On the propagation of social epidemics in social networks under S.I.R. model.

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Abstract

The S.I.R. model (Susceptible, Infected, Recovered or Died) was proposed by chemistry William Kermack (1927) and the mathematician G. Mc. Kendrick (1932). The model supposes to divide to the individuals of a population in three categories. Susceptible to be infected, Infected and Recovered (immune or died by the disease). On the other hand has been a similarity in the evolution of epidemics of infect aerial, the computer science propagation of virus and the propagation of social paradigms (fashion, rumor, etc.) it calls modernly “Social Epidemics”. In this work it is tried to use this model in different types from social networks, real or not. In order to evaluate an meta-analysis of results allows to investigate under which conditions the topology of the network is excellent and that networks are equivalent. The result obtained can have relevance in study of propagation of epidemics of different types.

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I. INTRODUCTION

The use of mathematical models to study the evolution of epidemics is not a newness. At the moment it is known enough on behavior of transmission of diseases according to its characteristics like knowing the limits and the possibilities these models. The S.I.R. model developed by Scottish chemistry William Ogilvy Kernack (1927) and mathematician A.G. Mc Kendrick (1932) was one on the first attempts. Unfortunately the articles fell in the forgetfulness until 1979 which a well-known article of Anderson and May in the Nature magazine turned east model in the departure point of the present studies. On the other hand, model S.I.R. generates a description in three phases of the course of an epidemic: starting (of slow growth), explosive and remission. Implicitly it is assumed that the contacts between the members of a population are purely random. This can even give relatively fit results for many diseases in virus transmission in networks of computers. Where it would be enough that it is considered to the users like susceptible individuals to the disease. This is thus because in general the electronic mail or the air (in the case of influenza) are opened environment that contacts to all with all with relative promiscuity then the randomness hypothesis can work enough. In this work different types from real social networks obtained by real or fictitious study (Scale-Free SF and Small World SW). Where a population of survivors was considered soon to carry out Meta Analysis of the data and thus to verify under which conditions the topology of the network is excellent and to investigate if the fictitious networks are equivalent to the real ones.

A. Theoretical bases

A network is a set of relations (bonds or edges) between a defined series of elements (nodes, vertices or actors). Formally a network is a graph defined as the triada $G = (V, E, \gamma)$ where $V$ is the set of vertices, $E$ is the set of edges and $g : E \rightarrow V$ so that $g(e) = \{v, w\}$. I.E., $g(.)$ assigns to each edge a pair of vertices. Nowadays to facilitate the study of the networks the binary matrices instead of the whole matrices are used. Then an isomorphism $f : G \rightarrow B_n$ can be defined, where $B_n$ is a binary and symmetrical matrix of well-known dimension nxn this matrix is called adjacency matrix (AM). The sociologists take like convention that in the rows is located the actors (exits or egos), however in the columns are located the attributes
or related actors (entered or alter), this convention is used in this work. As it is possible to be appreciated the AM contains all sensible information on the network reason why it allows to elaborate algorithms in MA without considering to the network. Another form to characterize to the network is through the well-known histogram of rows also named *prestige of an actor* who in the case of the graphs agrees with the histogram of columns or *popularity of an actor*. At the moment the connection probability is used, \( P(k) \). \( P(k) \) is the probability that a chosen vertex at random has \( k \) edges. According to the functional form of the tail of this histogram, \( k \to \infty \), the type of network can be classified in: *exponential*, when \( P(k) \approx e^{-\lambda k} \); *scale-free*, when \( P(k) \approx k^{-2-\gamma} \) with \( \gamma > 0 \); *broad-scale* when he is scale-free with a steep cut; and *single-scale* when it has a fast decay.

II. AN AD-HOC ALGORITHM OF EPIDEMIC

The algorithm of epidemic developed in this work supposes to know AM. This matrix can be obtained from investigations in a closed community, is to say does not interact with other communities, like as a list of electronic mail or an isolated population. Or of an opened community, it is to say interacts with with other communities, as it is a system of the news in Internet or countries connected by massive means of transport of people. To each actor has a structure of data with three following properties is assigned:

1. **Susceptibility or threshold** (U): It is the minimum value from which the actor interchanges information with its pairs.

2. **Internal state**: It is a state represented by a binary vector of 32 bits.

3. **Health**: It can have three possible states, alive or susceptible (state S), ill (state E) and dead (state M).

Of course when the actor dies automatically they eliminate the connections that connect with a the network. Unlike model S.I.R., in this work one assumes that an actor who becomes ill can cure itself but he does not stop being susceptible to return to become ill.

On the other hand the edges of the graph are characterized by the following properties:

1. **State**: It is a binary value that single taking two values “0” to indicate that there is not connection between actor ”i” with actor ”j”. Or “1” to indicate that a relation
between both exists.

2. **Infecting**: It is an assigned value of random form and uniforms in the rank \( C \in [0, 1] \). This it indicates the probability of infect between actors and it is not the same one for each pair of actors.

The algorithm consists of interacting all the population of connected actors (this is defined as epoc) considering that each pair of related actors interacts when in a Bernoulli raffle with probability given by value \( C \) be favorable. Soon the condition of **following proximity** is verified. Two actors are next or neighboring if the distance of Hamming between its vectors of state is minor that the minimum of its thresholds. Then if this condition is verified two actors can interact. In the following listing the pseudocode shown the algorithm of sharing of information between the proximity actors \( A_1 \) and \( A_2 \).

**Share Algorithm**

```plaintext
for each actor nondead I and each actor nondead J do
    U<- minimum(threshold(I), threshold(J));
    if Hamming_distance(I,J) < U then
        for each bit do
            q<- Bernoulli raffle with probability C(I,J)
            if q>0 then J.bit <- I.bit
            else q <- Bernoulli raffle with probability C(I,J)
            if q>0 then I.bit <- J.bit
        end if
    end if
end for
end Share
```

As it is possible to be appreciated the sharing of information is probabilistic and not deterministic as the case of the opinion model. However if the actors are not verified the following proximity condition the operation does not take place and their vectors of state
do not change. This criterion is of agreed with the sharing of information codified in a data channel.

The criterion of health adopted for an actor \( A \) is related to the value of the norm of Hamming of its internal state. It is to say an actor it remains in state S if the norm of Hamming of its internal state, \( H(A) \), is greater than the threshold than this has assigned, \( U_A \). However if it happened the opposite the actor turn to the state E and if after the next interaction it happened that \( H(A) < U_A \) the actor turn to state M soon to disappear of the network assigning the value “0” to all their possible connections. Of another form the actor recovers his state S.

In this model one takes like control parameter the common threshold value \( U \) to all the actors and the number of initial actors \( N \). On the other hand, initially the network consists of a population of \( K \) infected actors (that is to say, actors who have the state E as initial condition). In addition the location to infected actors is uniform in all the network to guarantee a random state in the population.

**III. METHODS AND RESULTS**

Four types of networks, two networks obtained in experimental works and two toy networks were used. the first toy model used it was a network Small-World type (SM) with \( N=4096 \) actors with probability of random reconexin of 10%. The second toy model was a network Scale-Free (SF) with \( N=4096 \) actors with \( \gamma = 0.1 \), this value is agreed with the experimental observations in real networks. Real social networks were obtained from two types of different societies in Internet. A society corresponds to a closed society as it happens in the lists of electronic mails (LM) and the other society corresponds to opened societies as it happens in news groups and the forums (DM). In the empirical networks they are not connected for that reason each experimental network was reduced to its connected maximum component.

In all the cases one test of 512 experiment by network of 2000 times where the threshold varying between \( 10 < U < 20 \). The used statistical estimators were the absolute frequency of survival, the absolute frequency of final ill, the absolute frequency of infected initial. Except for the last one, all these variates with probability distribution obtained empirically from the tests. In Table I the probability of survival based on the threshold for the different types
from networks can be appreciated.

| Threshold | SM | SF | LM | DM |
|-----------|----|----|----|----|
| 10        | 0.989 | 0.989 | 0.989 | 0.99 |
| 11        | 0.973 | 0.965 | 0.967 | 0.971 |
| 12        | 0.93  | 0.883 | 0.929 | 0.907 |
| 13        | 0.827 | 0.758 | 0.891 | 0.791 |
| 14        | 0.679 | 0.641 | 0.821 | 0.674 |
| 15        | 0.549 | 0.572 | 0.702 | 0.586 |
| 16        | 0.406 | 0.448 | 0.563 | 0.485 |
| 17        | 0.298 | 0.35  | 0.246 | 0.231 |
| 18        | 0.192 | 0.241 | 0.246 | 0.231 |
| 19        | 0.118 | 0.173 | 0.179 | 0.15 |
| 20        | 0.07  | 0.096 | 0.097 | 0.07 |

Table I: Survival Probability

In most of the networks for \( U = 15 \) the survival probability it is \( P(S) > 50\% \). On the other hand the variance of survivors (Table II), \( V(S) \), shown that is increased until reaching a maximum value soon to diminish. When one studied the final networks of survivors this increase of the variance was due to the great dispersion of final graphs is to say: by each successive test the final population of survivors was totally different.

Table II: Variance of Survival
Soon it was applied meta-analysis between networks of survivors for values of \(U=15\) by two reasons. \textit{First}: probability \(P(S)\) is greater than 50\% what allows to have a social structure not so destroyed. \textit{Second}: the \(V(S)\) is great this allows to guarantee a great variety of final societies.

In the following tables it is the comparative results in each particular situation. \(DM\) and \(LM\) correspond to the analysis group of which compares them with the control group given by networks \(SM\) and \(SF\). The dead and alive numerical values correspond to the mean value of each test. The variable \(Q\) represents the sum in a column and the variable \(R\) the sum in a row.

| Threshold | SM  | SF  | LM  | DM  |
|-----------|-----|-----|-----|-----|
| 10        | 2.23| 2.53| 3.01| 2.15|
| 11        | 5.37| 18.07| 25.94| 9.65|
| 12        | 29.37| 181.47| 132.2| 89.21|
| 13        | 160.84| 661.06| 425.17| 363.69|
| 14        | 498.03| 1224.94| 1634.64| 808.81|
| 15        | 665.51| 1769.68| 3704.39| 1444.53|
| 16        | 744.71| 1920.67| 6018.13| 2023.32|
| 17        | 876.2| 1906.55| 6992.23| 2180.64|
| 18        | 910.31| 1684.03| 5590.49| 1657.92|
| 19        | 849.35| 1194.13| 4565.42| 1301.69|
| 20        | 574.98| 700.03| 2713.59| 441.93|

Table III Network Meta-analysis of LM vs SM

|        | LM   | SM   | R    |
|--------|------|------|------|
| Dead   | 60   | 2398 | 2558 |
| Alive  | 140  | 1698 | 1838 |
| Q      | 200  | 4096 |

Table IV Network Meta-analysis of DM vs SM

|        | DM   | SM   | R    |
|--------|------|------|------|
| Dead   | 83   | 2398 | 2481 |
| Alive  | 117  | 1698 | 1815 |
| Q      | 200  | 4096 |
In a prospective analysis of data where the probability of death in one given network $X$ is:

$$p_X = P(M/X) = \frac{\text{Dead}}{Q_X} \quad (1)$$

After from previous tables $p_{SM} = 0.58; p_{LM} = 0.30; p_{DM} = 0.41$ and $p_{SF} = 0.60$, then if it is defined as null hypothesis, $H_0$, to not exist difference in probability between two networks. I.E. if $H_0$ is accepted soon is fulfilled a 95% of certainty that $p_1 = p_2$ or $DR = p_1 - p_2 = 0$ and both networks are equivalents. $DR$ is known as difference of proportions whose variance comes given by:

$$V(DR) = \frac{p_1(1-P_1)}{Q_1} + \frac{p_2(1-P_2)}{Q_2} \quad (2)$$

Here it is assumed that the random variables have statistical independence. Soon from the interval of following confidence:

$$I = DR \pm 1.96\sqrt{V(DR)} \quad (3)$$

If $DR = 0$ belongs at this interval it accepts in probability $H_0$ other wise it is rejected and it posible to conclude:

1. When it was compared networks LM and DM were $I = 0.02 \pm 0.09$. In this cituacin it is clear that $H_0$ cannot be rejected and both networks are equivalent.
2. When it was compared networks SF and SM were $I = 0.02 \pm 0.021$. Marginally it is possible to be accepted that both networks are equivalent, but to affection of the analyses they can be taken like equivalent.

3. When it was compared LM with SM were $I = 0.28 \pm 0.06$. That clearly shown that there is to reject the null hypothesis.

As a conclusion it is possible to be appreciated that there is no equivalence between the theoretical networks and the obtained ones by experimental work when the proposed algorithm is applied to them. It is to say in this prospective analysis the exposed actors to a network type DM or LM they have more probability of life then the behavior is different on surviving population of the found one in toy networks. This fact brings like consequence the nonreliability of the simulations on propagation of aerial epidemics of virus in theoretical, letting a door opened to find networks theoretical more realists.

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