

# **1 Tracing and testing the COVID-19 contact chain: cost- 2 benefit tradeoffs**

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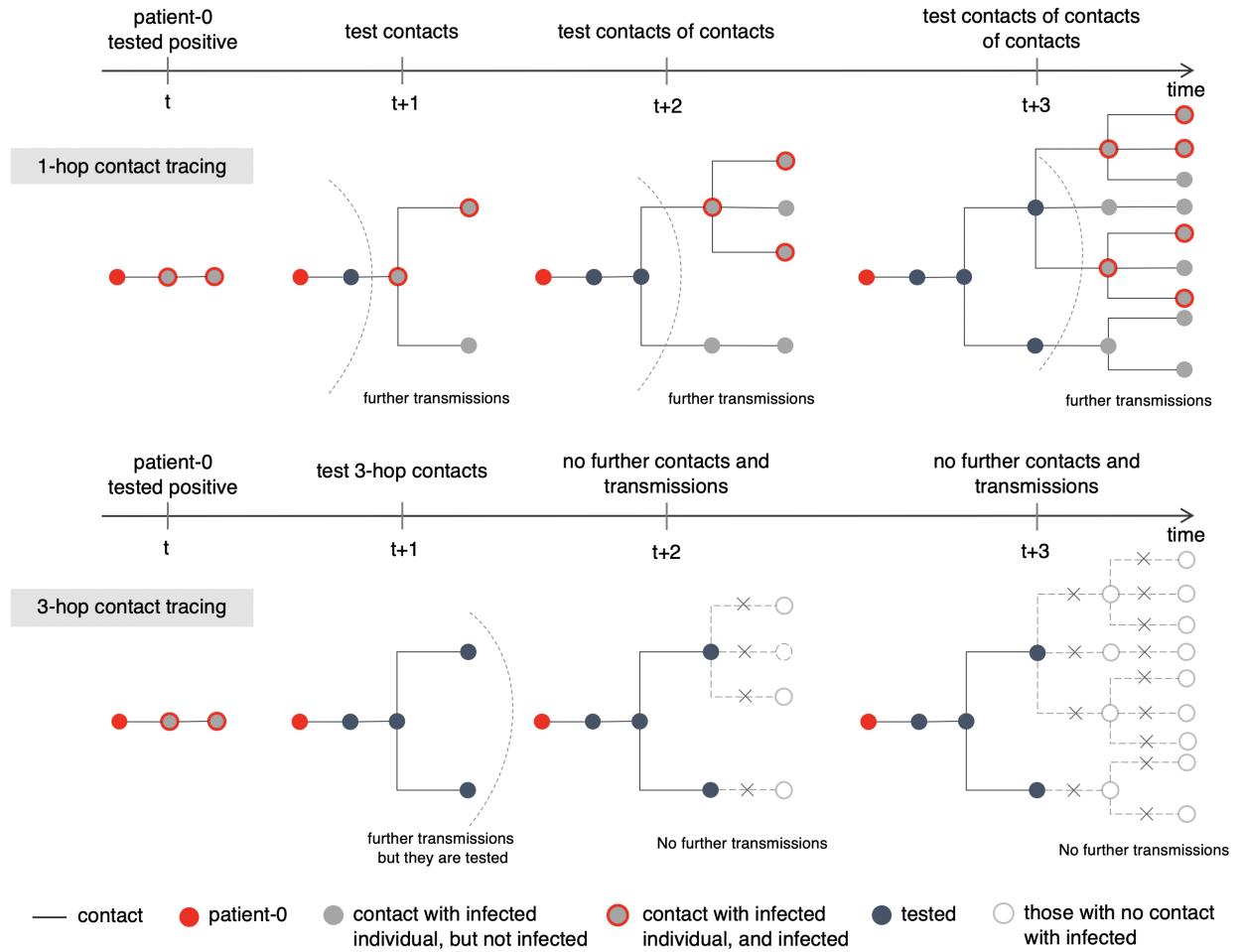
**6 Traditional contact tracing for COVID-19 tests the direct contacts of those who test positive  
7 even if the contacts do not show any symptom. But, why should the testing stop at direct  
8 contacts, and not test secondary, tertiary contacts or even contacts further down? The ques-  
9 tion arises because by the time an infected individual is tested the infection starting from him  
10 may have infected a chain of individuals. One deterrent in testing long chains of individuals  
11 right away may be that it substantially increases the testing load, or does it? We investigate  
12 the costs and benefits of testing the contact chain of an individual who tests positive. For  
13 this investigation, we utilize multiple human contact networks, spanning two real-world data  
14 sets of spatio-temporal records of human presence over certain periods of time, as also net-  
15 works of a classical synthetic variety. Over the diverse set of contact patterns, we discover  
16 that testing the contact chain can both substantially reduce over time both the cumulative  
17 infection count and the testing load. We consider elements of human behavior that enhance  
18 the spread of the disease and lower the efficacy of testing strategies, and show that testing the  
19 contact chain enhances the resilience to adverse impacts of these elements. We also discover  
20 a phenomenon of diminishing return beyond a threshold value on the depth of the chain to  
21 be tested in one go, the threshold then provides the most desirable tradeoff between benefit**

**22 in terms of reducing the cumulative infection count, enhancing resilience to adverse impacts**

**23 of human behavior, and cost in terms of increasing the testing load.**

24 To slow down the spread of COVID-19, public health authorities like the US Center for  
25 Disease Control and Prevention (CDC) have recommended to test those who have in the recent  
26 past been in physical proximity with a patient who has tested positive, even when the contacts  
27 do not exhibit any symptom [30]. This preemptive action, commonly known as contact tracing,  
28 is deployed because given how contagious the disease is, a patient is likely to have passed on  
29 the contagion to his contacts, and the infected contacts have the potential to infect others even  
30 before they show symptoms [12]. Moreover, the CDC estimates that up to 70% percent of the  
31 infected individuals are asymptomatic, showing no symptom throughout the entire course of the  
32 disease [25], and clinical research has revealed that the asymptomatic individuals can infect others  
33 [16, 29]. Testing and isolating the infected can stop these infected individuals from spreading the  
34 disease early on, that is, while they do not show symptoms, as compared to the strategy that tests  
35 only those who show symptoms and seek medical help. Slowing down the spread by testing the  
36 contacts comes at the cost of an increase in the testing load as compared to the latter policy, yet,  
37 the cost-benefit tradeoff for contact tracing is understood to be substantially favorable (cost is the  
38 testing load, benefit is the ability to contain the outbreak).

39 A question that naturally arises is if cost-benefit tradeoffs may be enhanced through general-  
40 izations of the core concept of contact tracing - this is what we seek to answer in this paper. In the  
41 time that elapses between when an individual is infected and until he is tested, the disease spreads  
42 from him through a chain of several hops - he infects those he is in contact with, those he infects



**Figure 1: Illustration of multi-hop contact tracing.** Illustration of 1-hop contact tracing (i.e., testing only the direct contacts of those who test positive) and 3-hop contact tracing (i.e., testing the direct, secondary and tertiary contacts of those who test positive). The time at which a health authority tests the patient-0 (red) was after the infection has propagated 2 hops. By  $t+3$  time units, both testing policies test 4 individuals (black) other than the patient-0; the 3-hop policy tests and isolates the positive ones in a shorter time, while 1-hop tests and isolates them progressively and therefore over longer times. Accordingly, only 3 individuals are infected under the 3-hop policy, while 10 individuals are infected under the 1-hop policy.

43 infect their contacts, the infected contacts infect their contacts, and so on. Fewer people are likely  
44 to be infected if we preemptively test not only the direct contacts of an individual who tests posi-  
45 tive, but contacts of the contacts and so on. Such testing will enable us to identify and isolate the  
46 individuals further down the chain who have imbibed the disease, earlier than if we had tested only  
47 the direct contacts of those who have tested positive and reached down the chain progressively.  
48 Earlier isolation of the infected reduces the number they infect. Does such aggressive preemptive  
49 testing schemes necessarily increase the overall number of tests? The answer is not apriori clear  
50 as reduction in overall infection spread through such a testing strategy may eventually reduce the  
51 number of tests required, as illustrated in Figure 1.

52 We formalize this aggressive preemptive testing scheme as *k-hop contact tracing (k)*, where  
53  $k = 0$  does not trace contacts and tests only those who show symptoms and seek medical help,  
54  $k = 1$  is the traditional contact tracing that tests the direct contacts of an individual who tests  
55 positive,  $k = 2$  additionally tests the contacts of the contacts,  $k = 3$  tests yet another hop of  
56 contacts, and so on. Our investigation will quantify the 1) benefits i.e., reduction in the number  
57 of individuals infected over time, 2) costs, i.e., increase in total number of tests, with increase in  
58  $k$ , for a wide variety of disease parameters, contact patterns, extent of willingness of individuals  
59 to cooperate with the health officials on testing. We investigate for a wide variety of the above  
60 parameters because values of the parameters that arise in practice are not definitively known at  
61 this nascent stage of research on the novel disease, and will in general be different for different  
62 ambiences. The goal of our investigation is to reveal if this natural generalization has any merit and  
63 provide specific policy recommendations with respect to testing strategies. We will also examine

64 whether there arises the principle of diminishing return, that is, increasing the number of hops  
65 beyond a certain *threshold* only marginally decreases the infection count but noticeably increases  
66 the testing load - if so, such threshold, which we seek to identify, provides the optimum cost-benefit  
67 tradeoff.

68 Human behavior plays an important role in determining the nature and extent of the spread  
69 of an infectious disease and the efficacy of tests:

- 70 • When a contagious individual interacts with a susceptible individual, the latter is infected  
71 with a probability whose value depends on various factors such as the duration, environment  
72 (e.g., indoor or outdoor) of the interaction, distance between interacting individuals, protec-  
73 tive gears worn by the individuals involved, personal hygiene like hand washing observed  
74 right after interactions etc. [28]. The probability is understood to be higher for longer du-  
75 rations, shorter distances, indoor environments and lower when appropriate protective gears  
76 are worn and good personal hygiene is observed [7, 26, 27]. But, ambiences that reduce  
77 probability of infection can not always be guaranteed owing to professional necessities and  
78 voluntary choices. For example, several societal interactions will have to be in indoor envi-  
79 ronments (e.g., among customers and staff of indoor businesses, fellow travelers in elevators,  
80 public transports), for long durations (inside business units, public transport, elevators), in  
81 close proximity (inside elevators, public transport). Protective gears like masks and personal  
82 hygiene like hand washing can be recommended but not enforced. The most effective masks  
83 like N95 masks may not be available for every individual and may also be inconvenient for  
84 daily use for common people, masks may not always be worn properly. The net effect of

85 all of these is that probability of infection can not be controlled and may be high in various  
86 circumstances.

- 87 • Human behavior also affects the reach of testing. It has been documented that only a frac-  
88 tion of contacts of patients who test positive can be tested, as many contacts either do not  
89 consent or can not be traced [14]; we refer to this fraction as *cooperativity*. Many contacts  
90 for example do not respond to outreach by public health authorities. Contact-tracing apps  
91 installed in wearable or hand-held devices can temporarily record contacts between individ-  
92 uals and communicate pertinent information to the centralized database once an individual  
93 tests positive [9]. Such contact tracing apps have been rolled out in Germany, Singapore,  
94 England and some states in the US. These increase the fraction of cooperativity, but still  
95 do not guarantee full cooperativity as individuals may function in areas of poor signal and  
96 may not carry their personal devices all the time. Besides downloading such apps can not be  
97 mandated owing to concerns on privacy and considerations of civil liberties and free choice.  
98 Thus their acceptance to the populace is unclear at this point. Hence cooperativity may be  
99 low in real life.

100 Resilience of a testing strategy to elements of human behavior that enhance the spread of the  
101 disease and lower the efficacy (i.e., reach) of testing constitutes an important benefit. We refer to  
102  $k$ -hop contact testing for  $k > 1$  as *multi-hop contact tracing* and ask if and in what sense multi-  
103 hop contact tracing enhances resilience compared to 1-hop contact tracing (that is, the traditional  
104 contact tracing), that is, can multi-hop contact tracing somehow offset the larger spread due to  
105 imponderables of human behavior?

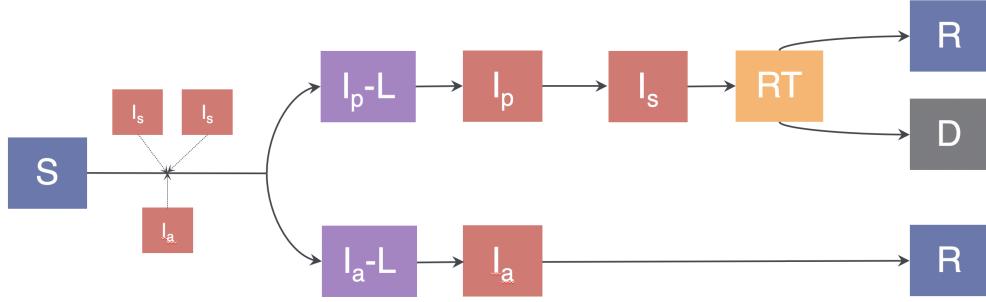


Figure 2: **Virus transmission model illustration.** The Compartmental model consists of the following compartments: Susceptible ( $S$ ), Presymptomatic-Latent ( $I_p$ -L), Presymptomatic ( $I_p$ ), Symptomatic ( $I_s$ ), Ready-to-Test ( $RT$ ), Asymptomatic-Latent ( $I_a$ -L), Asymptomatic ( $I_a$ ), Recovered ( $R$ ), and Dead ( $D$ ).

106       The significance of our investigation also draws from the fact that the testing recommendations by the regulating authorities have not been finalized yet, and recommendations are being  
 107       continually adapted as new facets are being discovered. For example, in the last few months the  
 108       CDC has changed its recommendation about testing the asymptomatic individuals multiple times  
 109       [29]. Thus, new findings about testing strategies are likely to find their way to practice now with  
 110       fewer legacy-related complications.

112       We consider a discrete time stochastic evolution of COVID-19 in a population that initially  
 113       consists of susceptible and a few contagious individuals. We model the progression of the disease  
 114       using a compartmental model (Figure 2). The disease spreads from the contagious to the suscepti-  
 115       ble individuals through mutual interaction. In any given interaction with a contagious individual,  
 116       a susceptible is infected with a probability. After a *latency period* (the presymptomatic-latent  
 117       and asymptomatic-latent are in this latency period), the newly infected individuals become conta-

118 gious. Specifically, at the end of the latency period, the individuals either become *presymptomatic*  
119 (the stage before exhibiting symptoms), or *asymptomatic* (that is, they never show symptoms).  
120 Presymptomatics proceed to become *symptomatics* in the next stage. Presymptomatics, asymp-  
121 tomatics, symptomatics all however are contagious.

122 We assume that test results are obtained in the same day, owing to the availability of reliable  
123 RT-PCR and antigen tests that are able to do so [11, 23] (recent antigen test authorized by the FDA  
124 under an emergency use can give results in 15 minutes with 97.1% sensitivity).

125 Given the imponderables of human behavior, we consider a range of values for the parameters  
126 they affect directly, namely, cooperativity and probability of infection. For the former we consider  
127 the following values: 0.2, 0.5, 1.0. In addition, we assume that the contacts who can be identified  
128 are identified within a day, contact-tracing apps can provide such turnaround times and can be  
129 easily modified to trace and alert indirect exposures through iterative algorithms. Tests can then be  
130 scheduled the next day through the same apps. As to the probability of infection, we use this term to  
131 denote the probability with which a symptomatic individual infects a susceptible individual during  
132 a contact, and consider the following values: 0.04, 0.2, 0.4. We consider that a presymptomatic  
133 individual infects a susceptible with the same probability as a symptomatic individual, and that an  
134 asymptomatic individual infects a susceptible with 0.75 times this probability [25].

135 We have simulated  $k$ -hop contact tracing for  $k = 0, 1, 2, 3$  to large values of  $k$  for con-  
136 tact patterns obtained from real-world data and various synthetic topologies. We consider two  
137 contact networks obtained from real-world data of: 1) physical proximity of university students

138 obtained from their smartphones equipped with Bluetooth over 28 days, as part of the Copenhagen  
139 Networks Study [22] (*University student contact network*), and 2) locations and time-stamps of  
140 individuals in Tokyo, Japan which they provide over a social network (Foursquare) over 100 days  
141 [32] (*Foursquare contact network*). These capture certain semblances of reality in that they are  
142 obtained from spatio-temporal records of actual human presence; here the contact patterns vary  
143 over time which is also what happens in reality. Yet, these are but constructed from only two sets  
144 of data, which may not be representative of all contact patterns. We therefore examine whether  
145 the phenomena observed in these also recur in some other very different networks, namely in two  
146 examples of classical synthetic networks: Erdős Rényi and scale-free networks. These two exam-  
147 ples complement each other in some fundamental characteristics such as in the nature of the degree  
148 distribution. The degrees of the nodes represents the number of contacts of the corresponding in-  
149 dividuals. The Erdős Rényi network is more regular, in that there is relatively low variance in the  
150 degree distribution. The scale-free network, on the other hand, has some nodes with high degrees  
151 (perhaps representing celebrities who interact with a large number of individuals) and many more  
152 nodes with low degrees (representing common folks); the degree distribution therefore has a high  
153 variance. For these the connections do not change over time, they are static in this sense. Any  
154 phenomenon that is observed in the four very different types of networks modeling human contact  
155 patterns is likely to recur extensively.

156 Refer to Methods for details on the systems we consider, the parameters we choose and  
157 further justification for the choices and the limitations thereof.

## 158 Results

159 We start with a summary of our important findings from the simulations for  $k$ -hop contact tracing  
160 that we perform for  $k = 0, 1, 2, 3, \dots$ . We observe the following for multi-hop contact tracing  
161 (which is  $k$ -hop contact testing for  $k > 1$ ):

162 • *Benefit of multi-hop contact tracing:* Multi-hop contact tracing considerably reduces the total  
163 number of infections over time compared to 1-hop contact tracing (that is, the traditional contact  
164 tracing). The reduction is higher with 1) increase in probability of infection 2) the decrease in  
165 cooperativity 3) decrease in the latency period. In addition, multi-hop contact tracing substan-  
166 tially reduces the average daily new infection count in the *peak infection period* (time until the  
167 daily new infection count peaks) compared to 1-hop contact tracing.

168 • *Cost of multi-hop contact tracing:* Over time the overall number of tests required in multi-  
169 hop contact tracing is usually *lower*, than that in 1-hop contact tracing. But, studying how the  
170 number of tests changes with time, initially the number of tests needed for multi-hop is somewhat  
171 (considerably in few instances) higher than for 1-hop contact tracing.

172 Increasing the value of  $k$  from  $k = 1$ , the number of infections and the number of tests over  
173 time decreases up to a threshold value of  $k$  (we observe that this threshold value is  $k = 2$  or  $k = 3$   
174 in our simulations). Formally, we define the threshold point as the value of  $k$  at which the overall  
175 number of tests required (cost) is minimized. As  $k$  increases beyond this threshold value, we see a  
176 phenomenon of *diminishing return*, that is, the number of infections only marginally decreases and  
177 number of tests increases (considerably, in some instances). We substantiate the above findings

178 with the results reported in Figures 3, 4, and 6; Figures 3 and 4 are for contact networks obtained  
179 from real-world data and Figure 6 is for synthetic topologies. In each case we report the average  
180 of 1000 simulation runs on given topologies.

181 We start with contact networks obtained from real-world data. We first consider the highest  
182 probability of infection (i.e., 0.4) and lowest cooperativity (i.e., 0.2) from our range of choices  
183 for the University student contact network. Recall that probability of infection and cooperativity  
184 are determined by human behavior and their respective increase and decrease enhance the spread  
185 of the disease and lower the reach of testing. Thus, this scenario represents a combination of  
186 elements of human behavior that render a populace most vulnerable to a pandemic (among our  
187 parameter choices). As  $k$  increases from 0 to 3, the cumulative number of infections considerably  
188 decreases, and subsequently decreases only marginally with further increase in  $k$ . 3-hop contact  
189 tracing achieves 80% reduction in the cumulative number of infections compared to 0-hop contacts  
190 tracing (i.e., no contact tracing), while 1-hop contact tracing achieves only 30% reduction (top left  
191 of Figure 3a). The total number of tests for  $k$ -hop contact tracing steadily decreases with increase  
192 in  $k$  from  $k = 1$  to  $k = 3$ , and subsequently steadily increases as  $k$  increases further. This number  
193 is minimized for 3-hop contact tracing, at which value 27% fewer tests are required, overall, than  
194 1-hop tracing (bottom left of Figure 3a). Thus, the threshold value is  $k = 3$ . Studying how the  
195 daily number of tests varies with time, it is somewhat higher initially for 3-hop contact tracing, but  
196 rapidly declines soon, as compared to 1-hop contact tracing (top of Figure 5a), leading to overall  
197 fewer number of tests for multi-hop contact tracing. These observations may be explained as  
198 follows. Multi-hop contact tracing may test greater number of individuals in early stages because it

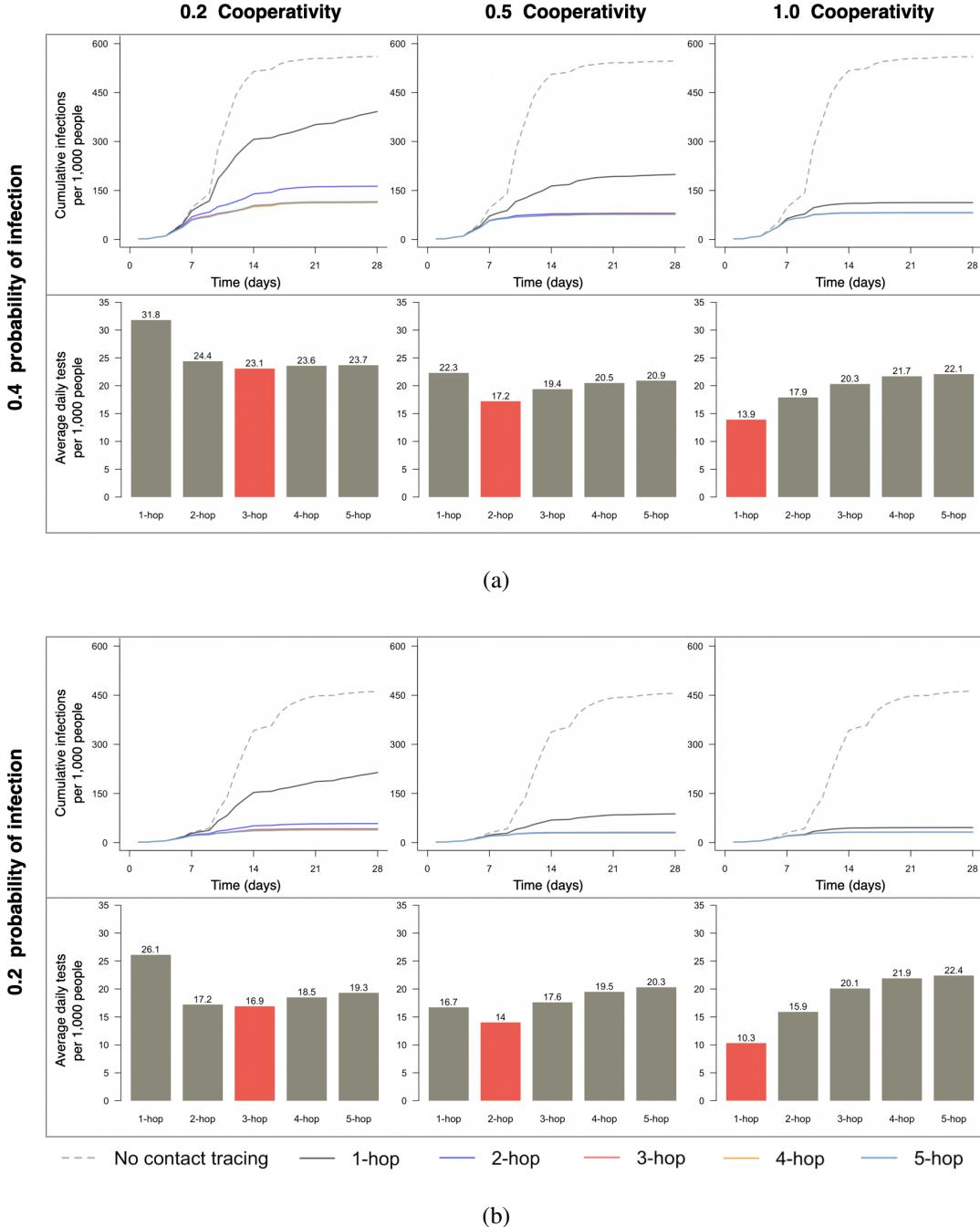


Figure 3: The cumulative number of infections and average daily tests required for  $k$ -hop contact tracing for various values of  $k$  for University student contact network. The red colored bar corresponds to the threshold value for  $k$ . For  $k$  exceeding the threshold value, the curves for the cumulative number of infections heavily overlap and become indistinguishable.

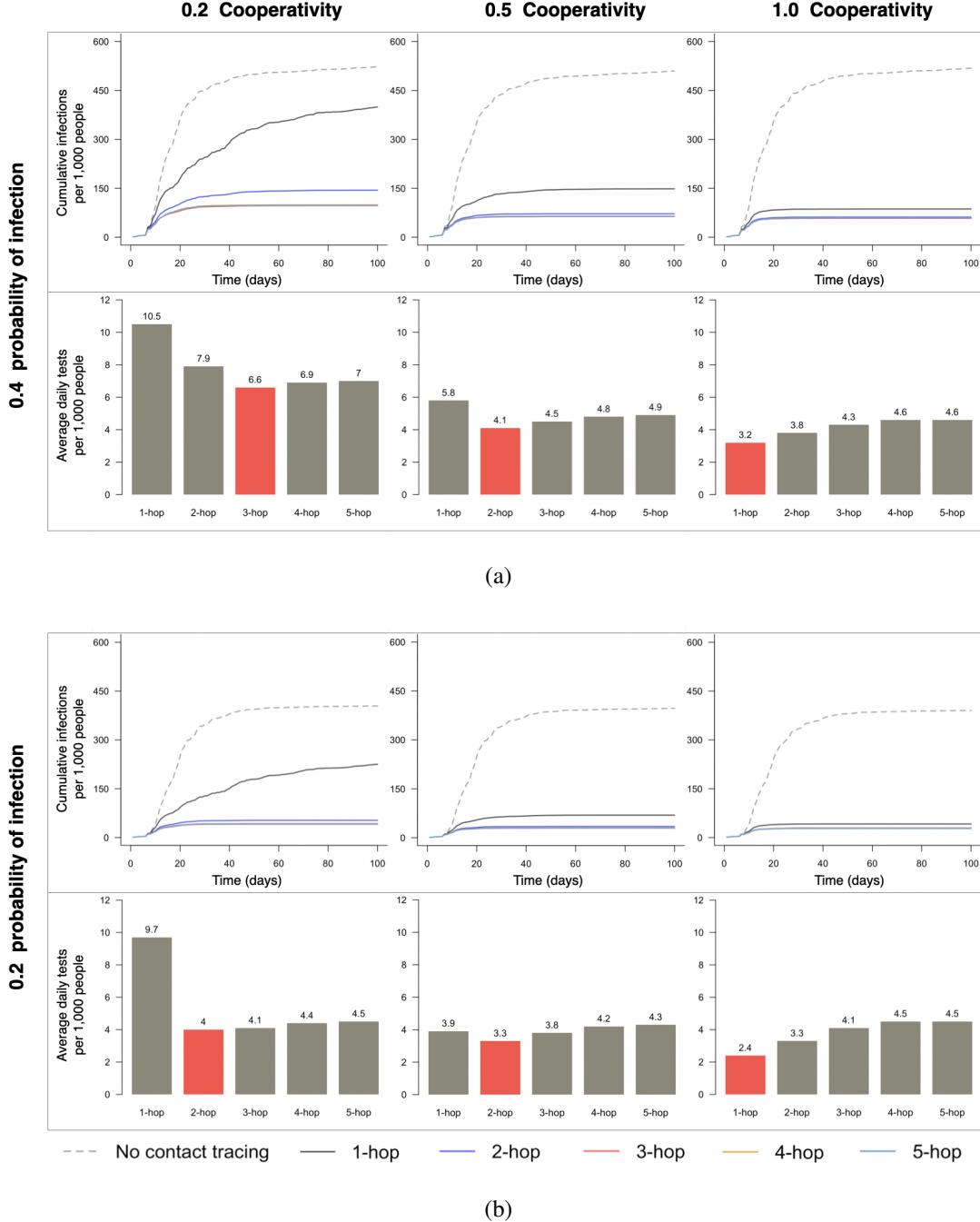


Figure 4: The cumulative number of infections and average daily tests required for  $k$ -hop contact tracing for various values of  $k$  for *Foursquare contact network*. The red colored bar corresponds to the threshold value for  $k$ . For  $k$  exceeding the threshold value, the curves for the cumulative number of infections heavily overlap and become indistinguishable.

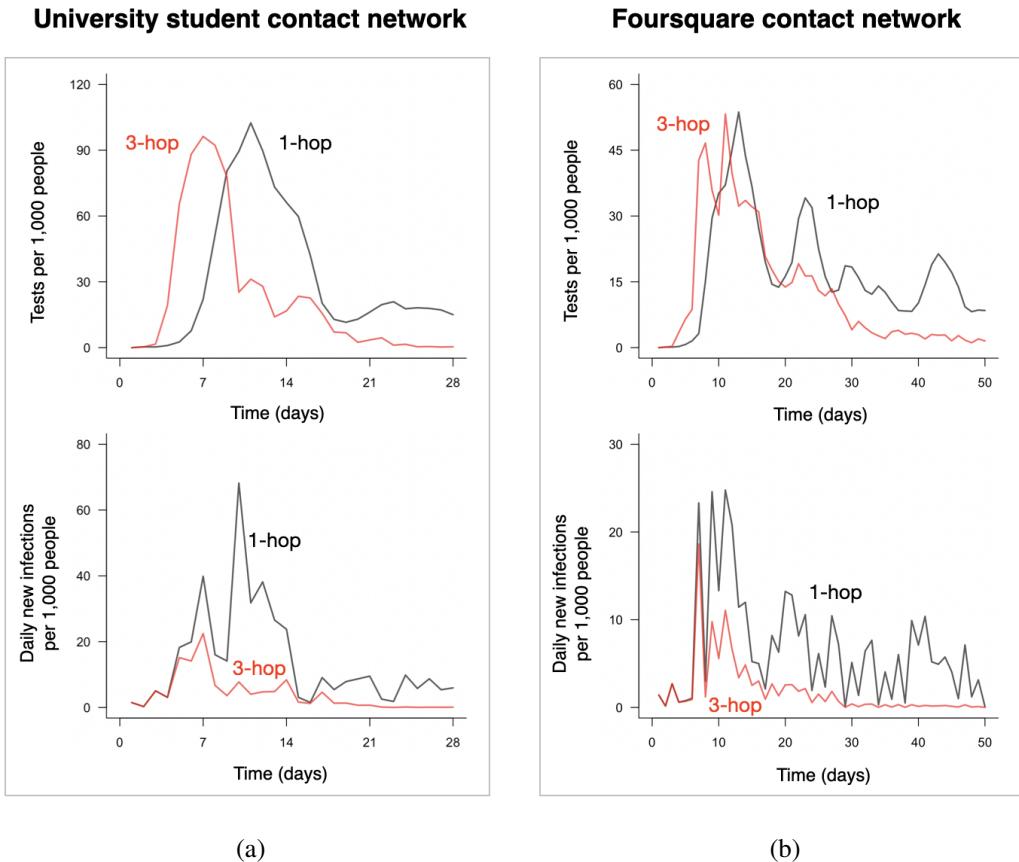


Figure 5: The number of tests over time and daily new infections over time for *University student contact network* and *Foursquare contact network*. The plots compare the numbers for 1-hop and  $k$ -hop contact tracings when  $k$  equals the corresponding threshold value. The first and the second column have been obtained for the same setups as the first column in Figure 3a and 4a, respectively.

199 traces up to more hops even from the same number of confirmed cases (top of Figure 5a). However,  
200 this aggressive preemptive testing from early stages can rapidly mitigate the spread of infection  
201 earlier than 1-hop contact tracing through early identification and isolation of the infected (bottom  
202 of Figure 5a), thus fewer number of individuals transmit the virus and need tests with passage of  
203 time. The latter phenomenon more than compensates for the larger number of tests required in  
204 early stage for multi-hop contacts of those who test positive.

205 The above phenomena also recurs in the other contact network we obtain from real-world  
206 data, namely the Foursquare contact network. Figures 4 and 5b for the Foursquare contact network  
207 show identical trend as Figures 3 and 5a respectively for the University student contact network.  
208 For the same probability of infection (i.e., 0.4) and cooperativity (i.e., 0.2), the threshold is again  
209  $k = 3$ . Again, the cumulative number of infections considerably decreases, as  $k$  increases from 0 to  
210 the threshold point of 3, and with subsequent increase in  $k$  the decrease in the cumulative number  
211 of infections is only marginal. 3-hop contact tracing achieves 81% reduction in the cumulative  
212 number of infections compared to 0-hop contact tracing, while 1-hop contact tracing achieves only  
213 24% reduction (top left of Figure 4a). 37% fewer tests are required, overall, for 3-hop contact  
214 tracing as compared to 1-hop tracing (bottom left of Figure 4a). Again, although as compared to  
215 1-hop contact tracing, 3-hop contact tracing initially needs somewhat higher number of daily tests,  
216 the number of daily tests in 3-hop contact tracing rapidly declines soon (top of Figure 5b), leading  
217 to overall fewer number of tests for 3-hop contact tracing. The higher number of tests in the early  
218 stages helps contain the spread of infection rapidly (bottom of Figure 5b).

219 All the phenomena reported above is replicated for other parameters for both the University

220 student and Foursquare contact networks (other subfigures of Figure 3 and Figure 4), but the extent  
221 of the advantage and values of the thresholds differ. The differences in the specific numbers reveal  
222 that multi-hop contact tracing is more *resilient* to components of human behavior that enhance the  
223 spread of the disease and lower the reach of testing:

- 224 • When cooperativity increases to 1, the reach of testing is higher, and the efficacy of 1-hop  
225 tracing increases substantially. In University student contact network, it reduces cumulative  
226 infections by 80% compared to 0-hop tracing (top right of Figure 3a). In Foursquare contact  
227 network, it reduces cumulative infections by 83% compared to 0-hop tracing (top right of  
228 Figure 4a). Comparing the results for cooperativities of 1 and lower, we note that multi-  
229 hop contact tracing can offset the limitation arising from the lack of available information on  
230 contacts. This is because decrease in cooperativity reduces the reach of tests while multi-hop  
231 contact tracing increases the reach.
- 232 • As probability of infection decreases, the disease spreads slower, and 1-hop contact tracing  
233 becomes more and more effective, and the threshold value generally decreases (or remains  
234 the same). For University student contact network, refer to Figure 3b for the intermediate  
235 value of 0.2 for the probability of infection, and to Figure 8 in Supplementary Information  
236 for the lowest value of 0.04. For Foursquare contact network, refer to Figure 4b for the  
237 intermediate value of 0.2 for the probability of infection, and to Figure 9 in Supplementary  
238 Information for the lowest value of 0.04. In other words, therefore, employing multi-hop  
239 contact tracing is more beneficial when probability of infection is high.

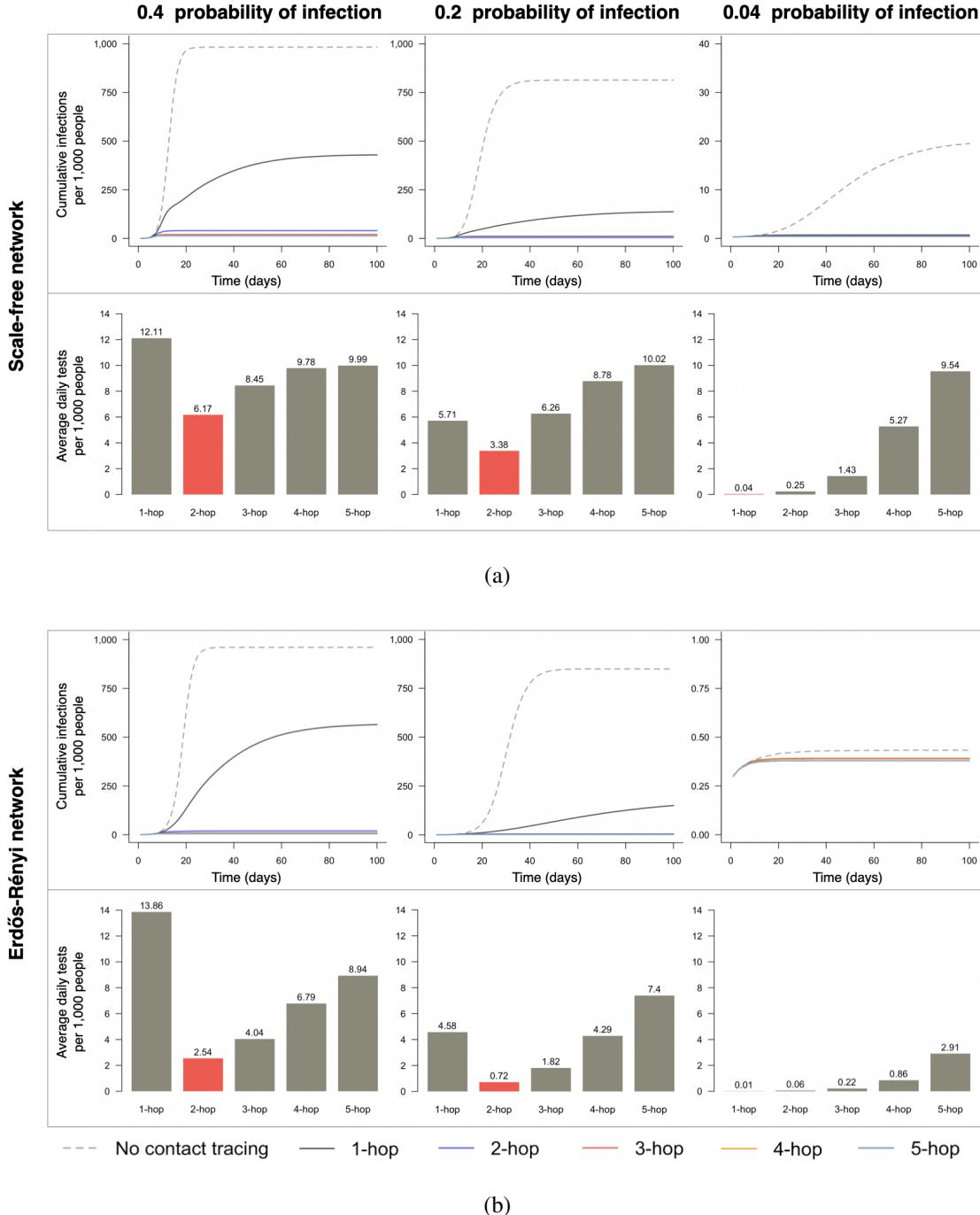


Figure 6: The cumulative number of infections and average daily tests required for  $k$ -hop contact tracing for various values of  $k$  for synthetic networks. The red colored bar corresponds to the threshold value for  $k$ . For  $k$  exceeding the threshold value, the curves for the cumulative number of infections heavily overlap and become indistinguishable.

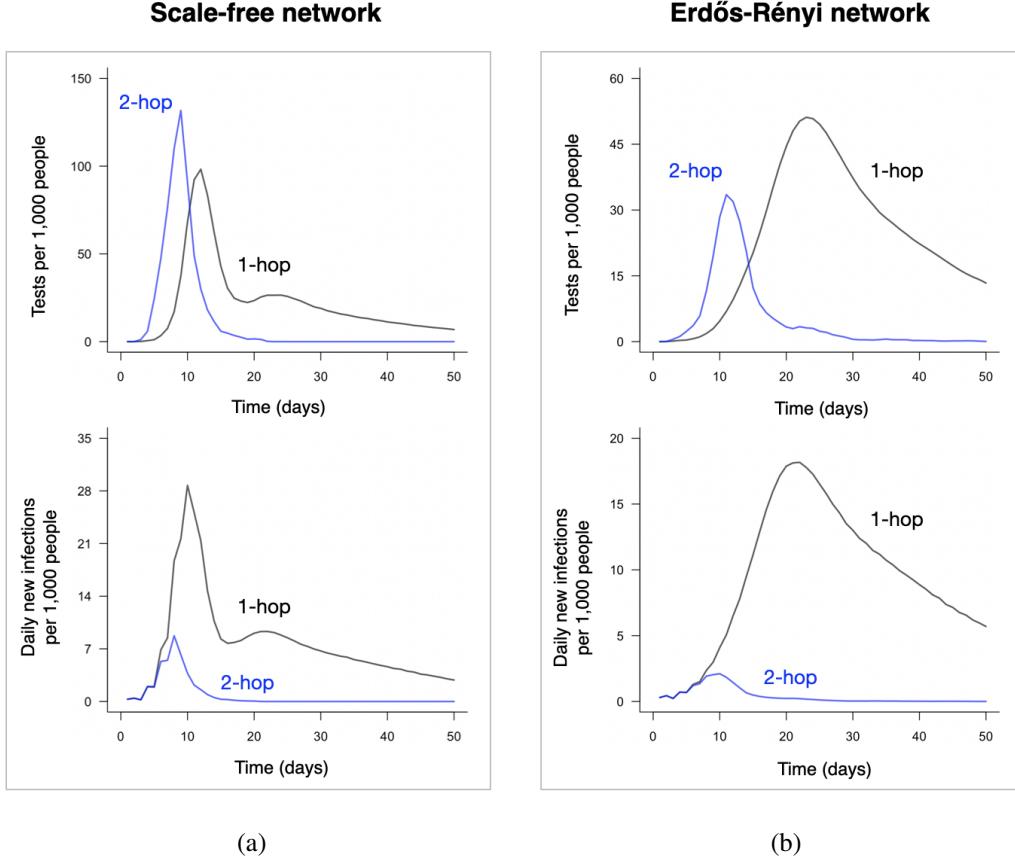


Figure 7: **The number of tests over time and daily new infections over time for synthetic networks.** The plots compare the numbers for 1-hop and  $k$ -hop contact tracings when  $k$  equals the corresponding threshold value. The first and the second column have been obtained for the same setups as the first column in Figure 6a and 6b, respectively.

240 We consider synthetic networks now (Figure 6). All the phenomena reported above is repli-  
241 cated, but the specifics differ. When probability of infection is 0.4, the threshold value is 2 for both  
242 the scale-free and Erdős Rényi networks (first column in Figure 6). In the two cases, despite the  
243 fact that the overall number of tests required in 2-hop contact tracing is significantly lower than  
244 that in 1-hop contact tracing, 2-hop contact tracing reduces the cumulative number of infections by  
245 96% and 98%, respectively compared to 0-hop tracing, while 1-hop tracing reduces by 56% and  
246 41%, respectively (top left of Figure 6a and 6b). The phenomenon of diminishing return is even  
247 more accentuated in these as the number of tests sharply increase with increase in  $k$  beyond  $k = 2$   
248 for  $k$ -hop contact tracing (bottom left of Figure 6a and 6b). Also, considering the variation of the  
249 number of tests over time, we notice that in scale-free networks, the number is significantly higher  
250 for multi-hop contact tracing than that for 1-hop contact tracing *initially* (top of Figure 7a). But,  
251 the decline in the number of tests required for multi-hop contact tracing becomes equally precip-  
252 itous over time, and the rapid decline starts in a short time from the start of the testing period as  
253 well. Figure 6 plots the average of 1000 simulation runs over 1 realization of the synthetic topo-  
254 logies, Figure 11 in Supplementary Information reports the average of 100 runs over 10 realizations  
255 of the same synthetic topologies, corresponding plots in Figure 6 and Figure 11 show identical  
256 trend.

257 We now focus on the peak infection period and the average daily new infection count during  
258 this period for all the contact networks considered above. The duration of this period is a measure  
259 of how soon the infection is contained. The average daily new infection count during this period  
260 is a measure of the treatment-load health care centers experience in a critical period in which

261 these have the potential to be overwhelmed. Under multi-hop contact tracing the peak infection  
262 period is shorter, in some cases considerably shorter, and the average daily new infection count  
263 during this period is invariably substantially lower, and therefore the healthcare facilities run lower  
264 risk of being overwhelmed. For example, in University student contact network and Foursquare  
265 contact network, considering the parameters as the first column in Figure 3a and 4a, respectively,  
266 for 3-hop contact tracing, the peak infection periods are 7 and 7 days, respectively, and an average  
267 of 8.8 (per 1000 population) and 3.6 (per 1000 population) daily new infections occurs during  
268 this period, respectively. On the other hand, for 1-hop contact tracing in these networks, the peak  
269 infection periods are 10 and 11 days, and an average of 18.6 (per 1000) and 8.6 (per 1000) daily new  
270 infections occurs during this period, respectively (Figure 5). Next, in scale-free and Erdős Rényi  
271 networks, considering the parameters as the first column in Figure 6, under 2-hop contact tracing,  
272 the peak infection periods are 8 and 10 days, respectively, and an average of 3 (per 1000) and 1.1  
273 (per 1000) daily new infection occurs during this period, respectively. On the other hand, for 1-hop  
274 contact tracing in these topologies, the peak infection periods are 10 and 22 days, respectively,  
275 and an average of 8.9 (per 1000) and 7.7 (per 1000) daily new infections occurs during this period,  
276 respectively (Figure 7). Note that multi-hop contact tracing substantially reduces the peak infection  
277 period in Erdős Rényi network.

278 We now examine how increase in the latency period affects the results. In this case, the in-  
279 fected individuals become contagious later, thus, the potential of 1-hop contact tracing to detect and  
280 remove individuals before they become contagious or in the early period of their becoming con-  
281 tagious increases. Comparing the results for randomized latency periods of two different means,

282 we note that this is indeed the case. In University student contact network, when the mean latency  
283 period is 1 day (2 days, respectively), 1-hop contact tracing can achieve 30% (43%, respectively)  
284 reduction in the cumulative number of infections compared to 0-hop contact tracing, and 3-hop  
285 contact tracing can achieve 80% (86%, respectively) reduction. In Foursquare contact network,  
286 when the mean latency period is 1 day (2 days, respectively), 1-hop contact tracing can achieve  
287 24% (33%, respectively) reduction in the cumulative number of infections compared to 0-hop con-  
288 tact tracing, and 3-hop contact tracing can achieve 81% (86%, respectively) reduction. In scale-free  
289 network, when the mean latency period is 1 day (2 days, respectively), 1-hop contact tracing can  
290 achieve 56% (71%, respectively) reduction in the cumulative number of infections compared to  
291 0-hop contact tracing, and 2-hop contact tracing can achieve 96% (98%, respectively) reduction.  
292 In Erdős Rényi network, when the mean latency period is 1 day (2 days, respectively), 1-hop con-  
293 tact tracing can achieve 41% (58%, respectively) reduction in the cumulative number of infections  
294 compared to 0-hop contact tracing, and 2-hop contact tracing can achieve 98% (99%, respectively)  
295 reduction. Refer to Figure 12 in Supplementary Information for a bar-graph representation of this  
296 data.

## 297 Discussion

298 Our findings obtained through extensive simulations over a diverse set of four contact networks,  
299 starting from those obtained from real-world data to synthetic networks show that multi-hop con-  
300 tact tracing has the potential to substantially reduce total number of infections (which would in  
301 turn reduce fatalities and treatment load on healthcare facilities) and reduce overall testing load. It

302 is more resilient to elements of human behavior that enhance the spread of the disease and lower  
303 the reach of testing. It also helps contain COVID-19 outbreaks within shorter times and reduces  
304 average daily new infection counts, specifically in the period up to when the daily new infection  
305 count peaks, which would in turn reduce the treatment load on healthcare facilities during the  
306 peak period. All these collectively have the potential to contain the outbreak without extensive  
307 lockdowns and economic downturns.

308 Our findings lead to the following recommendations for public health authorities:

- 309 • Deploy multi-hop contact tracing; usually testing up to secondary or tertiary contacts of  
310 those who test positive suffices.
- 311 • The recommended number of hops are on the higher end of the above range for lower latency  
312 periods and when human behavior enhances the spread of the disease and lowers the reach  
313 of testing, that is: 1) the probability of infection in each contact is high (e.g., from indoor  
314 contacts, longer durations of contacts, lack of protective gears and personal hygiene) 2)  
315 cooperativity is low. Given the imponderables in human behavior, the probability of infection  
316 and cooperativity can not usually be accurately estimated apriori. Thus, it is safer to err on  
317 the side of caution and opt for the higher end of the recommended range on the number of  
318 hops.
- 319 • Create the infrastructure for handling a larger testing load for limited periods, which will  
320 lead to a reduction in the overall testing load over time with the daily testing load expected  
321 to decline shortly after the testing starts (if multi-hop contact tracing is deployed).

322 Finally, multi-hop contact tracing may provide similar benefits for other infectious diseases which  
323 exhibit silent propagation (infection from individuals who do not show symptoms).

324 Note that the contact tracing recommendation of the CDC involves both testing and quar-  
325 antining (even when the test result is negative) the direct or primary contacts of those who test  
326 positive. Along the same lines, recent works considered tracing and quarantining (or testing) the  
327 direct contacts of those who tested positive [1, 6, 9, 13]. Another recent work considered tracing  
328 and quarantining both primary and secondary contacts of those who test positive, and found that  
329 quarantining secondary contacts decreases the cumulative infection count compared to quarantin-  
330 ing only the primary contacts, but also requires substantially higher number of quarantines [10];  
331 [10] appears to reject the notion of quarantining secondary contacts and did not therefore explore  
332 quarantining tertiary or even more distant contacts. It does not investigate testing the primary and  
333 secondary contacts, perhaps because they would be quarantined regardless of the test results. We  
334 instead explore tracing and testing multi-hop contacts, testing eliminates the need for extensive  
335 quarantining as only those who test positive need to be isolated. Our results show that multi-hop  
336 contact tracing even reduces the number of tests required. The difference between our finding  
337 and the recent work arises because quarantine is a cumulative process in which each contact is  
338 quarantined for several days, while tests related to each positive patient are done only once. As  
339 to the primary contacts of those who test positive, we take no position on whether they should be  
340 quarantined even when they test negative, and leave that to the policies of the relevant public health  
341 authorities.

342 We now discuss the scenarios in which some of our assumptions may not hold. Tracing con-

343 tacts and scheduling tests for those traced may require more than a day when individuals do not  
344 use contact tracing apps. PCR test results are not obtained same day if the testing site and labora-  
345 tory are not co-located, though this delay may not affect the broad nature of our findings if those  
346 tested quarantine until the test results are known. Antigen tests give results in an hour but some of  
347 them reportedly record non-negligible proportion of false negatives. Depending on classifiers such  
348 as duration, environment (indoor or outdoor), usage of protective gears, observance of personal  
349 hygiene, different contacts may pass on infection with different probabilities. Assuming that such  
350 a probability is identical for all contacts with same infectious categories, which is what we did,  
351 is equivalent to considering an average over all contacts. Explicitly investigating the impact of 1)  
352 delay in tracing contacts and obtaining test results 2) errors in test results 3) non-uniform infection  
353 probabilities constitute directions for future research.

354 **Methods**

355 **Construction of contact networks from real-world data.** Our goal has been to evaluate the  
356 multi-hop contact tracing strategy using publicly-available data of human contact patterns. For  
357 evaluating the impact of multi-hop contact tracing, data sets need to involve large population sizes,  
358 otherwise length of the contact chains will be limited by the size of the target populace. Also, in  
359 reality, pandemic spread involves large target populaces and over several days, weeks and months.  
360 Data of human contact patterns is not plentiful in the public domain due to privacy and other  
361 concerns, the availability becomes even less for contact patterns of even moderate population sizes  
362 and over moderate periods of times (e.g., even several weeks). Nonetheless, we construct two  
363 different contact networks from data of real-world spatio-temporal records of human presence

364 over certain periods of time: (1) University student contact network and (2) Foursquare contact  
365 network.

366 For the University student contact network, we utilize data collected by smartphones of Uni-  
367 versity students, as part of the Copenhagen Networks Study [22]. The smartphones were equipped  
368 with Bluetooth cards which recorded proximity between participating students at 5-minute reso-  
369 lution. According to the definition of *close contact* by CDC [30], we only used proximity events  
370 between individuals that lasted more than 15 minutes in a row in the same day to construct daily  
371 contact networks. We postulated that two individuals had a contact if there are at least three consec-  
372 utive proximity events with a 5-minute resolution between them. The constructed contact network  
373 has 2959.82 daily contacts on average among 672 individuals spanning 28 days. The strength of  
374 this data set is that it provides actual proximity events of a moderate number of individuals over  
375 several weeks (a moderate period of time).

376 For the Foursquare contact network, we utilized the data that users of Foursquare service (a  
377 Location-Based Social Networking or LBSN) made available in Social Media about their locations  
378 in Tokyo, Japan along with time-stamps. This dataset contains advertised locations (or check-  
379 ins) collected for about 10 months (from 12 April 2012 to 16 February 2013). Each check-in  
380 contains information about the time at which the user visited the location, the GPS coordinates of  
381 the locations, and the nature of the locations (e.g., coffee shops, restaurants etc.) [32]. We use the  
382 first 100 days of data with at least one check-in. The strength of this data set is that it provides actual  
383 time-stamped locations of a large number of individuals, more than 2000, over several months (a  
384 long period of time). The weakness is that the contacts are still sparser than what arises in reality

385 as the locations in question are usually crowded and much larger number of individuals actually  
386 visit these locations in overlapping time intervals but their whereabouts are not being reported in  
387 this dataset as they do not use this LBSN. The contact network will become denser if their presence  
388 can be considered. To compensate for this artificial sparsity we construct contact patterns based on  
389 the available data by postulating that people have had a contact if they have been at the same venue  
390 in the same day. Note that in reality individuals who have been at the same location in the same  
391 day do not always do so at the same time and are therefore not always in physical proximity to  
392 pass on the disease from one to another. Thus, the contact pattern we consider is denser than what  
393 the dataset actually provides, which may compensate for the artificial sparsity in question. The  
394 constructed contact network of Foursquare users has 5553.71 daily interaction on average among  
395 2120 individuals.

396 The University student network involves spatio-temporal records of a smaller number of  
397 individuals and over a shorter period of time as compared to the Foursquare contact network. The  
398 contacts in the former are however based on actual proximity, while those in the latter are based  
399 on visits to the same location during the same day. Thus these two networks have complementary  
400 strengths and weaknesses. The evaluations can be repeated on more accurate and expansive contact  
401 patterns, which would combine the strengths of the two contact networks above, as they become  
402 available through collective efforts and enrichment of existing data repositories.

403 Finally during the contacts in these two contact networks a contagious individual passes the  
404 disease on to a susceptible individual with a certain probability (we mention how we choose these  
405 probabilities where we provide details on the Compartmental model of virus transmission and in

406 Table 1 in Supplementary Information).

407 **Synthetic networks** The synthetic topologies consist of scale-free network [2, 3] and Erdős Rényi  
408 random network [3, 8]. Figure 6 have been provided for only one realization of scale-free network  
409 and Erdős Rényi random network, Figure 11 in Supplementary Information however shows plots  
410 of averages over 10 realizations of each.

411 The scale-free network topologies are generated by Barabási-Albert method where new  
412 nodes are added at each time step with  $m$  links that connect to existing nodes with a probabil-  
413 ity being proportional to the degree of the existing nodes; we set  $m = 2$  to generate the net-  
414 work. We consider topologies of 10,000 nodes and 19,997 edges, thus average degree of a node  
415 is  $\langle k \rangle = 3.9994$ . For the single realization we use in Figure 6a, diameter and average path length  
416 are 9 and 5.01, respectively. Figure 10a in Supplementary Information shows that for the one real-  
417 ization we consider in Figure 6a, the degree distribution is well approximated by power-law with  
418 degree exponent 3, as should be for scale-free networks with the same degree exponent. Thus, the  
419 single realization in question is a typical scale-free network.

420 The Erdős Rényi network consists of 10,000 nodes which are connected with 20,000 ran-  
421 domly placed edges, thus the average degree of a node is  $\langle k \rangle = 4$ . For the one realization we  
422 consider in Figure 6b, diameter (i.e., the greatest distance between pair of nodes of connected  
423 components) is 14 and average path length (i.e., average distance along the existing paths) is 6.76.  
424 Figure 10b in Supplementary Information shows that for the one realization we consider in Figure  
425 6b, the degree distribution is well approximated by Poisson distribution with parameter  $\langle k \rangle$ , as  
426 should be for Erdős Rényi random networks. Thus, the single realization in question is a typical

427 Erdős Rényi random network.

428 **Compartmental model of virus transmission.** We use a *discrete time compartmental disease*  
429 *model* to model the progression of COVID-19 where the transition from each compartment to  
430 the next happens after a random amount of time with a geometric distribution. Compartmental  
431 model is also used in [1, 31]. Different stages of the disease are shown in Figure 2. The Com-  
432 partmental model consists of the following stages: *Susceptible* ( $S$ ), *Presymptomatic-Latent* ( $I_p$ - $L$ ),  
433 *Presymptomatic* ( $I_p$ ), *Symptomatic* ( $I_s$ ), *Ready-to-Test* ( $RT$ ), *Asymptomatic-Latent* ( $I_a$ - $L$ ), *Asymp-*  
434 *tomatic* ( $I_a$ ), *Recovered* ( $R$ ), and *Dead* ( $D$ ). Only symptomatic individuals show symptoms, while  
435 presymptomatic, symptomatic and asymptomatic individuals infect others.

436 When a susceptible ( $S$ ) individual comes into contact with a symptomatic ( $I_s$ ) individ-  
437 ual, he is infected with the probability of infection  $\beta_s$ . Similarly, a presymptomatic ( $I_p$ ) and an  
438 asymptomatic ( $I_a$ ) individual infects a susceptible upon contact with probabilities,  $\beta_p (= \gamma_p \beta_s)$ ,  
439  $\beta_a (= \gamma_a \beta_s)$ , respectively, where  $\gamma_p$  and  $\gamma_a$  are respectively infectiousness of presymptomatic and  
440 asymptomatic individuals relative to symptomatic individuals. If a susceptible individual  $i$  inter-  
441 acts with  $l$  symptomatic,  $m$  presymptomatic, and  $n$  asymptomatic individuals at time  $t - 1$ , the  
442 probability that the susceptible individual is infected at time  $t$  is  $1 - (1 - \beta_s)^l (1 - \beta_p)^m (1 - \beta_a)^n$ .

443 Once an individual is infected he becomes contagious after a geometrically distributed la-  
444 tency time, whose statistics depends on whether he will develop symptoms at some point or  
445 otherwise. Following the nomenclature in compartmental models already utilized for COVID-  
446 19, we assume that an infected individual becomes asymptomatic-latent (with probability  $p_a$ ) or  
447 presymptomatic-latent (with probability  $1 - p_a$ ). The asymptomatic-latent ( $I_a$ - $L$ ) individuals never

448 develop symptoms, do not infect others for an mean latency duration of  $1/\lambda$ , and subsequently be-  
449 come contagious, at which stage we call them asymptomatic or  $I_a$  for simplicity. An asymptomatic  
450 individual remains contagious for a geometrically distributed random duration with mean  $1/r_a$ , af-  
451 ter which he recovers. We now consider the other compartment an individual enters after infection,  
452 the presymptomatic-latent compartment. A presymptomatic-latent individual becomes contagious  
453 after a mean latency period of  $1/\lambda$ , at which point we call him presymptomatic or  $I_p$ . He remains  
454 presymptomatic for a geometrically distributed duration with mean  $1/\alpha$ ; after this duration he de-  
455 velops symptoms and is called symptomatic. A symptomatic individual continues to infect his  
456 contacts until he opts for testing ( $RT$ ). The duration for which a symptomatic individual infects  
457 others is geometrically distributed with mean  $1/w$ . Once this duration ends, the patient quaran-  
458 tines himself and does not infect others. He ultimately dies ( $D$ ) with probability  $p_d$ , or recovers  
459 ( $R$ ) with probability  $1 - p_d$ , after a geometrically distributed duration whose mean is  $1/r_s$ . We do  
460 not consider that individuals can be reinfected.

461 In all the networks, except in the University student contact network, we consider that ini-  
462 tially all but three individuals are susceptible, among the three there is one each of presymptomatic,  
463 symptomatic and asymptomatic. Since the University student contact network involves fewer in-  
464 dividuals, we consider a fewer number of initially infected individuals. Specifically we consider  
465 that initially all but one symptomatic individual are susceptible.

466 The parameters we choose and further justification for the choices are listed in Table 1 in  
467 Supplementary Information.

468 **Multi-hop contact tracing process.** Every day individuals who are *ready to test* by virtue of  
469 showing symptoms are tested and isolated if they test positive. Considering an individual who  
470 tests positive on day  $t$ , we describe the process of tracing his  $k$ -hop contacts on day  $t$  and testing  
471 them on day  $t+1$ . On day  $t$  after the individual in question tests positive, the public health authority  
472 traces his  $k$ -hop contacts, over the last 14 days, and informs them that they may have been exposed.  
473 If cooperativity is  $q$ , only  $q$  proportion of interactions per day can be identified. Tests are scheduled  
474 on day  $t+1$ . Those scheduled to be tested are isolated from everyone else on the day of the test. The  
475 test results are available in the same day, and those who test positive are isolated until they recover  
476 and those who test negative can resume their normal activities. Individuals who test positive will  
477 not be tested again, but those who test negative can be tested again after 3 days from the test date if  
478 they have direct or indirect interactions with any one who tests positive or if they show symptoms.

#### 479 **Data availability**

480 The raw data used to construct University student contact network was previously published in  
481 [22]. The raw data used to construct Foursquare contact network was previously published in  
482 [32], which is available at <https://sites.google.com/site/yangdingqi/home/foursquare-dataset>. All other data generated or analyzed during this study are available  
483 from the corresponding author upon request.  
484

#### 485 **Code availability**

486 Custom code used to produce the results in this study is available from the corresponding author  
487 upon request.

488 **Supplementary Information**

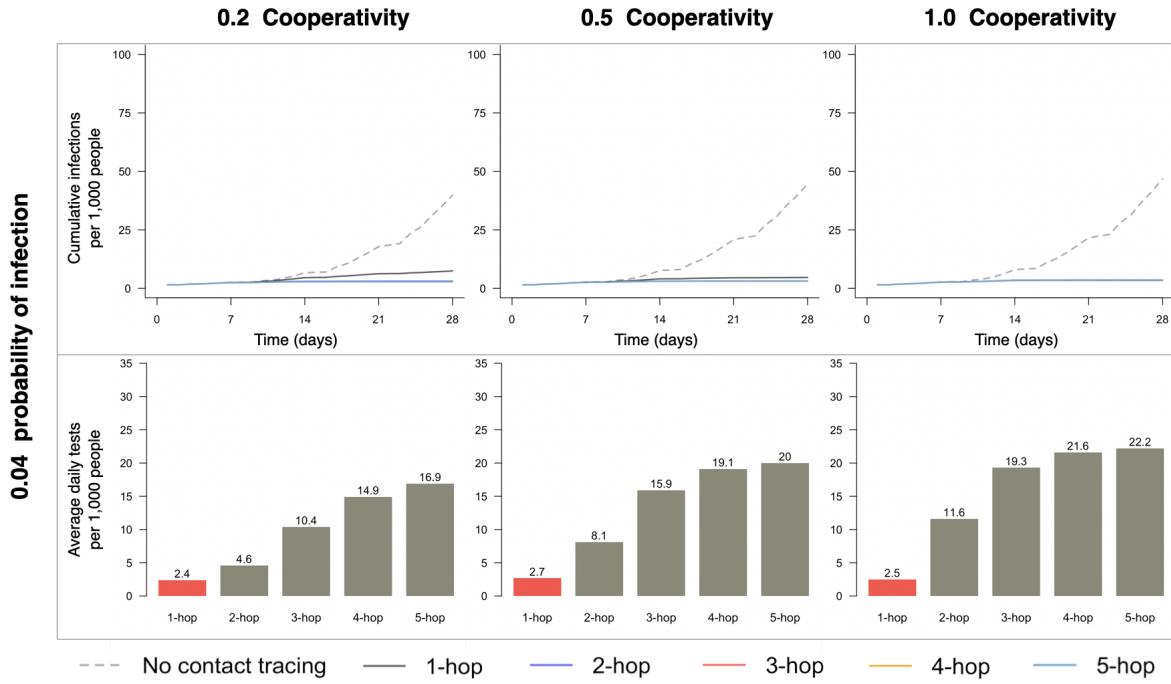


Figure 8: **The cumulative number of infections and average daily tests required for  $k$ -hop contact tracing for various values of  $k$  for University student contact network.** The probability of infection is 0.04. The red colored bar corresponds to the threshold value for  $k$ . For  $k$  exceeding the threshold value, the curves for the cumulative number of infections heavily overlap and become indistinguishable.

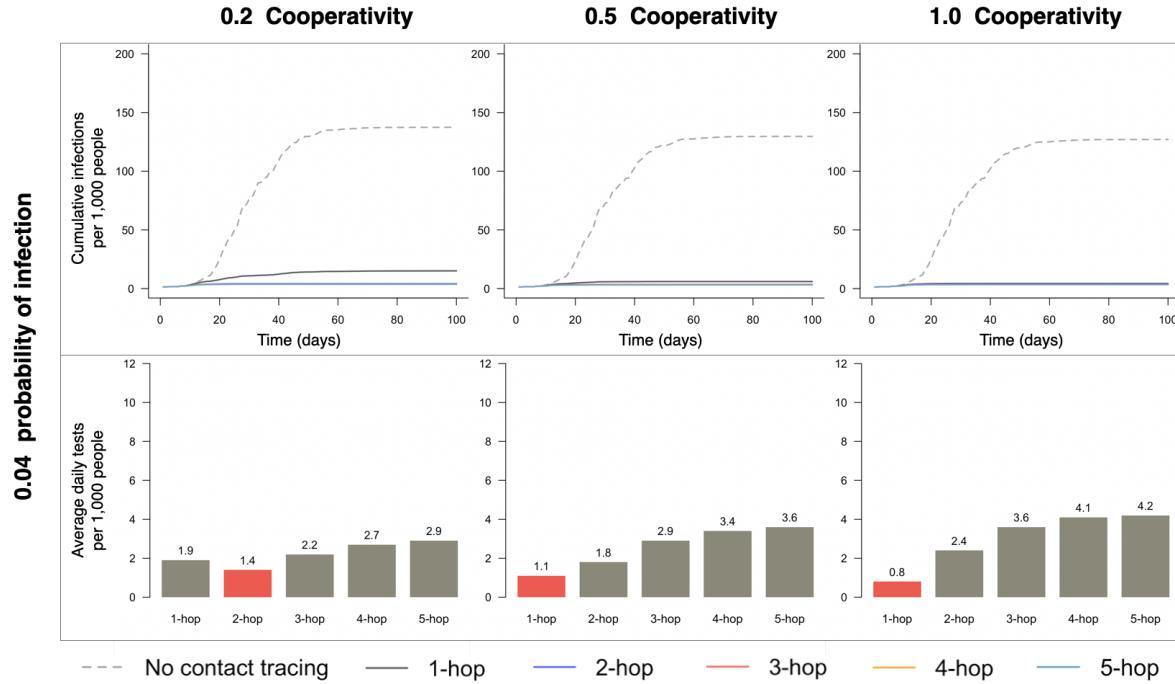
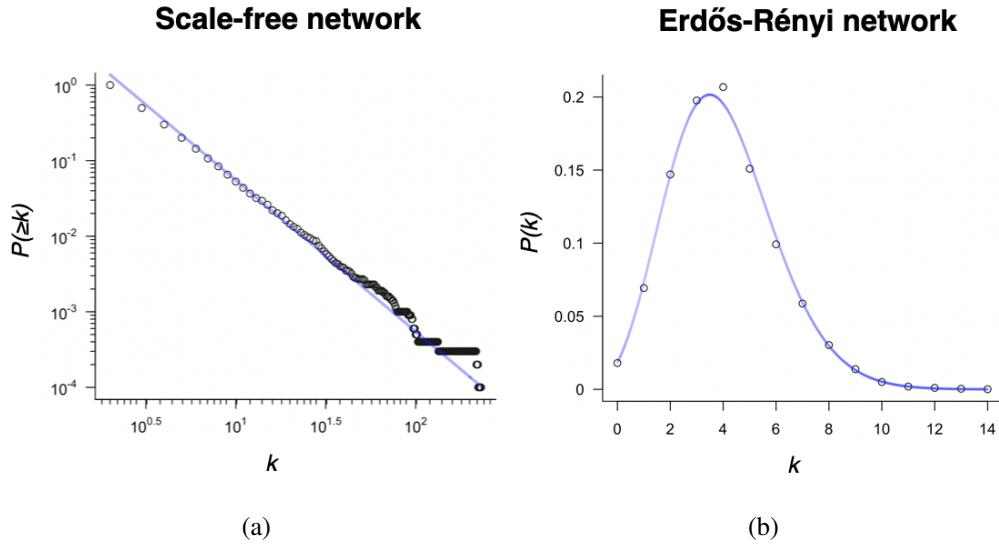


Figure 9: **The cumulative number of infections and average daily tests required for  $k$ -hop contact tracing for various values of  $k$  for Foursquare contact network.** The probability of infection is 0.04. The red colored bar corresponds to the threshold value for  $k$ . For  $k$  exceeding the threshold value, the curves for the cumulative number of infections heavily overlap and become indistinguishable.



**Figure 10: Degree distribution of the respective network realizations of the scale-free and Erdős Rényi network used for the data plotted in Figures 6 and 7.** (a) The points represent the cumulative degree distribution for the scale-free network, and the slope of the line is 2 which is the theoretical exponent of this power-law distribution. Those are plotted on a double logarithmic scale. (b) The points represent the degree distribution for the Erdős Rényi network, and the line represents the Poisson distribution with parameter 4.

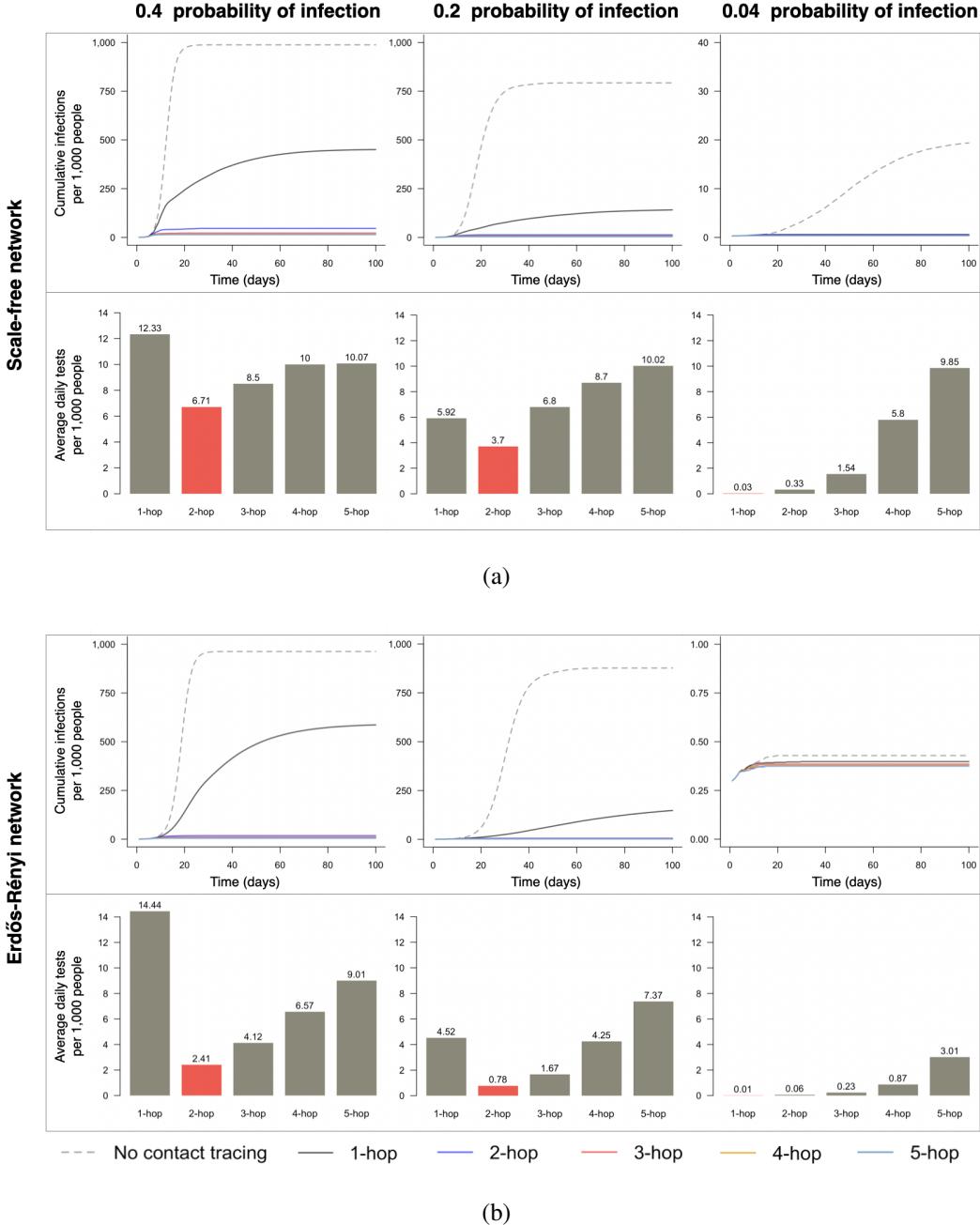


Figure 11: **Cumulative infection count and total number of tests needed for multi-hop contact tracing policy.** The data has been obtained for the same setups as in Figure 6, only difference is that this figure plots the results averaged over 10 network realizations and 100 simulation runs on each network realization, while Figure 6 plots the results averaged over 1000 simulation runs over 1 network realization. This figure closely resembles Figure 6 both in overall trends and specific values of the data points.

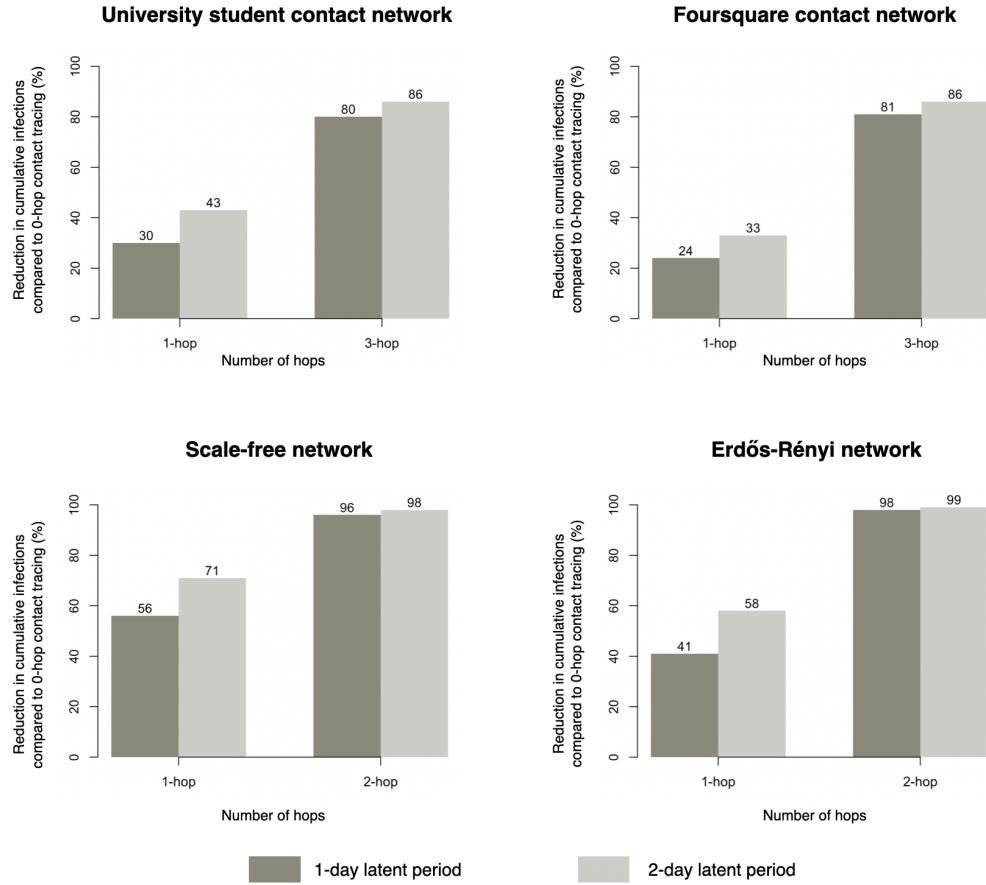


Figure 12: **Comparison of cumulative infection for different values of mean latency period.**

We use probability of infection as 0.4. The cooperativities are 0.2 and 1 respectively for ***University student & Foursquare networks*** and static synthetic networks. The plots compare the numbers for 1-hop and  $k$ -hop contact tracings when  $k$  equals the corresponding threshold value.

## Table 1: Values of disease parameters

Parameter	Notation	Value	Reference & Description
Probability of infection (Probability with which a symptomatic individual infects a susceptible in an interaction)	$\beta_s$	0.4, 0.2, 0.04	Assumed various scenarios
Infectiousness of presymptomatic individuals relative to symptomatic	$\gamma_p$	1	Inferred from [12] suggesting significant presymptomatic transmission
Infectiousness of asymptomatic individuals relative to symptomatic	$\gamma_a$	0.75	Best estimate by [25] from prior studies [16],[34],[33],[18],[20]
Proportion of infections that are asymptomatic	$p_a$	0.4	[25],[21]
Mean latency period †	$1/\lambda$	1, 2 days	Inferred from [19]
Mean duration in asymptomatic stage	$1/r_a$	7 days	Inferred from [5],[19]
Mean incubation period (period between infection and the onset of symptoms)	$1/\lambda + 1/\alpha$	5 days	[17],[15]
Mean duration from symptom onset to testing	$1/w$	4 days	Inferred from [4]
Mean duration of symptom onset to recovery or death	$1/w + 1/r_s$	14 days	Inferred from [24], [5]
Fraction of symptomatics who die	$p_d$	0.0065	[25]

† All Figures use a mean latency period of 1, except Figure 12 in which we compare the results for mean latency periods of 1 and 2.

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590 **Competing Interests** The authors declare no competing interests.

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