THE EUROPEAN SOCIETY OF MEDICINE
Medical Research Archives, Volume 13 Issue 3

RESEARCH ARTICLE

Vaccination Campaigns on Random and Scale-Free Networks

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PUBLISHED
31 March 2025

CITATION
Cornes, FE., Dorso, CO., et al., 2025. Vaccination Campaigns on Random and Scale-Free Networks. Medical Research Archives, [online] 13(3).
https://doi.org/10.18103/mra.v13i3.6405

DOI
https://doi.org/10.18103/mra.v13i3.6405

ISSN
2375-1924

ABSTRACT

The spreading of person-to-person infectious diseases (such as influenza) depends significantly on the contact network of the community. Any successful vaccination plan demands a complete understanding of how the disease can possibly propagate on this network. For this purpose, we examined vaccination actions on two specific community networks: scale-free networks and random networks. We applied a “random” vaccination plan and a “strategic” vaccination plan on both networks. The former corresponds to vaccine interventions regardless of the community structure, while the latter corresponds to preferential interventions according to the individual’s degree of connectivity. The “random” vaccination shows to be capable of reducing the infection peak, but the overall performance varies significantly if applied on a scale-free or random network. The “strategic” plan, on the contrary, prioritized vaccination actions on highly connected individuals. It showed more effective results since it slowed down the disease propagation while providing more time for immunization. We further applied the “strategic” plan to families instead of individuals alone. The plan appeared to perform nicely but not as effectively as vaccinating highly connected individuals.

Keywords: COVID-19, Complex networks, Small world.

1. Introduction

The spread of disease within large population groups is a complex phenomenon, shaped by the interactions between individuals and the internal dynamics of the disease within each person. These factors can vary widely across communities[1-4] and depend on the specific infectious agent involved[5-7]. This variability helps to explain the diverse outcomes observed during the COVID-19 pandemic in 2020[8-10].

Research indicates that a consistent pattern of contagion cannot be established without considering the role of human mobility. Mobility can create connections between individuals outside their immediate social environment, such as family or friends[2,5]. Studies on common mobility patterns suggest that these can differ depending on the spatial scale being examined[11]. Nonetheless, there is wide consensus in the literature that people tend to follow a “scale-free” spatial distribution within a typical urban environment[12-14]. In a nutshell, this means that a small number of individuals are responsible for the majority of social interactions, while most people only attain a few social contacts[15].

Human mobility introduces some degree of heterogeneity in the connectivity pattern. For instance, some groups may exhibit more connections than expected, leading to the formation of social communities. Consequently, epidemiological analysis must be conducted on two levels: a “global” scale that considers the overall progression of the disease and a “local” scale that focuses on the spreading within specific communities[16]. These scales are not necessarily spatial, as distinct “social layers” can overlap within the same geographic area[15].

Given these complexities, a microscopic approach to epidemiological modeling becomes essential. This approach considers each individual as part of an epidemiological environment similar to a “small world” network[17]. Within this framework, individuals may become infected, and the disease spreads according to established models, typically involving three stages (SIR models) or four stages (SEIR models), though additional stages may also be considered[18].

Incorporating vaccination strategies into this analysis adds another layer of complexity[19]. Vaccination can alter mobility patterns and social interactions by reducing the likelihood of disease transmission. For instance, vaccinated individuals may have fewer restrictions on their movement, which can impact how the disease spreads through different social groups[20].

Our investigation stands on the above perspective for the COVID-19 spreading. We simulated and compared different vaccination strategies in order to mitigate the disease propagation. The paper is organized as follows: Section 2 describes the epidemiological model and the different mitigation strategies. Section 3 details the simulation procedure. Section 4 displays the results of our investigation. These results are later discussed in Section 5. Finally, conclusions are drawn in Section 5.

2. The Model

This section outlines the presumed environment for the disease propagation. We first summarize the main features of the connectivity network (see Sections 2.1 and 2.2). We secondly detail the compartmental model of the disease (see Section 2.3).

2.1 RANDOM AND SCALE-FREE NETWORKS RANDOM AND SCALE-FREE NETWORKS

A network is essentially a collection of nodes (say, N) linked between each other in a specific manner. The random network and the scale-free network are possible examples that come up after establishing a rule for linking the nodes. The rules are as follows:

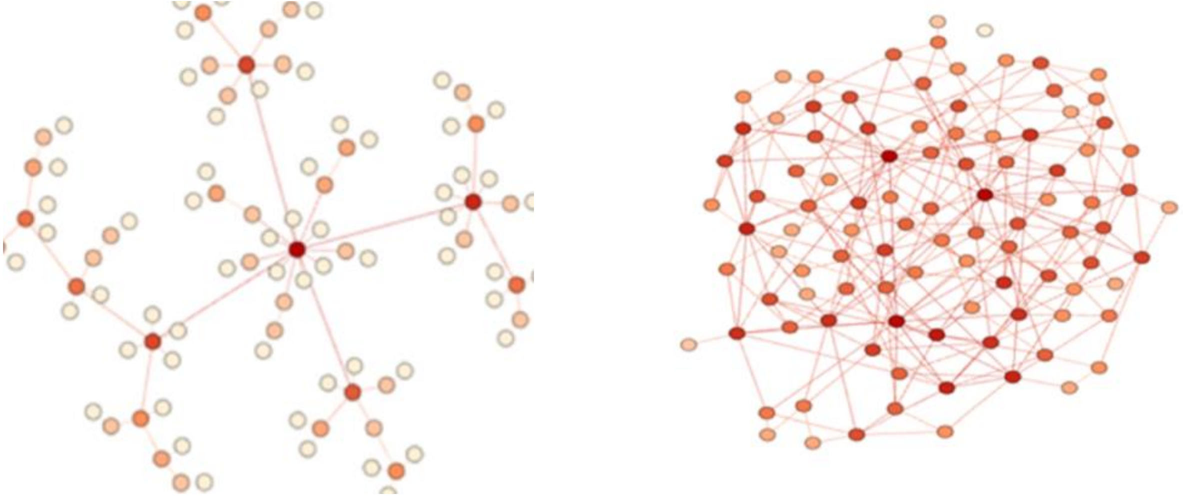
(a) Random linking: a fixed probability π is set, and nodes are connected according to this probability, as detailed in Ref. [21].

(b) Scale-free linking: the probability π of connecting an unlinked (new) node to an already attached node to the network depends on the degree of the latter[22-23]. That is, if the attached node i has an associated degree k_i, the probability of connection to this node is given by:

$$CB(i) = \sum_{j\neq k\in N} b_{ijk}/b_{jk} \tag{1}$$

This is called a *preferential* attachment[23]. It has been shown that this connection probability generates a scale-free (or power-law) connectivity distribution[24,25]. Real-world examples of such networks include the Internet and the human brain[26,27].

In network science, a node with an exceptionally high number of links is called a hub[24]. The existence of these hubs is the key difference between random networks and scale-free networks. Notice that the degree k in random networks is the same for all nodes. In scale-free networks, however, a few nodes (hubs) attain a high degree, while most of the nodes are scarcely linked. Fig. 1 exhibits a scheme for types of networks.



(a) Scale Free

(b) Random

Figure 1: Examples of a random network and a scale-free network[28]. Nodes with higher degrees are represented with more intense colors.

2.2 THE CAVEMAN MODEL

Disregarding the type of network (see Section 2.1), a caveman model can also be present in the network. This model captures the intra-family and inter-family social structure[29]. The common procedure to include the caveman model in the network is by first selecting randomly groups of four nodes (the family) and connecting them as a *cliqué*. Next, these family units were connected in a presumed fashion, allowing for interactions between different families, and thereby, reflecting a broader social network (see Fig. 2). It's important to note that every individual is embedded within a family structure after this model.

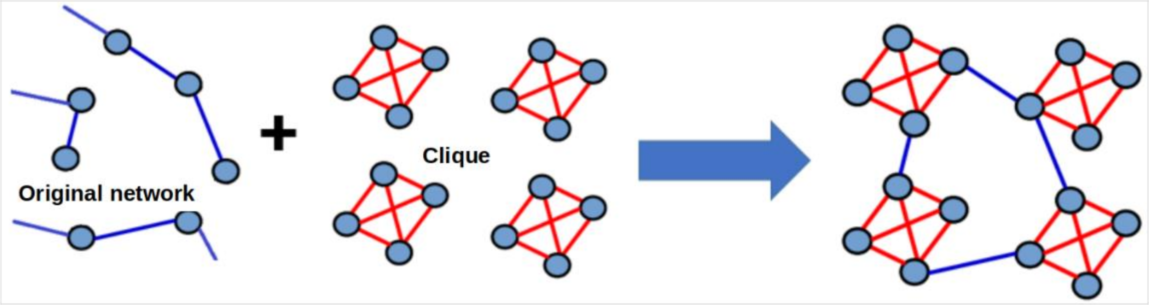


Figure 2: A schematic representation of a complex network consisting of four families. The subgraphs, which represent individuals' families, are interconnected by red links. These families are then integrated into the broader network through blue links.

2.3 THE SEIR EPIDEMIOLOGICAL MODEL

Throughout our investigation, we use the SEIRV epidemiological model to describe the disease evolution (see below). This model is widely used in epidemiology to simulate how diseases spread within a population. It offers a structured approach to understanding the dynamics of the disease transmission by categorizing the population into different stages[30,31].

In this context, each individual (out of a population of N) stands on a compartmental stage of the disease. The stage corresponds to some (discrete) step in the evolution of the disease. This is a kind of approximation that categorizes the complex evolution of the disease into major compartments of specific features. The number of compartments depends on the disease under study. We consider five compartmental stages, since this suits the behavior of a wide family of diseases like COVID-19. The compartmental stages are as follows:

(1) Susceptible $S(t)$: number of individuals who can become infected upon contact with an infected person.

(2) Exposed $E(t)$: number of individuals carrying the disease but not yet able to infect others.

(3) Infected $I(t)$: number of individuals capable of transmitting the infection to susceptible individuals.

(4) Recovered or removed $R(t)$: number of individuals who have recovered and are immune.

(5) Vaccinated $V(t)$: number of individuals who are immune due to vaccination.

where $S(t)+E(t)+I(t)+R(t)+V(t)=N$.

We stress that these basic compartments provide a preliminary approximation for the disease evolution. However, the specific complexities of each disease may require more detailed compartments for a more accurate description[5,7,32].

Notice that unlike other epidemiological models (SIS, SIR, etc.), the SEIR model fits better the behavior of the COVID-19 epidemic because it includes individuals in an incubation period of 5-6 days who are not yet infectious[33].

3 Methods

3.1 THE NETWORKS IMPLEMENTATION

As already mentioned in Section 2.1, we implemented the random and scale-free (preferential attachment) networks[22]. Recall that each one expresses a very different contact structure. The scale-free network, however, has been shown to express accurately human mobility patterns[22]. The random network, although naive, is useful as a comparison to other social situations.

We programmed both types of networks in low-level codes in order to simulate networks as big as one million nodes (*N*). These may represent cities the size of Rosario or Mendoza in Argentina. We further run at least 30 realizations for statistical sampling.

The detailed procedure for building the random and scale-free networks can be found in Ref.[34]. We just remind here that our implementation of the random network yields degrees that do not exceed $k \approx 10$. The scale-free network, instead, yields nodes of very high degree values acting as hubs ($k > 100$).

We also included *cliqués* for each kind of network, as explained in Section 2.2. These mimic the family structure in the network, although they do not change significantly the degree distributions in the network. Recall that the degree distribution for scale-free networks follows a power-law behavior (see Ref.[34] for details).

The minimum allowable degree for our simulations was $k=4$ due to the *cliqués*. The corresponding scale-free distribution (say, the network attaining preferential attachment and family structure) exhibited a power law with exponent $\gamma = -2.82$.

The paramount network attribute concerning our investigation is its “minimum path length”, that is, the shortest distance between any two nodes in the network. Fig. 3 illustrates the distribution of this magnitude for the random and scale-free networks.

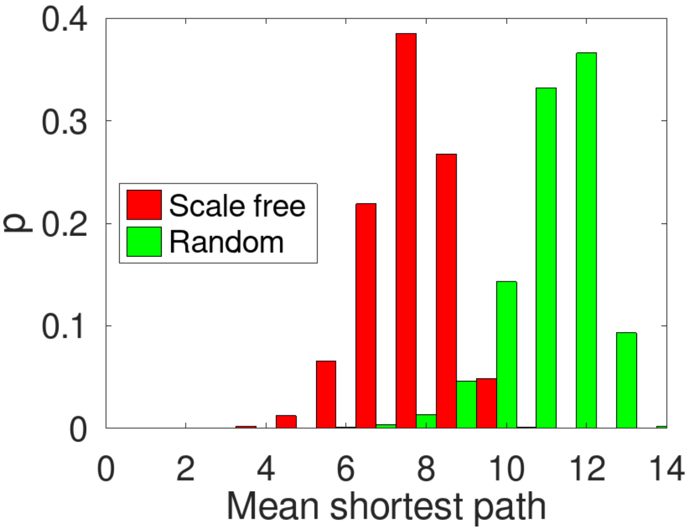


Figure 3: Shortest path distribution for the scale-free and random networks. 50 network realizations for each type were computed for building the histogram.

As can be noticed from Fig. 3, the average distance between any two nodes in the scale-free network is smaller with respect to the random network. This is due to the scale-free network’s structure, since the high-degree nodes, acting as hubs, enable more efficient and rapid dissemination of information across the network. Consequently, any “infection signal” or similar phenomenon within the scale-free network will spread more quickly than it would in the random network.

3.2 THE SEIR MODEL IMPLEMENTATION

The SEIRV model implementation follows the same steps as detailed for the SEIR model in Ref.[34]. But now we introduce the immunity stage due to vaccination (the ending V in the name of the model). We briefly resume the SEIR steps presented in Ref.[34].

(1) Start the simulation by randomly infecting an individual from a susceptible population.
(2) List the “susceptible” (S) individuals linked to the infected one and switch their stage to “exposed” (E) with fixed probability p (see Ref.[34]).
(3) Switch those exposed (E) individuals to the “infected” (E) stage after the incubation period.
(4) Repeat the above steps until the end of the simulation.

The average values of the incubation and infection periods for COVID-19 reported in Ref.[35] were considered.

The SEIRV model implements the vaccination strategy at step 2. Vaccination is applied exclusively on susceptible individuals since these are the ones at risk of becoming infected. However, we assumed that the vaccine provides immunity to the individual starting the day after its application.

The vaccines may be applied randomly on the population. However, an order of priority is also possible. For instance, the degree of connectivity in the network may establish an order of priority. Nodes are sorted according to the corresponding degree (in ascending or descending order), and the vaccines are strictly applied in this order.

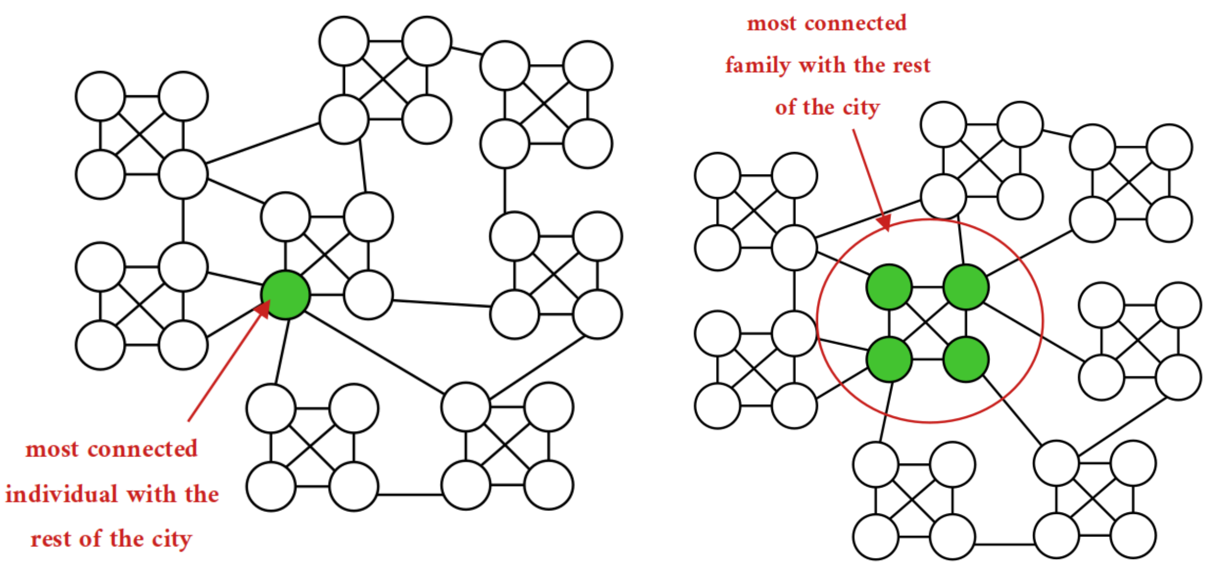
According to literature, it appears to be some kind of relation between people's age and the number of daily interactions they have (see, for example, Ref.[36]). Young individuals typically attain higher degrees of connectivity among the population than seniors. Thus, the order of priority based on the connectivity degree may be implemented by ordering people by their age. We will come back to this point in Section 4.2.

Complementary to random or priority vaccination of individuals, we may implement a family vaccination process. Fig. 4 shows the difference between both vaccination schemes (individual or family). Recall from Section 2.2 that families are present in the network by means of *cliqués* of 4 nodes.

We can summarize our implementation of the vaccination strategies as follows:

(a) Individual vaccination: may be random or prioritized. The former is self-explanatory. The latter sorts the individuals according to their degree and proceeds to vaccinate people in that order. Priority may be set in descending order (higher to lower degrees) or in ascending order (lower to higher degrees). Descending order may be envisaged as younger people first, while ascending order corresponds to seniors first.

(b) Family vaccination: similar to individual vaccination, but applies to *cliqués* (groups of 4 nodes). The degree of a family (*cliqué*) is defined as the sum of its members' degrees and ordered from lowest to highest (and vice versa). Thus, families were categorized as "young families" (high-degree) or "senior families" (low-degree).



(a) Individual vaccination (b) Family vaccination

Figure 4: Schematic representation of (a) individual vaccination and (b) family vaccination.

4. Results

Our results are divided into two parts. As a first step, we studied the disease spreading using a random vaccination strategy, where vaccines were administered regardless of the individual's connectivity. This approach, although naive, served as a baseline for the rest of the research. The "no matter who" intervention is the most elementary way of acknowledging how the disease propagates when a fraction of the population becomes immune.

As a second step, we focused on the more strategic intervention that prioritizes those (susceptible) individuals with a higher degree. This targeted strategy presumes that the mitigation efficiency depends on how fast the disease links can be broken. The higher the degree, the more links removed in a single shot.

4.1. RESULTS FOR THE RANDOM VACCINATION PROCESS

Fig. 5 presents the time evolution of the epidemic for different amounts of daily vaccinated people (see caption for details). The vaccination process exhibits a reduction in the peak number of infections for either the random network (dashed lines) or the scale-free network (continuous lines), as expected. However, this reduction is more pronounced in the case of the random network for an increasing number of daily interventions.

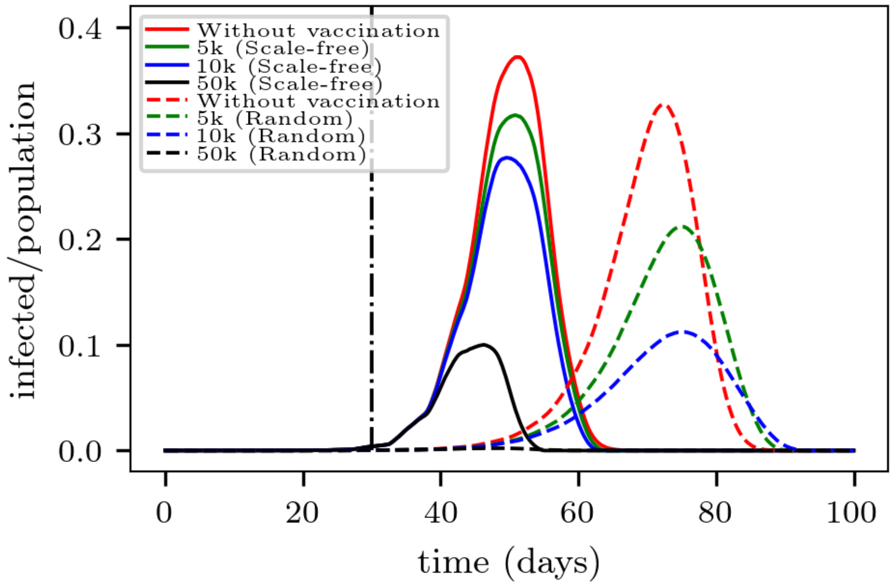


Figure 5: Evolution of infected individuals for different amounts of daily vaccinated people. The dashed lines correspond to random networks, while the continuous lines correspond to scale-free networks (see legend in the plot). The curves are normalized with respect to the population size (N = 1 million people). The black vertical line indicates the start of the vaccine interventions, say, once the number of infected individuals reached 5,000 (say, 5% of the population). The daily contagion probability was assumed to be $p_o = 0.8$ ($p = p_o / 24$). 50 realizations were performed for each network type.

The curves for the random network in Fig. 5 are a clear example of the commonly referred to "curve flattening" phenomenon that is known to be quite relevant when dealing with possible overcrowdings of medical-care centers. But also calls attention to the fact of the timing: the more people can be vaccinated daily, the better.

Fig. 5 further allows the comparison between the vaccination in the random network and in the scale-free network. For instance, in a random network, 50,000 daily interventions appear enough for an almost complete stop of the disease propagation (in the context of our model). But, surprisingly, this is not the case for the scale-free network where people may be easily reached, according to Fig. 3. This is an apparent paradox since many propagation links are now unavailable due to vaccination. We will discuss this point in Section 5.1.

Fig. 6 shows the number of vaccinated individuals over time for different vaccination rates (see caption for details). Notice that the maximum number of vaccinated people is always less in the scale-free network than in the random network (for the same rate). This means that many individuals were reached by the disease before the vaccination arrived, or say, the vaccination campaign did not arrive on time for them.

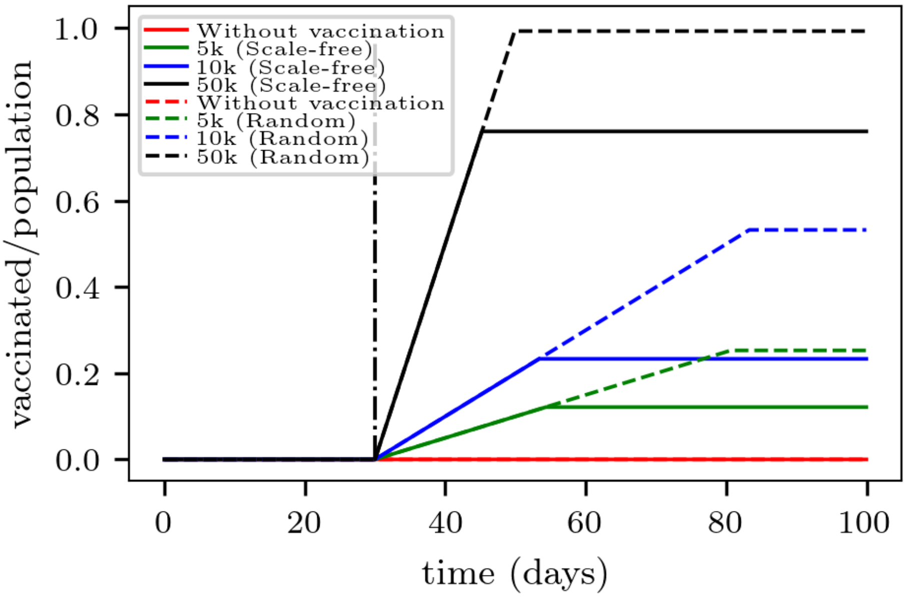


Figure 6: Evolution of vaccinated individuals for different amounts of daily vaccinated people. The random networks are shown in dashed lines, while the scale-free networks are shown in continuous lines. The slope of the curves indicates the vaccination rate (vaccinated people per day). The curves were normalized with respect to the whole population (N = 1 million individuals). The black vertical line indicates the starting point of the vaccination campaign. The daily contagion probability was assumed to be $p_o = 0.8$ ($p = p_o / 24$). 50 realizations were performed for each network type.

Fig. 7 completes the picture by showing the corresponding number of recovered individuals over time. It can be observed that the final effectiveness of the vaccination differs between the analyzed networks. For instance, applying 10,000 vaccines daily prevents 60% of the population from becoming infected in the random network, while this percentage drops to nearly 20% in the scale-free network (for the analyzed contagion probability).

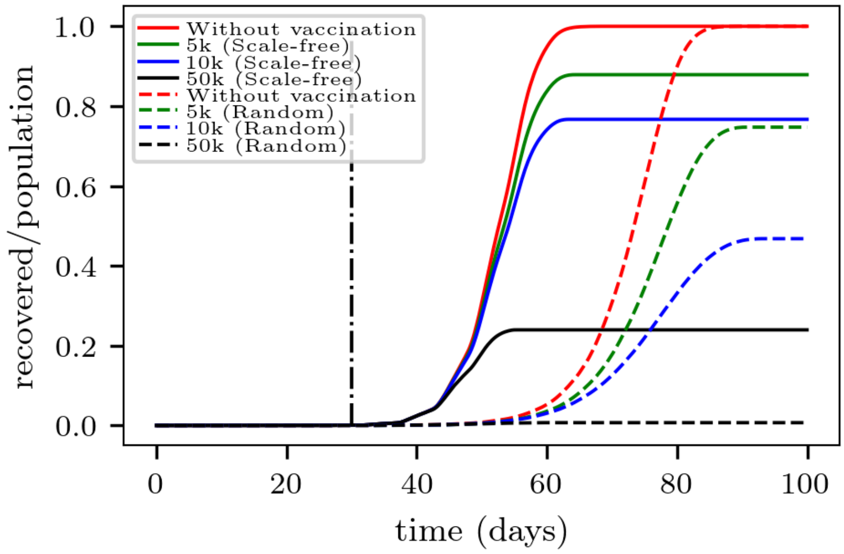


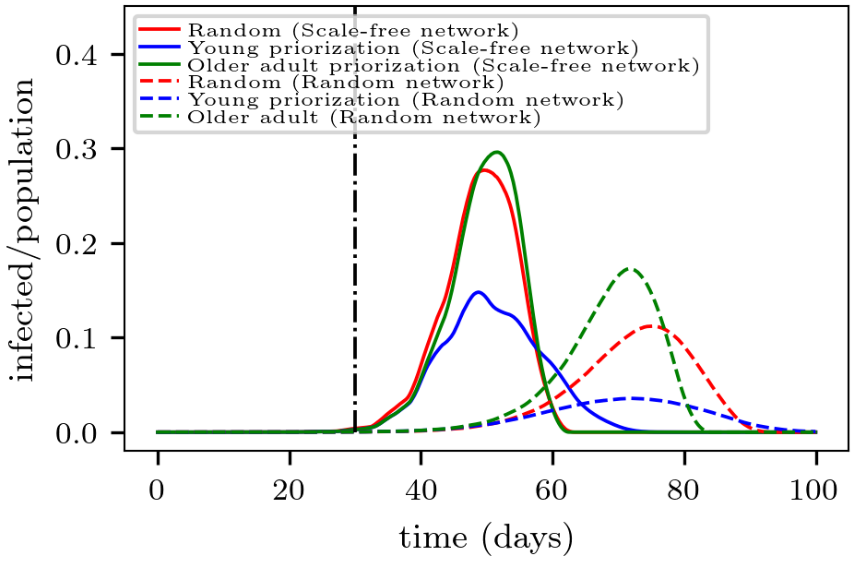
Figure 7: Evolution of recovered individuals for amounts of daily vaccinated people in scale-free (continuous lines) and random networks (dashed lines). The curves were normalized with respect to the population ($N = 1$ million people). The black vertical line indicates the start of vaccine interventions. The daily contagion probability was assumed to be $p_o = 0.8$ ($p = p_o/24$). 50 realizations were performed for each network type.

4.2 Results for the Strategic vaccination process

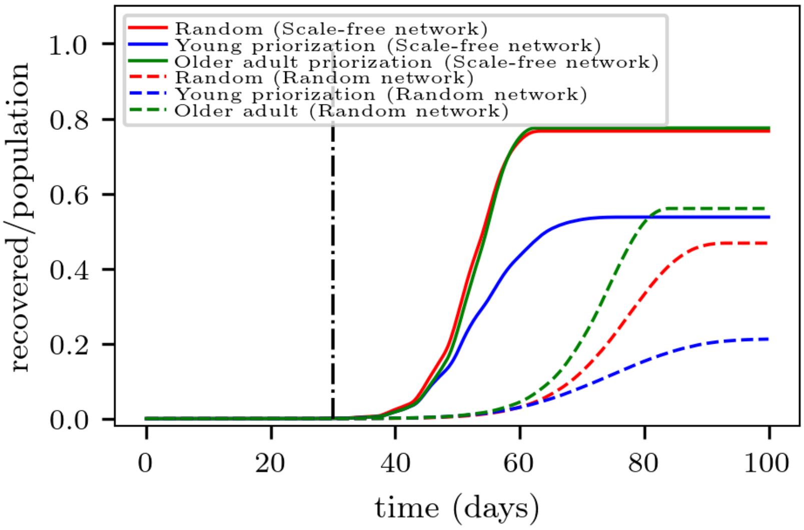
So far, we have analyzed the effectiveness of the vaccination campaign for a somewhat "no matter how" procedure. A step forward in our investigation is considering the degree of connectivity of each individual. We therefore turn to a vaccination procedure targeting individuals according to their degree of connectivity in the network.

We idealize the community as belonging to the following categories: senior or young individuals. The former are presumed to attain fewer contacts than the latter, as already mentioned in Section 3.2. Thus, in the context of our model, we will associate for a while low-degree nodes to seniors and high-degree nodes to young people. However, we want to make clear that this is just a simplifying hypothesis, although more complex situations may appear in practice.

Fig. 8 depicts the evolution of infected and recovered individuals for two vaccination strategies: time-priority of young people (blue color) or time-priority of seniors (green color). The random vaccination process is also shown in red color for comparison reasons (see caption for details).



(a) Infected



(b) Recovered

Figure 8: Evolution of (a) infected and (b) recovered individuals for different vaccination procedures. The red line corresponds to random vaccination, while the blue and green lines correspond to prioritizing young individuals and seniors, respectively. In all cases, 10,000 vaccines are supplied daily. The curves were normalized with respect to the population size ($N = 1$ million). The black vertical line indicates the starting point of the vaccination campaign. The contagion probability is assumed to be $p_0 = 0.8$ ($p = p_0/24$). 50 realizations were performed for each network type.

A first inspection of Fig. 8a shows that the vaccination campaign exhibits more "flattened" curves on the random networks (dashed lines) than on the scale-free networks (continuous lines) for the same priority strategy. This phenomenon was already present when analyzing the random vaccination process (see Section 4.1 for details). We observe that it remains present despite prioritizing seniors or youngers within the context of our model.

A closer examination of the random and scale-free networks in Fig. 8a shows that prioritizing younger people (blue lines) yields the most promising results (within the same kind of network). This means that starting the vaccination campaign on people attaining high-degree connectivity significantly improves the success of the campaign. The obvious reason is that vaccination gives immunity to highly connected people before the disease reaches them. However, not so obvious is that prioritizing younger people provides more time to vaccinate other larger portions of the population.

We emphasize that our hypothesis of associating low-degree nodes to seniors and high-degree nodes to youngers is quite ideal. There may exist in practice other reasons for prioritizing specific groups of individuals. However, from the logistic point of view, simply asking the age of the individual appears to be a feasible procedure.

Besides, a qualitative difference between the scale-free network and the random network can be noticed from Fig. 8a. The scale-free network does not show any significant difference between seniors priority and random vaccination. But this is not the case for the random network, where random vaccination somehow flattens the infection curve.

Fig. 8b confirms the above difference between the scale-free network and the random network. The former shows the same number of recovered individuals, regardless of proceeding with a seniors priority or a random vaccination. The latter, however, favors the random vaccination in comparison to seniors priority vaccination (say, by around 10% at the end of the campaign).

4.3 RESULTS FOR THE FAMILY VACCINATION PROCESS

The vaccination strategies discussed so far focus solely on individuals not considering the family social structure (see Section 2.2). We now turn our attention to vaccinating families based on their degree of connectivity, as defined at the end of Section 3.2. Fig. 9 depicts the evolution of recovered individuals under different vaccination strategies (see caption for details).

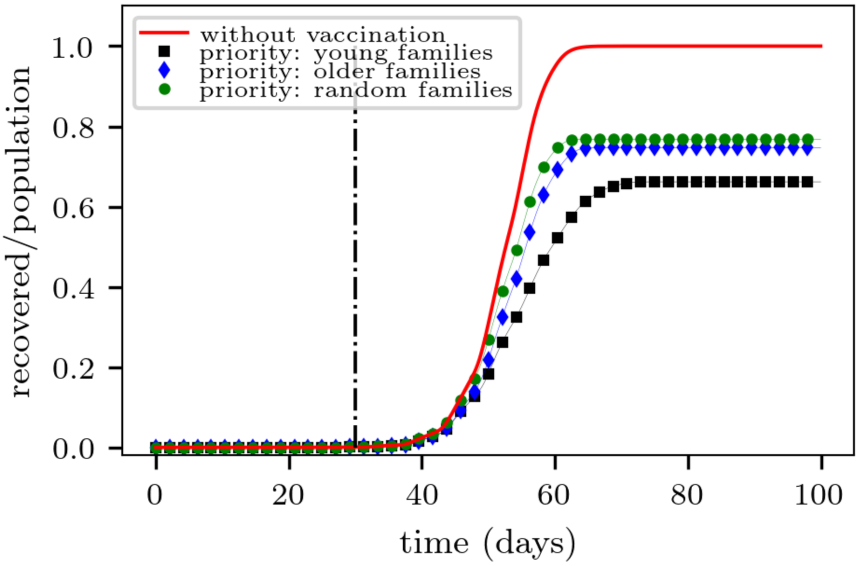


Figure 9: Evolution of recovered individuals in the scale-free network under different vaccination strategies (see legend for details). The red line represents the situation with no vaccination at all. In all cases, 10,000 vaccines are supplied daily. The curves were normalized with respect to the population (N = 1 million). The black vertical line indicates the starting point of the vaccination. The contagion probability was assumed to be $p_0 = 0.8$ ($p = p_0/24$). 50 realizations were performed for each network type.

We can see in Fig. 9 that priority vaccination of younger families appears as the most promising strategy. This is in agreement with the results shown in Section 4.2. Fig. 10 shows a more detailed comparison between both results.

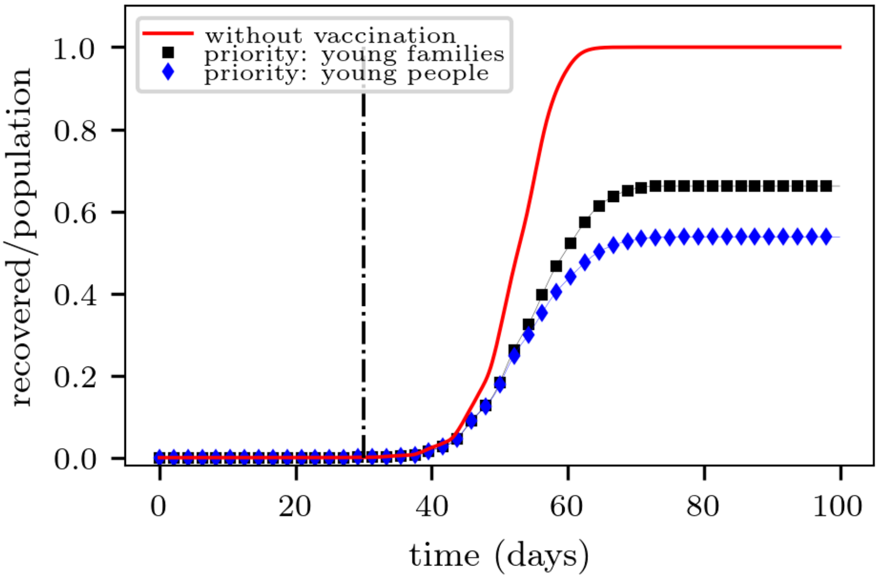


Figure 10: Evolution of recovered individuals in the scale-free network under different vaccination strategies (see legend for details). The red line represents a situation with no vaccination at all. In all cases, 10,000 vaccines are supplied daily. The curves were normalized with respect to the population (N = 1 million). The black vertical line indicates the starting point of vaccination. The contagion probability was assumed to be $p_0 = 0.8$ ($p = p_0/24$). 50 realizations were performed for each network type.

Notice from Fig. 10 that young individuals alone or young families attain a final recovery of roughly 60%. However, the "young families" vaccination appears slightly beyond the "young individuals" vaccination. Or in other words, the former appears as less effective than the latter (see Section 5.3 for a detailed discussion).

5. Discussion

5.1 THE RANDOM VACCINATION PARADOX

We noticed in Section 4.1 that the "no matter how" vaccination strategy performs better in the scale-free network than in the random network. Fig. 6 served to illuminate this point by showing that the random vaccination strategy fails to reach many individuals before the disease catches them. This is the key point of the paradox.

Recall that in the scale-free networks, only a few nodes (*i.e.* hubs) attain an extremely high number of connections (k>100), while many nodes only achieve a small number of connections. However, the vaccination process of "no matter how" yields equal immunity to individuals regardless of their degree of connectivity. Thus, some hubs may not be reached on time by the vaccination campaign while the disease continues spreading easily throughout the network. This is not the case in the random network, where the degree does not exceed $k \approx 10$, and consequently, there is more time for people to become immune.

In summary, this paradox expresses a somewhat competitive dynamic between the disease propagation and the vaccination rate. The "no matter how" vaccination at a fixed daily rate ignores the underlying contact structure, and thus, may lose effectiveness whenever the disease is allowed to spread easily throughout the network. We illustrated this phenomenon by means of a scale-free environment.

The message from the above reasoning is that a condition for the success of the vaccination campaign relies on its adaptability to the structure of the underlying network.

5.2 WHO TO VACCINATE FIRST?

We explored in Section 4.2 the priority vaccination strategy, targeting individuals according to their degree of connectivity in the network. We associated low-degree nodes to seniors and high-degree nodes to youngers, as a simplifying hypothesis. We emphasized that, although this is quite ideal and more complex situations may exist in practice, it appears as a reasonable starting point for the analysis.

Fig. 8 showed that starting the vaccination campaign on young people significantly improves the success of the campaign, regardless of the type of network (random or scale-free). This is not in question within our context, but other arguments may come into discussion in practice.

The most controversial arguments might involve seniors priority. Fig. 8 shows that the random vaccination procedure is preferred to seniors priority in the context of random networks. Thus, there are not *a priori* reasons to implement a seniors priority strategy if the network suggests some kind of linking randomness. But, as mentioned above, other reasons (out of the scope of our model) may exist for insisting on prioritizing seniors.

The scale-free network does not show any significant difference between seniors priority and random vaccination. This point is quite relevant when planning a campaign. The planner may prioritize the seniors, missing that the disease shortcuts through those younger, acting as hubs. Instead, the planner should consider thoughtfully if the random scheme is worth the logistics.

We conclude this Section emphasizing that priority procedures exhibit promising results. However, these should be considered with care according to the environmental conditions. As a guideline, any successful strategy should prioritize individuals attaining high degrees, such as young people in our model. But the precise vaccination procedure may deal with issues out of our model.

5.3 IS THE FAMILY VACCINATION AN EFFECTIVE STRATEGY?

We noticed in Fig. 10 that the fraction of recovered people at the end of the campaign is slightly higher for the "young families" target than for the "young individuals" target. This means that the former yields a less effective campaign than the latter. Recall that recovered people are those who were not vaccinated at all.

The above results are quite understandable since young families are expected to include mostly young individuals. However, some young people may not belong to young families, but to senior families (in a small fraction, though). Thus, they may still propagate the disease easily. This is the reason why the "young families" vaccination appears in Fig. 10 slightly beyond the "young individuals" vaccination. Or in other words, the former is less effective than the latter.

The priority vaccination of "senior families" shows somewhat no difference with respect to "random families" vaccination (see Fig. 9). This is also in agreement with the corresponding results shown in Fig. 8b for individuals alone. Indeed, the argument given in Section 4.2 remains valid here, say, that the disease shortcuts through younger people (belonging to younger families), acting as hubs. The priority of "senior families" makes no significant difference from a random family vaccination.

We arrive at two major conclusions in this Section. First, that the priority vaccination of young families is preferred over senior families priority or random families vaccination (in the context of our model). Secondly, and not intuitive, that vaccinating (young) individuals alone expects a more promising campaign than vaccinating the young families.

We call attention (once more) to the fact that our model neither considers logistic features nor social reasons for evaluating the effectiveness of the vaccination campaign.

6. Conclusions

The investigation studies the spatial-temporal evolution of an infection (similar to COVID-19) from a microscopic point of view. We focus on the analysis of vaccination strategies on different network structures. Two main strategies were considered: *(a)* the random vaccination strategy, where vaccines are applied regardless of the network connectivity structure, and *(b)* the priority vaccination, which targets individuals (or families) according to their connectivity degree within the network. We simulated random and scale-free networks for both kinds of strategies.

Our major conclusion is that prioritizing highly connected individuals (associated here with young people) appears as the most promising vaccination procedure within the context of our model. This is valid either for random networks or scale-free networks. We further noticed that prioritizing youngers not only slows down significantly the disease propagation, but also provides more time for the vaccination of other large portions of the population.

Whenever prioritizing highly connected individuals is not possible, we noticed that a random vaccination strategy is preferred with respect to prioritizing low-connected individuals (associated here to seniors). Random or "no matter how" vaccination does not actually have any advantage over seniors priority in scale-free networks. But it appears as a slightly more successful procedure in random networks.

We may feature a somewhat general rule from the above: the random vaccination is expected to be more effective in random networks, while targeted vaccination is expected to perform better in scale-free networks (according to our model). Thus, the campaign planner should analyze the nature of the connectivity structure and point to those highly linked individuals first.

Tailoring the vaccination procedures to target highly linked individuals is of paramount relevance when dealing with social groups. We compared a family-based procedure versus an individual-based procedure, prioritizing highly connected families or individuals, respectively (in the scale-free network). We noticed a loss of effectiveness in the former with respect to the latter. The reason is that highly linked families do not target *all* the highly linked individuals but a *fraction* of them. There is a remainder of highly linked individuals out of the highly linked families.

Our final conclusion concerns the planning of the vaccination campaign. A precise understanding of the underlying network structure allows for better tailoring of the vaccination strategy. However, our tailoring rule is limited to the scope of our model. Other issues may be relevant for the welfare of the population. Thus, the planner should thoughtfully weight our recommendations with those out-of-model arguments for the final decision.

Acknowledgments

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