown from $\mathcal{R}$. The spectral radii that result are displayed in the last column of Table 1. The districts that produce the greatest reduction in the spectral radius when in lockdown are Puente Alto and Pirque (near 1.56), followed by La Florida, La Pintana, Santiago, La Cisterna and El Bosque (all with spectral radii less than 1.60).

Next, we examined the accumulative affect of applying lockdowns successively. As in the previous paragraph, we examined the effect of putting a single district in lockdown and kept the one that provided the greatest reduction in the spectral radius. This was Puente Alto. Then, we considered all combinations of putting Puente Alto and a second district under lockdown together. We kept the combination that produced the smallest spectral radius, which was Puente Alto and Santiago. We then added a third district to the lockdown and continued adding districts until we obtained a spectral radius smaller than 1. Table 2 summarizes the results of this procedure. In the end, it was necessary to put eight districts under lockdown: Puente Alto, Santiago, El Bosque, Pirque, Maipú, Cerro Navia, La Cisterna and Ñuñoa. The spectral radius resulting from locking down these eight districts is 0.984. The matrix $\mathcal{R}$ corresponding to the districts that are not in lockdown is 32×32. Its row sums are shown in Table 3, where it can be seen that some are greater than 1 even though the spectral radius is less than 1 (see Remark 2).

Table 1: Summary statistics for rows of the reproduction matrix estimated for Santiago. The 'lockdown' column shows the spectral radius that results when the corresponding district is placed singly under lockdown.

District	Mean	Std	Quantiles					Row	Lock-
			Min	25%	50%	75%	Max	sum	down
CERRILLOS	0.031	0.064	0.000	0.004	0.012	0.020	0.313	0.451	1.615
CERRO NAVIA	0.042	0.103	0.000	0.002	0.009	0.021	0.525	1.525	1.609
COLINA	0.014	0.037	0.000	0.000	0.000	0.007	0.198	0.387	1.617
CONCHALÍ	0.036	0.087	0.000	0.001	0.010	0.019	0.486	1.095	1.613
EL BOSQUE	0.043	0.110	0.000	0.000	0.004	0.022	0.576	1.878	1.599
ESTACIÓN CENTRAL	0.039	0.088	0.000	0.005	0.013	0.036	0.433	1.291	1.609
HUECHURABA	0.029	0.068	0.000	0.001	0.006	0.021	0.349	0.739	1.616
INDEPENDENCIA	0.042	0.104	0.000	0.003	0.013	0.035	0.565	1.351	1.607
LA CISTERNA	0.045	0.094	0.000	0.001	0.006	0.029	0.387	1.628	1.598
LA FLORIDA	0.031	0.121	0.000	0.001	0.003	0.011	0.757	1.989	1.595
LA GRANJA	0.040	0.088	0.000	0.004	0.015	0.027	0.493	1.195	1.604
LA PINTANA	0.035	0.085	0.000	0.001	0.003	0.025	0.485	1.445	1.595
LA REINA	0.025	0.055	0.000	0.001	0.004	0.010	0.236	0.442	1.616
LAMPA	0.016	0.039	0.000	0.000	0.000	0.016	0.204	0.441	1.617
LAS CONDES	0.024	0.074	0.000	0.001	0.003	0.010	0.458	1.289	1.616
LO BARNECHEA	0.016	0.056	0.000	0.000	0.000	0.004	0.313	0.317	1.617
LO ESPEJO	0.043	0.077	0.000	0.005	0.016	0.040	0.352	1.301	1.604
LO PRADO	0.041	0.100	0.000	0.002	0.005	0.010	0.510	1.075	1.612
MACUL	0.029	0.064	0.000	0.002	0.006	0.014	0.324	0.766	1.614
MAIPÚ	0.035	0.143	0.000	0.001	0.005	0.011	0.905	2.798	1.610
PADRE HURTADO	0.023	0.063	0.000	0.000	0.001	0.009	0.314	0.424	1.616
PEDRO AGUIRRE CERDA	0.038	0.085	0.000	0.006	0.014	0.030	0.408	0.977	1.610
PEÑAFLOR	0.024	0.092	0.000	0.000	0.000	0.002	0.424	0.564	1.616
PEÑALOLÉN	0.031	0.088	0.000	0.003	0.005	0.013	0.518	1.718	1.612
PIRQUE	0.065	0.247	0.000	0.000	0.001	0.006	1.300	1.465	1.568
PROVIDENCIA	0.034	0.073	0.000	0.002	0.013	0.023	0.377	1.361	1.612
PUDAHUEL	0.036	0.099	0.000	0.002	0.006	0.015	0.576	1.462	1.611
PUENTE ALTO	0.041	0.220	0.000	0.000	0.000	0.005	1.393	3.361	1.559
QUILICURA	0.031	0.115	0.000	0.001	0.003	0.013	0.727	1.504	1.614
QUINTA NORMAL	0.041	0.093	0.000	0.002	0.013	0.033	0.528	1.140	1.608
RECOLETA	0.035	0.087	0.000	0.002	0.009	0.019	0.496	1.421	1.613
RENCA	0.038	0.095	0.000	0.003	0.012	0.031	0.474	1.330	1.609
SAN BERNARDO	0.034	0.096	0.000	0.001	0.005	0.019	0.559	1.824	1.602
SAN JOAQUÍN	0.038	0.087	0.000	0.005	0.015	0.035	0.510	0.852	1.609
SAN JOSÉ DE MAIPO	0.034	0.095	0.000	0.000	0.000	0.006	0.413	0.152	1.616
SAN MIGUEL	0.040	0.079	0.000	0.007	0.021	0.037	0.408	1.109	1.607
SAN RAMÓN	0.040	0.085	0.000	0.001	0.004	0.038	0.438	1.007	1.605
SANTIAGO	0.046	0.135	0.000	0.005	0.017	0.041	0.867	8.055	1.596
VITACURA	0.026	0.047	0.000	0.002	0.007	0.021	0.210	0.423	1.616
ÑUÑOA	0.036	0.093	0.000	0.003	0.008	0.021	0.528	1.949	1.609

Table 2: The spectral radius as districts are sequentially added to a lockdown. Each value in the 'Spectral radius' column corresponds to a lockdown including all districts on or above the line where it appears in the table. Spectral radii for only the first 9 lockdowns have been shown in the table.

District	Spectral radius after lockdown
PUENTE ALTO	1.559
SANTIAGO	1.354
EL BOSQUE	1.310
PIRQUE	1.161
MAIPÚ	1.111
CERRO NAVIA	1.076
LA CISTERNA	1.029
ÑUÑOA	0.984
RECOLETA	0.946
⋮	⋮

Table 3: The row sums (or local reproduction numbers R_i) for districts after a lockdown is imposed on eight districts.

District	R_i	District	R_i
CERRILLOS	0.611	PADRE HURTADO	0.549
COLINA	0.549	PEDRO AGUIRRE CERDA	0.963
CONCHALÍ	1.171	PEÑAFLOR	0.535
ESTACIÓN CENTRAL	0.892	PEÑALOLÉN	0.863
HUECHURABA	0.998	PROVIDENCIA	0.909
INDEPENDENCIA	1.005	PUDAHUEL	1.007
LA FLORIDA	1.027	QUILICURA	1.118
LA GRANJA	1.144	QUINTA NORMAL	0.899
LA PINTANA	0.932	RECOLETA	1.126
LA REINA	0.695	RENCA	0.934
LAMPA	0.604	SAN BERNARDO	0.879
LAS CONDES	0.810	SAN JOAQUÍN	0.863
LO BARNECHEA	0.618	SAN JOSÉ DE MAIPO	0.825
LO ESPEJO	0.988	SAN MIGUEL	0.972
LO PRADO	1.103	SAN RAMÓN	1.048
MACUL	0.808	VITACURA	0.731

Acknowledgments

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