International Journal of Mathematics and Computer Research

ISSN: 2320-7167

Volume 12 Issue 07 July 2024, Page no. –4354-4358

Index Copernicus ICV: 57.55, Impact Factor: 8.316

DOI: 10.47191/ijmcr/v12i7.04

Epidemiological Modeling on Networks with Vaccination Scenario

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ARTICLE INFO

Published Online:
22 July 2024

ABSTRACT

The world is facing health crises which have caused a lot of material and human damage. Modeling epidemics allows us to have control over the evolution and spread of the disease as well as its mode of operation. The susceptible-infected-recovered (SIR) mass action model is the basic model in mathematical epidemiology but it does not take into account heterogeneity of contacts.. However, the rate of contact between people is heterogeneous; it depends from one person to another. In this study we will introduce a compartmentalized model based on the edges and which takes into account the heterogeneity of the contacts. However, we will end up with a differential equation whose resolution of the system allows us to see the equilibrium points and the stability of the disease. We also introduce numerical simulations on different types of graphs to see the spread of the disease on the way in which contact rates are distributed. A vaccination scenario was approached to see the impact of the vaccine on an infectious disease.

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KEYWORDS: Epidemic SIR a compartmentalized model heterogeneity Networks Vaccination scenario

I. INTRODUCTION

In recent years, infection problems have become more and more frequent in our daily lives. These epidemic outbreaks result in an increase in mortality, sometimes catastrophic. This can be illustrated by the appearance of the plague which already caused devastation in the middle Ages. Numerous studies have been carried out to understand the phenomenon, reduce mortality rates or eradicate the disease.

Generally speaking, epidemiology is the study of the relationships between diseases or any other biological phenomenon and the different factors that can have an impact on its frequency, her distribution or its evolution. This field studies the factors affecting the health of populations and seeks to find solutions to mitigate their effects. Thus, better control of infectious diseases necessarily requires a better understanding of the way in which they spread. The primary tool for predicting the spread of an infectious disease is the Susceptible-Infected-Recovered (SIR) mass action model of Kermack and McKendrick Kermack and McKendrick (1927). The susceptibleinfected-recovered mass action model derives largely from its conceptual and mathematical simplicity. The principle of mass action implies that an individual infectious has the possibility of infecting each susceptible individual with equal probability. However, it is clear that things do not happen like this in reality. Once infectious, an individual can only transmit the viral agent (the disease) to a limited number of individuals. Furthermore, it is clear that there are individuals who are in contact with a very large number of people, while others interact with many fewer individuals. It thus appears obvious that the structure social status of a population is a determining factor for the spread of the disease. It must therefore be incorporated into a realistic mathematical model. It is in response to this problem that network epidemiology has developed.

Thus the objective of this dissertation is to model network epidemiology. To do this, we explain a recent modeling approach: Edge Based Compartiental Model (EBCM). This involves modeling all of the potential contacts of individuals in a given population such as a network or graph and studying the dynamics of the propagation of an epidemic through this network. We carry out the mathematical analysis of the EBCM model and the numerical simulation through different graphs using the Epidemic on Network (EoN) package available on python.

Then we base ourselves on the dynamics of the SIR model in random networks. simulation monitoring digital with a vaccination scenario.

II. RESEARCH METHOD

Network epidemic modeling with degree heterogeneity is generated with a network configuration model (CM) . It requires a certain number of hypotheses which allows it to describe the dynamics of the spread of the disease.

— Infection and recovery are assumed to occur at constant rates;

— Heterogeneous contact rates;

— Reduction in the number of contacts to be infected once the individual is infected;

— The cured individual is definitively immune;

Variations at the different states of the population ≪S≫, ≪I≫ and ≪R≫

The SIR model divides the population into three categories: individuals likely to become infected (S), infected individuals (I) and individuals who can no longer transmit the disease (R). (i.e. immunization which is valid throughout the epidemic period).

We choose a random target u and prohibit the infection of u to all its neighbors. We note that S(t) is the probability that a random test node u is in a state S. It is also the probability that none of u's partners have yet transmitted to u.

We define θ as the probability that a randomly chosen partner has not transmitted to u and if the degree of u is k, then the probability that u is still sensitive is $\theta(t)^k$. So the fraction of susceptible is:

$$S(t) = \sum_{k=0}^{\infty} P(k)\theta(t)^k = \varphi(\theta(t)), ou \quad \varphi(\theta(t)) = \sum_{k=0}^{\infty} P(k)\theta^k$$

is the generating function of the probability of the distribution of degrees; P(k) the probability of the distribution of degrees.

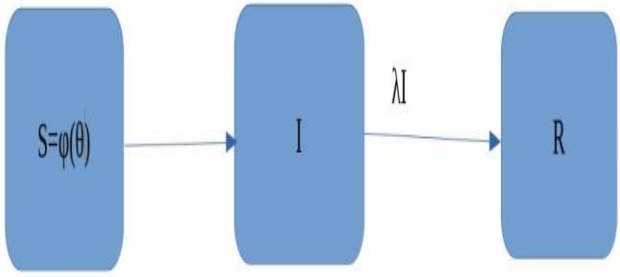

Figure 1 – The flow of susceptible to infected to recovered individuals with heterogeneous infection rate on network.

Explanation

The edges connect randomly to other neighbors using proportional mixing, so that the probability of selecting a neighbor of degree k is , where <k> denotes the mean of k. Now the probability that u is always susceptible is θ(t). Thus

$$S(t) = \sum_{k=0}^{\infty} \frac{kP(t)}{<k>}\theta(t)^k = \sum_{k=0}^{\infty} kP(k)\theta(t)^k \quad => \quad S(t) = \sum_{k=0}^{\infty} P(k)\theta(t)^k = \varphi(\theta(t)), ou\ \varphi(\theta(t))$$

is the probability generating function of the degree distribution.

We will have:

$$S(t) = \varphi(\theta(t))$$

$$R^{\cdot} = \lambda I$$

$$I = 1 - S - R$$

To calculate the probability that a random individual is sensitive, we choose a random test node uniformly from the population (i.e. a node chosen randomly and which is behaves like any other node). We alter u so that if it is infected, it does not transmit to its neighbors. This helps us assume that the status of its neighbors is independent, but does not affect the probability that it is susceptible. We define θ the probability that a random neighbor v of u has not transmitted an infection to u, and we decompose θ into three parties: the probability that a partner v is susceptible at time t, ϕS; the probability that v either infected at time t but did not transmit the infection to u, ϕI; the probability that v is recovered at time t but has not transmitted the infection to u, ϕR. Then θ = ϕS + ϕI + ϕR.

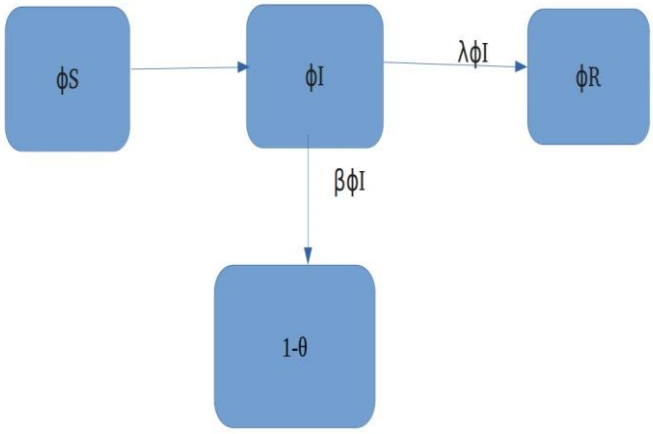

Figure 2– Graph representing variations at the network level

Compartment 1 − θ is the probability that it transmitted. The rate that an infected partner transmits to u is β; therefore the flux ϕ towards 1 − θ is βϕI. We conclude $\theta^{\cdot} = -\beta\phi I$. To find ϕI, we will use ϕI = θ − ϕS − ϕR and calculate ϕS and ϕR.

The rate at which an infected partner recovers is λ. Thus the flow ϕI towards ϕR is λϕI. This is proportional to the flow in 1 − θ with the proportionality constant $\frac{\lambda}{\beta}$. Since ϕR and 1 - θ start approximately with 0, we have ϕR = $\frac{\lambda(1-\theta)}{\beta}$. To find ϕS, recall that a partner v has a degree k with probability $P_n(k) = \frac{kP(k)}{<K>}$ where < k > designates the mean of k. Given that v is susceptible with probability θ^{k-1} (we prohibit transmission from u; therefore k − 1 nodes can infect v). A weighted average gives:

$$\phi S = \sum_{k=0}^{\infty} \frac{kP(t)}{<k>}\theta(t)^{k-1} = \sum_{k=0}^{\infty} P_n(k)\theta^{k-1} = \frac{\varphi(\theta)}{\varphi(1)} \ avec \quad \varphi(\theta) = \sum_{k=0}^{\infty} P(k)\theta^{k-1} \ et \ \varphi(1) = <k>$$

In this section, we will perform a numerical simulation to analyze the evolution of an infectious disease on graphs with different forms of degree distribution.

Model of graphs used

In this section, we will perform a numerical simulation to analyze the evolution of an infectious disease on graphs with different forms of degree distribution.

Graph with Poisson distribution

The graph with Poisson distribution has N nodes whose connection between the nodes is made with a probability P(k). The Poisson distribution is a distribution that rotates around its mean. However, the graphs with this distribution are relatively homogeneous with quite similar degrees.

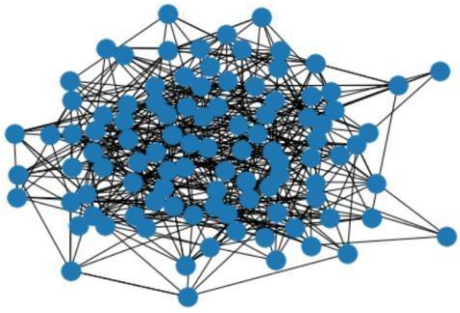

Figure 3 – Graph with a Poisson distribution

Scale free model

These graphs are characterized by a distribution of degree p(k) which follows a power law, that is to say graphs with a wide range of different degrees which detect slowly. The scale-free network is today the type of network most frequently found in studies carried out on real-world networks. They have the characteristic of providing a good modeling of social networks. The arabasi.albert.graph function on python allows you to automatically generate graphs of this type.

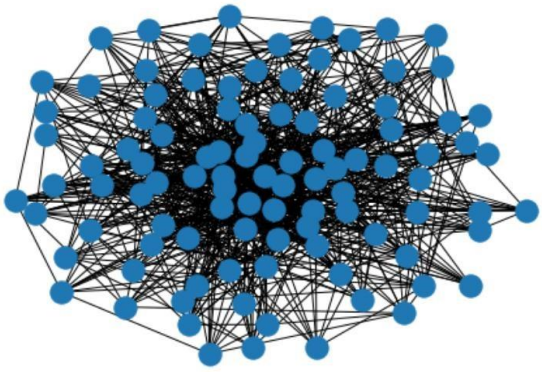

Figure 4 – Scalef ree type graph

Graph with exponential distribution

This type of graph can have N nodes with a distribution p(k) which follows an exponential law. The distribution of the exponential law models the lifespan of a phenomenon. The scipy-random-exponential function on python allows you to generate this distribution of degrees p(k)

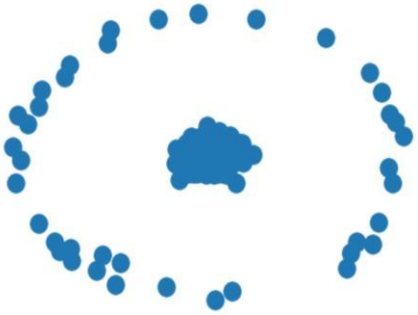

Figure 5 – Graph with an exponential distribution

III. RESULTS ANALYSIS

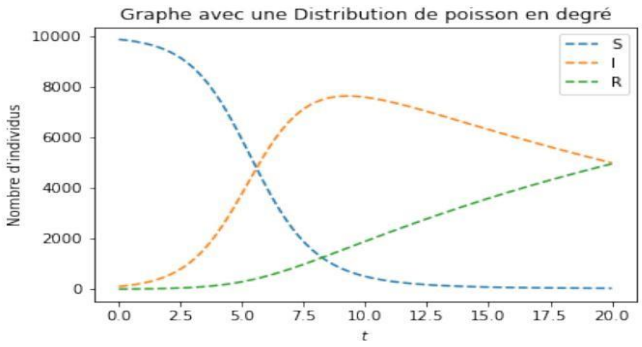

Figure 6 – Number of susceptible, infected and immunized individuals in a population following a fish distribution in degree

The figure shows us the SIR dynamics on a graph with a Poisson law degree distribution. The infected curve reaches its maximum in less than 10 days with 7,900 infected out of 10,000. The immune curve increases progressively and the susceptible people gradually decrease until reaching its minimum. (0).

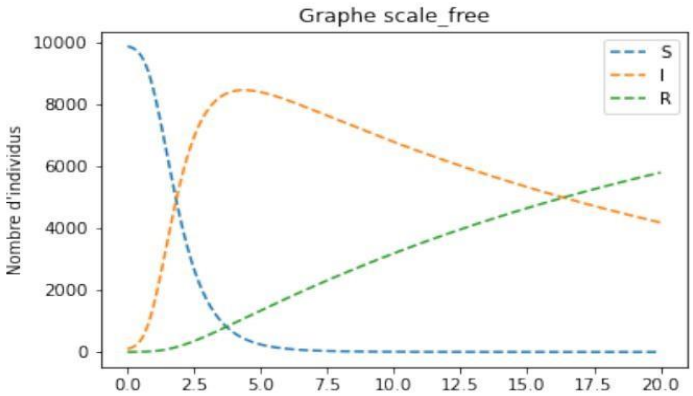

Figure 7 – Number of susceptible, infected and immune individuals in a population following a power distribution in degree

This graph represents the evolution of the SIR infectious dynamics on the network with a scalefree type graph. With a rate of 0.01 infected at the start, the population of infected reaches a maximum of 8100 infected per 1000 people after 4 days where the susceptible population tends towards 0. The number of recovered grows as a function of time.

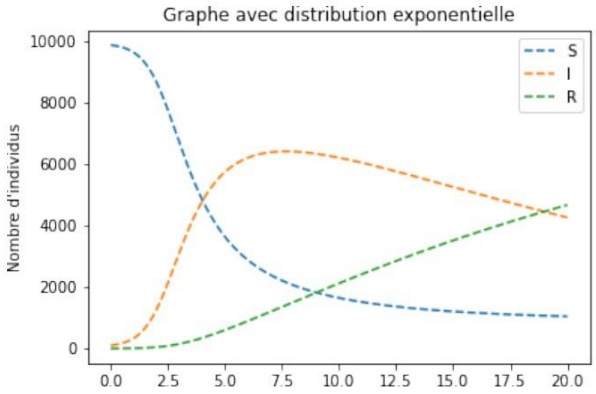

Figure 8 – Number of susceptible, infected and immunized individuals in a population following an exponential distribution

This graph represents the distribution of the population as a function of time (over 20 days) following an exponential distribution of degrees, i.e. the allocation of partners (or neighbor, or person in contact). Thus with a rate of 0.01 infected people at the start and an infection rate of 0.0964, the infected people reach a number of 6000 out of 10000 in 7 days and begin to decrease gradually.

In summary, we see that the disease evolves more quickly than with the scale free type distribution which reaches its maximum with 8100 infected in 4 days, then comes that of the distribution of poison which is quite similar due to the fact that the distribution of poison is centered around its average with 7900 infected in 9 days. The results with the simulation of the distribution graph of the exponential law are characterized by a weak evolution of the disease with a maximum number of infected 6000 infected in 7 days.

Vaccination scenario 1 Principle of vaccination

Vaccination is protection against infectious disease. It consists of injecting an infectious agent (virus or bacteria) into the body, in a harmless form (without effect) but stimulating the body's immune response. The immune system 1 has a form of memory, subsequent exposure to the infectious agent 2 will trigger a rapid and therefore more effective response. The agent is recognized by one or more specific molecules 3 and constitutes the antigen 4. The immune system responds by the production of antibodies 5 specially directed against it and manufactured by memory cells. A vaccine is therefore specific to a disease.

2 Approach used

We consider a SIR model with vaccination where the states are susceptible (Sus), infected (Inf), recovered (Rec) and vaccinated (Vac). We use Gillespie simple contagion which is in the EoN package to carry out the simulation.

In this model, susceptible people are vaccinated at a rate that is independent of state of the disease. Thus, the spontaneous transitions are 'Suc' to 'Vac' with a rate of 0.01 and 'Inf' to 'Rec' with a rate of 1.0. The induced transitions are ('Inf', 'Sus') to ('Inf', 'Inf') with a rate of 2.0.

3 Analysis and interpretation of results

We have a representation of the initial state of the disease on an SIR model with vaccination which corresponds to the start of the infection at the level of figure 3.9. The vaccination rate of susceptible people is equal to 0.01. At t = 0 the infected proportion is minimal unlike susceptible-vaccinated people who are at maximum. This is because the disease has not yet spread.

The immune system corresponds to the body's defense system

1. illness
2. A molecule is a set of elements linked to each other through chemical bonds
3. An antigen substance that can generate antibodies
4. An antibody is a substance produced by the immune system in an organism to detect and neutralize pathogens specifically

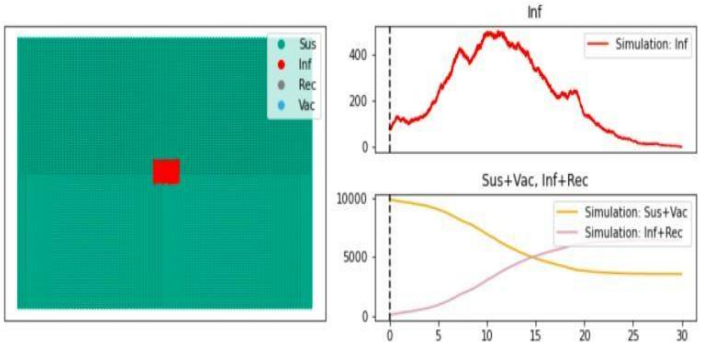

Figure.9 – SIR simulation on network with vaccination at t=0 at the start of the infection

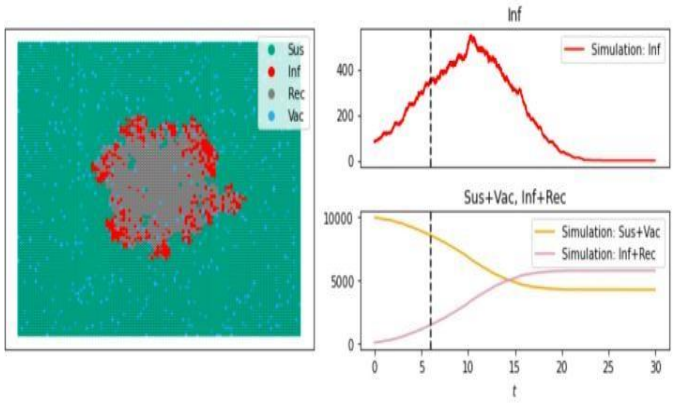

Figure 10 – SIR simulation on network with vaccination after 5 days

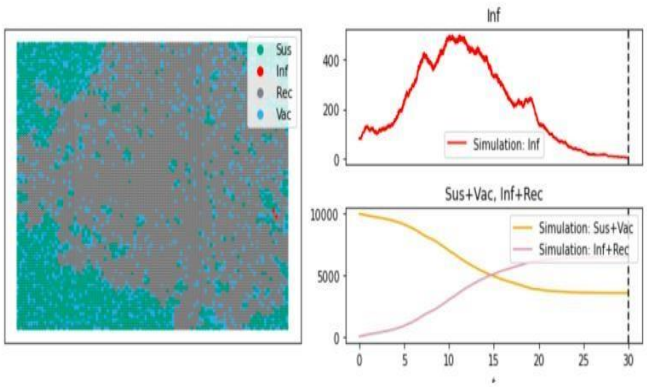

Figure 11 – SIR simulation on network with vaccination after 30 days

The two figures illustrate the spread of a disease using the SIR model with vaccination. On day 14, there is a peak with 450 infected individuals out of a population of 10,000. However, the number of infected individuals starts to decrease exponentially as they recover. After 30 days, the disease is nearly eradicated, with the number of infected individuals approaching zero. These figures demonstrate that the vaccine does not prevent infection but significantly slows down the spread of the disease. Furthermore, the vaccination plays a crucial role in ultimately neutralizing the disease, as the number of infected individuals tends towards zero after 30 days. Overall, the figures highlight the gradual increase and subsequent decline in the number of infected individuals, showcasing the effectiveness of the vaccine in curbing the spread of the disease.

IV. CONCLUSION

Network epidemiology modeling consists of modeling all possible contacts of individuals in a population and studying the spread of the disease through this network. So, in the resolution of our differential equations, we prove that the dynamics of the model is completely deterministic by a critical value R0. We find two points of balance $\theta_0 = 1$ and $\theta_1 = \alpha$ with α between 0 and c such that $c < 1$. When $R0 > 1$, we have stability at the equilibrium point $\theta_1 = \alpha$, while equilibrium at point $\theta_0 = 1$ is unstable. Then when $R0 < 1$, we have a stability of the equilibrium point $\theta_0 = 1$.days.

The simulation results on the different types of graphs used show that the evolution of the disease differs depending on the type of distribution used. Thus we could see that the disease progresses more quickly than with a power distribution which corresponds to the scale free type graph compared to the other graphs. For the exponential distribution, we have a low evolution of the disease. It is in this model that the lowest number of infected individuals was recorded.

Vaccination therefore plays a very important role in the spread of infectious disease. It helps reduce the number of people affected by this disease. It also makes it possible to neutralize (i.e. the number of infected people equal to zero) illness at some point.

ACKNOWLEDGEMENTS

All authors contributed equally to each part of the study, reviewed the results, and approved the final version of the manuscript

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