Probing into the effectiveness of self-isolation policies in epidemic control

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Abstract. In this work, we inspect the reliability of controlling and quelling an epidemic disease mimicked by a susceptible–infected–susceptible (SIS) model defined on a complex network by means of current and implementable quarantine and isolation policies. Specifically, we consider that each individual in the network is originally linked to individuals of two types: members of the same household and acquaintances. The topology of this network evolves, taking into account a probability $q$ that aims at representing the quarantine or isolation process in which the connection with acquaintances is severed according to standard policies of control of epidemics. Within current policies of self-isolation and standard infection rates, our results show that the propagation is either only controllable for hypothetical rates of compliance or not controllable at all.

Keywords: population dynamics (theory), critical phenomena of socio-economic systems, interacting agent models, epidemic modelling

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1. Introduction

Along with wars and natural disasters, plagues and epidemic (pandemic) diseases lie at the top of death toll lists in human history. By directly affecting the risk of death, such events or even their likelihoods are the source of acute distress among populations, which has been well documented by historians since ancient times [1]. As regards plagues and epidemic diseases, isolation of infected people has been applied since, at least, the Old Testament period as an instrument for controlling and quelling the spread of both viruses and contamination agents in such situations [2]. While for centuries it has been possible to separate people from their relatives and locations by means of a simple decree, social constructs based on the ‘Declaration of the rights of man and of the citizen’, which led to the ‘Universal declaration of human rights’, have urged discussion over the morality and legitimacy of compulsory quarantine and isolation (Q and I) practices [3]–[7]. Indeed, countries like Brazil and Japan have repealed previous laws on compulsory isolation, abortion and sterilization of patients suffering from leprosy as well as deciding to pay compensation and allowances to people subjected to these practices [8]–[10]. Accordingly, current Q and I practices strongly rely on the consciousness of the infected individual and her attitude towards the rest of the society, by imposing a self-isolation spell according to a medical recommendation (see [7] and references therein). Concomitantly, recent polls have shown that the willingness to comply with a self-isolation period depends very much on the social condition and literacy skills of the individual [11].

Quantitatively, the problem of reasoning over the spreading of an infectious and epidemic disease is generally based on standard models such as the susceptible–infected (SI), the susceptible–infected–susceptible (SIS) and the susceptible–infected–recovered (SIR) models [12,13] and their variants. Despite the simplicity of these models, they have been successfully applied to a variety of cases [14]–[21] in the assessment of the propagation of an epidemic disease. In the form of differential equations, their dynamics is well known in the literature on this topic, where they are usually called general solutions. When geometrical conditions are taken into account, namely the structure of the network of relationships between people, the critical behaviour changes [22,23]. Within this context, analytical and numerical results concerning the existence or absence of a non-zero transition for quenched scale-free networks have been in the spotlight [24]–[30].

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In our case, we have opted to base our model on the SIS model, which can represent situations wherein the virus responsible for the infection is able to mutate fast. Explicitly, although someone has recovered from the infection, she is at risk of being infected once again due to the newest mutation. As regards the topology in which the phenomenon endures, we have assumed a dynamical complex network with $N$ nodes, each one linked to $k$ other nodes in accordance with a distribution $P(k)$. Each node of the network represents an individual either in a susceptible, $S$, or in an infected, $I$, state. As usual, we start the dynamics with a single infected individual, randomly chosen among the $N$ nodes.

At first, all the remaining individuals are susceptible. In addition, we have considered that a density of the connections, $d$, in the network is fixed and thus they cannot be removed during the Q and I process. Two people connected by a fixed link are defined as members of the same household, whereas people linked by non-fixed links are dubbed acquaintances.

Recently, some works have studied the effect of isolation in the physics and computer science literature [31]–[37]. It was therein argued that such policies can be effective in controlling the spread of an epidemic disease. However, the conditions of these models rely on the total isolation of the infected patient, which is closer to academic proposals that also inspired several literary contemporary masterpieces [38, 39] than an actual implementable policy following international rules or recommendations. Alternatively, total isolation scenarios have also been studied in the context of small islands. In this case, it is argued that these policies might be successful, but in quite severe conditions demanding a complex and expensive logistics [40, 41]. On the other hand, the study of the impact of the household in the propagation of SIR epidemics and of adequate vaccination policies have been discussed in a biological and medical framework [42]–[47]. However, for the sake of analytical treatment [46], they often neglect the structure of social networks and assume random contacts between individuals. Complementarily, surveys stemming from the analysis of data on fatalities due to the ‘Spanish flu’ pandemic in cities of the United States of America and the relation to public health and non-pharmaceutical interventions have been presented [48, 49]. While these results provide important insights into the relevancy of coordinated interventions and the corresponding set-ups, (American) society has dramatically changed in the almost 100 years and thus so has its epidemic response to such interventions. Moreover, some of the measures adopted during that pandemic are now liable to be judged unethical or in breach of some fundamental law, as we have previously mentioned. Last but not least, it was impossible in these studies to separate out the impact of each measure.

Hence, with this work we intend to provide an answer to the fundamental question of to what extent Q and I policies abiding by World Health Organization (WHO) directives, which are prone to self-imposed isolation, can really hinder the spreading of an epidemic disease, contributing in this way to its control and suppression. Quantitatively, the task of answering this question is presented in the form of looking for an infection rate (or epidemic) threshold, $\lambda^*$, for a given rate of effectiveness of the isolation, above which the disease persists, it being quelled otherwise.

2. The model and numerical results

At each time step, $t$, the following automata rules control our model:

- We visit every node in the network.
For each infected node, we look for all susceptible neighbours of hers.

For each $I-S$ link connecting members of the same household, the susceptible individual becomes infected with probability $\lambda$.

On the other hand, we remove each $I-S$ link connecting acquaintance individuals with probability $q$ (quarantine). Then, the infected individual is isolated and the susceptible one is reconnected to another randomly chosen susceptible node, who is not a current contact of hers. For each surviving $I-S$ link, the susceptible individual becomes infected with probability $\lambda$.

After the verification of all neighbours of an infected individual, she returns to the susceptible state with probability $\alpha$.

Let us elaborate upon the parameters and the rules that we have established. We start by discussing the role of $q$, the main purpose of which is to reproduce the probability that a patient complies with the medical recommendation to stay at home. Ideally, people would strictly abide by the physician’s advice, but as recent polls have shown and given statistical significance to, the rates of compliance are different from 100% and can go as low as 50%. Two main factors for this change have been identified \([11,50]\); (i) more often than not, people do not understand or distort what they are expected to do due to inadequate literacy skills \([50]\); (ii) as occurs in life in general, people (patients included) perform a risk assessment \([11]\) before making a decision on stopping contact with a given individual. Accordingly, infected agents decide to sever the contacts that they have depending on the time for which they were asked to stay at home, the type and importance (circumstantial or not) of the relationship between the infected person and the susceptible individual, and the number of people that can be involved when the attendance at a given event is considered. Furthermore, this risk assessment is weighted by the hazard that the eventual non-compliance carries. Effectively, the perception of risk is quite strongly affected as the time of the self-isolation goes by, as well as the assessed performance of pharmaceutical interventions. As a matter of fact, enormous differences in the poll results concerning self-isolation before and after the introduction of a vaccine in the H1N1 pandemics were verified. A similar behaviour has been verified in polls on high risk unprotected sexual relations as well \([51]\).

Moving ahead, we now underpin the introduction of the rewiring process. As is very well known, social relationships arise because people need one another. Besides friendship, family and sentimental ties, people relate to other people because of their functions, skills and responsibilities. Previous studies have considered that after a link between susceptible and infected individuals has been destroyed, no new relation is established. From a sociological perspective, this option acts as though the needs of the susceptible individual can be dealt with within her current circle. Our option goes along another path that we consider more realistic and that is close to processes of rewiring studied in other works \([31,52,53]\). In spite of the fact that we could have considered a probability $f$ that a susceptible ‘stranded’ agent relinks, we have opted to limit the number of parameters of the problem and keep it constant and equal to 1.$^4$

As the majority of people live together, only in very few (and negligible) cases is it possible for someone to really isolate herself from the people with whom she shares an

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address. In this way, we justify the introduction of the parameter \( d \). Still, we would like to shed light on some aspects of this parameter. First, its introduction does not transform our network into a superposition of two networks (the household and acquaintances)\(^5\). The network remains unique, but there are a fraction \( d \) of the links that cannot be changed because they have been quenched. The household are the people who share the same residence whether they are relatives or not (e.g., people in student flats) and acquaintances are people with whom someone maintains contact on a close and regular basis, representing at its best a fraction of the so called Dunbar number, which is an anthropological/cognitive measure that quantifies the number of people with whom each person is able to keep up a relationship, i.e., preserving some information about his life. It is also important to emphasize that in establishing the network we have borne in mind important details, e.g., if two people are both members of the same household of a third individual, then a quenched connection between them is immediately established because they are obviously members of the same household.

As regards other computational details, we have applied a synchronous update, i.e., after having visited all the nodes on the network, we update all the individuals’ states simultaneously \(^5\),\(^5\),\(^5\). In other words, a new time step is considered only when the states of all of the individuals have been scrutinized. Furthermore, we have considered in this work a fixed \( I \rightarrow S \) transition probability \( \alpha = 0.2 \) and we have simulated the model on a Erdős–Rényi network with \( N = 10^4 \) nodes and \( \langle k \rangle = 5 \). The results presented herein have been obtained by averaging over \( 10^3 \) independent simulations, for each set of values presented. Please observe that we have only considered the epidemic spreading in the largest connected component of the network, i.e., the giant cluster \(^3\).

In figure 1, we exhibit the time evolution of the density of infected individuals \( I(t) \) for 20% of fixed links in the network (i.e., for \( d = 0.2 \)), two different values of the self-isolation probability, namely \( q = 0.3 \) and 0.8, and \( \lambda \) scanning the domain of infection rates. As can be observed, there are different values of \( \lambda \) above which we have \( I_{st} > 0 \). Here, the notation \( I_{st} \equiv I(t \rightarrow \infty) \) stands for the stationary density of infected individuals\(^6\). This defines the usual phase transition of epidemic models: for \( \lambda \leq \lambda^*(q) \), we have a disease-free phase with all the individuals presenting an \( S \) state, whereas for \( \lambda > \lambda^*(q) \), we have an epidemic phase, i.e., the disease spreads out and a finite fraction of the population are constantly infected. Pay heed to the fact that, for increasing values of \( q \), the time needed for the system to reach a stationary state increases. This kind of transition is best observed in figure 2 (left panel), wherein we exhibit the stationary density of infected individuals \( I_{st} \) as a function of \( \lambda \) for \( d = 0.2 \) and typical values of the self-isolation probability \( q \) of the Q and I process. In this case, we can see that for a fixed value of \( q \) the transition occurs at different values of \( \lambda \), which defines the transition points \( \lambda^* \). Analogously, the stationary density of infected individuals \( I_{st} \) can be represented as a function of the self-isolation probability \( q \) of the Q and I process for different values of \( \lambda \) (see figure 2, right panel). Once more, we perceive a transition at different values of \( q(\lambda) \). Notice that when we increase the self-isolation probability, the disease only disseminates through the network if we increase the infection probability \( \lambda \). In other words, the final size of the epidemic

\(^5\)From a coarse grained point of view, we could use this approach to define a network of households but this is not a superposition of networks either, since in this case each node is now a household and not an individual.

\(^6\)The quantity \( I_{st} \) was obtained from time averages of \( I(t) \) taken in the steady state, and in addition we also considered averages over \( 10^3 \) network realizations.

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Figure 1. Time evolution of the density of infected individuals for $d = 0.2$ and $q = 0.3$ (left side) and $q = 0.8$ (right side), and typical values of the infection probability $\lambda$ for random networks with $N = 10^4$ nodes and $\langle k \rangle = 5$. Notice that the time needed for the system to reach the steady states increases for increasing values of the self-isolation probability $q$ of the Q and I process. Results are averaged over $10^3$ realizations.

Figure 2. Left side: normalized stationary density of infected individuals $I_{st}$ as a function of $\lambda$ for $d = 0.2$ and typical values of $q$. We can observe a transition from $I_{st} = 0$ to $I_{st} > 0$ at different threshold points $\lambda(q)$. Right side: $I_{st}$ as a function of the self-isolation probability $q$ of the Q and I process, for $d = 0.2$ and typical values of the infection probability $\lambda$. We also observe a transition for each value of $\lambda$, at different points. In all simulations, $N = 10^4$, $\langle k \rangle = 5$ and averages are over $10^3$ realizations.

may be reduced, as was observed in the 2009 H1N1 pandemic [11] and as also discussed in some works [31]–[34], [52]. Nonetheless, in what follows, we will conclude that its outcome is limited when we take into account a more realistic model with a density of fixed links.

We have simulated the model for other values of the density of fixed links $d$, and we have also observed the above-discussed transition (see figure 3). Alternatively, we take into account the transition values $\lambda^*$ as functions of $d$ for fixed values of $q$ and we have noted that the data obtained from the simulations are well described by a stretched
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Figure 3. Normalized stationary density of infected individuals $I_{st}$ as a function of $\lambda$ for $d = 0.4$ and typical values of $q$. We can also observe a phase transition from $I_{st} = 0$ to $I_{st} > 0$ at different threshold points $\lambda(q)$. In all simulations, $N = 10^4$, $\langle k \rangle = 5$ and averages are over $10^3$ realizations.

Figure 4. The infection probability threshold $\lambda^*$ as function of $d$ for typical values of the self-isolation probability $q$ of the Q and I process. The lines are fittings based on the stretched exponential function $\lambda^* \sim \exp[-(d/a)^c]$.

For different values of the parameters $a$ and $c$ (see figure 4). In particular, for small values of $q$ like $q = 0.3$, the dependence of $\lambda^*$ on $d$ is almost purely exponential, since we have obtained an exponent $c = 0.91\pm0.08$. The values of $a$ and $c$ are shown in table 1. We have no first-principles justification for this dependence yet, but the justification for making such an approximation will be given later on.

Allowing for the transition values $\lambda^*$ obtained from the simulations, we exhibit the phase diagram of the model in the plane $\lambda$ versus $q$ for typical values of $d$ in figure 5. From this plot, it is possible to understand that a disease-free regime is achievable even for high infection rates and low compliances with the medical recommendations of home isolation, but only when the individuals are near to living alone or the ratio between the

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Figure 5. Phase diagram of the model, separating the disease-free and the epidemic phases, for typical values of the density of fixed links $d$. The symbols represent the threshold values $\lambda^*$ obtained from the numerical simulations and the lines are plotted as a guide to the eye.

Table 1. Values of the parameters $a$ and $c$ used in figure 4.

| $q$  | $a$      | $c$      | $\chi^2$       |
|------|----------|----------|-----------------|
| 0.3  | 0.62 ± 0.04 | 0.91 ± 0.08 | $1.13 \times 10^{-4}$ |
| 0.5  | 0.34 ± 0.01 | 0.93 ± 0.05 | $2.46 \times 10^{-4}$ |
| 0.8  | 0.11 ± 0.01 | 0.73 ± 0.09 | $6.28 \times 10^{-4}$ |

number of members of the individual’s household and the total number of relationships is small. As the fraction of fixed links (relationships) $d$ associated with the household soars, the size of the epidemic phase increases as well. This is easily comprehended: since the number of fixed links augments, the quenched part of the network becomes more dominant and so the number of ‘channels’ through which the epidemics can disseminate increases. Correspondingly, we can end up in a situation for which increasing the consciousness $q$ of the infected individual has little or no effect. In this respect, looking at the curve with $d = 0.3$, we verify that the threshold infection rate $\lambda^*$ barely varies with the rate $q$, for $q \gtrsim 0.6$.

On the other hand, in the interpretation of this diagram, we can also resort to the poll results published by Eastwood et al [11]. Looking to the data from Australia, during the H1N1 outbreak the lowest compliance rate with a public health request was of 62.6% for the avoidance of public gatherings. The rate of compliance decreases further to as much as 50% when household quarantine is considered [50]. As previously mentioned, in the same work by Kavanagh and co-workers [50], statistical significance was given to the fact that literacy skills influence the individual performance as regards proper compliance with a self-isolation recommendation as well as other public health interventions. Bearing in mind that Australia is one of the few countries with a Human Development Index (HDI) higher than 0.900, which in total account for less 10% of the world’s population (world HDI = 0.751), and that it is expected that the lower the HDI, the lower the compliance rates, assuming reasonable values for the parameters we evidence that it is extremely
unlikely that a Q and I policy under such conditions will induce a disease-free state. As a matter of fact, for infection rates of approximately 20%, such as those estimated for influenza, and $d = 0.2$ (eight acquaintances per ten relationships and a household composed of three people), we get an epidemic phase even if the probability of compliance is 1, which is basically a utopian value. As regards the value of $d$, we must allow for the fact that at present, people tend to actually (in a vis-à-vis sense) interact much less than in the past, particularly in countries where the Internet has become strongly implanted. In other words, although the world is apparently more connected, activities like home-working and on-line shopping, among others, have had boosted relevancy and, associated with that, there has been a decrease in the number of acquaintances (and casual contacts).

3. Analytical considerations

Following the rules of our model, we can carry out some analytical consideration regarding our problem, which corresponds to a network of $N$ individuals and $L$ dual flux links that are quenched for the household and allow rewiring for the other cases. At the initial time, $t_0$, the average degree of connectivity is $K_0 = 2L/N = \langle k \rangle$ and this can be split into

$$K_0 = K^h + K^a = dK_0 + (1 - d)K_0.$$ (2)

Assuming all individuals (nodes) to be equal, we can write a master equation reflecting the evolution of the number of infected people which reads

$$I_{t+1} = I_t + \lambda S_t I_t - \alpha I_t = I_t + \lambda (K_t - I_t) I_t - \alpha I_t,$$ (3)

which in the continuum limit yields

$$\frac{dI}{dt} = \lambda (K_t - I_t) I_t - \alpha I_t$$ (4)

where,

$$S_t + I_t = K_t.$$ (5)

When the individual preserves all links, $K_t = K_0$ (for all $t$), the stability limit of the solution to equation (3) yielding $I_{t \to \infty} = 0$ is given by the infection rate $\lambda = \alpha/K_0$ as given in [14]. In our case, we must focus on the dynamics of the connections of infected people as well. We know that at each time step, an infected person is given medical advice to self-isolate, which implies a cut of her acquaintances’ relations. In view of the fact that diseased individuals have a probability $q$ of severing these contacts, the evolution of $K^a$ of an infected person is on average given by

$$K^a_{t+1} = K^a_t - q K^a_t \quad \frac{dK^a}{dt} = -q K^a,$$ (6)

for which the solution is

$$K^a_t = (1 - d) K_0 \exp[-qt],$$ (7)

or

$$K_t = K_0[d + (1 - d) \exp[-qt]].$$ (8)
Now, the determination of the critical threshold from equations (4) and (6) can be tremendously simplified using the argument [31] that for the epidemic phase to persist over time, one must guarantee the infection of other people during the illness span, that lasts a time of the order of \(\alpha^{-1}\). In other words, the reproductive rate of infected people, \(R\), must be greater than 1. At time step \(t\), we can determine the mean-field reproductive rate,

\[
R_t = K_0 \frac{\lambda}{\alpha} [d + (1 - d) \exp(-qt)].
\]

Averaging \(R_t\) during the diseased cycle,

\[
\bar{R} = \alpha \int_0^\alpha R_t \, dt,
\]

and solving \(\bar{R} = 1\) with respect to \(\lambda\), we get

\[
\lambda_c = \frac{q}{K_0 [1 - d(1 - q/\alpha) - \exp(-q/\alpha)(1 - d)]}.
\]

the limits of which, namely, \(d \to 1\) (quenched network) and \(d \to 0\) (complete reconnection with probability \(q\)), are verified [12,14,31]. In figure 6, we depict \(\lambda_c\) as a function of \(d\) and \(q\). Comparing both panels with figures 4 and 5, we verify that only the qualitative behaviour of \(\lambda_c\) concurs with that of \(\lambda^*\). Specifically, the mean-field solution underestimates the critical values of the infection probability. To understand this discrepancy we avail ourselves of recently published work [56] where it is ascertained that mean-field-like approaches are more accurate for networks with high mean degree or high mean first-neighbour degree. As can be perceived from equation (8) and using the
Table 2. Values of the parameters $a'$ and $b$ used to numerically adjust the points of figure 4 with equation (15).

| $q$  | $a'$    | $b$       | $\chi^2$    |
|------|---------|-----------|-------------|
| 0.3  | 0.44 ± 0.02 | 0.13 ± 0.01 | 4.5 × 10^{-4} |
| 0.5  | 0.22 ± 0.01 | 0.25 ± 0.02 | 4.7 × 10^{-4} |
| 0.8  | 0.05 ± 0.01 | 0.89 ± 0.04 | 1.7 × 10^{-2} |

same parameter values in the simulations, the mean degree significantly fluctuates from susceptible to infected nodes. Therefore, at the stationary critical state and beyond it, the typical configuration of the network includes an important fraction of nodes with a small number of neighbours, a situation that tallies with the conditions of inaccuracy that we have referred to.

Nevertheless, we can provide an argument for our empirical adjustment of $\lambda^*$ as a function of $d$ from equation (11). Explicitly, for $q > \alpha$, that equation can be rewritten as

$$\lambda_c = \frac{q}{K_0 (1 - \exp[-q/\alpha])} \left[ 1 + \frac{\exp[-q/\alpha] + q/\alpha - 1}{1 - \exp[-q/\alpha]} - d \right]^{-1},$$

which in first order yields

$$\lambda_c \sim \exp \left[ -\frac{d}{D} \right],$$

with

$$D = \frac{1 - \exp[-q/\alpha]}{\exp[-q/\alpha] + q/\alpha - 1}. \quad (14)$$

A comparison between equations (11) and (13) is presented in the left panel of figure 6. Therein, for small $d$ the orange dotted line fits the initial points, but then decays faster. The stretching exponent $c < 1$ prolongs the curve. We can also confront our proposed equation (1) with equation (11). In figure 6 (left side), we have numerically adjusted the points given by equation (11) with equation (1). As can be seen, the adjustment matches the curve quite well with hardly perceptible deviations. Because of the qualitative similarity of the curves, we can be further tempted to consider an adjustment of the data in figure 4 with a mean-field-like dependence,

$$\lambda^* = \frac{b}{1 + d/a'},$$

the values of which are presented in table 2. Comparing the values of $\chi^2$ in the two tables, we verify that despite the good agreement of the mean-field curves, the stretched exponential clearly outperforms equation (15), especially for large $q$, which supports once again our previous choice.
4. Final remarks

In this work, we have studied a modified version of the SIS epidemic model that takes into account quarantine and isolation practices according to self-compliance with medical requests. For each person, their relationships are pigeonholed as with acquaintances or with members of the same household. For the former, there is a probability that the connection is broken, quantifying the degree of consciousness of the individual as regards the epidemic disease, whereas for the latter the connections are fixed—aiming at representing the possibility of a compulsory separation. For a susceptible–infected–susceptible process, our results have shown that quarantine following this structure, which agrees with WHO directives, is extremely unlikely to thwart the propagation of an epidemic infectious disease using standard figures regarding infection rate and compliance with medical (public health) requests. It should be stressed that our results must not be interpreted as arguing for the uselessness of self-isolation from an overall point of view. The outcome of our study indicates that self-isolation is likely to be ineffective per se and signals the importance of coordinated public health or non-pharmaceutical interventions in order to control the untamed spread of an epidemic.

That being said, we would like to highlight that our results could be further explored to take into account either different versions considering the impact of other public health (non-pharmaceutical) interventions or the joint impact of self-isolation and some other intervention(s). Besides scrutinizing epidemics of different types, we can also study the problem of isolation using mixed topologies [57] for the social network which depend on the type of relationship between people and institutions. Regarding this point, the problem can be honed by bolstering the acquaintance type connections, i.e., in the rewiring step, people are biased to rewire to acquaintances and members of the same household as people with whom they already have a relationship. Another important investigation concerning the dynamics respects the assumption of an (average) isolation time instead of the fixed (unitary) timescale that we have taken into consideration.

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