Containing Covid: "To trace or not to trace?" - That is not the question!

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The sudden onset of the Covid-19 pandemic disrupted the modern multi-national interconnected society and led the countries and societies to enforce unprecedented restrictions on movement. Among myriad containment measures, the policy of trace and quarantine found universal adoption among countries; the swift adoption of the policy was soon met with widespread criticism and opposition activists who questioned the utility and the risk associated with such a large scale collection of data and infringement on the movement of individuals. Consequently, one often tends to be either pro- or anti-trace and quarantine; the ensuing polarizing and politicized left little room for nuance. In this work, we undertake a methodology study to understand the nuances of the impact of different implementations of trace and quarantine. To this end, we design a user-friendly and intuitive tool that can be employed by experts to model the disease dynamics and societal structure. We focus on the study of the cost of policy with respect to quarantine degree, which captures the distance between the person required to quarantine after a person is detected to be infected. Our study results in a surprising conclusion: the cost is not necessarily monotone with respect to the degree of quarantine. Our analysis indicates that governments must curb the urge to adopt simplistic policy and the optimal policy of trace and quarantine for a country strongly depends on its societal structure and disease dynamics.

Additional Key Words and Phrases: Epidemics, Optimal Policy, Trace and Quarantine strategy, Agent networks

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1 INTRODUCTION

The interconnected nature of modern multi-national society acted as a strong catalyst in the pandemic of the Covid-19. The sudden onset of Covid-19 pandemic disrupted sophisticated human societies in all aspects: the high mortality among elder groups led to a stress on healthcare infrastructure that required the governments to take strong actions to curb the spread of the virus.[8] As such, the governments all over the world scrambled to devise policy to contain and mitigate the spread of virus [9, 26]. The inter-connected society was soon confronted with unprecedented restrictions of the movement at a global scale not witnessed in over half a century. [27]

Among the many policies employed by the governments, the policy of trace and quarantine (albeit in different forms) found near-universal adoption among the governments. Broadly, the policy of trace and quarantine focused on the

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usage of surveillance techniques to re-trace the movements of a confirmed infected patients to identify other close contacts. Once such close contacts are identified, the individuals in the contact graphs are often asked/required to (self-)quarantine. It is worth observing that the implementations of trace and quarantine have differed across countries:

- United States and England recommended quarantine of close contacts of the infected patients [7].
- Some states in India focused on tracing and quarantining contacts up to two degrees of identified cases, i.e., direct contacts of the infected patients[13, 31].
- Vietnam, on the other hand, has focused on tracing and quarantining contacts up to three degrees of identified cases [5].

While the policy of trace and quarantine found universal adoption, its impact on the containment and mitigation varied across the countries.[17] The varying impact attracted inquiry from the scientific community and general population alike on the potential benefits and costs of the policy of trace and quarantine. [2, 20] From epidemiological perspective, the usage of trace and quarantine is often viewed as crucial in containing outbreak. While there is a strong support for usage of trace and quarantine, there is no substantial agreement on the extent to which trace and quarantine should be employed. On one hand, requiring the entire population to quarantine for weeks at end may effectively end transmission of a virus but such a policy is untenable as the modern society has complex interdependence, which require a sufficiently large group of workers to return to workplace. Since not everyone can be quarantined, one may wonder if everyone except essential workers can be quarantined; such a policy, while feasible, has high cost as prolonged periods of quarantine is associated with increase in violence, poor mental and physical health in addition to significant loss in the productivity.[16, 28, 29] Consequently, since the early days of Covid-19 pandemic, the policy of trace and quarantine was met with polarized reception. On one hand, the proponents of trace and quarantine touted its ability to quickly identify and isolate potentially infected people, and thereby allowing to manage outbreak. On the other hand, the opponents of trace and quarantine resisted a broad surveillance of citizens by the governments as it enhanced the risk of leakage of sensitive private data. [10, 22] Since the trace and quarantine policies adopted political symbolisms, and consequently, the opposing viewpoints increasingly became polarized, and consequently, one often tends to be either pro- or anti-trace and quarantine. Since increased polarization left little room for nuance, the implementation details of trace and quarantine has not attracted detailed scientific scrutiny.

The primary contribution of this paper is a detailed methodological analysis of benefits of different models of trace and quarantine. In particular, we employ a contact graph wherein every node corresponds to a person, and two nodes are connected if they had direct contact with each other. The representation as a graph allows for a natural formalization of a given trace and quarantine policy wherein a policy enforces degree d of quarantine if all the nodes within d hops of node U are required to quarantine if u is confirmed to be covid positive. Since the connectivity characterstics differ across different socities, we employ different models of the graphs. We focus on analysis of the cost of a policy with respect to the different degrees of quarantine wherein the cost is expressed as a linear combination of cumulative person-hours spent as symptomatic infected, asymptomatic infected, and quarantined. Our analysis results into a surprising conclusion: the cost is not necessarily monotone with respect to the degree of quarantine, i.e., depending on the underlying structure of the contact graph, higher degree of quarantine may lead to higher cost. In fact, we observe that even cumulative quarantine time is non monotonic with respect to degree of quarantine.

Our analysis indicates that the implementation of trace and quarantine requires a nuanced analysis, and the governments must curb the urge to adopt simplistic policy. In particular, the optimal degree of quarantine is closely dependent on the underlying social structure of a given society as well as the characteristics of the disease. In addition

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to the detailed analysis, we also release the associated software system via web (https://contact-tracing.herokuapp.com/) with an intuitive interface that allows experts to perform such studies for different underlying networks, infection transmissions, and different cost functions.

The rest of the article is organized as follows: We first provide background to the underlying contact graph structure, infection transmission models, and trace and quarantine strategies in Section 2. We then present, in Section 3, a discussion of the simulation study and analyze a paradoxical behavior with respect to cumulative quarantine time. We then analyze, in Section 4, the optimal degree of quarantine with respect to different costs. We finally conclude in Section 5.

2 DESCRIPTION OF OUR MODEL AND PARAMETERS

2.1 Ground networks

In this article, we consider different models for static networks of people defined by physical proximity. A pair of two persons would be viewed as neighbors in these networks if they spend sufficient time in close physical proximity so that infection can directly transmit from one to the other. Suppose there are n people in the network. We will consider different network topology, ranging from two-dimensional grids to Erdos-Renyi random graphs and hybrid graphs modelled on real world countries. In case of the grid, there is no other network parameter, whereas the random graph models would have additional parameters, e.g. the connectivity parameter p for Erdős-Rényi (ER) random graph G(n,p) on n nodes.

2.2 Infection spreading mechanism

In the literature, several agent-based stochastic models have been proposed and studied to capture different aspects of the infection spreading mechanism. Examples include (i) SI (susceptible-infected), (ii) SIR (susceptible-infected-removed), (iii) SIS (susceptible-infected-susceptible), (iv) SIRS (susceptible-infected-removed-susceptible) epidemic models and their variants [30]. In case of Covid, it was noticed that a significant portion of the infected people do not show any symptoms[32], and after recovering from the infection individuals retain immunity for some time (the immunity is not permanent [12]). Keeping these features in mind, we would consider a variant of the SIR model, which is referred to as the SEYAR model [11]. In this model, each person has one of the five possible states – susceptible (S), exposed (E), symptomatic infected (Y), asymptomatic infected (A), and removed (R). An individual moves from S compartment to E compartment at rate β times the number of Y and A neighbors, and from E compartment to either Y compartment (with probability p) or A compartment (with probability $q = 1 - p$). Finally, people move from Y or A compartment to R compartment at rate γ_Y and γ_A respectively. We modify this model to incorporate the disease progression patterns which have been observed specifically in the case of Covid-19. Instead of using fixed rates for the transitions between different states (e.g., from E (resp. E, Y, A) to Y (resp. A, R, R)), we use random samples from the respective distributions (see the following table), which have been empirically shown to fit the corresponding real world observed data [3, 21], for the holding times at states E, Y, and A. Furthermore the model considers that 30% of all infections are asymtomatic which is an aggregation from many studies[23]. The rates of infection of an asymptomatic individual has been set to 80% of that of an symptomatic individual due to a lack of consensus of studies for the same.

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Period or Transition	Compartment	Distribution
Incubation period	Exposed (E)	Lognormal with mu 1.63 and sigma 0.5 [21]
Symptomatic duration	Symptomatic (Y)	Normal distribution with mean 13.4 days[3] and variance of 3 days
Asymptomatic duration	Asymptomatic (A)	Uniform distribution between 6.5 and 9.5 days[3]

2.3 Trace and Quarantine Strategies

In the trace and quarantine policy, if a person is detected to have the infection, then that person, his/her recent contacts, and their subsequent contacts etc. are immediately quarantined. The stringency of the policy depends on how many levels of contacts one traces. In the

- zero degree policy, neither tracing nor quarantining anyone occurs.
- first degree policy, people who are symptomatic or tested positive are quarantined.
- k-degree policy (for any $k \geq 2$), people who would be quarantined according to the $(k-1)$-degree policy as well as all of their neighbors are quarantined.

One can extend the definition of the degree of contact tracing to any non-integer positive number k by adopting the $[k]$ policy, and additionally quarantining each of the persons, whose graph distance from the originally detected person is $k+1$, with probability $k-[k]$. Note that int he real world each level of tracing has a time delay as the agents in question have to be contacted and appropriate actions have to follow. Thus an additional parameter representing delay in subsequent tracing called 'tracing delay' has been included in the model. Additionally, 'quarantine time' has been set to 14 days unless otherwise stated and refers to the duration of quarantine after being identified in the trace and quarantine strategy.

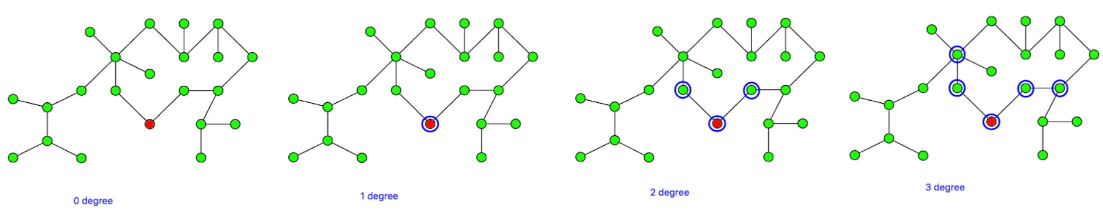

Fig. 1. Different degrees of quarantine where the nodes represent people and the edge between two nodes represents contact between the corresponding two people. A node is red if the corresponding person has been identified to be infected, and a node is blue encircled if the corresponding person is quarantined.

2.4 Simulation Parameters

We consider a finite horizon with a fixed time frame of 100 days. Furthermore to ensure verifiable results every simulation has used a fixed random seed. The logs of each simulation have been stored and can exactly reproduce each simulation and corresponding figures shown int he paper. Throughout this paper, in order to reduce variance in this complex non-deterministic system with largely inherent stochasticity or randomness, all shown results are averaged

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over multiple instances of the simulation. The number of instances were determined by the convergence of the final result. Although variance can be introduced as a risk metric, this is not in the scope of this paper.

3 SIMULATION STUDY

We empirically study SEYAR disease dynamics on the agent network and compare different degrees of the trace and quarantine strategy[1]. This paper deals with 3 types of graphs namely Erdos-Renyi random graph, a structured 2D grid graph of degree 4, and a hybrid country graph inspired by real countries.

3.1 Understanding the simulation

We consider a SEYAR model with the chance of an Exposed becoming Asymptomatic being 3 times higher than becoming Symptomatic. The underlying agent network is represented by a Erdos-Renyi graph with 5000 persons and a 0.001 probability of an edge(Bernoulli,iid) between any two persons. The average degree is 5. This simulation runs through for 100 days or time-steps. We present the simulation of perfect contact tracing with no error while applying the strategies.

We choose a closed world with the above priors. Each simulation starts with a small number of initial exposed agents after which there is no interference from outside the system. Each time step the people run through the SEYAR model and accordingly change states. For each strategy the simulations are averaged multiple times to reduce variance and noise.

The figure 2 shows the comparison between the strategies with different degrees of quarantine. The three bars in the histogram refer to the cumulative time of all agents being Symptomatic(Blue), Asymptomatic(Orange) and Quarantined(Green). Note that an agent cannot be both Symptomatic and Asymptomatic at the same time but can be in one of those states along with being quarantined at a given time step.

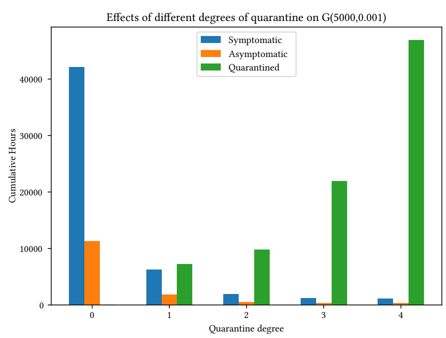

Fig. 2. Comparison of different degrees of quarantining based on the cumulative time spent by all the nodes of a G(5000,0.0015) Erdos-Renyi random graph in different states. There is a trace delay of 2 days and a quarantine time of 14 days. It is clearly seen that increasing the degree of quarantine results in an improved control over the spread of the disease as seen by the cumulative infection.

As expected we see that increasing the degree of quarantine naturally increases the cumulative quarantine hours as we are quarantining more and more people. This strategy naturally results in lower disease spread resulting in lower total cumulative Symptomatic and Asymptomatic time. It is a standard phenomenon for any disease that

[1]Our tool is available at https://contact-tracing.herokuapp.com/

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spreads through exposure to infected people such that it occurs irrespective of the disease dynamics. One can also notice a significant improvement in the first degree of quarantine and marginal improvement thereafter. This result is related to the underlying structure or the graph in conjunction with the disease dynamics and shall be explored further.

3.2 Cumulative quarantine paradox

As seen in figure 2 it is intuitively clear at to why the cumulative quarantine time increase with increase in quarantine degree. This effect can be attributed to the simple fact that we have more agents under our purview. But the counter-intuitive fact is that under certain ranges of parameters which include the edge probability in an Erdos-Renyi graph or the underlying disease dynamics(rate of infection, rate of recovery) we see that the cumulative quarantine time is non-monotonic.

This phenomenon illustrated in figure 3 can be explained using the following mathematical reasoning. If a higher degree of quarantining policy is adopted, then, on the one hand, there would be the fewer total number of infections which in turn reduces the total quarantine hours, but on the other hand, more people would be quarantined per infection detection which would increase the total quarantine time. The argument can be made more precise using a "coupling argument" [18]. Let ξ_t^k (resp. ζ_t^k) denotes the set of infected (resp. quarantined) people at time t when degree k quarantine policy is adopted. For any set of values of the SEYAR model parameters and $k < l$, the infection and contact tracing processes corresponding to degree k and l quarantine policy can be coupled so that $\xi_t^l \subset \xi_t^k$ for all t. Moreover, if $A_t := \zeta_t^l \setminus \zeta_t^k$ and $B_t := \zeta_t^k \setminus \zeta_t^l$, then both A_t and B_t are possibly nonempty. A_t consists of people belonging to $\xi_t^k \setminus \xi_t^l$ who would be quarantined under the degree l quarantine policy. On the other hand, B_t consists of people who would be quarantined in the degree k quarantine policy and whose infection trail remains within $\cup_{s<t}\xi_s^k \setminus \xi_s^l$. The SEYAR model parameters and the parameters of the underlying graph determines whether the expected values $E(|A_t|)$ and $E(|B_t|)$ satisfy $E(|A_t|) \leq E(|B_t|)$ or not, which in turn determines whether $E(|\zeta_t^l|) \leq E(|\zeta_t^k|)$ or not.

Thus, the cumulative quarantine time (green bar) is expected to be decreasing (resp. increasing) as a function of the quarantine degree when the quarantine degree is small (resp. large). The minima of the curve may occur before the first degree as seen in Figure 2 or it may occur at a higher degree as noticeable in the plots of figure 3.

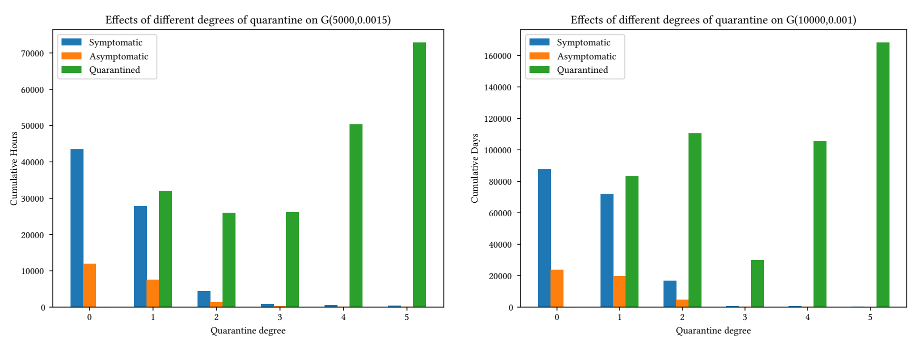

Fig. 3. Both plots on G(5000,0.0015) and G(10000,0.001) show the non-monotonic behaviour of cumulative quarantine time. This figure shows that it is not a pure artifact of a random run on a specific graph as these results have been averaged over multiple individual simulations. The trace delay is 1 day and quarantine time 14 days.

3.3 A more practical scenario

We introduce a hybrid graph modelled on the family structure of respective countries. A family is considered as a completely connected network and is modelled as a clique. Each agent is assigned a clique based on the distribution of family sizes in the country(Figure 4). To this we append an underlying Erdos-Renyi random graph connecting the agents.

Country\Family Size	1	2-3	4-5	6+
Nederland	35%	46%	18%	1%
USA	27%	49%	20%	5%
India	4%	24%	42%	31%
Afghanistan	0%	6%	17%	77%

Fig. 4. The distribution of family sizes in each country./citeunited nations The orange highlight shows the distribution of over 80% of the population in the respective country. Notice that Netherlands(country with smallest average family size) has a significantly different structure from Afghanistan(country with largest average family size).

The family structure and rate of interaction in a region heavily impact the spread of the disease.[19] This interaction results in varying effects of the same strategies across different regions. In figure 5 note the significant variation in effects of strategies from top to bottom and also left to right. This plot shows us that average interaction and family size play an important role in determining the effect of the strategy. One should notice that the weather, diet, health and infrastructure of Netherlands and Afghanistan are very different which will even further vary the outcomes of disease spread. The bottom right plot shows us that there is no significant effect in the first degree quarantine while the top left shows us that the first degree quarantine has the most effective increase in controlling spread. Furthermore the monotonicity of cumulative quarantine hours varies drastically across all plots.

3.4 Other observed behaviours

Sparseness of graph in conjunction with rate of recovery drastically determine how many people get infected over the course of the epidemic.[6] This effect is due to a high rate of recovery, which essentially results in cutting off of sections of sparse graphs resulting in a local notion of herd immunity. A classic example is of a village where only the shopkeeper interacts with the outside world. If the shopkeeper recovers and becomes immune before transmitting the disease into the village the only path of the disease into the village is now blocked(assuming no carriers and that the disease spreads only by contact). Furthermore the rate of infection determines how fast the disease can spread while the ratio of symptomatic to asymptomatic shows the extent to which we can identify a disease without testing. All of this further begs the questions regarding the best course of action. It is clear that every region is unique in it's own way and must take a decision on which strategy to implement. This observation calls for an optimal degree of trace and quarantine which is discussed in the following section.

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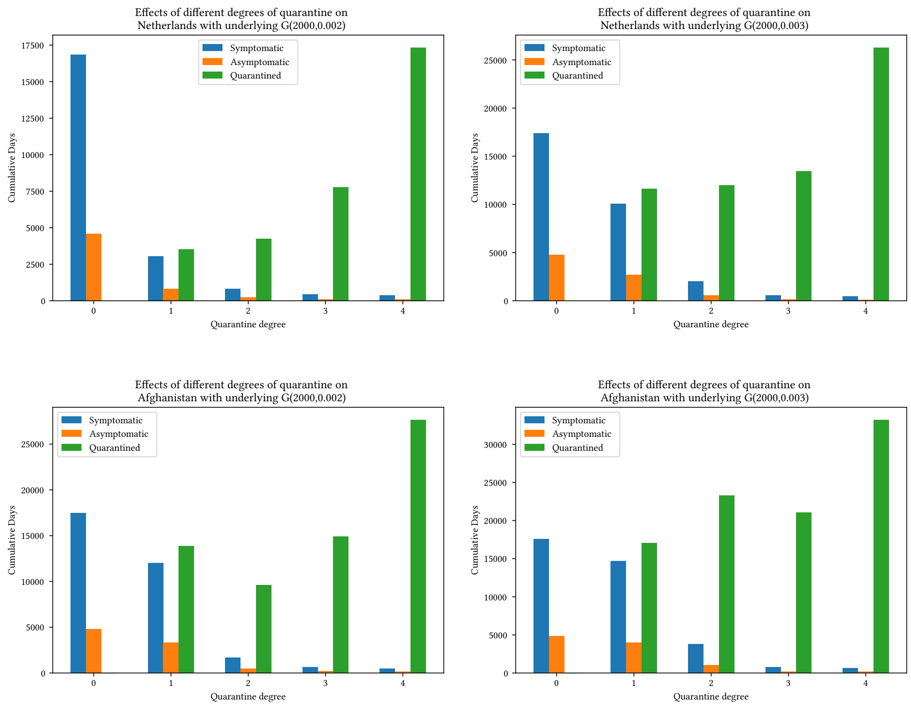

Fig. 5. Comparing strategies of different quarantine across interaction networks modelled on different countries.
The 4 plots are put in the following order for easy and quick visual comparison. The top two plots consider a graph structure modeled on the family size distribution of Netherlands. The bottom two consider a graph structure modeled on the family size distribution of Afghanistan. Both plots on the left assume more interactions outside the family on average($p = 0.003$ for the underlying ER graph). Both plots on the right assume sparser interactions outside the family($p = 0.002$ for the underlying ER graph). All plots have been averaged over multiple individual simulations to reduce variance and noise. The trace delay is 1 day and quarantine time 14 days.

4 OPTIMAL DEGREE

4.1 Policies are not free

Every quarantine policy enacted in a region would be associated with a cost to the overall economy of that region which needs to be considered before deciding whether the policy should be adopted or not. Broadly speaking, there can be two kinds of costs in this context, namely "economic costs" and "health costs." If a person is quarantined, then he/she would not be able to take part in the economic activities and contribute to the economy during the quarantine period. Moreover, the policymaker may need to arrange for food, other subsistence, medical supplies, etc. for the quarantined persons. These constitute the economic cost. The economic cost associated with a person would depend on the employment status, socio-economic status, health status, etc. of that person. The health cost associated with a quarantine policy stems from the associated rates at which critical patients (belonging to different age and comorbidity groups) requiring hospitalization show up, rates at which the necessary equipment and medical supplies for the treatment of infected patients would be needed, etc.

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Although, in theory, any level of quarantine can be considered, all policies may not be feasible to enact in a given region due to a lack of necessary infrastructure and capability. Keeping such practical concerns in mind, we need to consider only the feasible policies to choose from. In many cases, the economic costs and health costs are not readily available. Depending on the proportion of different contributing factors, the cost structure can vary from place to place, and it needs to be estimated carefully. The accuracy of the overall estimation procedure would depend on the noise present in the measurements of the predictor variables, the kind of relationship (linear or nonlinear) between the overall cost and its components, and the noise involved in the execution of the contact tracing procedure. In this paper, we would not address the estimation problem; rather, we demonstrate the consequence of a particular kind of cost structure. The overall cost is a linear combination of the components. Similar behavior is expected for other relationships. Other contributors to the overall cost include human resources and logistics for carrying out the contact tracing procedure, but these factors would not be considered here, as they do not seem to be a major factor.

4.2 Cost Structure

For every policy the community seeks to implement, there is an associated cost borne by the community. Here, cost does not imply the mere monetary expense but a total encoding of all effects. This cost structure encodes the priorities, expenses and constraints of a community.[4]

- Priorities : Every community is unique in their needs, vulnerabilities and abilities which determine their priorities. Quarantine for an affluent community with savings is not as harsh as quarantine of a less fortunate community that lives on a day to day wage. Furthermore communities differ in inherent strengths and weaknesses. For example a nursing home is much more likely to result in deaths as compared to an undergrad college with the same of number of cases.
- Expenses : The expenses associated with a community depends on many other factors including the demographic composition, socio-economic factors, healthcare infrastructure, the level of awareness, perception, and sensitivity of people. At a basic level the GDP, technological progress, infrastructure and resources of a country determine various expenses. Even at a local level expenses can vary across neighbourhoods due to availability of labour, demand and supply of resources and transport. An example is that of transport, tracing personnel, quarantine and machine expenses.
- Constraints : A variety of factors like Infrastructure, Availability of resources, Demand and Supply, Government Regulations constrain the possible policies a community can implement. Constraints could include a minimum number of infections, deaths, quarantine days and could also include bounds on the total number of false quarantine.

We consider a cost structure that is composed of the following four components:

(1) cost for quarantining people (C_1) – this cost stems from the fact people will not be able to take part in economic activities involving physical interactions. So, financial support need to be arranged for such people.
(2) cost incurred by the asymptomatic infected people (C_2) – this cost stems from the fact that the asymptomatic infected people spread infection at relatively faster rate to their susceptible neighbors which comes with health cost dues to hospitalizations, health hazards, and fatalities.

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(3) cost incurred by the symptomatic infected people (C_3) – this cost stems from the fact that the symptomatic infected people, who are not quarantined, spread infection at relatively slower rate to their susceptible neighbors which comes with health cost dues to hospitalizations, health hazards, and fatalities.

Another main component is the fixed costs that includes setting up the tracing and identification system and other processes like information dissemination. Since it is fixed, we formalise our cost structure with only the three components as a tuple (C_1, C_2, C_3).

4.3 Cost Function

Given a policy, the cost function returns the total cost borne by the community, which is determined by the cost structure.

We consider the cost function as the linear combination of the cost components.

$$C = n_1C_1 + n_2C_2 + n_3C_3 \tag{1}$$

Where, n_1, n_2 and n_3 are the total number of quarantined days, asymptomatic infected days, symptomatic infected days and infections respectively. With a semblance of sanity we can assume certain conditions on n_1, n_2 and n_3. Clearly they are non-negative as no community will will want to increase any of the above components. Also as quarantine is preferred over being infected and furthermore a symptomatic person will bear higher cost than an asymptomatic person we can naturally incite the condition $n_1 < n_2 < n_3$. Additional constraints like an significantly higher cost for infected over quarantine can be placed which shall be discussed in future works. Furthermore the logistic cost of tracing is negligible with today's technology and can be subsumed in the cost for quarantine itself.

We have considered linear cost components but this may be appropriately adjusted to capture the community's utility. For example a community which shuns excessive deaths could penalise the cost function with a quadratic component in the number of deaths. Note that one can easily extend this cost to encode the cost of death which occurs as a proportion of the total infected population. But constraints like hospital space and medication might affect this resulting in a non linear piece-wise cost function. The simplest linear cost function is enough to show the non-monotonic nature of cost with respect to degree of quarantine. A more complex function will further exacerbate these observations.

Goal : Find the optimal degree of trace and quarantine that minimizes the cost function. Given the parameters of the underlying population network, infection spreading process, and the different kinds of costs, we want to obtain the value of k (the degree of contact tracing) for which the combined cost would be minimized.

4.4 Comparing Cost Structures

As discussed above for each region the cost structure varies vastly. We consider $G(2000, 0.006)$, the Erdos-Renyi random graph on 2000 nodes, as the underlying agent network. The cost structure that we use considers of the following. A unit time of quarantined, asymptomatic, and symptomatic period spent by one person costs 1, 2, and 3 units respectively. We obtain the cumulative cost for all the agents of the underlying network for different degrees of quarantining. See Figure 6(b) for the comparison of cumulative costs under different quarantine strategies.

We see that the cost of quarantine is not monotonic. Instead we see that the cumulative cost minimizes at quarantine-degree 3. If one would change the cost structure, then the optimal quarantine-degree would change accordingly. Thus,

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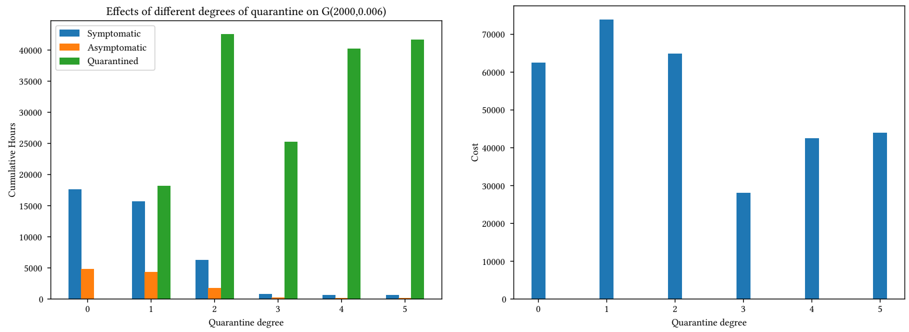

Fig. 6. Left: Comparison of different degrees of quarantining based on the cumulative time spent by all the nodes of an ER random graph in different states. Right: Comparison of different degrees of quarantining based on the cost structure (1,2,3). The trace delay is 1 day and quarantine time 14 days.

the best quarantine strategy depends on both of the factors: (a) relative costs of being symptomatic and asymptomatic relative to the quarantine-cost, and (b) the underlying structure of the graph.

Next we consider the 40×40 Grid graph on 1600 nodes, as the underlying agent network. The cost structure that we use considers of the following. A unit time of quarantined, asymptomatic, and symptomatic period spent by one person costs 1, 2, and 3 units respectively. This comparison has been shown in figure 7.

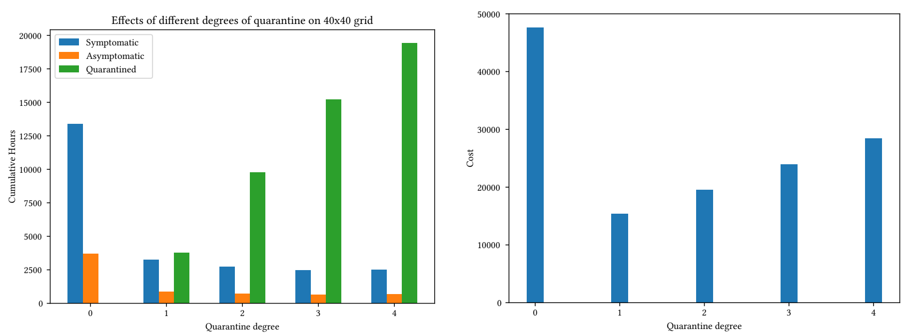

Fig. 7. Left (6a): Comparison of different degrees of quarantining based on the cumulative time spent by all the nodes of a 40x40 Grid graph in different states. Right (6b): Comparison of different degrees of quarantining based on the corresponding cost. The trace delay is 2 days and quarantine time 14 days.

We observed that the non-monotonic cost structure is not restricted to random graphs. We see that degree 1 strategy is optimal. The optimal strategy changes according to associated costs. This analysis shows that the phenomenon is not an innate quality of certain kinds of graphs but instead a result of the strategy under the dynamics of an epidemic spreading along the agent network.

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It is also possible that doing neither contact-tracing nor quarantine is the optimal strategy. Effectively a 0 degree trace and quarantine strategy may be treated as a baseline. As seen in the bottom two plots of figure 8 we see that the 0 degree strategy can be optimal as seen with cost structure (1,2,5). Though counter-intuitive we have considered multiple cost structures and shown how the optimal degree can vary. This phenomenon can be attributed to the fact that 1 degree quarantine does not show significant improvement, while later degrees show great improvement in disease control but a high cumulative quarantine increases the cost. But on further inspection we see that based on the structure we see how the monotonicity of the cost changes with trace delay and structure of graph. This is most evident with the (1,2,10) cost structure which drastically changes shape across all plots. Additionally observe how the optimal degree varies as we change the cost structure, graph structure and delay in tracing.

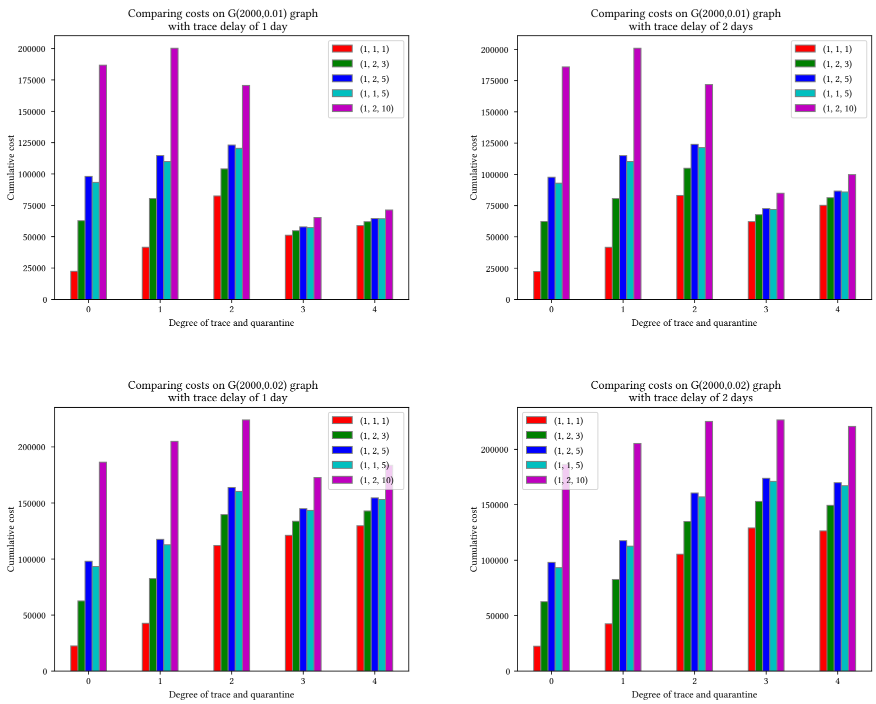

Fig. 8. Left: Comparison of different degrees of quarantining based across cost structures, trace delay and connectivity parameter p. The left plots assume a trace delay of 1 day while the right two plots assume a trace delay of 2 days. The top plots are run on G(2000,0.01) while the bottom two are on G(2000,0.02). The colors from Red, Green, Blue, Cyan and Violet represent the cost structures (1,1,1),(1,2,3),(1,2,5),(1,1,5) and (1,2,10) respectively.

4.5 Error in Tracing

We have considered a wide variety of factors in our attempt at modelling 'trace and quarantine' strategies of different degree's across structural variations in the underlying agent network. We shall now explore a natural extension to the current model.

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Contact tracing is never perfect.[14, 15, 17] A wide variety of factors ranging from lack of coordination among the various hierarchies of policy making, delay in quick tracing of contacts, lack of cooperation from the public and normal human error it is nearly impossible to find every contact. We define error in tracing as follows : a k% error corresponds to finding a contact with probability $1 - k/100$. This error model applies for finding contacts at any degree. This error is further magnified as we propagate to the next level of contacts . As seen in figure 9 change in error results in an unpredictable change in the final cost and thus optimal degree of trace and quarantine strategy.

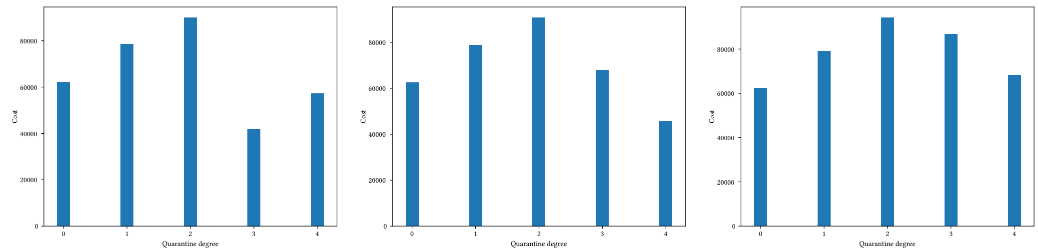

Fig. 9. We consider a SEYAR model on G(2000,0.007) ER graph. From Left to Right the plots represent error 0%, 20%, and 40% with optimal degree 3, 4, and 0 respectively. All 3 plots consider the same dynamics with the same random seed and was averaged over multiple simulations. The cost structure is 1, 2, and 3 per unit time of quarantined, asymptomatic, and symptomatic respectively.

4.6 Optimal Region

We see the formation of optimal regions based on the cost structure for Erdos-Renyi graphs. Although dependent on the disease dynamics and graph parameters we can find the optimal degree.

In figure 10 we can see the optimal degree under different cost structures. The plots show that based on the associated costs either degree 0 or degree 3 is optimal. Thus under the certain cost structures it is optimal to do no quarantining at all. We can clearly see the shift in quarantine degree as we change the associated costs. There is thus an optimal degree which varies largely with the cost structure. Furthermore the difference between the plots show the large impact the underlying structure has on the final cost and thus the optimal strategy.

5 DISCUSSION

In this paper, we have analyzed the effects of different degrees of quarantine policy for a region on the total quarantine time and on the associated cost for the economy of that region. We have considered the SEYAR model the infection spreading mechanism, and used different (random and deterministic) graphs as models for physical proximity network. We have demonstrated that the optimal (or near-optimal) quarantine policy is far from any obvious choice. It depends on the parameters of the disease spreading mechanism, the topology of the underlying proximity network, and the cost structure in a nontrivial way. The cost structure associated with a region in turn would depend on many other factors including the demographic composition, socio-economic factors, healthcare infrastructure, the level of awareness, perception, and sensitivity of people, measures taken by law enforcing agencies. So, any adhoc choice of quarantine policy may inflict unnecessary burden on the economy. Our framework helps to find out the optimal (or any near-optimal) policy once the associated cost structure and disease spreading mechanism are understood. The framework also allows to check how robust the optimal policy is by perturbing the influencing factors in any

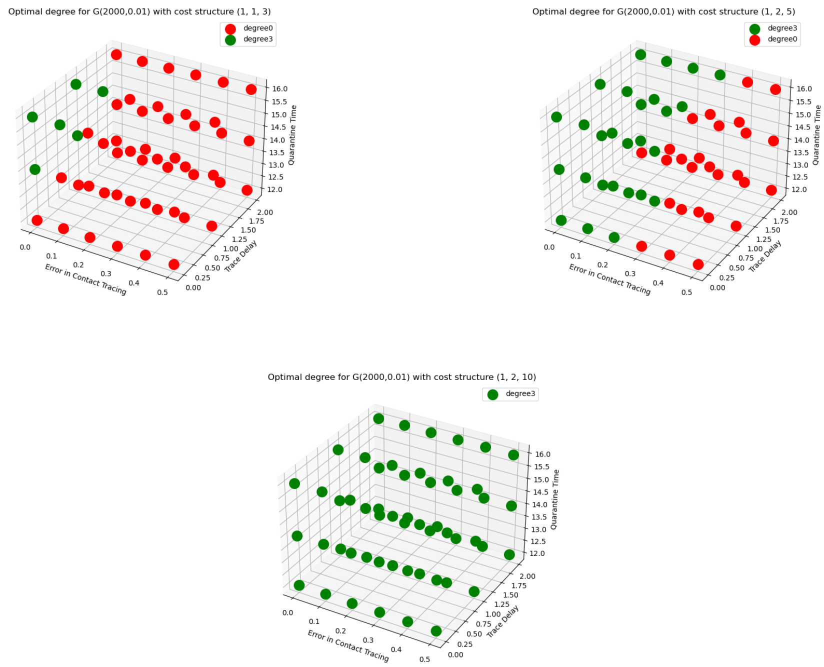

Fig. 10. Optimal Quarantine degree given error in tracing, trace delay and duration of quarantine.
Method: We consider a SEYAR model on a G(2000,0.01) graph. We run the simulations on respective Erdos-Renyi graphs with different cost structures varying from (1,1,3), (1,2,5) and (1,2,10) from left to right. We find the optimal degree out of 0,1,2 and 3 based on the minimum cost averaged over multiple simulations. We vary the error in tracing, trace delay and duration of quarantine to get the parameters for each point.

direction and comparing the resulting optimal degree of quarantining. The framework can also incorporate any available information about the proximity network, disease spreading mechanism, or the cost structure into the optimal policy determination procedure. For example, if the physical proximity network for a region can be estimated in a better way using the relevant transportation data, movement data obtained from cell phone locations of individuals, or aggregated visit data, the our analysis can be conducted on the resulting deterministic proximity network. Instead, if some characteristics (e.g. degree distribution) about the proximity network is known only, then we can choose a random graph having those characteristics and conduct our analysis on that. In conclusion, we present a flexible and useful framework for obtaining optimal (and near-optimal) quarantine policy based on information about the proximity network, disease spreading mechanism, and cost structure. The policymaker needs to understand these components better in order to arrive at any rational conclusion about whether to adopt any quarantine policy or not.

Our work opens up several interesting avenues of future work; we sketch out three directions of interest:

Compliance Human behaviour is erratic and unpredictable. Furthermore in challenging times, people tend to function irrationally.[1, 25] Thus compliance to quarantine, test or even name contacts is not a task for enforcers and must be accounted for by policymakers.

Heterogeneous population Humans are heterogeneous, even identical twins vary in multiple attributes. Demography(Age, Gender, Profession) plays a crucial role in interaction and risk measure of a person. Furthermore genetic markers and innate factors like the blood group or HLA type may determine the susceptibility of a person to Covid-19 and also the chances of recovery.[24]

Other policies Trace and quarantine is not a stand alone policy. Other interventions and strategies like testing, vaccination, curfew, and lockdown affect the result of any other policy. It is imperative to consider the larger amalgamated picture before taking any decision.

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In mid-March of 2020, with the aim of combating Covid-19, approximately 150 members from around the world organically converged to form the "cure COVid-19 for Ever and for All" (RxCovea:https://rxcovea.org/) Group, a rigorous community of scientists, clinicians, AI-specialists, mathematical and computational/data modelists, pharmaceutical, public and digital health intelligence representatives from multiple institutions, countries and scientific training. Within the network, self-organized task forces continue to conduct core projects, structured around hypotheses and minimal viable products (MVP's), mentored and examined by experienced senior members. We thank RxCovea for useful comments and encouragements.

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