Containing COVID-19 Pandemic using Community Detection

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Abstract. Diseases such as COVID-19 that quickly spread through social contact where infections remain undetected for long pose new kinds of challenges. Traditional epidemic models when applied to COVID-19 not only give highly alarmist predictions but also fail to indicate any way to target interventions. The models also do not factor social structure/context/dynamics. To address this challenge we propose a novel Social Infection Analysis Model explain the intuition behind it and a methodology that factors social structure while performing the analysis. SIAM is particularly beneficial as standard epidemic models are dependent on wide-spread testing. Our methodology includes (i) modelling society/localities using social network paradigm and analysis at macro level (ii) detecting communities and (iii) analysis of infection spread within a community over time. To arrive at an outlook for infection spread within communities we make use of the NK Model for solving complex, long term problems coupled with agent based modeling for member behavior. We make use of NetLogo to run simulations. We intend to validate our research in Indian context.

Keywords. clustering coefficient, community detection, social network, N-K problem, containment, small world networks

1. Introduction
There was a general expectation that COVID-19 Pandemic will subside within a few months when Government after Government imposed lock-downs all over the world in the early part of 2020. However, the last few months have indicated that neither short term approaches nor macro level approaches work well. Governments can no longer afford to keep their entire economy in...
suspended animation. The course of pandemic spread typically gets compared with forest-fires with containment by isolation between infectious and susceptible populations. Recent trends have shown we not only have a scale issue but also issues related to high dispersion. Thus, we need to put out many small fires. Hence we need strategies that operate at the local level which can guide us to design interventions at the level of communities.

In addition to the pervasive mode of spreading another challenge with COVID-19 is that many infected people do not display any symptoms for long periods. Table 1 below compares COVID-19 with other viruses [1]. You can see that COVID-19 has the longest incubation period during which the person is infectious even before the onset of symptoms.

General information on COVID-19 is presented lucidly by Robert Roy Britt [2]. Most of the literature connected to epidemics makes use of models such as Susceptible-Infectious-Recovered (SIR), Susceptible-Exposed-Infectious-Recovered (SEIR) and Susceptible-Infectious-Recovered-Susceptible (SIRS). There have also been attempts to improvise these models by adding more compartments and factoring social structure. Our earlier paper [3] has done a detailed survey on COVID-19 literature. In addition, the epidemic models run into difficulties in the absence of wide-spread testing and information on immunity levels.

Most studies are related to prediction and rarely factor into social structure. This paper is about containment and factors, social structure and the underlying social contact networks. The aim is to guide communities on striking trade-offs between the spread of epidemic and societal inconvenience/economic distress. In this study, we make use of NetLogo to model diffusion of infection over underlying social networks/communities.

Further, the approach we have taken is to look at the problem of COVID-19 as a long-term complex problem instead of looking at it as a short-term problem. The complex problems can be represented using the NK Model [4] and individual behavior using agent based modeling. We also draw on learning from the course on Network Dynamics of Social Behavior by Damon Centola [5], a Coursera course ongoing in August 2020.

The remaining part of the paper is structured as follows. Section 2, covers Related work on epidemics and impact of social structure on spread of epidemics. Section 3 deals with the Proposed Methodology for COVID-19 Pandemic containment using Community Detection. Section 4 presents Results on application of the proposed methodology in a simulated community environment. In Section 5, we make a list of Recommendations for better containment of COVID-19 Pandemic in India. Section 6 concludes the paper.

2. Related Work
Tom Britton [6] in his survey article has analyzed how epidemic models behave on social networks and what inferences we can draw. As elaborated by Britton there are two models for the spread of infections. They are the Discrete Time Reed-Frost model and Continuous Time Markovian model. With Reed-Frost, model infections happen sequentially in generation. With the Markovian model, they happen continuously with no generational boundaries. Britton describes a method to estimate the final size (the size of the population that gets infected) by factoring social structure. He considers degree distribution, degree correlation and clustering to be the three important network properties that bear the final size.

Table 1: Comparing COVID-19 with other diseases.

|                  | COLD  | FLU   | NOROVIRUS | COVID-19 |
|------------------|-------|-------|-----------|----------|
| Incubation period| 1-3 days | 2-4 days | A few hours | 2-14 days |
| Symptom Onset    | Gradual | Abrupt | Abrupt    | Gradual |
| Typical illness duration | 7-10 days | 3-7 days | 1-2 days | undetermined |
Whereas Tom Britton has done his study on Random Network, there are other studies who make use of small-world networks [7]. Bing Wang et al. [8] have studied the spread of epidemics on clusters using the 2-disease dynamic model. Guizani et al. [9] made use of an ad hoc network as an underlying model for their study on epidemic dynamics. Zhen-peng Li et al. [10] have studied the spread of a disease on extensive transportation networks, where the modelling is hierarchical. The objective of their paper is to halt infections in social networks. Zhaoyang Zhang et al. [11] have studied the spread of an epidemic over social contact networks and proposed the ISIR (Improved SIR) model. Nicole Bohme Carnegie [12] did a study on what are the important network properties that can affect the spread of epidemics. She makes use of the transmission tree model. Prem et al. [13] have done a study on the impact of social mixing on the spread of epidemics to arrive at control strategies for the epidemic. They provide recommendations to the government on how to stagger return to work by residents of Wuhan, where the virus is supposed to have originated. Michaela Hoffman et al. [14] applied Cohen’s $\kappa$ to community detection, where two nodes are considered similar based on a similar relationship with neighbourhood(s) under consideration. Zhuanlian Ding et al. [15] in their paper cover the detection of overlapping communities using network decomposition, which can prove critical in arresting the epidemics. Kponyo et al. [16] use NetLogo modelling approach to investigate the epidemic spread.

3. Proposed Model
We propose a novel Social Infection Analysis Model (SIAM) to analyze the spread of infection in communities. The SIAM Model is illustrated in Figure 1.

Algorithm 1: SIAM Mathematical Model

Procedure: SiamModel()

Initial Conditions: Let P be the size of the general population. C be the size of Calling Population, S be the size of Infectious chamber, I be size of Infected Chamber, R be the size of Immune Chamber and D be the size of Drop-outs chamber.

Assumption: In a given social context and within a limited time duration $\alpha$, $\beta$, $\gamma$, $\delta$, and $\xi$ are constant. We can reach containment faster if we can work on these parameters.

Objective: Flatten the curve to move towards $dI/dt=0$

(i) $C = \alpha P$ ($\alpha$ is social contact rate i.e. what fraction of population are generally connected to each other, approximated by largest connected cluster or aggregate of groups of clusters).

(ii) $I = I_0 + \beta C$ ($I_0$ is initial/previous value of infected people, $\beta$ is infection rate fraction of community who gets infected in the infectious chamber and move to the infected chamber. $\beta$ depends on the potency of virus and vulnerability of people).

(iii) $D = \gamma C$ (Here $\gamma$ is the drop-out rate and Drop-out chamber is a transit chamber. People quickly move back to general population. The value of $\gamma$ depends on individual behaviour and immunity status).

(iv) $R = R_0 + \delta I$ (Here $\delta$ depends on how well the health-care facilities are).

(v) $S = S_0 + \xi I$ ($S_0$ is initial/previous value of infectious people, $\xi$ is infectiousness rate - new people who are joining them to serve more infections).

In the SIAM model, we make use of Queuing Theory concepts and constructs in an unconventional manner. The compartments and states of the model are described below.

Compartments in SIAM:

- General Population - The General Population is the social group/society/locality/community under study.
Calling Population - The calling population is a subset of General population. In the queuing theory paradigm they may be treated as customers (who are unaware that they are treated). When we model society as a social network, the calling population can be considered equivalent to a reachable cluster relative to infectious persons.

Infectious Chamber - The Infectious chamber has people who are already infected and hence infectious. In the queuing theory paradigm, this is a service center with each infectious person acting as a server (serving infection) without awareness. There could be multiple service centers, each having over one server. Customer after receiving the infection departs to the infected chamber. Each service center has a certain system capacity. Here, we refer to it as infection capacity. This is because of infectious servers being available for time duration to serve infection. Some customers may drop-out.

Infected Chamber - The Infected chamber consists of customers departed with infection. Here the infected isolate themselves and do not cause further infections. However, some customers may move back to the infectious chamber and act as servers.

Drop-outs Chamber - As when we apply queuing theory to a retail store, some customers may balk, jockey or renege from their queues and therefore escape from being served infection. We have added a “decline” behavior, which can be correlated to immune members. Some may decline by rigorous adherence to social norms. This they do by minimising the contact time within the infectious chamber. They then join back the general population. These continue to be susceptible if they were so before they entered the chamber.

Immune Chamber - Some infected people recover and become immune. After achieving immunity (knowingly or unknowingly) join back the general population.

Further SIAM goes through the following states:

Initial State: The model kicks in when there is at least one infectious person in a social group/general population.
• Terminal State: In this state, the infectious chamber is empty and the general population constitutes only susceptible or immune people.

• Containment State: Here the size of the infected population is bounded, and that size is manageable from economic, social and governance considerations.

SIAM is applied to study the process of diffusion of infection in a social context. Here the overall size of the social group/community can be considered as a control variable. In addition, at any point in time we will have some numbers of people who are already infected, which act as initial values to the problem. To contain further infections, reachable clusters and infection capacity requires to be managed. In addition, the dynamics of networks (because of rewiring) and growth of networks (because of new nodes) play a crucial role in the spread of infection. The number of people who drop out may be a stochastic variable which varies with the level of immunity and adherence of social norms related to personal protection as well as limiting inter-personal engagement both in spatial and temporal sense. Overall, the interventions need to take the model towards containment/terminal state.

4. Proposed Methodology

Our methodology comprises 3 steps. In the first step, we model society as social contact networks. In the second step, we analyze social contact networks and detect communities. In the third step, we make an analysis of spread of infection within the communities. In each of these phases, we discuss aspects related to containment of COVID-19 like Pandemic.

4.1. Modeling Society as Social Contact Networks

The social group/locality we are analyzing can be modeled using a social network model which enables representation of a variety of social contexts. Table 2 illustrates the representation of social contexts using Social Network Models.

Any network where average path lengths are low can lead to infection of large numbers of people. Any network where the clustering coefficient is high may present a lot more opportunities for a susceptible person to get infected. In the SIAM model, the reachable cluster is influenced by the clustering coefficient. The service rate of infection is determined by short average path lengths. We can imagine that the far off nodes either balk or renege and move to the drop-outs chamber. Thus given characteristics of the underlying Social Network and the properties using the SIAM model, we can analyze the infection spread in different social contexts. We can provide guidance to societies to calibrate interventions at societal level.

4.2. Detecting Communities in Social Contact Networks

Persisting with societal interventions is unsustainable. Hence it is essential to design interventions in communities and micro-networks. Communities in social networks form due to a variety of shared characteristics. We can detect stable communities by using any of the common techniques such as Girvann Neumann. To model ephemeral interactions, we may need more complex techniques such as label propagation. Therefore, we may use Girvann Neumann in a relatively static scenario and use label propagation when there are more interactions. We can simulate the formation and detection of communities over different networks.

4.3. Analysis of Infection Spread within Communities

The way a Pandemic like COVID-19 spreads in a new region in the following 3-stage pattern. In the first stage there are small pockets of infections spread in different areas, which were presumably visited by infected persons. In the second stage, some of these pockets grow phenomenally, possibly showing formation of a giant component within a locality and many such localities add to the scale of infection. In the third stage infection, instead of being restricted to
Table 2: Social Contexts and Social Network Models

| Sr. No. | Social Context                                           | Social Network Model       | Remarks                                                                 | Lockdown implication                                      |
|---------|----------------------------------------------------------|----------------------------|------------------------------------------------------------------------|----------------------------------------------------------|
| 1       | Row of houses that are isolated                          | One dimensional linear lattice. | Here a node may also directly relate to a neighbour’s neighbour.       | Stay-at-home social groups can be represented as lattice networks. |
| 2       | Households arranged in a circular fashion                | One dimensional circular lattice | Here a node may also directly relate to a neighbour’s neighbour.       | Enables greater diffusion compared to linear organization, even in stay-at-home scenarios. |
| 3       | Households organized in a spacious layout                | Lattice grid               | Here a node may be connected to 4 other neighbours.                   | Limited mobility and limited diffusion in stay-at-home scenarios. |
| 4       | Households in a congested locality                      | Moore’s neighbourhood       | Here a node may interact up to 8 other neighbours.                    | Stay-at-home scenarios may even spread the infection more. |
| 5       | Neighbourhoods with free movements for necessities.     | Random Networks             | Here nodes get randomly connected to each other and rewired frequently. | Possibility of diffusion many times more compared to regular networks of the same degree. |
| 6       | Communities with no restriction on allowing migrants    | Random Networks with growth | In this there are no restrictions of movement in the broader region    | Here diffusion of infection may be lot more if infected nodes join |
| 7       | Households/work-places arranged in concentric circles. | Ring Lattice Network        | Here a node is connected to its neighbours in the same ring and next ring. | Typical of stay-at-home scenario with limited proximate movement. |
| 8       | Neighbourhoods where people commute to workplaces on a daily basis. | Small World Network | Here short ties are replaced by long ties and then vice-versa via rewiring. | This can lead to greater spread of infection between households and work-spaces. |
| 9       | Neighbourhoods allow occasional visitors from far away regions | Small World Additive Network | Here long ties are added without letting go off short ties. | This can add to the prevailing infection. |
| 10      | Health-care centers, banks and service centers          | Disassortative Networks     | Here people with high degrees interact with people with low degrees, who visit them. | Here relatively large numbers of people are serviced by visiting small numbers of serving people. |
| 11      | Communities that allow postal service, courier service, deliveries and service calls. | Scale-free networks with hubs | Here people serve a given locality. | Postal zones with households can be represented as hubs and spokes. Generally sparse networks. |
| 12      | Politicians and celebrities who may meet/interact with people in magnitudes multiple orders more than that commonly happens | Power Law Networks | Here small number of people have large number of interactions and large numbers have very few. | This makes the prominent persons a lot more vulnerable to infection. |
| 13      | Schools, Colleges and congregations.                    | Assortative Networks        | Here people with high degrees interact with other people with high degrees and people with low degrees interacting with people with low degrees. | Here some are highly social and some are aloof and generally people may relate to or interact with people with similar social characteristics. |

few pockets, is dispersed in many communities. In stage 3, it is important to model the spread of infection within a community and perform the analysis.

One reason pandemics get the upper hand is while infection spreads as a simple contagion, the adoption of social norms such as masks and social distance follow the process of complex contagion. Simple contagious spread particularly well through long ties, weak ties and networks. For complex contagions, local interactions, repeated reinforcements are much more important. The analysis of infection spread in a community we leverage the NK problem modelling applied in innovation context [5] and re-purpose it in infection context. Table 3 illustrates our model.

It is necessary to solve the complex, long-term model and aim for a calibrated relaxation of
Table 3: NK Problem Modelling in Infection Context

| Parameters          | Innovation Context                                                                 | Infection Context                                                                 |
|---------------------|------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------|
| Entities in the Model | Explorers and Exploiters                                                          | Explorers and Exploiters                                                          |
| Explorers’ Behavior | They explore and invent on their own. The process of arriving at inventions is a complex problem with many parameters with inter-dependencies. | Explorers get infected directly or indirectly. How an infection happens is a complex problem and depends on many parameters with inter-dependencies. |
| Exploiters’ Behavior | They exploit others inventions thus avoid inventing themselves. To exploit inventions it is important that inventions are made public. | They may keep away from infected people, or follow social norms and avoid being infected. To exploit infections, it is important that infections are publicized. |
| Key Metrics         | Unique explorations can be measured. Co-inventors may need to be counted as collectives. | Unique infections can be measured. Those who infect each other can be counted as collectives than individually |
| Simple, Short term problem model | Here inventions rise quickly and saturate quickly. | Here infections rise quickly and saturate quickly. |
| Complex, Long term problem model | Here inventions rise slowly and continue to rise for longer periods | Here infections rise slowly but continue to rise for longer periods |

restrictions. Otherwise communities switch back and forth into restrictions, making the matters worse.

The likelihood of any person in a community can be modeled as the N-K problem as follows. Here we identify N predictor variables which may have K inter-dependencies among them. The entire process is stochastic. Table 4 illustrates the infection prediction Model.

While exploration is a combination of active and passive phenomena, exploitation depends on how individuals protect themselves in the infectious chamber as active agents. They have a choice to avoid or minimize contact time with the infected. They respond by greater adherence to social norms, isolation or through prevention/immunity. Table 5 compares member behavior to behavioral constructs described in the Social Infection Analysis Model.

The following characteristics of communities have an influence on relative success of exploration (infection) vs exploitation(avoiding/preventing infection) as shown in Table 6.

The overall formulation of our problem is to arrive at a time-bound by which the disease will subside. This needs to be managed with a trade-off. If the networks are well-connected infection may spread rapidly but they stop because of crowding effect with a cost to pay in terms of mortalities. Alternatively, if a network is sparsely connected with a low average degree, the infection may continue to spread over longer periods as members may get freshly infected without reaching terminal state.

Thus a balance can be achieved by having a social structure with moderate degree and adherence to social norms so that infections die out without causing too many infections while allowing for some degree of immunity due to spread of infection in a contained manner among less vulnerable populace.

In summary, we have presented a 3 step methodology to analyze infection spread and arrive at strategies to achieve containment of infection by working on calibrated management of social structure. We also model infection spread in a community as a complex, long-term problem and arrive at an approach to assess the final size of the infected component.
### Table 4: Infection(Exploration) Prediction Model

| Sr. No. | Predictor Variable                  | Inter-dependencies | Remarks                                                                 |
|---------|------------------------------------|--------------------|-------------------------------------------------------------------------|
| 1       | Age                                |                    | Older people are more vulnerable. People of any age may get infected.   |
| 2       | Gender                             |                    | No particular correlation in most cases                                |
| 3       | Diabetes High Blood Pressure       |                    | If both conditions exist it makes matters worse                        |
| 4       | High Blood Pressure Diabetes       |                    | If both conditions exist it makes matters worse                        |
| 5       | Lung diseases or low immunity      |                    | Weak lungs can make people vulnerable and let the infection persist for longer. |
| 6       | Job Role                           |                    | We can classify as intramural, extramural, frontline and migratory     |
| 7       | Social Profile                     |                    | Stable interactions or changing interactions.                         |
| 8       | Infectious Neighbour Infected family member |                | Neighbours and family members are more likely to get infected and stay infected. |
| 9       | Infectious Family Member Infected neighbour |                | Neighbours and family members are more likely to get infected and stay infected. |

### Table 5: Member Behaviour and SIAM construct

| Sr. No. | SIAM construct | Members Behavior                          | Social Network Construct                                                                 |
|---------|----------------|-------------------------------------------|------------------------------------------------------------------------------------------|
| 1       | Balk           | Very few close connections                | Path lengths relative to members are high or average path lengths are high                 |
| 2       | Renege         | Does not stick to connections for long    | Low degree or generally isolated or low average degree                                    |
| 3       | Jockey         | Keeps switching connection               | Constant rewiring                                                                         |
| 4       | Decline        | Adherence of Social Norms, Proactive Testing | Part of the complex contagion who focus on prevention and protection                        |
Table 6: Community Characteristics

| Sr. No. | Predictor                      | Remarks                                                   |
|---------|--------------------------------|-----------------------------------------------------------|
| 1       | Size of largest component      | Large component/giant component can result in wide-spread infection |
| 2       | Average path lengths           | If average path length is low people are less likely to get infected via intermediaries. |
| 3       | Size of reachable cluster      | Low size here can help limit the infection spread through intermediaries. |
| 4       | Average Clustering coefficient | If the clustering coefficient is on the lower side, people are less likely to get exposed to infected people directly. |

5. Results

We ran NetLogo Simulations on a variety of Social Network Models followed by analysis within the communities by factoring underlying social structure. We look at the epidemic as a complex problem. Exploration is modeled as the NK problem and minimally modeled exploitation. NK problems can be simulated in different social contexts. We select prominent kinds of communities and explain them in terms of popular social networks. We compare multiple social contexts and how infection spreads such as all movements allowed, schools and congregations, commute and migrations allowed, stay-at-home. In our simulation we assumed a population size of 100. The results we are illustrating are indicative.

A community where all kinds of movement is allowed, can be modelled as a random network as depicted in Figure 2. Everyone can move freely in this neighbourhood and has no travel restrictions. The network depends on the probability of an individual coming in contact with other people. Here, it shows two common probabilities - 0.05 and 0.2. The network with a higher probability is dense, showing that there are too many random interactions between people and the disease will spread quickly because the average path length is low.

When the same community is restricted to a place where there are very few people meeting many people in less time, it becomes a scale-free/power law network. We can observe in Figure 3 that this network explodes because there are major hubs with a huge number of connections and few others with noticeably less number of connections. The growth is almost exponential and this kind of pattern will lead to immediate scarcity of resources.

On adding more restrictions to the random network community, we get a small-world network. Figure 4 depicts another neighbourhood where people commute to workplaces and allow visitors from far away regions too. We model it as a Small World Additive network with short and long ties. People are more connected to their neighbours through small ties which increases the clustering coefficient; they are also in contact with the visitors which decreases the average path length. The more are the long ties, the faster is the spread of the disease.
Figure 2: Random Network with wiring probabilities - 0.05 and 0.2

Figure 3: Scale free/Power Law Network
Figure 4: Small World Network in N-K Space - Commute and Migration allowed

Figure 5: Ring Lattice with limited ties
Table 7: Social Network Models and Network Metrics from NetLogo Simulation

| Sr. No. | Network Type                          | Control Variables                                      | Average Path Length | Giant Component | Reachable Cluster | Clustering Coefficient |
|---------|---------------------------------------|--------------------------------------------------------|---------------------|-----------------|-------------------|------------------------|
| 1       | 1-Dimensional Circular Lattice        | # of agents = 100, Degree = 2                          | 25                  | NA              | NA                | 0                      |
| 2       | Ring Lattice (Concentric Circles)     | # of agents = 100, Degree = 4                          | 12.995              | NA              | NA                | 0.67                   |
| 3       | Random Network with growth            | # of nodes = 100, # of links = 100, wiring probability = 0.2, max degree = 5, min degree = 0 | 1.79               | 80              | 90                | 0.203                  |
| 4       | Small World Network with rewiring     | # of nodes, rewiring probability = 0.30                | 3.974               | NA              | 15                | 0.207                  |
| 5       | Small World Network without rewiring  | # of nodes, rewiring probability = 0.0                 | 12.879              | NA              | NA                | 0.5                    |

Figure 6: Ring Lattice in N-K Space - Stay at home

For a community which has households or workplaces spaced out like concentric circles with each house interacting with four other neighbours, we can see in Figure 5 that even with limited movement, the contagion can spread swiftly. We model this stay-at-home community as a Ring lattice network with degree 4 as shown in Figure 6. The spread of disease is very rapid but due to high clustering coefficient and high average path length, the disease often gets stuck within this neighbourhood and eventually dies out.

More work is needed to take this work to the next level of maturity. Table 7 illustrates analysis of Social Network Model simulation. Table 8 deals with the results of NK Problem simulation on explorations and exploitations.

Through the aforementioned simulations, we have observed different kinds of communities and how any contagion can spread in a given fashion. How random and power-law networks grow rapidly while small worlds with lockdown take a significant amount to grow. If we draw parallels to COVID-19 situation, we find nothing different. COVID-19 also follows the same epidemic behaviour and its spread is dependent on the community it is spreading in. All neighbourhoods can be modelled using a network in NK space. There are various other communities and we are working on modelling them in future.
Table 8: Community Infection Dynamics using Netlogo Simulation

| Sr. No. | Social Structure/Model/Context | Control Variables | Simulation Period | Total No of Infections | Unique Infections or No of Infectious clusters | Remarks |
|---------|--------------------------------|-------------------|-------------------|------------------------|-----------------------------------------------|---------|
| 1       | Ring Lattice                   | # of agents = 100, Degree = 4, N =10, K=5 | 9 units           | Full Network i.e all 100 nodes | Start with 106 unique cases, goes down to 0 | The average score goes up till 0.87. As the number of neighbours increase, the disease spreads much faster but tends to get stuck at the local maxima and dies out eventually |
| 2       | Small World Network            | # of agents = 100, Degree = 6, N =10, K=5 | 3.96 units        | Full Network i.e all 100 nodes | Start with 107 unique cases, goes down to 0 | Reaches the average score of 1 in just 3.6 units of time. The spread of disease is very fast. |

6. Discussion

The aim of this work is containment in a bounded manner while recognizing the long term and complex nature of the problem. The worst nightmare is when either infections, hospitalizations or deaths happen in a power law pattern. Instead of looking at the total population in one go, we break it down into multiple sects. The idea here is to contain infection, one community at a time.

Stay-at-home community is depicted as a lattice network with concentric circles, with nodes heavily connected to all the neighbours. Ring lattice is a powerful network because of immediate ties between neighbouring nodes. Exploration is much suited, and a disease spreads rapidly, infecting the entire community in a brief span of time. But it often gets stuck in the local maxima and causes the disease to die out soon or later.

Small world additive network is an example of a community which allows regular movement of people from their homes to a fixed destination, e.g. workplace. They also allow others to enter their neighbourhood. Spread of disease in such a neighbourhood is much sooner than ring lattice because many ties are present between immediate and far away neighbours. Usually, a small-world network has a high clustering coefficient because the nodes are connected to their neighbours tightly. Clustering coefficient and average path length decrease as the number of ties increase, making it an optimal condition for the spread of diseases. With more open movement inside and outside the community, a small-world (special case of random network) starts behaving like a typical random network with minimal clustering.

Because of the high incubation period and major asymptomatic infections, curbing the spread of COVID-19 is an arduous task. Being unaware of infections themselves, individuals lead to the quicker exploration of their infection, instead of exploiting their detection and cure. The rate of spread depends on the community one is living in. In an epidemic with strict restrictions, the infection seems to follow a bell curve whereas in a situation with no restraints; it shoots up first and later comes down. The lock-down is a great way to curb, but not the strongest one because the spread happens, nevertheless. Maintaining adequate distance is of utmost importance, and that can be accomplished by using a proximity calculating mobile app [17] or by following social-distancing. A community under lock-down with casual movement and no incoming migrant population is an optimal case to contain COVID-19.
7. Conclusion
In this paper we have addressed the challenge of COVID-19 containment by factoring the underlying social network structure over which epidemic spreads. By making use of concepts and constructs of queuing theory, we have proposed a novel Social Infection Analysis Model. It comprises Infectious, Infected, Drop-outs and Immune chambers through which people from calling population transit through and join back the general population. Variety of social contexts which are differentially treated by Governments during COVID-19 pandemic have been represented using the most amenable social network model. Then the Network properties are studied using NetLogo simulations. Finally, transmission within communities is analyzed by modelling infections using NK problem and behavior of the susceptible using agent-based models. We intend to apply the Community Infection Spread Model to more social contexts in future. We believe that this work can lead to further research in this challenging problem of containment of COVID-19 pandemics.

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Appendix A. Popular Social Networks Simulated using Netlogo

(i) Virus in a directed 2D graph

(ii) Small World Network with rewiring

(iii) Small World Network with no rewiring
(iv) Virus on a Network

(v) Epidemic Model
(vi) Epidemic with lockdown and travel restrictions

(vii) Epidemic with no lockdown and travel restrictions
(viii) Erdos-Renyi Random Network

(ix) Virus - Alternative Visualisation

(x) Spread of a Disease - Hubnet Model
