Network Based Framework to Compare Vaccination Strategies

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Abstract. We propose a network based framework to model spread of disease. We study the evolution and control of spread of virus using the standard SIR-like rules while incorporating the various available models for social interaction. The dynamics of the framework has been compared with the real-world data of COVID-19 spread in India. This framework is further used to compare vaccination strategies.

Keywords: Network based framework · Vaccination strategies · Disease spread modelling

1 Introduction

Pandemics are rapidly spreading diseases which are results of disorders caused by various germs. COVID-19, the ongoing pandemic is due to a novel coronavirus named *Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)*. Modeling of infection spread, prediction of disease spread by inferring data at early stages of endemic, quantifying and forecasting the spread of infectious disease, are some of the basic direction of study when a disease outbreak occurs. These studies help to understand and identify various mechanisms to slow down the spread and flatten the curve of spread until antivirals/vaccines are developed. For some diseases, it takes quite a large amount of time to establish a certified antiviral medication or develop a vaccination. In the meantime, if the basic reproduction number of disease is not small enough (≤ 1), it doesn't die on its own. The basic reproduction number of COVID-19 has been estimated in early studies [11,14] to be around 1.8–2.7. Therefore, even if one infected case remains on the planet, there will be a chance of next wave of outbreak until a major fraction of the global population is immunized. Once some certified vaccine has been developed, the next challenge is to deliver it to the people to slow down

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the spread and further make the disease disappear. While there are several constraints involved in producing a vaccine on a large scale for the world population, countries with a higher population, like India, faces the same challenge severely. In the beginning, due to scarcity and limited availability of vaccines, an optimal strategy to vaccinate people plays a crucial role.

In this paper, we first propose a network based modular framework for modeling spread of COVID-19. Then we use real-world data in the context of India to fine tune various input parameters in the model to simulate similar spread dynamics as in the real-world. Afterwards, we apply this framework to compare performance of various existing immunization strategies. The paper is organized in 6 sections after the introduction. Section 2 discusses a few related works. Next, in Sect. 3, we discuss the design of framework. Section 4 mentions considered vaccination strategies. Simulation results are compiled in Sect. 5. We conclude and discuss future direction in Sect. 6.

2 Related Work

In a similar study, Yang et al. [16] used a network developed from empirical social contact data and applied fixed choice designs to identify contacts. They considered conventional SIR model where infection seeding started from 1% of the population. Kherani et al. [7] recently proposed a queuing model to study the spread of an infection. Vaccination is a mechanism to provide immunity to a person. It reduces the spreading rate by reducing the susceptible population which may also increase the likelihood that the disease dies out. Random immunization strategy may demand to vaccinate a large portion of the overall population, at times almost the whole population, to control a disease outbreak [1]. Therefore, due to scarcity in the availability of vaccine soon after the invention of the vaccine, it is not feasible to follow random immunization. Few target immunization strategies exist that suggest vaccinating highly connected people in the population but due to the unavailability of related data, these approaches might not be practical [4]. Several evolutionary algorithms have been designed to find optimal vaccination strategies [3,5,10,12] some of which rely on genetic paradigm.

3 Network Based Framework

In this section, we propose a network based modular framework to model spread of disease in context of pandemic and use it further to compare various vaccinations strategies. Several challenges are involved while designing such a framework. Few are mentioned next. There is a huge uncertainty in the number of parameters involved. The germs may mutate over a period of time and it may affect spreading rate, severity etc. The disease might end in a single wave of spread or there might be multiple waves of the infection. For spreading diseases due to novel viruses, there is an uncertainty in the availability of vaccination. In the early days, there is non-availability of sufficient clinical proofs regarding reinfection and quantification of the volume of reinfection. The duration after taking the vaccination shot when vaccine becomes effective and the duration for which the immunity due to vaccine or recovery holds is not well established. One of the major challenge is the unavailability of accurate contact network in real world. In this paper, we generate synthetic contact network based on the following three standard network generation models:

- Small World Network Model by Watts-Strogatz (WS)
- Scale Free Network Model by Barabasi-Alberts (BA)
- Random Network Model by Erdos-Renyi (ER)

In the proposed framework, social interaction among individuals in a population is assumed to be similar to a real-world social network. Each individual is considered as a node of a network and the link of the network represent the interactions among people. Nodes are classified as Susceptible(S), Exposed(E), Infected(I), Recovered(R), and, Vaccinated(V) based on SEIRV model in order to mimic the various state of a person during disease propagation as shown in Fig. 1. Every node is initially classified as susceptible. The disease starts at seed nodes by changing the status to exposed. In this paper, exposed nodes denote those people who have caught the infection post exposure but yet have not been detected as infected in the system based on testing. A person would be only in any one of these states at a time. In order to control the spread of the epidemic, different strategies like lockdown, containment, and immunization enforced by government authorities are also incorporated into our system. All these process are incorporated as modules.

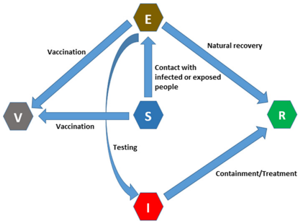


Fig. 1. SEIRV MODEL

Model: Any framework requires to capture following functionalities to show the dynamics of disease propagation similar to the real-world. It should capture the availability and scarcity of testing kits in the initial days of spread. It should have the provision to start vaccination only after a counter day in simulation that captures the start of vaccination drive and in parallel the daily availability of vaccination should be taken into account. Mutation of virus is a common phenomenon and due to it after the initial days of spread, spreading virus exist in the form several strains/variants. The mutation may cause change in the transmission rate which needs to be captured. An exposed person doesn't recover immediately, the duration of recovery varies from person to person. A right mechanism to capture the duration of natural recovery when the exposed person remains undetected or the duration of medicated recovery after testing positive is required. Lockdown and unlock are a globally known modus operandi in the early days of pandemic when there is scarcity of testing kits and yet there is no sign/scarcity of vaccine. During COVID-19 it has been used widely by various countries and states to contain as well as control the spread. It is very important to capture the restrictions imposed during lockdown and versions of unlocking periods. The possibility of developing symptoms or remain asymptomatic during infection and the capacity/duration for being active to transmit infection is another essential feature which is required in any such framework. In the proposed framework, all of the above discussed requirements are encapsulated as modules. Being modular in nature, the framework has the flexibility to easily modify a module representing a functionality based on the real-world requirement while disturbing other functionalities. There is not sufficient clinical studies exist that shed light on the reinfection post vaccination or post immunity after recovery in the case of COVID-19. Although, this framework easily allows to add the possibility of limited time immunity due to vaccination/ natural recovery, we have left it for future work. Algorithm 1 portrays the skeleton of the proposed framework where the modules are present in an abstraction form.

Algorithm 1: Modular Network-based Framework for COVID-19 Spread

```
INPUT: Parameters, Network Type Choice and Vaccination Strategy Choice
Generate Synthetic Interaction Network.
Contact_Profile()                          ▷ Initialise contact probability on the links
Seeding_Profile()                          ▷ Choose seed nodes to start disease propagation.
Set $Counter = 0$                          ▷ Day of seeding counts as the zeroth day.
while Number of Infected/Exposed nodes at the end of $Counter$ day $\neq 0$ do
    Mutation_Profile()                     ▷ Change in transmission rate due to mutation.
    Lockdown_Profile()                     ▷ Change in interaction probability due to lockdown.
    for Each Infected/Exposed node do
        if Node is Exposed then
            Natural_Recovery_Profile()     ▷ Does node recovers today naturally?
            if Naturally Recovered Today then
                Change State of this node from $Counter + 1$ day : $\boldsymbol{E} \rightarrow \boldsymbol{R}$
            else                           ▷ Node did not recover yet and is still exposed.
                Symptomatic_Profile()      ▷ Does node develop Symptoms?
                Testing_profile()          ▷ Does testing option available?
                if Tested Positive then
                    Change State pf this node from $Counter + 1$ day: $\boldsymbol{E} \rightarrow \boldsymbol{I}$
                else
                    for Each Susceptible Neighbor do
                        Transmission_Profile()   ▷ Does transmission happen?
                        if Disease transmits to that Neighbor then
                            Change state of neighbor from $Counter + 1$ day: $\boldsymbol{S} \rightarrow \boldsymbol{E}$
                        end if
                    end for
                end if
            end if
        else                               ▷ Node is Marked Infected
            Medicated_Recovery_Profile()   ▷ Does node recovers today?
            if Recovered Today then
                Change State of this node from $Counter + 1$ day: $\boldsymbol{I} \rightarrow \boldsymbol{R}$
            end if
        end if
    end for
    Vaccination_Profile()                  ▷ Vaccinate Susceptible nodes as per availability.
    Counter=Counter+1
end while
```

Input Parameters. Following parameters are required before starting the algorithm: number of nodes denoting the population (N), choise of synthetic network and parameters to generate it, ratio of population to be made as seed nodes (r), initial testing capacity and weekly incremental value, threshold day for recovery (after which an E or I node definitely recovers), scaling factor in case of medicated recovery, days when lock down and versions of unlock is placed, scaling factor for transmission probability when virus mutates, days when mutations occur, scaling down factor for meeting probability during lockdown and various versions of unlock, containment threshold, that checks whether the no.of infection are sufficient to declare containment zone, choice of vaccination strategy, parameters for vaccination (starting day of vaccination, initially available quantity and daily increment factor), and fraction of overall population to be classified into various age category.

Modules. The modules present in abstraction in Algorithm 1 representing various functionalities are described below:

- **Contact_Profile():** This module is to set daily contact probability as weights on the links. In the real-world, people make contact with other people during their daily activities which happens in different forms, for different duration, and in different environment set-ups. These interactions would be different for each individual based on the role they play in a society like a law-enforcer, or a health professional might have a lot of interaction than a common man. Also this social connection varies with the nature of the population like urban, semi-urban and rural. As the number of contact increases, a person is more likely to spread the influenza and might be called a super spreader[2]. In this paper, we have assigned uniformly random interaction probability values on the links. The values are generated based on Gaussian random number distribution.
- **Seeding_Profile():** This module chooses the seed nodes to start disease propagation. The fraction of the nodes to be initially made exposed to the disease for further transmission needs to be given as input to the framework. The approximate number of initial reported cases in the beginning of spread could be given as inputs in order to simulate for an actual condition prevailing in a region under study. In this paper, we have considered uniformly random selection for choosing seed nodes among the population to start the disease propagation.
- **Mutation_Profile():** The virus for spreading infectious disease mutates over time and its spreading rate as well as severity due to infection changes over time post mutation. This framework is mainly designed to understand the performance of vaccinations strategies in controlling propagation of a pandemic. Therefore, we consider a simplified version of mutation where the transmission probability is scaled up/down by a tuning factor. In this assumed model, effect of mutation is activated when the day counter in simulation reaches to the preset days given as input in the framework for mutation.

- **Lockdown_Profile():** Infectious disease often traverse from human to human if people interact within a distance limit for some duration. There might be undetected yet exposed people, therefore, staying away from close interaction is the best available solution to reduce the virus attack [6]. During COVID-19 spread, different lockdown restrictions have been imposed to reduce the interaction among people. In this paper, we have modelled a simplified version of real-world lockdown imposition. This version scales down contact probability of every link by a multiplicative tuning factor $0 \leq LF \leq 1$. $LF \in [0, 1]$ denotes the scale of lockdown restriction. $LF = 0$ means that all interactions are severed while $LF = 1$ means that no lock down restrictions, i.e., contacts are made with the initial assigned probability values. Lockdown restrictions and unlock relaxations are activated when the day counter in simulation reaches to the preset days given as input in the framework for applying restrictions and relaxations.
- **Natural_Recovery_Profile():** This module is to check if an exposed node naturally recovers on a counter day based on the number of days since when it has been exposed. We computes the conditional probability that a node recovers on Xth day since exposure, given that it had not recovered on previous days. Based on this computed probability value, this module decides if the exposed node under consideration recovers on this counter day or not. Naturally recovering probability is assigned based on a exponential function.
- **Medicated_Recovery_Profile():** This module is to check if an infected node on medication recovers on a counter day based on the number of days since when it has been exposed and since when it has been detected as infected. The decision is made based on a conditional probability that a node recovers on Xth day since exposure and Yth day since infected, given that it had not recovered on previous days. Based on this computed probability value, this module decides if the infected node under consideration recovers on this counter day or not. The medicated recovery probability is computed similarly to the probability value for natural recovery while taking into account the speed-up effect in recovery due to medication after detection. We have assumed to consider a linear scaling of natural recovering probability value based on the day since when this exposed node got detected and started using medication.
- **Symptomatic_Profile():** This module aims to bring in the functionality of symptomatic and asymptomatic case. It considers the factor that every exposed node does not develop symptoms due to varying immunity across the population. In this paper, we implement this functionality with the help of symptomatic probability and consider that only the nodes that develop symptoms get tested if testing kits are available. We assume that probability of developing symptoms after x counter days since exposure is generated similarly as the transmission probability, i.e., the symptomatic probability value is also assigned based on a normal distribution.
- **Testing_Profile():** This module incorporates the capacity of testing. In the early days of COVID-19, due to scarcity of testing kits/ long procedure and limited testing centers, not anyone could be tested for the disease. One of the essential condition was to have the established symptoms. Once sufficient

many centers were established and capacity of testing was increased sufficiently, then this requirement was relaxed. We try to model the capacity of testing in the form of the chance of getting tested given the symptoms are present. Only symptomatic exposed cases are tested based on the availability of testing. The capacity of testing on the current day counter is computed based on the initial capacity of testing and daily increment factor given as input. In this paper, we assume that the capacity of testing is increased linearly and after a threshold counter day, the capacity reaches sufficient that any one can be tested.

- **Transmission_Profile():** This module checks if an exposed node transmits disease successfully to a susceptible neighbor. The success of transmission depends on the contact probability value on the link between these two nodes and the transmission probability of the exposed node representing the capability of spreading the disease. The transmission probability of an exposed node is computed based on the current day counter and the day counter when that node was moved to exposed category. In this paper, we have assumed that the transmission probability is assigned based on a normal distribution.
- **Vaccination_Profile():** This module applies considered vaccination strategies which are discussed in next section. Before starting the vaccination it checks whether the current day counter is higher than the day counter when the vaccination drive starts. It also computes the number of vaccine vials available on the current day counter. This quantity is computed based on the initial vaccination quantity and daily increment factor given as input. In this paper, we assume that the production of vaccine as well as the availability of vaccine vials is increased linearly after the start of vaccination. This module vaccinates Susceptible/Exposed nodes as per the chosen vaccination strategy and availability of vaccine. Change state of these chosen nodes from $Counter + t$ day: $\boldsymbol{S} \rightarrow \boldsymbol{V}$ if these nodes remain susceptible for the next t days, where t is the number of days after which vaccine becomes effective.

Let N^t_{SV}, N^t_{EV}, N^t_{SE}, N^t_{ER}, N^t_{IR} be the number of susceptible nodes vaccinated, exposed nodes vaccinated, susceptible nodes exposed to disease, exposed nodes showed symptom and tested positive, exposed nodes naturally recovered, and infected nodes recovered with medicines respectively at the end of counter day t. Similarly, let N^t_S, N^t_E, N^t_I, N^t_R, and N^t_V be the number of, susceptible, exposed nodes, infected, recovered, and vaccinated nodes in the beginning of counter day t. As per the proposed model and algorithm, these values are related as follows: $N^1_S = N - SEED$, $N^1_E = SEED$, $N^1_I = N^1_R = N^1_V = 0$ where N denotes the population size and $SEED$ denote the number of seed infections

$$\begin{aligned}
N^{t+1}_S &= N^t_S - N^t_{SV} - N^t_{SE} \\
N^{t+1}_E &= N^t_E + N^t_{SE} - N^t_{EI} - N^t_{ER} - N^t_{EV} \\
N^{t+1}_I &= N^t_I + N^t_{EI} - N^t_{IR} \\
N^{t+1}_R &= N^t_R + N^t_{ER} + N^t_{IR} \\
N^{t+1}_V &= N^t_V + N^t_{SV} + N^t_{EV}
\end{aligned}$$

4 Considered Vaccination Strategies

Vaccines actually simulate the bodies natural immune system to create antibodies that could effectively fight against pathogens. The distribution of vaccine doses during a pandemic needs to be optimized when the demand is high and supply is less especially in a highly populated country like India. The proposed system would vaccinate the susceptible and exposed people based on the availability of doses and type of vaccination strategy. In the current framework, vaccination begins with an initial quantity that is calculated from the average of first week vaccines distributed in India, collected from https://www.covid19india.org/. The increment in the number of available dose is assumed to follow a linear curve. In this paper, we compare following vaccination strategies.

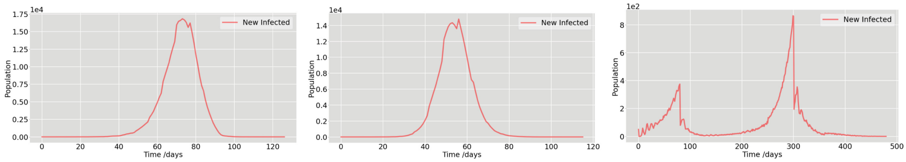
Random Vaccination: Individuals are randomly selected from the subject population, based on the quantity of vaccine doses available. In this approach, no information about the network structure is required, hence nodes are selected without any knowledge about its position [16]. Thus, no preference is given to any of the nodes.

Age-Based Vaccination: Government of India initially vaccinated all COVID-19 Front-line Warriors followed by elder population above 60 and people with comorbidities [8]. In subsequent phases, the target population were people above 45 and 18 years of age. Although to reduce the mortality rate the elderly should be given initial preference, it would be better to vaccinate the youth responsible for spreading the virus [9]. In the system, nodes are randomly classified into four age groups, namely, 65 and above (6.72%), 55–64 (7.91%), 18–54 (59.07%) and below 18 age groups. In order to mimic the actual age based vaccination followed in India the elder group is vaccinated first, followed by the 55–64 and 18–54 groups.

Ring vaccination: As per medical definition, Ring vaccination is a type of vaccination that vaccinates all susceptible individuals in the demarcated area of an epidemic outbreak. If an individual gets infected, the probability of infection getting transmitted to all the neighbouring nodes is high. Hence, all these neighbours need to be vaccinated immediately. A ring of protected people would act like a buffer to cover the infected person and stops further spreading of the virus [15]. This is a traditional vaccination strategy that had been used to control small pox.

Acquaintance Vaccination: This vaccination is applied in networks with large heterogeneity. First, a node is randomly selected like in the case of random vaccination and then, from its connected neighbours a new random node is selected for vaccination. This is based on the assumption that the acquaintance node might be more exposed to infections [15]. In actual scenario, this vaccination is implemented by asking a random person to nominate one of his friend for vaccination. Hence, it is also called as Nominated vaccination [16].

High Degree Vaccination: The number of contact a person have depends on the nature of his occupation and social behaviour. If the interaction is more,



(a) ER (b) BA (c) SW

Fig. 2. Comparison of daily New Infection in ER, BA, SW synthetic networks with Random Vaccination starting from day:300 and the real-world data of Indian COVID19 daily new confirmed cases.

there is more chance to get exposed from an infected person and spread to others. In this vaccination strategy, all the nodes having degree above a threshold value, say average degree, are tracked and immunized to break the viral chain [16].

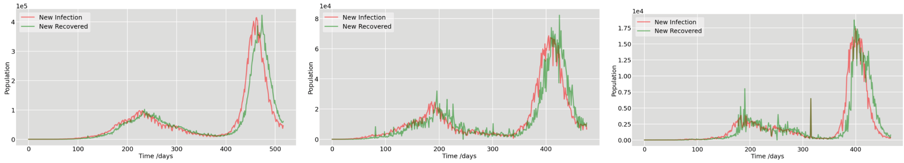
Top Degree Centrality Vaccination: The rate of transmission of pandemic could be reduced by identify and vaccinating those people with the highest number of contacts. These super-spreader would, otherwise spread the virus to a large group of people. Conventionally it selects some fraction of highest degree nodes for vaccination. [16]. In this paper, we implement it by choosing the highest degree nodes, vaccinate them if vaccines are available and, follow the same for next lower highest degree. Similar strategies based on other type of centrality measures [13] can be implemented in future.

5 Results and Discussion

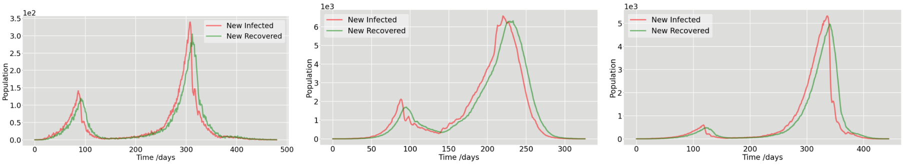
In this section, we compile and discuss the acquired simulation results. The simulation results achieved using the proposed framework scales linearly.

5.1 Comparison with the Real-World Data

In this section, first we plot simulation results for the three considered synthetic network generators and compare to identify the one that shows most similar disease dissemination as in the real-world. Figure 2 contains plots for ER, BA and WS network generator models. The networks were generated with same number of nodes and similar average degree, i.e., similar number of links. It is evident from the plots that results on synthetic small world networks generated based on WS model deliver most similar disease diffusion as observed in the real-world data in context of India given in Fig. 3a. In this simulation, the average degree has been considered 16 across all models. For higher average degree, even network generated based on WS model also exhibits a single wave due to faster disease dissemination in denser network.



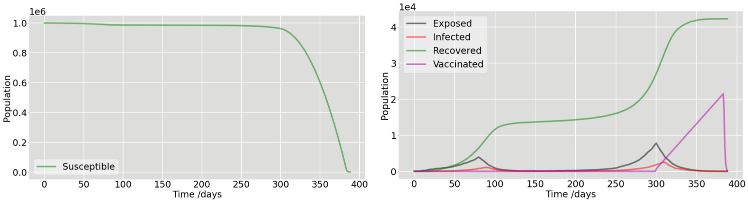
(a) Real-world (India) (b) Real-world (Maharashtra) (c) Real-world (Chhattisgarh)



(d) Simulated Data for India (e) Simulated (Maharashtra) (f) Simulated (Chhattisgarh)

Fig. 3. Comparison of real-world new daily infection and recovery count of India, Maharastra and Chhattisgarh data with simulated data

Next, we show the plots for daily new infection and daily new recovery for India as well as two states (Maharashtra and Chhattisgarh) of India where the proposed framework using WS small world network has exhibited similar dynamics for disease spread as happened in the real-world. The plots are compiled in Fig. 3. Apart from capturing the two waves of the real-world data, it is also observed that the daily new recovery curve (detected cases) follows the daily infected curve by few counter days similar to how it occurs in the real-world data. The real-world data has been curated from https://www.covid19india.org/. The detail list of input parameters for these simulations have been given in the full-version paper available on www.iitbhilai.ac.in/index.php?pid=csonet2021.



(a) Plot of Active S (b) Plot of Active E,I,R and V

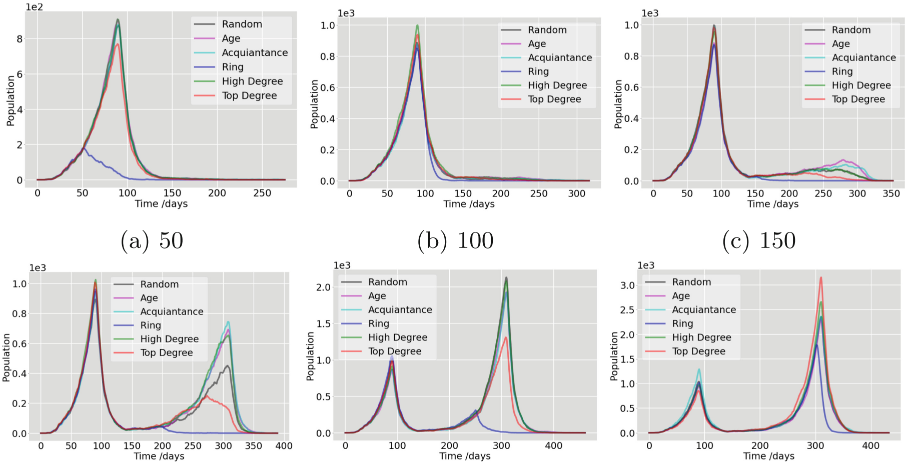
Fig. 4. Plot of SEIRV model in WS small world network with random vaccination starting from day:300

5.2 Disease Spread

In this section we show plots depicting the changes in the number of nodes belonging to various class in SEIRV model in a simulation on WS model based synthetic small world network. The plots are given in Fig. 4. It is observed that the plots for active exposed cases and active infected case look similar. The plot for infected nodes seems to lag by few days than the plot for exposed nodes. It is also observed that the peaks for active exposed nodes arrives few days earlier than the corresponding peaks for active infected nodes.

5.3 Comparison of Vaccination Strategies and Effect of Starting Date of Vaccination

In this section, we compare performance of vaccination strategies using the proposed framework. We also analyse the effect of the starting date of vaccination on the performance of vaccination strategies and the containment power against spread of disease. The plots are compiled in Fig. 5 and the expected number of total infected nodes for various strategies applied from different starting days has been compiled in Table 1.



(a) 50 (b) 100 (c) 150

(d) 200 (e) 250 (f) 300

Fig. 5. Plot of Daily Active Infection when different vaccination strategies are applied from day X = 50, 100, 150, 200, 250, and 300 in WS Small world Network

The expected results are generated by averaging the results over 5 runs of each simulation. It is evident from the plots that starting vaccination at early stage helps contain the disease quickly and in most of the cases there occurs a single wave of disease spread. But as we delay the start of vaccination process, the chance as well as the size of second wave increases. Ring vaccination has turn out to be most efficient among the considered strategies but it is not a realistic strategy to implement in most of the cases. The high degree vaccination strategy comes next in minimizing the expected number of total infection cases which is a more realistic approach. In India, the front-line workers were vaccinated first which is similar to vaccinating high degree nodes.

Table 1. Expected number of infected nodes when various vaccination strategies are applied from day X = 50, 100, 150, 200, 250, and 300

Type of vaccination	Day 50	Day 100	Day 150	Day 200	Day 250	Day 300
Random	31871.92	32688.17	43847.83	60724.67	130430.42	134503
Age	32799.22	33621.10	43979.57	73105.28	116993.64	127114
Acquaintance	31956.15	32376.68	45000.64	74050.65	113310.40	145875
Ring	7140	29634.84	31809.37	36775.42	53171.70	103298.92
High degree	32541.70	38092.75	42786.47	75622.65	124645.70	150917.08
Top degree	28787.8	34831.84	39820.14	56640.85	99415.98	142957.00

6 Conclusion and Future Directions

We proposed a network based framework to compare performance of vaccination strategies during a pandemic. It has been observed that the results for the dynamics of disease spread on small-world networks were the most similar to the real-world spread among the considered synthetic network generators. Although, Ring vaccination has turnout to be most efficient among the considered strategies, top-degree seems most realistic yet efficient approach to consider. Simulation results show that if the vaccination starts early, it may contain the dissemination of disease quickly. The dynamics of the spread scales linearly in the proposed model. Considering more accurate probability generation functions based on real-world behaviour is one of the future directions. A synthetic network generator that can depict the real-world physical social relationships better than the general synthetic generators considered in this paper is desired.

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