Epidemic models with restricted circulation and social distancing on some network topologies*

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Abstract. A model to simulate the spreading of a disease on a network is proposed. The SIS and SIR models, a social distancing factor and network circulation restrictions are considered. We perform some experiments that give us an idea of how a disease spreads on different network topologies and social distancing factors.

Keywords: Epidemic models · Networks · Experiments

1 Introduction

Nowadays we are witnessing a pandemic. The health system and the economy of the region affected by a disease can suffer serious damage without proposals to control its spreading. So, control policies to lead this spreading are necessary. The ideal is that public agents and society together act quickly applying suggested policies as fast as they can to avoid that a disease reaches people and advances on territory.

Follow the real numbers of infected people, recovered people, the real number of occupied and empty beds in hospitals are important statistics in combat to pandemic. Other important question is the possibility to estimate with quality such numbers given some initial conditions. Hethcote [5] describes three fundamental epidemiological mathematical models which are used to follow the dynamic of a disease. The models classify people in groups and they depend on the following scenario: 1. a person is subject to contract a disease even if he (she) was already cured; 2. a person is subject to contract a disease, however, if he (she) contracted it in the past and he (she) is now cured then he (she) cannot contract the disease again; 3. a healthy person can be immune or can be vaccinated, thus avoiding to contract a disease. In the first scenario, we have the model named SIS. In this model people are classify as *susceptible* (those that are subject to contract a disease) and *infected* (those with a disease). In the second scenario, we have the SIR model. In this case, people are classify as susceptible, infected and *recovered* (those that were infected and will not be infected anymore). The class recovered can include dead people. In the third scenario, the SIRV model, people are classify as susceptible, infected, recovered and vaccinated.

It is common to find ordinary differential equations models to simulate the dynamic of a disease and to estimate the numbers of susceptible, infected, recovered and vaccinated people (when it is the case) over time. A classic epidemiological model which uses differential equations is the Kermack and McKendrick model [6]. In their work, they consider the groups of people that are susceptible, infected and recovered. The Linge and Langtangen' book [7] have a section dedicated to the treatment of spreading disease through the numerical solution of ordinary differential equations. Other models use cellular automata to study the spatial effects of an epidemic. White, del Rey and Sánchez [9] introduced a cellular automata model to simulate the epidemic spreading. Beauchemin, Samuel, and Tuszynski [3] used cellular automata to study the influenza A spreading. There are other works on this subject such as [1], [10] and [8].

This work follows the same direction of the models based on cellular automata. Here we study the disease effect in a *network* with different *topologies*. We highlight two points whose turn more difficult the disease spreading by the network: the *circulation restrictions* remaking a real network topology to a particular network topology, turning the network strongly structured; and the *social distancing* through the possibility of people answer positively requests from public agent, media, academy, etc. We perform experiments on the SIR model and illustrate its characteristic graphics on different network topologies and in different social distancing levels.

To finish this section, we describe how this work is divided. In Section 2, we start with the application of SIS model in a network. In Section 3, we describe how we treat the social distancing in the model. In this work, we suppose that a disease is spread by meeting between two people, a susceptible an another infected. So, in Section 4, we add to the model the meeting between people. Section 5 considers the SIR model in a network. We describe some network topologies and analyze the experimental results in Section 6. The conclusions are in Section 7.

2   The SIS model and the network

The SIS model supposes, for each time t, a set of infected people I^t and a set of susceptible people S^t. The people set maintains constant $N^t = I^t \cup S^t$. A susceptible person on time t can become infected on time $t+1$ and vice versa. We know that a susceptible person becomes infected when he (she) has a contact with the disease virus. However, in this work we concentrate the infections occurring in the meeting of a susceptible person and an infected person. There is a *virulence rate* $v \in [0,1]$ that represents the potential infection of a meeting. A *recovered rate* of infected people from the time t to $t+1$, $\varepsilon \in [0,1]$, is also considered. In this way, next it is given a simple model to estimate the number of susceptible and infected people for each time t (here yet considering such numbers as real numbers)

$$|I^t| = |I^{t-1}| - \varepsilon|I^{t-1}| + v|X^{t-1}|,$$
$$|S^t| = |S^{t-1}| - v|X^{t-1}| + \varepsilon|I^{t-1}|$$

where X^{t-1} is the set of people $p \in S^{t-1}$ that have a meeting with some infected person. Note that $|N^t| = |I^t| + |S^t| = |I^{t-1}| - \varepsilon|I^{t-1}| + v|X^{t-1}| + |S^{t-1}| - v|X^{t-1}| + \varepsilon|I^{t-1}| = |N^{t-1}|$. Therefore, the model maintains the total number of people constant over time. For a while, we allow $|I^t|$ and $|S^t|$ be real numbers. Since this not reflect the reality of the world, in the following sections, we will keep these numbers as integer numbers.

We use networks (or graphs) to represent the proximity concept among people. Consider a network $G = (V, E)$. The vertex set is formed by $V = \{1, 2, \ldots, n\}$. The edge set is formed by $E = \{\{i, j\} : i \text{ is adjacent to } j\}$. The set of vertices adjacent to vertex i is denoted by $\chi(i)$. A real value in interval $[0, 1]$ is associated to each vertex. We discuss the representation for these values in the end of this section. Additionally, a group of people is associated to each vertex (people from the same neighborhood, same city, etc). They can be susceptible or infected. A certain proportion from these people answer to social distancing. Two vertices are adjacents if the two people groups have some proximity (neighborhoods or cities sharing a frontier). This network will be used to simulate, for each time, the dynamic of susceptible and infected sets in each vertex. The group of people in a vertex i and on time t is denoted by the set $N_i^t = S_i^t \cup I_i^t$ (the intersection $S_i^t \cap I_i^t$ is empty). The number of elements in the sets S_i^t and I_i^t can vary over time, however, there is no removal in N_i^t.

As previously described, each vertex has a real value, denoted by α_i^t, and it represents the social distancing factor of people in vertex i and time t. Although we have a time associated to the problem, the graph structure is static. However, the number of susceptible, the number of infected people and the social distancing factor can be changed over time. In the following, we describe how the distancing factor is considered in the model.

3   The social distancing factor in the model

The social distancing factor partitions the sets of people in two: those people that answer to social distancing and those that do not answer. The people that do not answer the distancing could go out its vertex and could keep going through the network. However, we will simplify the model supposing that a person can go through adjacent vertices. So, or a person is in his (her) own vertex or in some adjacent vertex.

Now we add to the model the social distancing factor. We denote by $\dot{S}_i^t \subseteq S_i^t$ ($\ddot{S}_i^t \subseteq S_i^t$) the set of susceptible people in N_i^t that answer (do not answer) to social distancing. The set denoted by $\dot{I}_i^t \subseteq I_i^t$ ($\ddot{I}_i^t \subseteq I_i^t$) is the set of infected people that answer (do not answer) to social distancing. We will assume that the social distancing factor of each vertex i on time t, α_i^t, is applied equally on the sets S_i^t e I_i^t, that is, $|\dot{S}_i^t| = \lfloor \alpha_i^t |S_i^t| \rfloor$, $|\ddot{S}_i^t| = |S_i^t| - |\dot{S}_i^t|$, $|\dot{I}_i^t| = \lfloor \alpha_i^t |I_i^t| \rfloor$ and $|\ddot{I}_i^t| = |I_i^t| - |\dot{I}_i^t|$ (the function $\lfloor x \rfloor$ takes the integer part of x). Therefore, we will have, for each time t, the set of people from N_i^t that answer to social distancing $\dot{N}_i^t = \dot{S}_i^t \cup \dot{I}_i^t$; and the set of people from N_i^t that do not answer to

social distancing $\ddot{N}_i^t = \ddot{S}_i^t \cup \ddot{I}_i^t$. Next section, we highlight how the model treats the meeting between susceptible and infected people.

4   About the meetings

In our scenario, for each time t, some people that answer to social distancing ($\lfloor \lambda_{\dot{S}} | \dot{S}_i^t | \rfloor$ and $\lfloor \lambda_{\dot{I}} | \dot{I}_i^t | \rfloor$) can be infected. This happens due to situations that require a person having to go out home (he (she) goes to drugstore, supermarket, etc). For the people that do not answer to social distancing ($\ddot{S}_i^t$) can become infected (on his (her) own vertex or in some adjacent). Therefore, for each vertex i, we can have people circling in i coming from the set N_i^t and from the set $\bigcup_{j \in \chi(i)} \ddot{N}_j^t$. Given such observation, it is important to us know the total number of people that are circling in each vertex of the network and in each time. This can be estimated by a tool that identifies the number of people in regions such that parks, shopping malls, workplaces, residences, transit, etc. Note that, it is not required the position where each person is but a *community mobility report*, such as in [4], giving the total number of people located in regions for each considered time.

Our experiments consider, for each time t, the following number of people circling in vertex i (people from N_i^t and from $\bigcup_{j \in \chi(i)} \ddot{N}_j^t$):

a. $\dot{\mathcal{S}}_i^t = \lfloor \lambda_{\dot{S}} | \dot{S}_i^t | \rfloor$: susceptible people that answer to distancing (from $\dot{S}_i^t$);

b. $\dot{\mathcal{I}}_i^t = \lfloor \lambda_{\dot{I}} | \dot{I}_i^t | \rfloor$: infected people that answer to distancing (from $\dot{I}_i^t$);

c. $\ddot{\mathcal{S}}_i^t = \left\lfloor \frac{|\ddot{S}_i^t|}{|\chi(i)|+1} \right\rfloor + (|\ddot{S}_i^t| \mod (|\chi(i)|+1))$: susceptible people that do not answer to distancing (from $\ddot{S}_i^t$);

d. $\ddot{\mathcal{I}}_i^t = \left\lfloor \frac{|\ddot{I}_i^t|}{|\chi(i)|+1} \right\rfloor + (|\ddot{I}_i^t| \mod (|\chi(i)|+1))$: infected people that do not answer to distancing (from $\ddot{I}_i^t$);

e. $\dddot{\mathcal{S}}_i^t = \sum_{j \in \chi(i)} \left\lfloor \frac{|\ddot{S}_j^t|}{|\chi(j)|+1} \right\rfloor$: susceptible people from adjacent vertices that do not answer to distancing;

f. $\dddot{\mathcal{I}}_i^t = \sum_{j \in \chi(i)} \left\lfloor \frac{|\ddot{I}_j^t|}{|\chi(j)|+1} \right\rfloor$: infected people from adjacent vertices that do not answer to distancing.

The values in items a and b represent the people that answer the distancing but, for some unavoidable reason, they have to go out home. By items c and d we know that people in i that do not answer the distancing are distributed in own vertex and in adjacent vertices leaving, possibly, the own vertex with more people (the rest of division remains on own vertex). The items e and f show to us that each vertex receives from its adjacents an amount equally distributed. Let us denote by $\dot{\mathcal{N}}_i^t = \dot{\mathcal{S}}_i^t + \dot{\mathcal{I}}_i^t$, by $\ddot{\mathcal{N}}_i^t = \ddot{\mathcal{S}}_i^t + \ddot{\mathcal{I}}_i^t$ and by $\dddot{\mathcal{N}}_i^t = \dddot{\mathcal{S}}_i^t + \dddot{\mathcal{I}}_i^t$.

In the model presented in Section 2, we denote by X^t the set of susceptible people that meeting an infected person on time t. Now, we consider the distancing factor in the meetings. Denoted by $\dot{X}_i^t$ ($\ddot{X}_i^t$) the set of people from

$p \in \dot{S}_i^t$ ($p \in \ddot{S}_i^t$) that meeting an infected person in vertex i (in adjacent vertices of i). The set of people $p \in S_i^t$ that meeting infected people is denoted by $X_i^t = \dot{X}_i^t \cup \ddot{X}_i^t$. Thereby, the model is updated to:

$$|I_i^t| = |I_i^{t-1}| - \varepsilon|I_i^{t-1}| + v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|)$$
$$|S_i^t| = |S_i^{t-1}| - v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|) + \varepsilon|I_i^{t-1}|.$$

Next, we analyze the *expected value* of $\mathbb{E}[|\dot{X}_i^{t-1}|]$ and $\mathbb{E}[|\ddot{X}_i^{t-1}|]$. The probability to occur an event Y is denoted by $\mathbb{P}\{Y\}$.

The meetings of a person who answers to social distancing are restricted to the vertex that he (she) belongs. Let $\dot{Y}_{pi}^t$ be an indicator random variable which is equal to 1 if a susceptible person $p \in \dot{S}_i^t$ meets an infected person; and it is equal to 0 otherwise. Thus, $|\dot{X}_i^t| = \sum_{p=1}^{\dot{\mathcal{S}}_i^t} \dot{Y}_{pi}^t$ for all vertex i and for all time t. The meetings of a person who does not answer to distancing can occur in his (her) own vertex or adjacent vertices. In a similar way, let $\ddot{Y}_{pi \to i}^t$ ($\ddot{Y}_{pi \to j}^t$) an indicator random variable which is equal to 1 if a susceptible person $p \in \ddot{S}_i^t$ meets an infected person in vertex i (in vertex $j \in \chi(i)$). So, $|\ddot{X}_i^t| = \sum_{p=1}^{\ddot{\mathcal{S}}_i^t}(\ddot{Y}_{pi \to i}^t) + \sum_{j \in \chi(i)}(\sum_{p=1}^{\left\lfloor \frac{|\ddot{S}_i^t|}{|\chi(i)|+1} \right\rfloor} \ddot{Y}_{pi \to j}^t)$.

The expected value of $|\dot{X}_i^t|$ is

$$\mathbb{E}[|\dot{X}_i^t|] = \mathbb{E}[\sum_{p=1}^{\dot{S}_i^t} \dot{Y}_{pi}^t] = \sum_{p=1}^{\dot{S}_i^t} \mathbb{E}[\dot{Y}_{pi}^t] = \sum_{p=1}^{\dot{S}_i^t} \mathbb{P}\{\dot{Y}_{pi}^t\} = \dot{\mathcal{S}}_i^t \mathbb{P}\{\dot{Y}_{pi}^t\}.$$

Similarly, we have

$$\mathbb{E}[|\ddot{X}_i^t|] = \ddot{\mathcal{S}}_i^t \mathbb{P}\{\ddot{Y}_{pi \to i}^t\} + \sum_{j \in \chi(i)} \left\lfloor \frac{|\ddot{S}_i^t|}{|\chi(i)|+1} \right\rfloor \mathbb{P}\{\ddot{Y}_{pi \to j}^t\}.$$

Therefore, we need to calculate the probability to occur a meeting between a susceptible person $p \in \dot{S}_i^t$ and an infected person ($\mathbb{P}\{\dot{Y}_{pi}^t\}$) and the probabilities to occur a meeting between a susceptible person $p \in \ddot{S}_i^t$ and an infected person ($\mathbb{P}\{\ddot{Y}_{pi \to i}^t\}$ and $\mathbb{P}\{\ddot{Y}_{pi \to j}^t\}$). Before that, we rewrite the model in function of the expected value of susceptible and infected people over time. It is important to note that we can work with lower and upper bounds for the expected values. These bounds can always be integer numbers (as long as they are initially integer number). Given $|I_i^{t-1}|$ and $|S_i^{t-1}|$, and given constants ε and v, the model is:

$$\begin{aligned}
\mathbb{E}[|I_i^t|] &= \mathbb{E}[|I_i^{t-1}| - \varepsilon|I_i^{t-1}| + v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|)] \\
&= |I_i^{t-1}| - \varepsilon|I_i^{t-1}| + v(\mathbb{E}[|\dot{X}_i^{t-1}|] + \mathbb{E}[|\ddot{X}_i^{t-1}|]) \\
&\geq |I_i^{t-1}| - \lceil\varepsilon|I_i^{t-1}|\rceil + \lfloor v(\mathbb{E}[|\dot{X}_i^{t-1}|] + \mathbb{E}[|\ddot{X}_i^{t-1}|])\rfloor \\
&= |I_i^t|, \\
\mathbb{E}[|S_i^t|] &= \mathbb{E}[|S_i^{t-1}| - v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|) + \varepsilon|I_i^{t-1}|] \\
&= |S_i^{t-1}| - v(\mathbb{E}[|\dot{X}_i^{t-1}|] + \mathbb{E}[|\ddot{X}_i^{t-1}|]) + \varepsilon|I_i^{t-1}| \\
&\leq |S_i^{t-1}| - \lfloor v(\mathbb{E}[|\dot{X}_i^{t-1}|] + \mathbb{E}[|\ddot{X}_i^{t-1}|])\rfloor + \lceil\varepsilon|I_i^{t-1}|\rceil \\
&= |S_i^t|.
\end{aligned}$$

The previous model uses *floor* and *ceiling* functions. Observe that, if $|I_i^{t-1}|$ and $|S_i^{t-1}|$ are integer numbers then $|I_i^t|$ and $|S_i^t|$ are also integers. Moreover, the expected value of infected (susceptible) people of vertex i and on time t is at least (at most) $|I_i^t|$ ($|S_i^t|$). Now, we describe the probabilities.

The Probabilities $\mathbb{P}\{\dot{Y}_{pi}^t\}$, $\mathbb{P}\{\ddot{Y}_{pi\to i}^t\}$ *and* $\mathbb{P}\{\dddot{Y}_{pi\to j}^t\}$. Fixed a time t, we know that the number of infected in any vertex i is $\dot{\mathcal{I}}_i^t + \ddot{\mathcal{I}}_i^t + \dddot{\mathcal{I}}_i^t$; and we know that the total number of possible meetings (without repetition) between two people (one being susceptible) is

$$\dot{\mathcal{N}}_i^t + \ddot{\mathcal{N}}_i^t + \dddot{\mathcal{N}}_i^t - 1.$$

Therefore, the probability of a susceptible people to be infected in any vertex is

$$\mathbb{P}\{\dot{Y}_{pi}^t\} = \frac{\dot{\mathcal{I}}_i^t + \ddot{\mathcal{I}}_i^t + \dddot{\mathcal{I}}_i^t}{\dot{\mathcal{N}}_i^t + \ddot{\mathcal{N}}_i^t + \dddot{\mathcal{N}}_i^t - 1}.$$

Since the last probability holds for any vertex, we have the same result to

$$\mathbb{P}\{\ddot{Y}_{pi\to i}^t\} = \frac{\dot{\mathcal{I}}_i^t + \ddot{\mathcal{I}}_i^t + \dddot{\mathcal{I}}_i^t}{\dot{\mathcal{N}}_i^t + \ddot{\mathcal{N}}_i^t + \dddot{\mathcal{N}}_i^t - 1}, \text{ for all vertex } i; \text{ and}$$

$$\mathbb{P}\{\dddot{Y}_{pi\to j}^t\} = \frac{\dot{\mathcal{I}}_j^t + \ddot{\mathcal{I}}_j^t + \dddot{\mathcal{I}}_j^t}{\dot{\mathcal{N}}_j^t + \ddot{\mathcal{N}}_j^t + \dddot{\mathcal{N}}_j^t - 1}, \text{ for all } j \in \chi(i).$$

Next, we extend this proposal for SIR model.

5   The SIR model

In SIR model we have, a set of susceptible people S_i^t, a set of infected people I_i^t and a set of *recovered* people R_i^t, for each vertex i and each time t. Once again, the total people number $N_i^t = S_i^t \cup I_i^t \cup R_i^t$ is maintained constant over time. In this case, a susceptible person on time t can be infected on time $t+1$. An infected person on time t can be recovered on time $t+1$. A recovered person does not become infected again. Now, given $|I_i^{t-1}|$, $|S_i^{t-1}|$ and $|R_i^{t-1}|$, and given the constants ε and v, the model can be write as:

$$\begin{aligned} |I_i^t| &= |I_i^{t-1}| - \varepsilon|I_i^{t-1}| + v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|), \\ |S_i^t| &= |S_i^{t-1}| - v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|), \\ |R_i^t| &= |R_i^{t-1}| + \varepsilon|I_i^{t-1}|, \end{aligned}$$

where $\dot{X}_i^{t-1}$ ($\ddot{X}_i^{t-1}$) is the set of susceptible and distancing people (without distancing) of vertex i that meeting an infected person. The expected value of the number of infected people ($\mathbb{E}[|I_i^t|]$) is equal to that given in the previous

section. For the remaining expected value sets we have

$$
\begin{aligned}
\mathbb{E}[|S_i^t|] &= \mathbb{E}[|S_i^{t-1}| - v(|\dot{X}_i^{t-1}| + |\ddot{X}_i^{t-1}|)] \\
&= |S_i^{t-1}| - v(\mathbb{E}[|\dot{X}_i^{t-1}|] + \mathbb{E}[|\ddot{X}_i^{t-1}|)]) \\
&\leq |S_i^{t-1}| - \lfloor v(\mathbb{E}[|\dot{X}_i^{t-1}|] + \mathbb{E}[|\ddot{X}_i^{t-1}|)]) \rfloor \\
&= |S_i^t|, \\
\mathbb{E}[|R_i^t|] &= \mathbb{E}[|R_i^{t-1}| + \varepsilon|I_i^{t-1}|] \\
&= |R_i^{t-1}| + \varepsilon|I_i^{t-1}| \\
&\leq |R_i^{t-1}| + \lceil \varepsilon|I_i^{t-1}| \rceil \\
&= |R_i^t|.
\end{aligned}
$$

Once again, if $|I_i^{t-1}|$, $|S_i^{t-1}|$ and $|R_i^{t-1}|$ are integer number then $|I_i^t|$, $|S_i^t|$ and $|R_i^t|$ will also be. Observe that the expected value of infected (susceptible, recovered) people of vertex i and on time t is at least (at most, at most) $|I_i^t|$ ($|S_i^t|$, $|R_i^{t-1}|$).

In our experiments of model SIR, the social distancing factor is applied on sets S_i^t, I_i^t e R_i^t of the following way: $|\dot{S}_i^t| = \lfloor \alpha_i^t|S_i^t| \rfloor$, $|\ddot{S}_i^t| = |S_i^t| - |\dot{S}_i^t|$, $|\dot{I}_i^t| = \lfloor \alpha_i^t|I_i^t| \rfloor$, $|\ddot{I}_i^t| = |I_i^t| - |\dot{I}_i^t|$ and $|\dot{R}_i^t| = \lfloor \alpha_i^t|R_i^t| \rfloor$, $|\ddot{R}_i^t| = |R_i^t| - |\dot{R}_i^t|$. The set of people that answer to distancing is $\dot{N}_i^t = \dot{S}_i^t \cup \dot{I}_i^t \cup \dot{R}_i^t$ and the set of people that do not answer is $\ddot{N}_i^t = \ddot{S}_i^t \cup \ddot{I}_i^t \cup \ddot{R}_i^t$.

For the people that circulate in vertex i, all items of Section 4 still hold (items a – f). Additionally, the following number of people also circulate in vertex i

g. $\dot{\mathcal{R}}_i^t = \lfloor \lambda_{\dot{R}}|\dot{R}_i^t| \rfloor$: recovered people that answer to social distancing (from $\dot{R}_i^t$);

h. $\ddot{\mathcal{R}}_i^t = \left\lfloor \frac{|\ddot{R}_i^t|}{|\chi(i)|+1} \right\rfloor + (|\ddot{R}_i^t| \mod (|\chi(i)| + 1))$: recovered people that do not answer to social distancing (from $\ddot{R}_i^t$);

i. $\dddot{\mathcal{R}}_i^t = \sum_{j \in \chi(i)} \left\lfloor \frac{|\ddot{R}_j^t|}{|\chi(j)|+1} \right\rfloor$: recovered people that do not answer to distancing.

Now, we denote the total of people circling in vertex i by $\dot{\mathcal{N}}_i^t + \ddot{\mathcal{N}}_i^t + \dddot{\mathcal{N}}_i^t$ where $\dot{\mathcal{N}}_i^t = \dot{\mathcal{S}}_i^t + \dot{\mathcal{I}}_i^t + \dot{\mathcal{R}}_i^t$, $\ddot{\mathcal{N}}_i^t = \ddot{\mathcal{S}}_i^t + \ddot{\mathcal{I}}_i^t + \ddot{\mathcal{R}}_i^t$ and $\dddot{\mathcal{N}}_i^t = \dddot{\mathcal{S}}_i^t + \dddot{\mathcal{I}}_i^t + \dddot{\mathcal{R}}_i^t$. The meetings of a susceptible person and an infected and the probabilities of these events still hold. Next, we describe the results obtained for some network topologies.

6   SIR model experiments

In this section we describe the experiments performed on different *network topologies*. For us, network topology is the way how the network connections are organized and how they define a structure (if any). Our motivation for this experimental analysis is that the topologies analyzed and real topologies (i.e. format connections of neighborhoods, cities, etc) can have similarity. For a case of extreme necessity, some topology could by applied in practice (and in emergency way), changing temporarily the usual network connections.
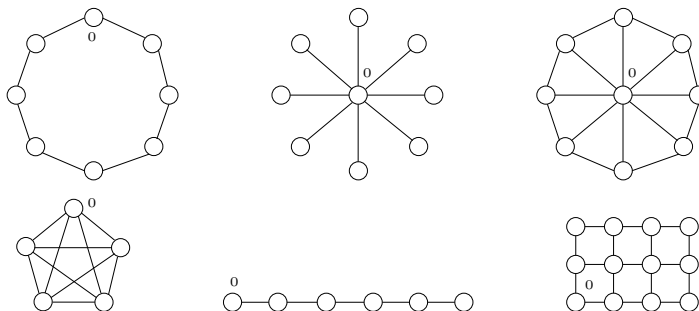
Fig. 1. The cyclical, star, wheel, complete, line and grid topologies.

The topologies analyzed were the following: *cyclical, star, wheel, complete, line* and *grid.* All this topologies are *planar networks* unless the complete topology. We illustrate each one of them in Fig. 1.

Next we illustrate some characteristic graphics for the SIR model ($t \times n$ where t represents a day from 0 up to 200 and n represents the number of susceptible, infected or recovered people). The graphics in Fig. 2 correspond to the total number of susceptible, infected and recovered people on the wheel, star, grid, cyclical and complete topologies. The first scenario did not consider social distancing ($\alpha_i^t = 0$ for all i and all t). Each topology has 100 vertices and each vertex i has $N_i^t = 3000$ people. Initially, the number of infected are 400 for all topologies (in vertex labeled 0 in Fig. 1). When this is not the case, we explicitly describe for which topology this value was changed. All other people are initially susceptible and there is no recovered people. The daily recovered rate and the daily virulence rate are respectively $\varepsilon = \frac{29}{200}$ and $v = \frac{91}{200}$. Such rates have been recently used and they are related to the COVID-19 disease (see, for example, in [2]). The line topology results were similar to cyclical topology: low number of infected people and almost constant over time. The curves of susceptible and recovered people for the line case were less steep. The characteristic curves to SIR model did not appear for the complete topology (400 infected). In this case, the number of people circling each vertex was not enough to increase the expected value of infected people. However, increasing the initially infected number to 500 for complete topology, the infection spreads (in Fig. 2 bottom middle graphic).

The social distancing was considered for the experiments illustrated in Fig.2 (bottom right graphic) and Fig. 3. The people that do answer to social distancing but still circulate in their vertex (for some unavoidable reason) are $\lambda_{\dot{S}} = \frac{2}{5}$, $\lambda_{\dot{I}} = \frac{1}{10}$ and $\lambda_{\dot{R}} = \frac{3}{5}$. The constants ε and v are the same as previous. Moreover, the social distancing considered over time was constant in $\alpha_i^t = \frac{2}{5}$ for all i and all t (40% of people do answer to social distancing). Once again, each vertex has 3000 people and a single vertex has 400 infected people. The distancing in these conditions was enough to control the infection spreading on star, wheel and complete topologies. For the complete topology and when the initially number

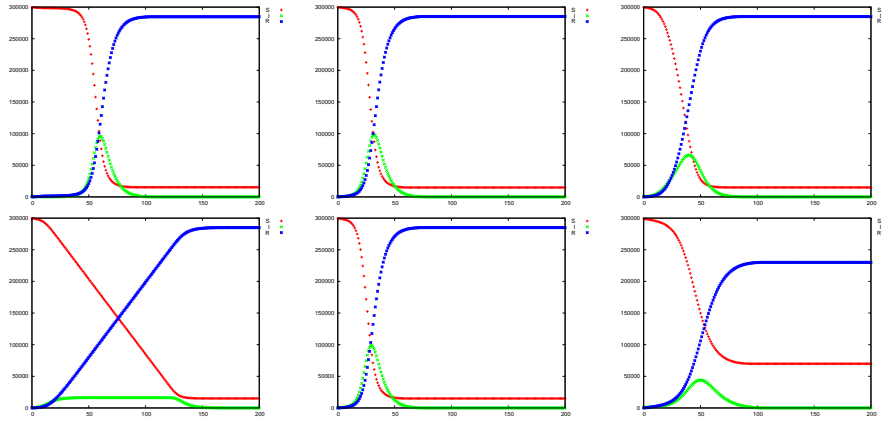**Wheel, Star, Grid, Cyclical and Two Complete**

Fig. 2. Graphics without social distancing unless the bottom right graphic.

of infected people is 1000, we obtain the bottom right graphic in Fig. 2. For the cyclical (right graphic in Fig. 3) and line (not shown), the curve for infected people was lower than the same topologies without social distancing. For the grid topology (left in Fig. 3), the curve was lower and smoother (compare to the top right graphic in Fig. 2).
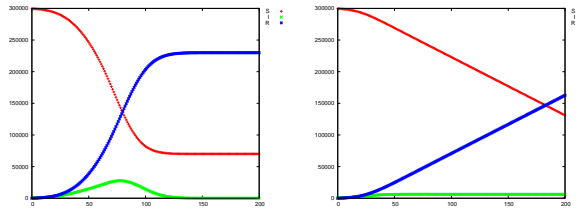
Grid e Cyclical

Fig. 3. Social distancing in 40% over time. On the right, the curves continue its trajectory although the interruption on time 200.

The graphics in Fig. 4 illustrate a periodical social distancing case applied to grid and complete topology (the last, initially 1000 infected people). In the begin of the period, there is no social distancing factor. Over time, the social distancing factor gradually increases until to reach the peak (day five) with distancing factor in 70%. After, the distancing factor starts to gradually decrease until to cancel the factor (day ten). This behavior repeats over time.
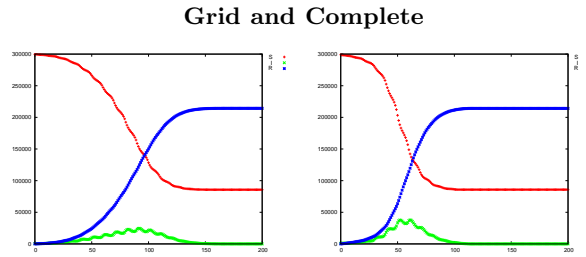
Grid and Complete

Fig. 4. Social distancing given by a periodical function (sine module function). The function period is ten days. The peak occurs on day five and corresponds to factor social distancing equal to 70%

7   Conclusion

In this paper we proposed SIS and SIR models considering social distancing factor and circulation restrictions on different network topologies. These parameters can be used to control the number of infected people. The topologies analyzed were cyclical, star, wheel, complete, line and grid. Our experiments showed that if people circulation is allowed around a region on cyclical and line topologies, then the number of infected people is controlled.

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