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<sup>2</sup> **Supplementary Information for**  
<sup>3</sup> **Interacting Policies in Containing a Disease**

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<sup>7</sup> **This PDF file includes:**

<sup>8</sup>      Supplementary text

<sup>9</sup>      SI References

10 **Supporting Information Text**

11 **1. Theorem Details and Proofs**

12 **A. Model and Definitions.**

13 **People and Interactions.** There are  $n > 1$  nodes (individuals) in an unweighted, and possibly directed,  
14 network.

15 We study the course of a disease through the network. Time is discrete, with periods indexed by  
16  $t \in \mathbb{N}$ . An initial infected node, indexed by  $i_0 \in V$ , is the only node infected at time 0. We call this  
17 node the *seed*.

18 We track the network via neighborhoods that expand outwards via (directed) paths from  $i_0$ . Let  
19  $N_k$  be all the nodes who are at (directed) distance  $k$  from node  $i_0$ . Let  $n_k$  denote the cardinality of  
20  $N_k$ .

21 For any node in  $j \in N_{k'}$ , for  $k' < k$ , let  $n^j$  be the number of its direct descendants and  $n_k^j$  be  
22 the number of its (possibly indirect) descendants in  $N_k$  that are reached by never passing beyond  
23 distance  $k$  from  $i_0$ .

24 Unweighted network models are admitted here. Additionally, the results below extend to any  
25 weighted model in which weights are bounded above and below (e.g., probabilities of interaction).  
26 Note also, that the network can be directed or undirected.

27 The infection process proceeds as follows. In every time period  $t \in \{1, 2, \dots\}$ , an infected node  $i$   
28 transmits the disease to each of  $i$ 's neighbors independently with probability  $p$ . A newly infected  
29 node is infectious for  $\theta \geq 1$  periods after which the node recovers and is never again infectious. The  
30 model can easily be extended to accommodate renewed susceptibility.

31 There may be a *delay* in the ability to detect the disease. The number of periods of delay is given  
32 by  $\tau$  with  $0 \leq \tau \leq \theta$ . Delay is a general term that can capture many things. For example, it can  
33 correspond to (a) asymptomatic infectiousness, (b) a delay in accessing health care given the onset  
34 of an infectious period, (c) any delay in the administration of testing, and so on.

35 In the first period of an infected node's infectious period – after delay ( $\tau$ ) – there is a probability  
36  $\alpha$  that the policymaker detects it as being infected. So, potential detection happens exactly once  
37 during the first period in which the node can be detected. Detection is independently and identically  
38 distributed. Our results are easily extended to have a random period for detection after the delay.

39 Finally, the policymaker may face some error in their knowledge of the network. This can come  
40 from their limited enforcement capacity, random noise in data collected to estimate interaction  
41 networks, or from network model misspecification. If there is error, we will track a share  $\epsilon$  of nodes  
42 that are within a  $k$ -neighborhood of the seed but are estimated by the policymaker to be outside  
43 the  $k$ -neighborhood.

44 **Regional Quarantine Policy.** Let a *regional policy of distance  $k$  and threshold  $x$*  be such that once  
45 there are at least  $x$  infections (other than the seed) detected within distance  $k$  from the initial seed,  
46 then all nodes within distance  $k + 1$  of  $i_0$  are quarantined for at least  $\theta$  periods. A quarantine implies  
47 all connections between nodes are severed to avoid any further transmission, the infection lasts its  
48 duration  $\theta$  and dies out.

49 Implicit in this definition is that a quarantine is not instantaneous, but that infected people could  
50 have infected their neighbors before being shut down, which is why the nodes at distance  $k + 1$  are  
51 quarantined. All the results below extend if we assume that it is instantaneous, but with quarantines  
52 moved back one step and path lengths in definitions correspondingly adjusted.

53 We have assumed the policymaker knows the “seed,” for simplicity - but this knowledge may  
54 take some time in reality. This provides an advantage to the policymaker, but we see substantial  
55 containment failures despite this advantage.

56 **Growth Balance.** In order to conduct asymptotic analysis, a useful device to study the probabilities  
57 of events in question in large networks, we study a sequence of networks  $G(n)$  with  $n \rightarrow \infty$  and an  
58 associated sequence of parameters  $(\alpha, p, \tau, \theta, k) = (\alpha(n), p(n), \tau(n), \theta(n), k(n))$ .

59 Consider a network and a distance  $k$  from the initially infected node  $i_0$ . A *path of potential*  
60 *infection to  $k + 2$*  is a sequence of nodes  $i_0, i_1, \dots, i_\ell$  with  $i_\ell \in N_{k+1}$ ,  $i_{j+1}$  being a direct descendant of  
61  $i_j$  for each  $j \in \{0, \dots, \ell - 1\}$ , and for which  $i_\ell$  has a descendant in  $N_{k+2}$ .

62 Consider a sequence of networks and  $k(n)$ s. We say that there are *bounded paths of potential*  
63 *infection* from  $i_0(n)$  to  $k(n) + 2$  if there exists some finite  $M$  and for each  $n$  there is a path of potential infection to  $k(n) + 2$ ,  $i_0(n), i_1, \dots, i_\ell$  of length less than  $M$ , with  $n^{i_j} < M$  for every  $j \in \{0, \dots, \ell - 2\}$ .

64 We say that a sequence of networks is *growth-balanced* relative to some  $k(n)$  (and sequence of  
65  $i_0(n)$ ) if there are no bounded paths of potential infection to  $k(n) + 2$ . This is equivalent to stating  
66 that there exists a sequence  $m(n) \rightarrow \infty$  such that each path of potential infection from  $i_0(n)$  to  
67  $k(n) + 2$  is either of length at least  $m(n)$  or has some node with degree at least  $m(n)$ .

68 If  $k(n)$  grows without bound, then the condition is satisfied trivially, so the bounded case is the  
69 one of interest; it is also the one of practical interest given the small diameter of real-world networks.

70 Also note that the condition is stated with respect to a sequence of seed nodes. The results extend  
71 directly if one wants things to hold with respect to sets of seeds by requiring that the conditions  
72 hold for sequences of sets of seeds.

73 Growth balance is essentially a condition that requires a minimum bound of expansion along all  
74 potential paths of infection to escape a regional quarantine from some initial infection. The intuition  
75 behind the condition is clear: to ensure detection of an outbreak before it reaches a distance  $k + 1$   
76 from the seed, many of the nodes within distance  $k$  must be exposed to the disease by the time it  
77 reaches distance  $k$ . What is ruled out is a relatively short path that gets directly to that distance  
78 without having many nodes be exposed along that path.\*

79 Figure S1 presents an illustration of a network that is not growth-balanced.

## 80 **B. Results.**

81 **A Benchmark: No Delay in Detection; Perfect Information and Enforcement.** We begin with a benchmark  
82 case in which there is no delay in detection ( $\tau(n) = 0$ ) and the policymaker can completely enforce  
83 a quarantine at some distance  $k(n) + 1$ .†

84 We allow the size of the quarantine region  $k$  to depend on  $n$  in any way, as the theorem still  
85 applies. We work with an arbitrary but fixed infection threshold  $x$ . What is important is that  $x$  not  
86 grow too rapidly, as otherwise the likelihood of observing  $x$  infections within proximity  $k$  to the seed  
87 is extremely low.‡

88 **THEOREM 1.** Consider any sequence of networks and associated  $k(n) < K(n) - 1$  where  $K(n)$  is  
89 the maximum  $k(n)$  for which  $n_k > 0$ ,§ such that each node in  $N_{k(n)+1}$  has at least one descendent at  
90 distance  $k(n) + 2$ , and let  $x$  be any fixed positive integer. Let the sequence of associated diseases have

\* This is very different from conditions that concern long paths within short distances, such as (1), as ours is ruling out *short* paths with low expansion.

† Note that this requires knowledge of the neighborhood structure around the seed node, but no other knowledge of the network by a policymaker.

‡ The theorem extends to allow  $x = x(n)$  to grow with  $n$ , provided the growth is sufficiently slow. Then that growth balance condition becomes more complicated, as the  $M = M(n)$  in the definition adjusts with the rate of growth of  $x$ .

§ Otherwise, it is actually a global policy.

92  $\alpha(n)$  and  $p(n)$  bounded away from 0 and 1,<sup>¶</sup> no delay in detection, and any  $\theta(n) \geq 1$ . A regional  
 93 quarantining policy of distance  $k(n)$  and threshold  $x$  halts all infections past distance  $k(n) + 1$  with a  
 94 probability tending to 1 if and only if the sequence is growth-balanced with respect to  $k(n)$ .

95 Note that the growth balance condition implies that the number of nodes within distance  $k(n)$   
 96 from  $i_0$  must grow without bound. Theorem 1 thus implies that in order for a regional policy to  
 97 work, the region size must grow without bound, and also must satisfy a particular balance condition.  
 98 (Rates at which this growth must occur as a function of  $k$  and  $n$ , can be deduced from the relevant  
 99 infection probabilities and network structure.)

100 *Proof of Theorem 1.* To prove the first part, note that if the infection never reaches distance  $k(n)$   
 101 then the result holds directly since it can then not go beyond  $k(n) + 1$ . We show that if the sequence  
 102 of networks is growth-balanced relative to  $k(n)$ , then conditional upon an infection reaching level  
 103  $k(n)$  with the possibility of reaching  $k(n) + 2$  within two periods, the probability that it infects more  
 104 than  $x$  nodes within distance  $k(n)$  before any nodes beyond  $k(n)$  tends to 1. Suppose that infection  
 105 reaches some node at distance  $k(n)$  that can reach a node in  $N_{k+1}$ . Consider the corresponding  
 106 sequence of paths of infected nodes  $i_0, i_1, \dots, i_\ell$  with  $i_\ell \in N_{k+1}$ ,  $i_{j+1}$  being a direct descendant of  
 107  $i_j$  for each  $j \in \{0, \dots, \ell - 1\}$ , and note that by assumption  $i_\ell$  has a descendant in  $N_{k+2}$ . By the  
 108 growth balance condition, for any  $M$ , there is a large enough  $n$  for which either the length of the  
 109 path is longer than  $M$  or else there is at least one  $i_j$  with  $j \leq \ell - 2$  along the path that has more  
 110 than  $M$  descendants. In the latter case, the probability that  $i_j$  has more than  $x$  descendants who  
 111 become infected and are detected is at least  $1 - F_{M,m}(x)$  where  $F_{M,m}$  is the binomial distribution  
 112 with  $M$  draws each with probability  $m$ , where  $p(n)\alpha(n) > m$  for some fixed  $m$ . Given that  $x$  and  $m$   
 113 are fixed, this tends to probability 1 as  $M$  grows. In the former case, the sequence exceeds length  
 114  $M$ , all of which are infected and so given that  $\alpha(n)$  is bounded below, the probability that at least  
 115  $x$  of them are detected goes to 1 as  $M$  grows. In both cases, as  $n$  grows, the minimal  $M$  across such  
 116 paths of potential infection to  $k(n) + 1$  grows without bound, and so the probability that there are  
 117 at least  $x$  infections that are detected by the time that  $i_{\ell-1}$  is reached tends to 1 as  $n$  grows.

118 To prove the converse, suppose that the network is not growth-balanced. Consider a sequence of  
 119 bounded paths of potential infection to  $k(n) + 2$ , with associated sequences of nodes  $i_0, i_1, \dots, i_\ell$  of  
 120 length less than  $M$  with  $i_\ell \in N_{k+1}$ ,  $i_{j+1}$  being a direct descendant of  $i_j$  for each  $j \in \{0, \dots, \ell - 1\}$ ,  
 121 with  $n^j < M$  for every  $j \in \{0, \dots, \ell - 2\}$ , and for which  $i_\ell$  has a descendant in  $N_{k+2}$ . The probability  
 122 that each of the nodes  $i_1, \dots, i_{\ell-2}$  becomes infected and no other nodes are infected within distance  
 123  $k(n) - 1$ , and that all infected nodes are undetected is at least  $(p(n)(1 - \alpha(n))(1 - p(n))^M)^M$ . This  
 124 is fixed and so bounded away from 0. This implies that probability that the infection gets to nodes  
 125 at distance  $k(n)$ , and  $i_{\ell-1}$  in particular, without any detections is bounded below. Thus, there is a  
 126 probability bounded below of reaching  $i_\ell$  before any detections, and then by the time the quarantine  
 127 is enacted, there is at least a  $p(n)$  times this probability that it escapes past  $N_{k+1}$ , which is thus  
 128 also bounded away from 0.  $\square$

129 We note that Theorem 1 admits essentially all sequences of (unweighted) networks. Thus, for  
 130 every type of network, one can determine whether a regional policy of some  $(k(n), x)$  will succeed or  
 131 fail. The only thing that one needs to check is growth balance. If it is satisfied, a regional policy  
 132 works, and otherwise it will fail with nontrivial probability.

133 This has implications for some prominent random network models. Consider a randomly chosen  
 134 sequence of seeds and networks from the associated networks:

<sup>¶</sup>The cases of  $p(n)$  or  $\alpha(n)$  equal to 1 are degenerate.

- 135 1. For a sequence of stochastic block models in which all nodes have expected degree  $d(n) > \log(n)$   
 136 so that the network is path connected (with Erdos-Renyi as a special case),<sup>||</sup> a regional policy  
 137 with a bounded  $k(n)$  has a probability going to 1 of halting the disease on the randomly  
 138 realized network if and only if the seed node's expected out degree  $d(n) > 1$  is such that  
 139  $d(n)^{k(n)} \rightarrow \infty$ .
- 140 2. For a regular expander graph with outdegree  $d(n) > 1$ , a regional policy works if and only if  
 141 the expansion rate  $d(n)^{k(n)} \rightarrow \infty$ .
- 142 3. For a regular lattice of degree  $d(n) > 1$ , a regional policy works if and only if  $d(n)^{k(n)} \rightarrow \infty$ .
- 143 4. For a rewired lattice with  $d(n) > 1$  for all nodes and with a fraction links that are randomly  
 144 rewired, a regional policy with a bounded  $k(n)$  has a probability going to 1 of halting the  
 145 disease on the randomly realized network if and only if  $d(n)^{k(n)} \rightarrow \infty$ .
- 146 5. For a sequence of random networks with a scale-free degree distribution with average degree  
 147  $d(n) > \log(n)$ , a regional policy works (with probability 1) if and only if  $k(n) \rightarrow \infty$ .

148 Thus, whether a regional policy works in almost any network model requires that either the degree  
 149 of almost all nodes grows without bound, or else the size of the quarantine grows without bound.  
 150 For a scale free distribution, there is always a nontrivial probability on small degrees, and hence in  
 151 order for a regional policy to work, the size of the neighborhood must grow without bound.

152 In practice, even very sparse networks will have a large  $d(n)^{k(n)}$  (e.g., if people have hundreds of  
 153 contacts,  $100^3$  is already a million and even with a very low  $\alpha(n)$  many infections will be detected  
 154 within a few steps of the initial node).<sup>\*\*</sup> What the growth balance condition rules out is that some  
 155 nontrivial part of the network have neighborhoods with many fewer contacts - so there cannot be  
 156 people who have just a few contacts, since that will allow for a nontrivial probability of undetected  
 157 escape (e.g.,  $2^3 = 8$  and so with only 8 infections, it is possible that none are detected and the disease  
 158 escapes beyond 3 steps). As many real-world network structures have substantial heterogeneity,  
 159 with some people having very low numbers of interactions, such an escape becomes possible even  
 160 under idealized assumptions of no delay in detection and no leakage (2–6).

161 **Delay in Detection.** The detection delay,  $\tau(n)$ , is distributed over the support  $\{1, \dots, \tau^{\max}(n)\}$ . This  
 162 includes degenerate distributions with  $\tau^{\max}(n)$  being the maximal value of the support with positive  
 163 mass. The policymaker may or may not know  $\tau^{\max}(n)$  and we study both cases. The latter is  
 164 important as in practice we estimate delay periods so there is bound to be uncertainty. When  $\tau(n)$   
 165 is known, we can simply say  $\tau(n) = \tau^{\max}(n)$ .

166 Let a *regional policy with trigger  $k(n)$ , threshold  $x$ , and buffer  $h(n)$*  be such that once there are at  
 167 least  $x$  infections detected within distance  $k(n) + h(n)$  from the initial seed, then all nodes within  
 168 distance  $k(n) + h(n) + 1$  of  $i_0$  are quarantined/locked down for at least  $\theta(n)$  periods.

169 There are two differences between this definition of regional policy from the one considered before.  
 170 First, it is triggered by infections within distance  $k(n) + h(n)$  (not within distance  $k(n)$ ), and it also  
 171 has a buffer in how far the quarantine extends beyond the  $k(n)$ -th neighborhood.

172 We extend the definition of growth balance to account for buffers.

173 Consider a network and a distance  $k(n)$  from the initially infected node  $i_0$  and an  $h(n) \geq 1$ . A *path*  
 174 of potential infection to  $k(n) + h(n) + 2$  is a sequence of nodes  $i_0, i_1, \dots, i_\ell$  with  $i_\ell \in N_{k(n)+h(n)+1}$ ,  
 175  $i_{j+1}$  being a direct descendant of  $i_j$  for each  $j \in \{0, \dots, \ell - 1\}$ .

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<sup>||</sup> Consider a sequence of block models such that the ratio of expected out degree of a node in one neighborhood compared to another in some other block cannot grow without bound.

<sup>\*\*</sup> This is still extremely sparse, as having 100 contacts out of millions or billions of potential other nodes is a small fraction.

176 Consider a sequence of networks,  $n$ , and associated  $k(n), h(n)$ . We say that there are *bounded*  
 177 *paths of potential infection* to  $k(n) + h(n) + 2$  if there exists some finite  $M$  and for each  $n$  there is a  
 178 path of potential infection to  $k(n) + h(n) + 2$ ,  $i_0, i_1, \dots, i_\ell$  of length less than  $M$ , with  $n^j < M$  for  
 179 every  $j \in \{0, \dots, \ell - h(n) - 2\}$ . We say that a sequence of networks is *growth-balanced* relative to  
 180 some  $k(n)$  and buffers  $h(n)$  if there are no bounded paths of potential infection to  $k(n) + h(n) + 2$ .

181 **THEOREM 2.** *Consider a sequence of diseases that have  $\alpha(n)$  and  $p(n)$  bounded away from 0 and*  
 182 *1,  $\theta(n) \geq 1$ , and have a detection delay distributed over some set  $\{1, \dots, \tau^{\max}(n)\}$  with  $\tau^{\max} > 1$*   
 183 *(with probability on  $\tau^{\max}(n)$  bounded away from 0).<sup>††</sup> Consider any sequence of networks and*  
 184  *$k(n) < K(n) - \tau^{\max}(n) - 1$  where  $K(n)$  is the maximum  $k(n)$  for which  $n_k > 0$ , such that each*  
 185 *node in  $N_{k'}$  for  $k(n)' > k(n)$  has at least one descendant at distance  $k(n)' + 1$ , and let  $x$  be any*  
 186 *fixed positive integer. A regional policy with trigger  $k(n)$ , threshold  $x$ , and buffer  $\tau^{\max}(n)$  halts all*  
 187 *infections past distance  $k(n) + \tau^{\max}(n) + 1$  with a probability tending to 1 if and only if the sequence*  
 188 *is growth-balanced with respect to  $k(n)$ .*

189 The Proof of Theorem 2 is a straightforward extension of the previous proof and so it is omitted.

190 This result shows several things. First, if the detection delay is small relative to the diameter  
 191 of the graph, one can use a regional quarantine policy – adjusted for the detection delay – along  
 192 the lines of that from Theorem 1 and ensure no further spread. This is true even if the period is  
 193 stochastic as long as the upper bound is known to be small.

194 Second, in contrast, if the detection delay is large compared to the diameter of the graph, then  
 195 a regional policy is insufficient. By the time infections are observed, it is too late to quarantine a  
 196 subset of the graph. This condition will tend to bind in the case of real world networks, as they  
 197 exhibit small world properties and have small diameters (7, 8). As a result, even short detection  
 198 delays may correspond to rapidly moving wavefronts that spread undetected.

199 **Leakage in the Quarantine.** Next we turn to the case of in which there is some leakage in the quarantine,  
 200 which may happen for a variety of reasons. First, the policymaker may have measurement error in  
 201 knowledge of the network structure and thus who should be quarantined. Second, and distinctly,  
 202 lockdowns are imperfect, and some transmission still happens. Third, the network may cross  
 203 jurisdictional borders and some nodes within distance  $k(n)$  of  $i_0$  may be outside of the policymaker's  
 204 jurisdiction.

205 To keep the analysis uncluttered, we assume no detection delay, but the arguments extend directly  
 206 to the delay case with the appropriate buffer.

207 **THEOREM 3.** *Consider any sequence of networks. Let the sequence of associated diseases have  $\alpha(n)$*   
 208 *and  $p(n)$  bounded away from 0 and 1, and be such that  $\theta(n) \geq 1$ , with no detection delay. Consider*  
 209 *any  $k(n) < K(n) - 1$  where  $K$  is the maximum  $k(n)$  for which  $n_k > 0$ , and suppose that each node*  
 210 *in  $N_{k(n)}$  has at least one descendant at distance  $k(n) + 1$ , and let  $x$  be any positive integer.*

211 *Suppose that a random share of  $\varepsilon_n$  of nodes within distance  $k(n)$  of  $i_0$  are not included in a regional*  
 212 *quarantine policy and are connected to nodes of distance greater than  $k(n) + 1$  – because of a lack of*  
 213 *jurisdiction, misclassification by a policymaker, or lack of complete control over people's behaviors.<sup>‡‡</sup>*  
 214 *Then:*

- 215 1. *If  $\varepsilon_n = o((\sum_{k(n)' \leq k(n)} n_{k'})^{-1})$  and the network is growth-balanced, then a regional policy of*  
 216 *distance  $k(n)$  and threshold  $x$  halts all infections past distance  $k(n) + 1$  with a probability*  
 217 *tending to 1.*

<sup>††</sup>A special case is in which  $\tau^{\max}(n)$  is known.

<sup>‡‡</sup>The misclassification can be that if some node within distance  $k(n)$  is controlled by the quarantine, but connects to nodes that are not included and were thought to be of greater distance, but then allow the disease to escape beyond the quarantine.

218    2. If  $\varepsilon_n \geq \min[1/x, \eta]$  for all  $n$  for some  $\eta > 0$  or the network is not growth-balanced, then a  
 219    regional policy of distance  $k(n)$  and threshold  $x$  fails to halt all infections past the regional  
 220    quarantine with a probability bounded away from 0.

221    Proof of Theorem 3. Part 1 follows from the fact that if  $\varepsilon_n = o((\sum_{k(n) \leq k(n)} n_{k'})^{-1})$  then the proba-  
 222    bility of having all nodes in  $N_k$  correctly identified as being in  $N_k$  tends to 1, and then Theorem 1  
 223    can be applied.

224    For Part 2, suppose that some  $x$  infections are detected. The probability that at least one of them  
 225    is misclassified is at least  $1 - (1 - \varepsilon_n)^x$ . Given that  $\varepsilon_n \geq \min[1/x, \eta]$  for some  $\eta > 0$ , it follows that  
 226     $(1 - \varepsilon_n)^x$  is bounded away from 1. There is a probability bounded away from 0 that at least one  
 227    of the infected nodes is misclassified, and not subject to the quarantine, and connected to a node  
 228    outside of distance  $k(n) + 1$ .  $\square$

229    The theorem implies that the effectiveness of a regional policy is sensitive to any small fixed  $\varepsilon$   
 230    amount of leakage.

## 231    2. Simulation Details

232    To illustrate the processes described in the main text, we run several simulations. First, we construct  
 233    a large network with many jurisdictions. We directly study the content of the theorems with several  
 234    versions of  $(k, x)$  quarantines with a SIR infection process on a network. We use the same process  
 235    and network to show the issues with jurisdictional policies, studying reactive and proactive policies.

236    **A. Network Model.** We model the network structure as follows.

- 237    1. There are  $L$  locations distributed uniformly at random on the unit sphere. Each location has  
 238    a population of  $m$  nodes with a total of  $n = mL$  nodes in the network.
- 239    2. The linking rates across locations are given as in a spatial model (2, 9). The probability of  
 240    nodes  $i \in \ell$  and  $j \in \ell'$  for locations  $\ell \neq \ell'$  linking depends only on the locations of the two  
 241    nodes and declines in distance:

$$q_{\ell, \ell'} = \exp(a + b \cdot \text{dist}(\ell, \ell'))$$

242    where  $\text{dist}(\ell, \ell')$  is the distance between the two locations on the sphere and  $a, b < 0$ .

243    Every interaction between every pair of nodes is drawn independently from the observed spatial  
 244    distribution, with distances measured along the surface of the unit sphere.

- 245    3. The linking patterns within a location are given as in a mixture of random geometric (RGG)  
 246    (3) and Erdos-Renyi (ER) random graphs (10). Specifically, as spheres are locally Euclidean,  
 247    we model nodes in a location (e.g., in a city) as residing in a square in the tangent space to  
 248    the location. The probability that two nodes within a location link declines in their distance  
 249    in this square.

We set  $d_{RGG}$  as the desired degree from the RGG. Nodes are uniformly distributed on the unit square  $[0, 1]^2$ , and links are formed between nodes within radius  $r_\ell$  (3). Let  $d_\ell$  be the desired average degree for all nodes within location  $\ell$  with  $m_\ell$  as the population at location  $\ell$ , which we take as equal for all locations in our exercises. We define

$$\pi = \frac{d_\ell - d_{RGG}}{m_\ell}$$

which is the probability with which remaining links within location are drawn (i.i.d.). To obtain the desired degree we set

$$r_\ell = \sqrt{\frac{d_{RGG}}{m_\ell \pi}}.$$

- 4. Next, we uniformly add links to create a small world effect, with identical and independently distributed probability  $s = \frac{1}{cn}$ , where  $c$  is an arbitrary constant and  $n$  is the total number of nodes in the network (11).
- 5. Finally, we designate a single location as a “hub,” to emulate the idea that certain metro areas may have more connections to *all* other regions. To do so, we select a hub uniformly at random and add links independently and identically distributed with probability  $h$  from the hub location to every other location.
- 6. To avoid the possibility of multiple links between the same two nodes, we remove any duplicate links.

We first take  $L = 40$  and  $m = 3500$  for all locations. We set  $a = -4$  and  $b = -15$ . Next, we calibrate the network to data by setting  $d_\ell = 15.5$ , and  $d_{RGG} = 13.5$  for all locations. Next, we set  $c = 2$ . Finally, we set  $h = 2.85 \times 10^{-6}$ . This process results in a graph that very roughly emulates the connectivity of real world networks in the United States and India (12–15). This includes data from India during the COVID-19 lockdowns about interactions within six feet, meaning that it is conservative (15).

We fix this network to use in all versions of the simulations. The network we generate is sparse, clustered, and has small average distances, as demonstrated by information detailed in Table S1.

Finally, we recalculate the connection probability matrix between locations to reflect realized rates of connection across regions, denoted by  $q$ . The entry that denotes the probability of linking between locations  $\ell$  and  $\ell'$  is  $q_{\ell,\ell'}$ .

**B. Disease Process.** We set parameters as follows: the duration of infection is  $\theta$ , detection delay (when incorporated) is  $\tau$ , and set quarantine thresholds  $x$  depending on the simulation.

We set transmission probability  $p$  as

$$p = 1 - \left(1 - \frac{R_0}{\bar{d}}\right)^{\frac{1}{\theta}}$$

where  $\bar{d}$  is the mean degree. We take  $R_0 = 3.5$ , based on estimates of COVID-19 (16).

Following estimates from the literature (5–15%), we set  $\alpha = 0.1$  (17, 18). In the simulations, each node is either detected or not during the first period in which it can be detected. Nodes that are detected are classified as such until recovery. Nodes that are undetected remain undetected (and so the  $\alpha$  probability of detection is realized in the  $\tau + 1$ st period, and only in that period).

As outlined in the main text, we begin by using  $\theta = 5$  and  $\tau = 3$  (17–20).

**C. Simulation Progression.** Each time period in the simulation progresses in four parts, which happen sequentially. The simulations run as follows:

- 283 1. The policymakers see the newly detected infections from the previous period, and update their  
 284 estimates of current infections (in all jurisdictions if proactive), and then determine whether  
 285 a quarantine is necessary in their own jurisdiction in the next period (if there is not one  
 286 already in place). This quarantine decision is done based on estimated infections for proactive  
 287 jurisdictions, and internally observed infections for reactive jurisdictions.
- 288 2. The disease progresses for a period. This includes new infections and recoveries.
- 289 3. Infected nodes that have just finished their detection delay of  $\tau$  periods are independently  
 290 detected with probability  $\alpha$ .
- 291 4. New quarantines are enacted based on decisions made in step one of the process in this time  
 292 period. Quarantines that have taken place for  $\theta$  periods end.

293 A node that becomes infected in period  $t$  with a detection delay of  $\tau$  and total disease length  $\theta$ , is  
 294 tested in period  $t + \tau$ , results are processed in  $t + \tau + 1$ , and they will be quarantined (if necessary)  
 295 starting at the end of  $t + \tau + 1$  (under the fourth item above). This means that they have  $\tau + 1$   
 296 time periods during which they can infect other nodes. For instance, if  $\tau = 0$  this allows a node that  
 297 becomes infected (but that was not already under quarantine for other reasons) one opportunity  
 298 to infect others. This process reflects that neither detection nor quarantining of individuals (or  
 299 jurisdictions) happens instantaneously. In addition, we stipulate that the seed node,  $i_0$  is not counted  
 300 in the quarantining testing and calculations. This is meant to reflect that it may be unclear whether  
 301 the disease is spreading or not. Nodes that are detected are marked as such until recovery.

302 **D. Containment Policies.** A random node  $i_0$  is selected and the epidemic begins there. We study the  
 303 epidemic curve, the number total node-days of infection, and the number of node-days of quarantine  
 304 for a variety of containment strategies. In all cases, the policymaker does not detect  $i_0$ , to emulate  
 305 the difficulty of detecting an infection seed in real time.

306 **( $k, x$ ) Policies.** We examine a number of scenarios using the  $(k, x)$  policy model outlined in Theorems  
 307 1-3.

308 If a quarantine fails, and there are infections outside of the quarantine radius, the policymaker  
 309 deals with each escaped infection individually. The policymaker treats each detected case outside of  
 310 the initial quarantine as a new seed, and immediately quarantines all nodes with the same radius as  
 311 the initial quarantine.

312 We begin by picking our threshold for triggering the initial quarantine by using a simple objective  
 313 function. We minimize a linear combination of the number of infected person periods and quarantined  
 314 person periods. For all linear combinations where some weight is given to both terms, the optimal  
 315 threshold is  $x = 1$ . The logic is as follows: if the initial quarantine is successful, the number of  
 316 quarantined person periods will be fixed and also the minimum number of quarantined person  
 317 periods. Therefore, the problem reduces to minimizing the number of infections, which is done by  
 318 setting  $x = 1$ .

319 We study three versions of a  $(k, x)$  policy. First, we simulate the  $(k, x)$  policy with no detection  
 320 delay and no buffer. Then, we incorporate a detection delay of  $\tau$ , still using a  $(k, x)$  without a buffer.  
 321 We do not include a buffer because the resulting quarantine on our network with  $k = \tau = 3$  would  
 322 encompass 99.98% of nodes on average, since almost all nodes are within distance 6 of each other.  
 323 Lastly, we study a  $(k, x)$  policy with enforcement failures and no buffer. In this case, a fraction  
 324  $\epsilon = 0.05$  of nodes do not ever quarantine.

325 While the policymaker is unable to detect the infection seed in real time, once the policymaker  
 326 decides to quarantine, we give them the advantage of perfect information with knowing the location  
 327 of  $i_0$ . As a baseline, we set  $k = 3$ , but then also examine the case where  $k = 2$ .

328 **( $k, x$ ) Policies with an Unknown Seed.** We also simulate the case where the policymaker is unable  
 329 to trace back to find the initial seed  $i_0$  to use as the center of the quarantine region. In this case,  
 330 once at least  $x$  cases are detected, the policymaker calculates the pairwise distance between the  
 331 set of all detected nodes. The most central node is defined as the one with the minimum average  
 332 distance to the other detected nodes. The policymaker then quarantines all nodes within distance  
 333  $k + 1$  of the most central node. If there are multiple nodes with the same average distance, the  
 334 policymaker picks one at random. If the initial quarantine fails, the policymaker proceeds the same  
 335 way as when they do know  $i_0$ , instituting quarantines of radius  $k + 1$  around detected nodes.

336 Again, we examine three cases: the first with no detection delay, the second introducing  
 337 a delay (still without a buffer), and the third including enforcement failures. In the third case, a  
 338 fraction  $\epsilon = 0.05$  nodes never quarantine just as with the standard  $(k, x)$  policies. Again, we do not  
 339 include a buffer in any of the simulations as it would result in nearly global quarantines. As in the  
 340 scenario where the seed is known, we set  $(k, x) = (3, 1)$  as a baseline but then also examine the case  
 341 where  $(k, x) = (2, 1)$ .

342 **A Global Quarantine Policy.** In a global quarantine policy, every node is quarantined for  $\theta$  periods as  
 343 soon as at least  $x = 1$  infections are detected globally. We study this in the case with a detection  
 344 delay, to compare it to the  $(k, x)$ , reactive, and proactive policies.

345 **Reactive and Proactive Quarantine Policies.** For both the reactive and proactive policies, we take each  
 346 location on the graph to be a separate jurisdiction.

347 **Reactive Quarantine Policies.** Reactive jurisdictions respond only to detected infections within their  
 348 own borders. We set  $x = 1$  for all jurisdictions, the most conservative possible threshold, unless  
 349 otherwise specified.

**Proactive Quarantine Policies.** Proactive jurisdictions quarantine based on estimated infection rates  
 within their own borders, with estimates that account for the history of infections observed in all  
 jurisdictions and knowledge of the network connection rates. In each period, each jurisdiction  $\ell$   
 observes the number of actual detected infections at time  $t$ ,  $z_{\ell,t}$ , and then calculates their estimated  
 infections  $w_{\ell}$  as follows:

$$w_{\ell,t} = \max\{w_{\ell,t-1} + y_{\ell,t} - r_{\ell,t}, z_{\ell,t}\},$$

350 where  $y_{\ell,t}$  denotes the number of expected new infections in region  $\ell$  at time  $t$ , given the history  
 351 of infections observed in all jurisdictions and knowledge of the network connection rates, and  $r_{\ell,t}$   
 352 denotes the number of expected recoveries in  $\ell$  at  $t$ . The max updates the infection rate upwards if  
 353 the estimated infection rate is lower than the actual observation. This is not fully sophisticated, as  
 354 the adjustment could also backwardly update previous infection rates in light of the new information,  
 355 but this would require introducing a probability space and more machinery that might improve the  
 356 proactive policy's accuracy, but would not qualitatively change the results.

Each jurisdiction calculates  $y_{\ell,t}$  as:

$$y_{\ell,t} = p \sum_{\ell' \text{ s.t. } \ell' \text{ not quarantined at t-1}} m_{\ell'} q_{\ell,\ell'} w_{\ell',t-1}$$

The summation includes the term for spread from  $\ell$  to still within  $\ell$ . If  $\ell$  is quarantined at time  $t$ , then  $y_{\ell,t} = 0$ . Expected recovery at each period  $r_{\ell,t}$  is calculated as:

$$r_{\ell,t} = w_{\ell,t-\theta} - w_{\ell,t-\theta-1} + r_{\ell,t-\theta}.$$

Finally, we set  $w_{\ell,t} < 0.01$  to be zero, to avoid implementation issues with floating point calculations. Setting a lower value to truncate at would improve the performance of the proactive jurisdiction policies, as they would be more sensitive to detected cases in other jurisdictions. We set  $w_{\ell,1} = 0$ , for all jurisdictions. Thus, the  $w_{\ell,t}$  values remain at zero until at least one infection is detected somewhere.

**Uniform and Lax Policies** We run two simulation variants for both the proactive and reactive policies: one in which all states are as conservative as possible, setting  $x = 1$  and a second in which four regions set a higher threshold of  $x = 5$ . In the proactive case, the lax jurisdictions follow a reactive policy in addition to using the higher threshold value.

We choose  $x = 5$  to simulate lax thresholds. In the United States, New York state issued a stay at home order when 0.07% of the state population was infected, which scaled to our populations of 3500 that is equivalent to a threshold of 2.73 (21, 22). When scaled to match our population of 3500, Florida began re-opening with a threshold of 6.15, and some countries never locked down (22–24). The quarantines in our stylized model are more aggressive, as they cut contact completely.

**E. Results and Sensitivity Analysis.** We run 10000 simulations with the parameters detailed in the main text: using  $\theta = 5$ ,  $\tau = 3$ ,  $\alpha = 0.1$ , and  $R_0 = 3.5$ , plus  $(k, x) = (3, 1)$  where appropriate. Each simulation begins with a singular infection, selected uniformly at random. In the simulations where there are lax jurisdictions, four of the forty are selected to be lax uniformly at random. For all the additional sets of parameters reported below, we run 2500 simulations.

We include the results of the simulations detailed in the main text in the tables below. In addition, we run simulations with several sets of varied parameters: first, we take  $\alpha = 0.05$  and  $\alpha = 0.2$ ; second we take  $\theta = 8$  and  $\tau = 5$ ; finally, we set  $R_0$  equal to 2, 5, and 15 while holding all other parameters fixed. Within the United States, estimates for the detection rate range from 5% to 15%, and in countries with less developed testing infrastructure, the detection rate is undoubtedly lower (17). Because disease parameters are estimated, we use a different estimate of the disease lifespan of COVID-19 (20). We also examine an alternate  $(k, x)$  policy, setting  $(k, x) = (2, 1)$  and using the disease and detection parameters outlined in the main text, to mimic an attempt at a more targeted intervention. Full results are shown in Tables S2-S7, and in Figure S2.

There are two key trends among the single regime policies. While the results from single jurisdiction policies in terms of infection and quarantined person-days are similar, regardless of whether or not the seed is known, knowing the seed node improves the effectiveness of the initial quarantine. This result is consistent with the theory. The similar results in terms of infections and quarantine person days is a result from the overall high effectiveness of the policymaker's response if the initial quarantine fails. Because the policymaker treats every escaped, detected infection as a new seed, no matter how it treated the initial quarantine, the overall results for infection and quarantine person-days are similar.

Second, as shown through the visuals of Figure S2, the effectiveness of the single policymaker policies varies depending on the disease parameters. For larger values of  $R_0$ , as demonstrated by the cases where  $R_0 = 5$  and  $R_0 = 15$ , the single policymaker regional quarantine policies perform worse than the proactive, multiple jurisdiction simulations. With high values of  $R_0$ , the single jurisdiction policies perform better in terms of infected person-days, but have significantly more quarantine

398 person days. This is because with a high  $R_0$ , precise targeting becomes much more difficult leading  
 399 to many rounds of ineffective quarantines. In essence, the single jurisdiction is trying its best to halt  
 400 the spread, but with a regional quarantine fails to get it under control. The multiple jurisdiction  
 401 setting moves far more slowly, and so does not have the same number of quarantine days (but  
 402 very similar infections). This is less a product of successful policy, and more a reflection that with  
 403  $R_0 = 15$ , the only real effective policy is complete global quarantine.

404 There are several notable points about the reactive and proactive policies. First, the relationship  
 405 between the reactive and proactive policies is robust to different sets of simulation parameters. In  
 406 all cases, there is a significant gap between the proactive and reactive jurisdictions, along both the  
 407 number of quarantine and infection person-days. Second, proactive policies are strictly better in  
 408 terms of infections, regardless of the disease and administration parameters. Third, the impact of lax  
 409 jurisdictions on quarantined person-days with reactive jurisdictions depends on the set of parameters.  
 410 When  $\alpha = 0.2$ , we see that adding lax jurisdictions to reactive policies increases the number of  
 411 quarantine person-days. However, in all other cases, there are outcomes similar to those described in  
 412 the main text: because of the high connection rate between jurisdictions, lax jurisdictions serve as  
 413 super spreaders that cause coincidental large scale shut downs. Finally, lax jurisdictions uniformly  
 414 increase the number of quarantined person-days for proactive jurisdictions.

415 Finally, we note that decreasing the quarantine radius from  $k = 3$  to  $k = 2$  has large effects on  
 416 both the number of infection and quarantine person-days, increasing both by orders of magnitude.  
 417 The more targeted single jurisdiction intervention achieves similar results to the reactive multi-  
 418 jurisdiction policies. Introducing delays and leakage impose a much large cost in terms of both  
 419 infection and quarantine person-days for the more targeted policy. Knowing the location of the seed  
 420 still improves the failure rate, but again, the overall results are similar due to the high effectiveness  
 421 of the policy if the initial quarantine fails. With  $k = 4$ , the policy would be extremely large relative  
 422 to the size-limited networks that we are able to simulate. In fact, it would initially quarantine  
 423 approximately 54 percent of people, making all the variants look similar. For our relatively small  
 424 networks the range of radii that span parts of the network but not a majority of it are limited.  
 425 On networks with billions of nodes, it would be a much larger range.

### 426 3. Supplementary Tables

**Table S1: Graph Statistics**

Property	Value
Average Degree	20.49
Average Local Clustering Coefficient	0.208
Diameter	9
Average Path Length	5.33

**Graph statistics for the graph used in all simulations. Similar to real world networks, it is sparse, clustered and has short average distances between nodes.**

**Table S2: (3, 1) Regional Policy (Known Seed) Simulation Results**

$R_0$	$\theta$	$\tau$	$\alpha$	$\epsilon$	Percent Infected	Infection Person Days	Quarantined Person Days	Escape Rate
3.5	5	0	0.1	0	0.0276	1384.05	803955.61	0.0953
3.5	5	3	0.1	0	0.226	11282.19	2301413.60	0.458
3.5	5	3	0.1	0.05	0.514	25688.08	6478054.64	0.551
3.5	5	0	0.05	0	0.0684	3421.10	11231131.73	0.225
3.5	5	3	0.05	0	2.81	140667.17	20297075.03	0.623
3.5	5	3	0.05	0.05	7.80	390155.83	66067046.93	0.706
3.5	5	0	0.2	0	0.0097	483.96	698551.61	0.022
3.5	5	3	0.2	0	0.064	3196.86	1024409.97	0.260
3.5	5	3	0.2	0.05	0.096	4794.23	2027933.31	0.352
3.5	8	0	0.1	0	0.0277	2213.92	1243574.65	0.0904
3.5	8	5	0.1	0	0.285	22834.58	4187189.53	0.506
3.5	8	5	0.1	0.05	0.559	44709.41	10653981.92	0.582
2	5	0	0.1	0	0.0611	3057.36	737563.73	0.102
2	5	3	0.1	0	0.149	7473.47	931141.96	0.226
2	5	3	0.1	0.05	0.156	7784.11	1185778.89	0.252
5	5	0	0.1	0	0.027	1349.74	800273	0.074
5	5	3	0.1	0	1.607	80333.14	10826074.49	0.622
5	5	3	0.1	0.05	6.795	339788.66	63996541.26	0.746
15	5	0	0.1	0	0.0849	4245.51	712741.24	0.004
15	5	3	0.1	0	74.615	3730767.57	115033210.96	0.998
15	5	3	0.1	0.05	75.809	3790452.76	187358575.83	1.000

Results for the parameters used in the main text are the average over 10000 simulations. Results for the parameters only used in this section are the average over 2500 simulations. Infection person days and quarantined person days are scaled to be per million individuals. The escape rate is defined as the frequency with which the disease escapes the initial quarantine.

**Table S3: (3, 1) Regional Policy (Unknown Seed) Simulation Results**

$R_0$	$\theta$	$\tau$	$\alpha$	$\epsilon$	Percent Infected	Infection Person Days	Quarantined Person Days	Escape Rate
3.5	5	0	0.1	0	0.0181	903.66	907418.73	0.191
3.5	5	3	0.1	0	0.209	10425.09	2474174.31	0.524
3.5	5	3	0.1	0.05	0.503	25147.99	6733925.78	0.597
3.5	5	0	0.05	0	0.052	2602.33	1434418.54	0.349
3.5	5	3	0.05	0	2.689	134472.07	20800069.91	0.676
3.5	5	3	0.05	0.05	8.038	401918.94	69666034.17	0.736
3.5	5	0	0.2	0	0.0086	428.81	748090.71	0.067
3.5	5	3	0.2	0	0.061	3056.09	1141315.7	0.329
3.5	5	3	0.2	0.05	0.097	4873.17	2221095.64	0.416
3.5	8	0	0.1	0	0.007	562.29	708870.95	0.09
3.5	8	5	0.1	0	0.228	18237.83	4193253.6	0.555
3.5	8	5	0.1	0.05	0.561	44886.81	11767810.56	0.616
2	5	0	0.1	0	0.0095	477.09	669783.94	0.117
2	5	3	0.1	0	0.029	1427.07	830410.44	0.244
2	5	3	0.1	0.05	0.034	1680.93	996141.17	0.263
5	5	0	0.1	0	0.024	1202.11	952173.23	0.207
5	5	3	0.1	0	1.807	90371.77	12607529.19	0.718
5	5	3	0.1	0.05	7.074	353675.16	66430323.4	0.789
15	5	0	0.1	0	0.1239	6195.7	1248499.49	0.266
15	5	3	0.1	0	73.99	3699513.54	123395786.67	0.998
15	5	3	0.1	0.05	75.482	3774094.57	191925875.01	1.000

Results for the parameters used in the main text are the average over 10000 simulations. Results for the parameters only used in this section are the average over 2500 simulations. Infection person days and quarantined person days are scaled to be per million individuals. The escape rate is defined as the frequency with which the disease escapes the initial quarantine.

**Table S4: (2, 1) Regional Policy Simulation Results**

$i_0$	$R_0$	$\theta$	$\tau$	$\alpha$	$\epsilon$	Percent Infected	Infection Person Days	Quarantined Person Days	Escape Rate
Known	3.5	5	0	0.1	0	0.394	19706.76	1147303.53	0.363
Known	3.5	5	3	0.1	0	27.165	1358241.87	105221845.94	0.790
Known	3.5	5	3	0.1	0.05	29.809	1490432.74	119489225.66	0.810
Unknown	3.5	5	0	0.1	0	0.0935	4676.53	1029432.17	0.491
Unknown	3.5	5	3	0.1	0	27.204	1360209.23	108372918.63	0.801
Unknown	3.5	5	3	0.1	0.05	29.983	1499166.90	122945457.44	0.818

Results are the average over 2500 simulations. Infection person days and quarantined person days are scaled to be per million individuals. The escape rate is defined as the frequency with which the disease escapes the initial quarantine.

**Table S5: Global Policy Simulation Results**

$R_0$	$\theta$	$\tau$	$\alpha$	Percent Infected	Infection Person Days	Quarantined Person Days
3.5	5	3	0.1	0.0778	3890.51	4730000.00
3.5	5	3	0.05	0.1518	7591.79	4702000.00
3.5	5	3	0.2	0.044	2199.23	4716000.00
3.5	8	5	0.1	0.0847	6772.11	7545600.00
2	5	3	0.1	0.0207	1035.57	3708000.00
5	5	3	0.1	0.1937	9685.63	4922000.00
15	5	3	0.1	5.1639	258192.87	5000000.00

Results for the parameters used in the main text are the average over 10000 simulations. Results for the parameters only used in this section are the average over 2500 simulations. Infection person days and quarantined person days are scaled to be per million individuals. There are fewer quarantined person days on average with  $\alpha = 0.05$ , rather than  $\alpha = 0.1$  as there is a greater chance of the disease going completely undetected before dying out.

**Table S6: Reactive and Proactive Policy Simulation Results**

Policy	$R_0$	$\theta$	$\tau$	$\alpha$	Percent Infected	Infection Person Days	Quarantined Person Days
Reactive	3.5	5	3	0.1	29.89	1494552.99	131303637.50
Proactive	3.5	5	3	0.1	1.71	85526.78	51328755.00
Reactive	3.5	5	3	0.05	44.91	2245276.69	132165200.00
Proactive	3.5	5	3	0.05	5.45	272265.56	73938850.00
Reactive	3.5	5	3	0.2	10.63	531685.96	59927450.00
Proactive	3.5	5	3	0.2	0.56	27845.97	33333750.00
Reactive	3.5	8	5	0.1	27.66	2213177.60	194385520.00
Proactive	3.5	8	5	0.1	2.50	200369.76	35172320.00
Reactive	2	5	3	0.1	2.03	101275.14	13037500.00
Proactive	2	5	3	0.1	0.20	10104.91	5300750.00
Reactive	5	5	3	0.1	50.74	2537078.07	157829850.00
Proactive	5	5	3	0.1	4.14	206837.40	38021550.00
Reactive	15	5	3	0.1	81.66	4082954.97	16475250.00
Proactive	15	5	3	0.1	71.10	3555090.86	12125500.00

Results for the parameters used in the main text are the average over 10000 simulations. Results for the parameters only used in this section are the average over 2500 simulations. For all simulations, every jurisdiction sets  $x = 1$ . Infection person days and quarantined person days are scaled to be per million individuals.

**Table S7: Reactive and Proactive Policies with Lax Jurisdictions Simulation Results**

Policy	$R_0$	$\theta$	$\tau$	$\alpha$	Percent Infected	Infection Person Days	Quarantined Person Days	Low Threshold Case Fraction
Reactive	3.5	5	3	0.1	34.06	1702933.48	123051062.50	0.853
Proactive	3.5	5	3	0.1	9.19	459435.15	87241700.00	0.724
Reactive	3.5	5	3	0.05	46.16	2308090.83	111742450.00	0.867
Proactive	3.5	5	3	0.05	21.65	1082529.07	133660250.00	0.757
Reactive	3.5	5	3	0.2	19.71	985572.76	101214350.00	0.846
Proactive	3.5	5	3	0.2	1.93	96453.34	36203450.00	0.748
Reactive	3.5	8	5	0.1	32.78	2622535.7	192823440.00	0.852
Proactive	3.5	8	5	0.1	11.99	958939.79	138729440.00	0.761
Reactive	2	5	3	0.1	6.76	337947.53	34866850.00	0.857
Proactive	2	5	3	0.1	1.62	81059.37	19606550.00	0.810
Reactive	5	5	3	0.1	53.23	2661322.79	139446200.00	0.863
Proactive	5	5	3	0.1	10.67	533748.29	69943200.00	0.717
Reactive	15	5	3	0.1	83.63	4181626.60	15395600.00	0.885
Proactive	15	5	3	0.1	73.66	3683186.66	10949990.00	0.871

**Results for the parameters used in the main text are the average over 10000 simulations. Results for the parameters only used in this section are the average over 2500 simulations. For all simulations, 36 jurisdictions use  $x = 1$  and the lax remainder use  $x = 5$ . In the proactive case, jurisdictions with  $x = 5$  follow reactive policies. Infection person days and quarantined person days are scaled to be per million individuals.**

## 427 4. Supplementary Figures

Figure S1: Growth Balance

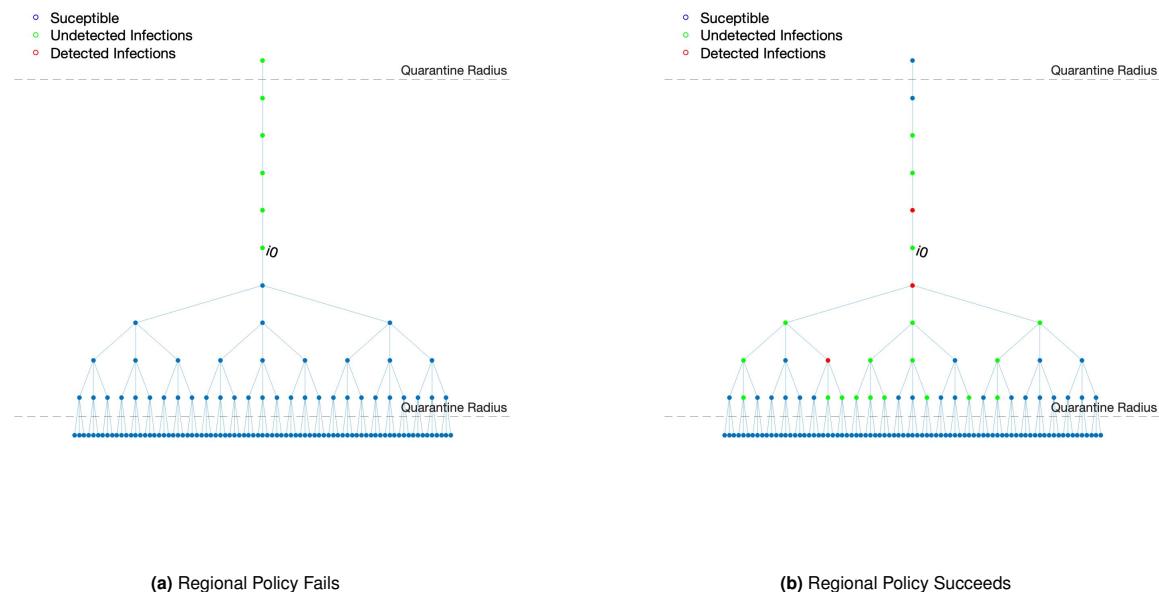
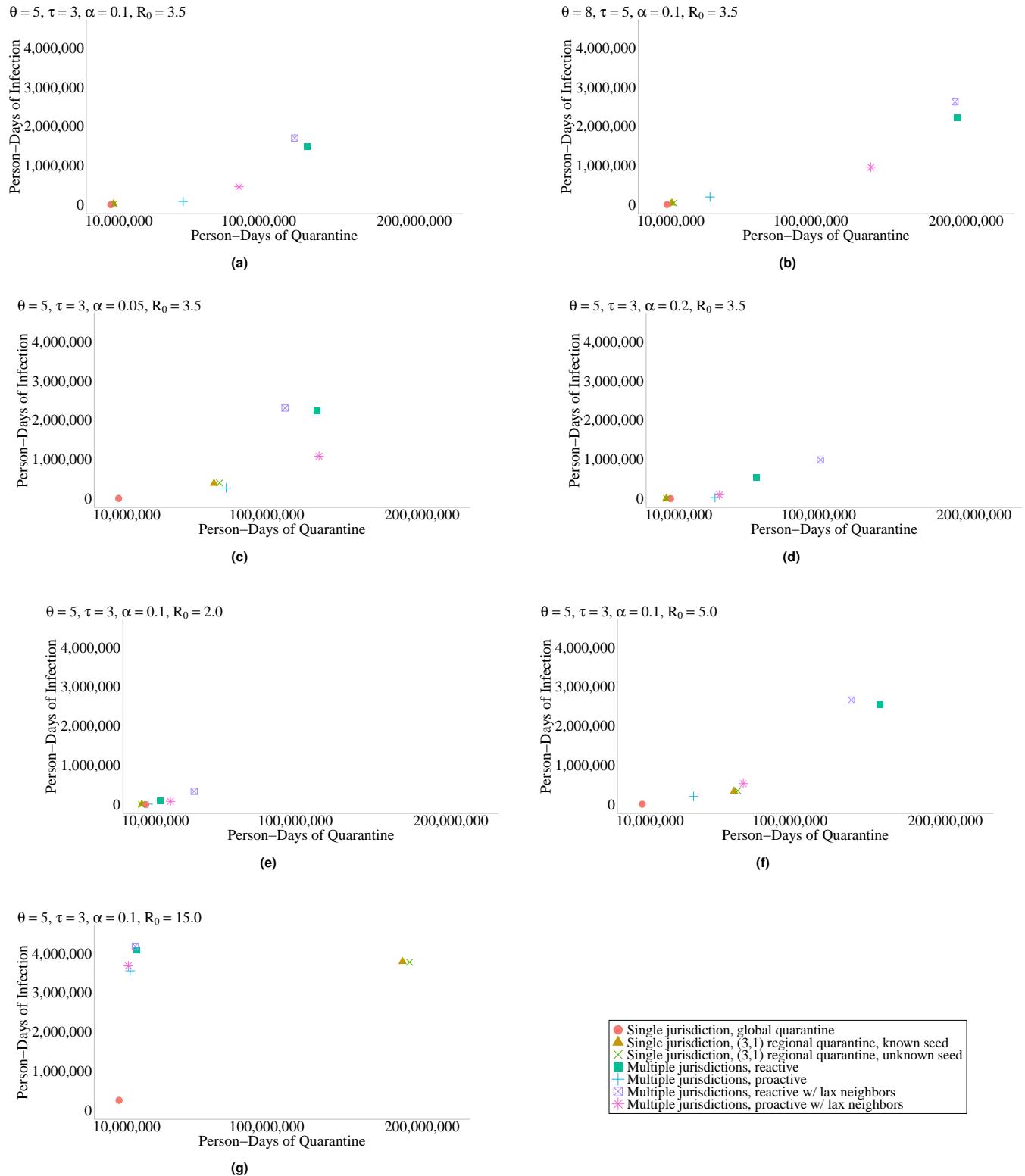


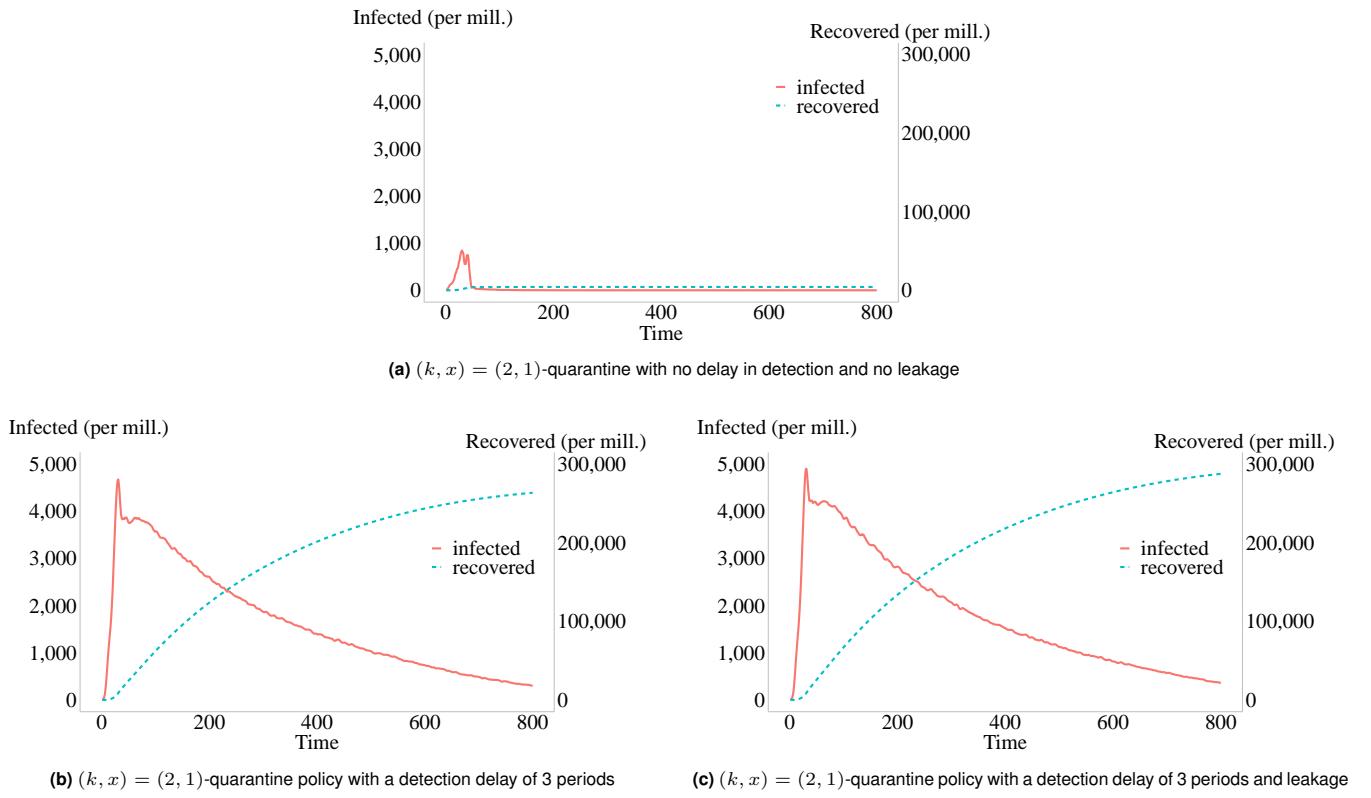
Figure S1: Panel (a) demonstrates the possible failure of growth balance. The infection escapes up the line undetected beyond the quarantine radius. If the infection happens to spread downwards, as in Panel (b), it is much more likely to be detected. However, that only happens with some moderate probability in this network, and so growth balance fails.

**Figure S2: Impact and Costs of Quarantines with Different Simulation Parameters**



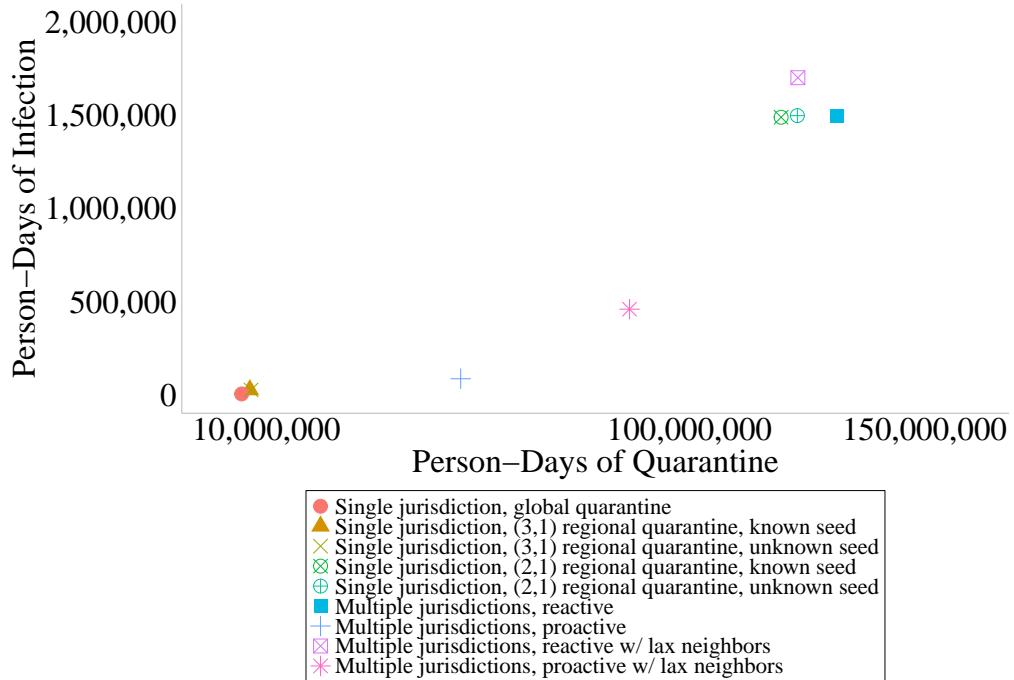
This figure plots the number of person-days of quarantine (per million) and the number of person-days of infection (per million) for seven different policy scenarios. Both single jurisdiction policies include leakage of a fraction  $\epsilon = 0.05$  people who never quarantine. Simulations in (a) are the average from 10000 simulations, while in (b)-(g), the results are the average over 2500 simulations.

**Figure S3: The Impact of Delay and Leakage on a  $(k, x) = (2, 1)$  Policy**



We picture daily infections and cumulative recoveries under three scenarios. As in the main text, we take  $\theta = 5$ ,  $\tau = 3$ ,  $\alpha = 0.1$  and  $R_0 = 3.5$ . The entire network is governed by a single policymaker using a  $(k, x) = (2, 1)$ -regional quarantine. In Panel (a), there is no detection delay and no leakage. In Panel (b), we introduce a detection delay of  $\tau = 3$ . Panel (b) adds leakage to the setup of Panel (c), by having a randomly selected fraction  $\epsilon = 0.05$  never quarantine. For each figure, we simulate 2500 times on the same network with random initial infections, and present the average number of infections and recovered people over time, scaled per million.

**Figure S4: Impact and Costs of Different  $(k, x)$  Policies**



We examine the  $(k, x) = (2, 1)$  policy scenario in contrast with other policy options, using  $\theta = 5$ ,  $\tau = 3$ ,  $\alpha = 0.1$  and  $R_0 = 3.5$ . All of the  $(k, x)$  regional policies include a fraction  $\epsilon = 0.05$  of people who never quarantine. Using a smaller radius of  $k = 2$  with all parameters held fix is significantly less effective than with  $k = 3$ , along both the number of person-days of infection and quarantine. Note that the  $(k, x) = (2, 1)$  policies are simulated 2500 times, while the rest are simulated 10000 times.

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